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Molecular Mechanisms Involved in the Interaction Effects of HCV and Ethanol on Liver
Cirrhosis

A thesis submitted in partial fulfillment of the requirements for the degree of Master of
Science at Virginia Commonwealth University.

by

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List of Abbreviations

ADH.....	Alcohol Dehydrogenase
ALD.....	Alcoholic Liver Disease
APC.....	Antigen Presenting Cell
C.....	Core protein of HCV
cDNA.....	Complementary DNA
cRNA.....	Complementary RNA
Ct.....	Cycle threshold
CTL.....	Cytotoxic T Lymphocyte
CYP2E1.....	Cytochrome P450 2E1
DC.....	Dendritic Cell
dsRNA.....	Double Stranded RNA
E.....	Envelope protein of HCV
ECM.....	Extra-cellular Matrix
ER.....	Endoplasmic Reticulum
EtOH.....	Ethanol
HBV.....	Hepatitis B Virus
HCC.....	Hepatocellular Carcinoma
HCV.....	Hepatitis C Virus
HSC.....	Hepatic Stellate Cell
IFN.....	Interferon
IPA.....	Ingenuity Pathway Analysis
IRF.....	Interferon Regulatory Factor
ISG.....	Interferon Stimulated Gene
JAK.....	Janus Kinase

KC.....	Kupffer Cell
MDA.....	Malondialdehyde
NF- κ B.....	Nuclear Factor-kappa B
NS.....	Non-Structural protein of HCV
NK.....	Natural Killer Cell
OLT.....	Orthotopic Liver Transplantation
PAMP.....	Pathogen Associated Molecular Pattern
QPCR	Quantitative Reverse Transcriptase 'Real Time' Polymerase Chain Reaction
RIG-1.....	Retinoic-Acid-Inducible-Gene-1
RdRp.....	RNA-dependent RNA polymerase
RMA.....	Robust Multiarray Averaging
rRNA.....	Ribosomal RNA
ROS.....	Reactive Oxygen Species
S.....	Structural protein of HCV
SOCS.....	Suppressor of Cytokine Signaling
ssRNA.....	single-stranded RNA
STAT.....	Signal Transducer and Activator of Transcription
Th.....	T helper cell
TLR.....	Toll-Like Receptor
TRIF.....	Toll/IL-1 Receptor-Domain-Containing Adaptor Inducing IFN- β
TYK.....	Tyrosine Kinase
UNOS.....	United Network of Organ Sharing

ABSTRACT

MOLECULAR MECHANISMS INVOLVED IN THE INTERACTION EFFECTS OF HCV AND ETHANOL IN LIVER CIRRHOSIS

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A thesis submitted in partial fulfillment of the requirements for the degree of Master of Science at Virginia Commonwealth University

Virginia Commonwealth University, 2010

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The leading causes of liver disease are Hepatitis C virus infection and chronic alcohol abuse. Alcohol accelerates liver disease in HCV but the mechanisms are poorly understood. The identification of molecular gene expression profiles on human liver tissue was performed using microarrays. Samples were obtained from alcoholic-cirrhotic, HCV-cirrhotic, HCV/alcohol-cirrhotic and control non-cirrhotic liver tissue. Probe set expression summaries were calculated using RMA. Probe set level linear models were fit where probe set expression was modeled by HCV status, alcohol status, and the interaction between HCV and Alcohol. HCV cirrhosis was associated with up-regulation of genes related to viral and immune response, apoptosis and inflammation. There were down-regulation of genes in the ubiquitin-proteasome system in alcoholic cirrhosis. The interaction of HCV and alcohol revealed negative interaction for genes involved in

apoptosis and immune response. There was a negative estimate for genes involved in class II restricted antigen presentation.

Introduction

Chronic Liver diseases of any etiology are the 9th leading cause of death in the United States (1). The leading causes of liver disease are Alcoholic Liver Disease (ALD) and chronic Hepatitis C Virus (HCV) infection, either alone or in combination, as they account for close to two-thirds of deaths from and patients with chronic liver diseases (1,2,3).

The liver is vulnerable to sustained, chronic injury because the hepatocyte is the primary site of HCV replication as well as the metabolism of ethanol; thus it is intuitive that there is an interaction in the pathogenesis of HCV and alcohol (4). Despite clinical evidence of exacerbated injury, higher mortality rates and increased risk of hepatocellular carcinoma (HCC), liver disease mediated by the interaction of alcohol and HCV is complex and not completely understood. Pathogenesis of alcohol and HCV have similar effects of injury but arrive at those effects via different mechanisms as both etiologies manifest the four sequential hallmarks of liver disease: steatosis (fatty liver), steatohepatitis (inflamed fatty liver), fibrosis and HCC (5).

What is the Hepatitis C virus?

Hepatitis C is a single stranded positive sense RNA virus (6) that was discovered in 1989. The virus is transmitted through bodily fluids, and most of those infected are intravenous drug users (7). Over 170 million people worldwide are infected with the virus (8). The progression of the virus is slow, most people are not aware of their infection until presented with a compromised liver; the onset of chronic liver disease can take at least 20 to 30 years to develop (7,9). This progression is dependent on genetic and environmental factors and tends to proceed at a faster rate in males, in obese, in persons with diabetes, individuals with co-infections such as Hepatitis B (HBV) and HIV, and in alcoholics (10). A small portion (15-25%) of persons infected will spontaneously clear acute infections the virus, and of those that are chronically infected, only about half of them will respond to therapy such as pegylated interferon (IFN) with ribavirin (11,12).

The ssRNA (single-stranded RNA) of the virus is translated into a single polyprotein that is further processed by proteases belonging to both the cellular host and the virus in the endoplasmic reticulum of the host (13). The virus is composed of ten proteins: four structural (S) and six nonstructural (NS) proteins. The core protein(C), Envelope 1 and 2 (E1 and E2), and p7 protein are the four structural proteins, while the six NS proteins are NS2, NS3, NS4A, NS4B, NS5A, and NS5B (6,13,14). E1 and E2 form a heterodimer that is the glycoprotein envelope and the virus is unable to enter the host cell with out the envelope proteins (6). The core protein forms the nucleocapsid of the virus and binds RNA. Core protein has been associated with the interference of many cellular mechanisms such as cell signaling, viral response and induces oxidative stress through metabolism and apoptosis (6). The p7 protein

contains two transmembrane domains and separates the structural proteins from the NS proteins. The function of p7 has not been fully determined, although it is thought to be an ion channel (13).

The NS proteins consist of proteases and other enzymes involved with viral reproduction. The role of NS2 is to form the NS2/NS3 enzyme that cleaves the NS2/NS3 junction (13). Other than its viral assembly role in the NS2/NS3 protease complex, the functions NS2 protein has not been fully investigated (13). NS3 has two domains, a protease domain and a helicase/NTPase domain. Not only does it form a complex with NS2, NS4 is an important cofactor for NS3. The NS3/4A protease plays an important role because it is responsible for the downstream cleaving of the polypeptide, which consists of the rest of the NS proteins (15). Not much is known to date about protein NS4B besides its structure and that it is an integral trans-membrane protein that associated with both the lumen and cytosolic side of the ER (endoplasmic reticulum) and can alter intracellular membranes (12). NS5A is also involved in disrupting host cellular processes (6). NS5B is a RNA-dependent RNA polymerase (RdRp) (7).

Pathogenesis of Hepatitis C Virus Infection

There are many arguments that suggest HCV is not directly cytopathic to the hepatocyte and the main focus of pathology of HCV infection has been on inflammation from the immune response as the main contributor of reactive oxygen species (ROS) from macrophages and neutrophils (16). Recently more attention has been given to the role viral proteins play in oxidative stress because the serum and hepatic tissues of patients with HCV contain levels of markers for ROS (17). There is evidence of ROS production as levels of malondialdehyde (MDA)-adducts (18), and lipid peroxidation protein adducts (19) are higher and antioxidant markers such as GSH are reduced in those with the virus (20). The prevalence of hepatocellular carcinoma in HCV is also indicative of ROS production; increased levels of 8-hydroxy-deoxyguanosine, a marker of DNA oxidative damage, have been found in circulating leukocytes of HCV patients (21).

The most extensively studied protein in the proteome of HCV is the Core protein. Core induces cellular damage by oxidative stress, mitochondrial injuries, misfolded proteins, ER stress, and lipid peroxidation (22,23,24,25). Core's association with the mitochondria causes a direct uptake of Ca^{++} , inducing the electron transfer chain to increase production of ROS. NS5A can also increase ROS production, but through release of ER Ca^{++} which is then taken up by the mitochondria (20,22). NS3 contributes to ROS by up-regulating NADPH oxidase (NOX-2) in macrophages (17). The cytotoxicity of the viral proteins is somewhat controversial and more research is needed in this area.

Another area under investigation is the suppression of T-lymphocytes. An early strong, sustained and virus specific CD4+ T-helper cell (Th) response and an early, broad CD8+ CTL

(cytotoxic T-cell) viral clearance is associated with acute viral clearance (7). In chronic carriers of the virus, the responses of T-lymphocytes are much weaker and impaired (15). The weak CD4+ T-cell mediated response is thought to be from T-cell exhaustion or impaired antigen presentation from dendritic cells (DC)(7,14). The impaired CTL viral clearance might be from an inefficient antigen presentation, hampered CD4+ cell mediated priming of CTLs, or viral escape through mutation (14,26). The lack of proofreading in the RdRp of viral protein NS5B and the hyper-variable region of E2 are thought to promote viral escape (6,15).

A virus, like any parasite, must be able to circumvent the host's defense in response to foreign invaders. The host's attempt to clear viruses and the virus' need to persist have faced evolutionary selection pressures in this battle: Host cells have developed different strategies for clearance of viruses and to slow their entry and reproduction, while viruses have evolved methods of evading the immune system and counteracting antiviral pathways (12,15). The anti-viral pathway in hepatic cells involves the induction of Type 1 IFN and ISGs (interferon stimulated genes).

Surveillance of pathogens by cell is by proteins that can recognize and bind pathogen-associated molecular patterns (PAMP) (26). Viral PAMPs include single and double stranded RNA (dsRNA) and polyuridine nucleotide motifs. Hepatitis C is specifically recognized extracellularly by the Toll-like receptor (TLR)-3 and intracellularly by Retinoic-acid-inducible gene 1 (RIG-1) and by intracellular compartments containing TLR-3 (14). TLR-3 and RIG-1 recognize and bind dsRNA, and even though HCV RNA is single stranded, there are secondary structural motifs that can be recognized by these receptors. Down stream signaling and transcription of IFN- β occurs through the transcription factors IRF (Interferon Regulatory factor)-3 and NF- κ B (Nuclear Factor-kappa-B) (27)

HCV proteins NS3/4A will cleave adaptor proteins Toll/IL-1 receptor-domain-containing adaptor inducing IFN- β (TRIF), of TLR-3 signaling , and Cardif, of RIG-1 signaling, to attenuate the IFN- β transcription (27). Even if IFN- β is transcribed, HCV can also prevent the paracrine and autocrine effect of IFN signaling by inhibiting the JAK/STAT (Janus Kinase/ Signal Transducer and Activator of Transcription) pathway activated by IFN.

ISG expression is activated through the Jak/STAT pathway, initiated by the binding of IFN to the IFN receptors. Jak proteins, JAK-1 and TYK (tyrosine kinase)-2 phosphorylate the STAT proteins STAT1 and STAT 2 (26). Core protein can block this pathway by inducing a negative regulator of the JAK/STAT pathway SOCS (suppressor of cytokine signaling)-3 (15).

Mechanisms of Hepatic Cirrhosis

Liver regeneration induces activation of a non-pathological inflammatory response during acute injury. Normal parenchymal cells are eventually replaced after resolution of the inflammatory response. However, during sustained, chronic injury the resulting deregulation of the wound healing response leads to liver cirrhosis, eventually compromising the structure and function of the organ. The progression of liver disease can take decades (28) and eventually lead to fibrosis, cirrhosis, liver failure, and ultimately hepatocellular carcinoma (29). Although some level of reversibility has been shown if the insult is removed, the only effective cure for advanced liver disease is orthotopic liver transplantation (OLT) (30,31).

Fibrosis occurs in many different tissues and organs. The pathway of fibrogenesis can be stereotyped, as all types of tissue follow a common string of events. Persistent, repeated or chronic injury to tissue is followed by infiltration of immune cells due to the wound healing response, These release soluble cellular signals that activate myofibrogenic cells which start to proliferate and migrate to the injury site and begin synthesis of extracellular matrix proteins (ECM) (18,32,33).

In the liver, the parenchymal cells are hepatocytes. When damaged, Kupffer cells (KC), the resident macrophage of the liver, are among the inflammatory infiltrate that migrate to the site of the injury releasing cytokines (34) that attract and promote the differentiation of hepatic stellate cells (HSC), the main source of ECM proteins (35). The continuation of this general cascade will result in the build up of ECM, mainly type I collagen, resulting in fibrosis (36,37). The hepatocytes can be damaged from viral, toxemia, metabolic disorders or iron overloads (38). Fibrogenic stimuli can vary depending on the etiology of the insult. Processing of cellular

toxins, such as ethanol, not only inflict cellular damage but also promote the generation of ROS, which can have a direct stimulatory affect on HSCs (33). In the case of a viral attack, infected hepatocytes are cleared by immune cells such as CTL and natural killer (NK) cells (39). When a cell is damaged beyond repair, the apoptotic bodies are released as signals during the death process and are important stimuli for macrophages that are constantly monitoring the organ (40). The death of hepatocytes used to be viewed as passive consequence of liver injury, however, apoptosis and necrosis of hepatocytes have been implicated as a stimulus to fibrosis as apoptotic bodies can be engulfed by KCs and HSCs. (41,42). Kupffer cells phagocytose damaged cells and apoptotic bodies and become activated. As a result they transcribe cytokines, which have effects on other cells of the liver and initiate the innate immune response.

Oxidative Stress

Oxidative stress is central to both HCV and ALD pathogenesis and is proposed as a synergistic mechanism in liver disease mediated by the addition of alcohol to HCV. Oxidative stress is defined as an imbalance between the generation of ROS and the antioxidant defense capacity of cell. ROS affects all cellular components including lipids, proteins, and DNA. As a result lipid and protein adducts can cause cytotoxicity, break autoimmunity and lead to cell death.

Oxidative stress in ALD results from two main sources; the metabolism of ethanol itself and the inflammatory response from immune cells. Ethanol is metabolized by alcohol dehydrogenase (ADH) in the cytosol and Cytochrome P450 2E1 (CYP2E1) in microsomes. Both enzymes are inducible and reduce ethanol to acetaldehyde. Considered a second messenger within the cell, generated ROS are important factors in the initiation of HSCs. Sources of ROS are recruited by neutrophils from the wound healing response, activated Kupffer cells, CYP2E1 and mitochondria (16,17). ROS can up-regulate the production of pro-inflammatory cytokines through activation of the transcription factors NF- κ B and c-Myb (43,44).

Oxidative stress is directly related to the metabolism and break down of ethanol to acetaldehyde. ADH and CYP2E1 carry out this reaction through oxidation-reduction (45). The oxidation of ethanol to acetaldehyde by these enzymes results in the reduction of the cofactors NAD to NADH and NADP to NADPH respectively (45,46,47,48). The oxidation of NAD(P)H to NAD(P) takes place in the mitochondria by reducing oxygen to H₂O via the electron transfer chain (46). Intermediate reactive oxygen species such as superoxide, the hydroxyl radical and

peroxide are formed during this process (49). Chronic ingestion of ethanol leads to a red-ox imbalance due to a high NAD(P)H/NAD(P) ratio and a generation of ROS that surpasses the anti-oxidant systems in cells. A high NAD(P)H/NAD(P) ratio promotes fatty acid synthesis (47) and ROS generation (49).

Cytotoxicity is the result of oxidative stress from the build up of ROS intermediates from ethanol metabolism as well as acetaldehyde itself (45,50).

Immunomodulation

Both acute and chronic ethanol intake modulates the immune system (51,52). Alcoholics have a higher chance of post-surgical complications due to surgery and also exhibit decreased ability to clear bacterial and viral pathogens (51). Studies have shown a reduction of class I presentation partially due to inhibition of the proteasome which may hamper the ability of CTLs to recognize infected cells (53,54). The hepatitis C virus also exhibits its remarkable ability to evade host defenses by causing persistent infection in 75-80% of individuals acquiring the disease. Viral proteins have been shown to interfere with viral recognition and antiviral pathways such as NF- κ B and IFN signaling (55,56,57). In studies with chimpanzees and humans, successful clearance of the virus is associated with a strong, vigorous CD4+ T helper cell response and broad, multi-epitope specific CD8+ CTL response. Persistent infection is associated with weak narrowly focused T-cell response. DC, the most potent APC (antigen presenting cell) for priming T-cells, are shown to be incapacitated in their ability to present and antigens by both HCV and alcohol (58,59)

Alcohol and HCV

Not all alcoholics will develop fibrosis and cirrhosis can take decades to develop in some hepatitis C infected individuals. The fibrogenic process is a very complex web and researchers have looked to environmental and genetic co-factors in the progression of liver fibrosis. Alcohol is considered an accelerant of fibrosis in individuals infected with HCV (10,42). There is a higher rate of HCV infection among alcoholics than the general population and there is a 40% increased odds of mortality in alcohol abusers with HCV (10). Additionally, the response rate of HCV therapy and compliance is much lower in alcoholics.

There is a large body of evidence that alcohol exacerbates liver injury in patients with HCV. However, the mechanisms of synergism and/or additivity of the two etiologies are still unclear (60). There have also been conflicting findings in areas such as the effect of alcohol use and viral load and replication (61,62,63).

Hypothesis and Aims

The current study intends to identify molecular pathways affected by the addition of alcohol in HCV positive individuals. Gene expression profiling was modeled for the separate conditions (EtOH vs Normal and HCV vs Normal) as well as for their interaction term (HCV*EtOH).

Due to the impairment of the immune system from alcohol consumption, and HCV's ability to evade and abrogate the immune response, **our hypothesis is that the combination of chronic alcohol abuse and HCV infection may result in gene expression suggestive in immunomodulation, specifically in the activation of the adaptive immune response. Alcohol abuse may increase an individual's susceptibility to infections.**

Although alcohol use and abuse is a major risk factor for cirrhosis in individuals infected with HCV, not much is known about the molecular mechanisms. There are practically no studies on gene expression in with concurrent alcohol use in HCV infection. We propose to:

AIM 1: To identify characteristic molecular signatures individually associated with HCV cirrhosis and Alcoholic cirrhosis.

AIM 2: To build molecular pathways associated with the direct effect of the interaction of alcohol and HCV in liver disease.

Patients, Materials, and Methods

Patients and Samples

We used samples obtained from explanted liver from patients undergoing liver transplantation for ALD, end-stage hepatitis C, and combined hepatitis C and alcoholic cirrhosis at from the Hume-Lee Department of Transplantation at Virginia Commonwealth University. The study evaluated seventy-eight human liver tissues, including 23 (29.5%) from patients with HCV mediated cirrhosis, 13 (16.7%) from patients with ALD, 23 (29.5%) from patients with cirrhosis due to both HCV and alcohol, and 19 (24.4%) were non-cirrhotic, normal donor livers acquired from the United Network of Organ Sharing (UNOS) to be used for comparison analyses. Written informed consent was obtained from all patients prior to surgery. The institutional review board approved the research protocol.

All normal liver donors were sero-negative for HCV Antibody and were shown to have normal liver function and histopathology. None of the HCV-infected patients were receiving anti-viral treatment at the time of surgery. Significant alcohol consumption was defined as > 50g/day for a period of > 5 years or >80 g/day for a shorter time period. Alcohol intake was assessed by the attending physician prior to the transplant.

Liver tissue samples were obtained through Liver Tissue Cell Distribution system (Richmond, VA) which is funded by NIH contract #No1-DK-7-0004/HHSN267200700004C.

Sample Preparation.

Samples from cirrhotic liver tissue were collected in liquid nitrogen or RNA later solution (Ambion, Inc., Austin, TX) and stored at -80 C until use.

Sample preparation protocol follows the Affymetrix GeneChip Expression Analysis manual (Santa Clara, CA). Total RNA was extracted from liver tissue samples using TRIzol (Life Technologies, Rockville, MD). RNAs were purified using Rneasy kit (Qiagen, Valencia, CA). To facilitate hybridization to the U133A 2.0 GeneChip probe arrays, the purified RNA was reverse-transcribed using T7-polydT primer and then converted to double stranded cDNA by using Superscript Choice System (One-Cycle Target Labeling and Control Reagents, Affymetrix, Santa Clara, CA). The cDNA (complementary DNA) served as template to construct biotin-labeled antisense cRNA (complementary RNA) by way of an *in vitro* transcription reaction. The labeled cRNA was then chemically fragmented and made into a hybridization cocktail according to the Affymetrix GeneChip protocol, which was then hybridized to HG-U133A 2.0 GeneChip probe arrays (Affymetrix, Santa Clara, CA). The array image was generated by the high-resolution GeneChip[®] Scanner 3000 by Affymetrix[®] (Affymetrix, Santa Clara, CA). After all chips passed quality control, the data were analyzed using Affymetrix Microarray Suite software, version 5.0 and Bioconductor packages (Gentleman 2004) available in the R programming environment (R Development Core Team 2007).

Quality Assessment:

RNA purity as measured by spectrophotometer was deemed sufficient, providing the ratios satisfied the criteria $A_{260\text{nm}}/A_{280\text{nm}} > 1.8$ and $A_{260\text{nm}}/A_{270\text{nm}} > 1.3$. Additionally, the RNA integrity, assessed by capillary electrophoresis using the Agilent Bioanalyzer, had to meet the criteria that the 28S/18S ratio ≥ 1.5 , with an rRNA (ribosomal RNA) contribution greater than 30%. Assessment of RNA quality will also be made using data from the hybridized GeneChips.

Microarray Data Analysis:

Probe set expression summaries were calculated after image analysis using robust multiarray averaging (RMA).

Conducting an unsupervised analysis generated a dendrogram and associated heatmap. The data set was filtered by retaining the most variable probe sets (the probe sets having the top 1% range was retained). Agglomerative hierarchical clustering using Ward's method and using 1-Pearson's correlation as the dissimilarity measure was applied to the filtered data set.

For differential gene expression of HCV cirrhotic liver tissue vs normal liver tissue, each probe set was compared using a two-sample t-test with Satterwaites's approximation to the degrees of freedom to account for unequal variances. Differential gene expression of alcohol cirrhotic liver tissue vs. normal liver tissue was compared in the same manner.

To examine the interaction of HCV and alcohol (HCV*EtOH), probe set level linear models were fit by modeling probe set expression by HCV status, EtOH status, and the interaction between HCV and Alcohol. The model is taken to be as

$$y_{ij} = m_j + b_{1j}HCV_i + b_{2j}EtOH_i + b_{3j} (HCV_i)(EtOH_i) + e_{ij}$$

where j represents a probe set and i represents an individual subject. HCV_i and $EtOH_i$ are dichotomous variables representing the HCV or Alcohol status, respectively, for a given individual. b_{1j} represents the effect due to HCV status on probe set j and b_{2j} represents the effect due to alcohol status on probe set j , while b_{3j} represents the effect of the interaction of HCV and alcohol on given probe set j . y_{ij} represents the \log_2 intensity of probe set j for subject i and m_j represents the baseline \log_2 intensity for probeset j . Random error term was represented by e_{ij} . Probe sets that were significant for the term b_{3i} were of particular interest as this was an indication of the effect of the interaction of HCV and EtOH on gene expression being

synergistic or antagonistic, as opposed to being additive. A Bonferroni correction was used for all comparisons as control for multiple hypothesis tests.

Gene Annotation:

Gene ontology and gene interaction analyses for genes identified as differentially expressed were examined using Ingenuity Pathway Analysis (IPA) tools 7.0 (<http://www.ingenuity.com>).

In addition, an HTML page listing all significant probe sets with their associated Entrez ID, gene symbol, Unigene ID, chromosomal location, and gene name with appropriate hyperlinks was produced to expedite follow-up.

Verification of Microarray Data:

Reverse Transcriptase (RT) real time PCR Analysis. To validate our microarray results, we carried out a quantitative reverse transcriptase “real time” PCR (QPCR) for genes selected for relevance and biological significance. We selected Caspase 1 (CASP1), interleukin 8 (IL8), interleukin 15 (IL15), platelet derived growth factor (PDGFC) myxovirus (influenza virus) resistance 1 (MX1) and transforming growth factor beta 1 (TGFB1). We used the same mRNA from the stock RNAs samples that were subjected to microarray study. Total RNA from each sample was subjected to reverse transcription using TaqMan® Reverse Transcription Reagents (Applied Biosystems, Foster City, CA) according to the manufacturer’s protocol. Real-time PCR reactions then were carried out in a 25µL reaction mixture in an ABI Prism 7700 Sequence Detection System (Applied Biosystems, Foster City, CA), using TaqMan® Pre-Developed Assay Reagents for Gene Expression (Applied Biosystems). Each assay is a 20x mix of forward primer, reverse primer, and 6FAM™ dye - MGB labeled probe. Data were analyzed according to the comparative cycle threshold (Ct) method and normalized by Beta 2-microglobulin (B2M) expression in each pool sample. We used QPCR to determine the relative expression levels of some of the prognostic genes obtained from the microarray data analysis among multiple randomly chosen samples from each group. Pearson’s correlation coefficient (r) was calculated to examine the relation between microarray and real-time PCR results, $P < 0.05$ were considered significant.

Results

Analysis of gene expression patterns between alcoholic cirrhotic and normal liver tissues

The Top over expressed genes between alcoholic cirrhotic tissue and normal liver tissue are involved in immune response (IGKC, IGL@, IGHM), antigen presentation (HLA-C) and inflammation (IL8). Genes involved in the immune response were down regulated in alcoholic cirrhotic tissue. The top canonical pathways in alcoholic cirrhotic tissue were Jak/Stat signaling (P=5.39E-04), Protein Ubiquitination Pathway (P=8.22E-04), and VEGF signaling (P=1.06E-3). Jak/Stat signaling is intracellular signal transduction used by cytokines, interferons and growth factors, and certain aspects of the immune response.

In the protein ubiquitination pathway there was a down regulation of genes that code for protein subunits of the Proteasome. The proteasome plays a role in the turnover of cellular proteins and also in processes antigenic peptides for MHC class I antigen presentation. The down-regulated genes code for proteins subunits that make up the 26S proteasome, including subunit members of the proteolytic 20S core particle (PSMA1, PSMA3, PSMB1, PSMB2, PSMB4, PSMB7) the 19S regulatory particle (e.g. PSMC2, PSMD1, PSMD2, PSMD4, PSMD12, PSMD14). The 26S proteasome degrades ubiquitinated proteins in an ATP – dependent manner; we also found under-expression of several genes encoding proteins involved in ubiquitin mediated proteolysis (e.g. UBE2L3, UBE2A, UBE3A) as well as the regulatory subunits PA28gamma (PSME3) and PA200 (PSME4).

Chronic ethanol abuse induces genes for enzymes that metabolize ethanol, notably members of the cytochrome P 450 family, alcohol dehydrogenase and aldehyde dehydrogenase;

we found representatives of this group ALDH3B1, CYP2W1, and CYP2C9 to be up-regulated compared to normal liver tissue.

The presence of other immune cells was suggested by the up-regulation of CD7, CD8B, CD72, CD163, FCER2, ITGA3, KLRB1.

Differential gene expression between HCV cirrhotic liver tissue and Normal liver tissue

The top canonical pathway for HCV cirrhotic tissue was Hepatic Fibrosis/ Hepatic stellate cell activation ($P=9.17E-06$). Top over expressed genes were involved in the immune response (CXCL10, IGHM, IGL@, IGC, HLA-DQB1), response to virus (IFI27, IFIT1), and antigen presentation (HLA-DQB1). Many genes were up-regulated in the Hepatic Fibrosis/Hepatic stellate cell activation pathway including those encoding for extracellular matrix proteins (COL1A1, COL1A2, COL3A1), cell receptors (e.g. CD40, FAS, TGFBR2, TNFRSF1, LY96, FGFR1, IL10RA), signal transduction (STAT1, SMAD2, SMAD7) as well as cytokines and chemokines (CCL5, CCL21, TGFB1, IL8).

There was an over-abundance of cytokines and chemokines in HCV cirrhotic tissue. Chemokine signaling ($P=0.0433$) and CCR5 signaling ($P=1.67E-03$) canonical pathways emerged as significant in the analysis. XCL1, CCL3 (MIP1a), CCL4 (MIP1b), CCL5 (RANTES), CCL21 (ALP) CXCL9 (MIG), and CXCL10 (IP10) were all up-regulated and suggest an inflammatory state. Interleukins that were present in HCV cirrhotic tissue include over-expression of IL8, IL15, IL18 and under-expression of IL4 and IL19.

HCV infection induces interferon signaling. We found up-regulation of IFN induced genes (e.g. IFI27, IFI35, IFITM1, IFIT1, OAS1) and for genes associated with viral response (e.g. MX1, IFIH1, PTPRC, ISG15). Moreover, IFN signaling ($P=0.0132$) was identified as a significant canonical pathway. A cartoon representation of this pathway can be seen in Figure 2

T-cell receptor signaling ($P=0.00298$) was also a top canonical pathway. Up-regulated genes in this pathway include CD3G, CD8A, ITK, LYK, FYN, LCP2, PTPRC (CD45), and TRA@. Genes involved with CTL and NK killing of target cells were up-regulated (FAS,

GZMB, PFR1) Additionally, CTL-mediated apoptosis of target cells was another significant canonical pathway (P=0.049).

Genes encoding proteins expressed by B-cell presence is suggested by the up-regulation of BST2, CD24, and CD72. Macrophage and monocyte presence is suggested by over expression of CD300A and CSF1R.

Genes involved in the significant interaction of HCV and Ethanol

Probe set linear models were used to determine any synergistic or antagonistic effect of the interaction of HCV and ethanol in cirrhotic tissue set based on HCV status, Alcohol status, and interaction of Alcohol and HCV status.

The top canonical pathways of genes involved in the interaction between HCV and alcohol were antigen presentation pathway, IL-4 signaling , hepatic fibrosis/hepatic stellate cell activation, fatty acid biosynthesis, Protein ubiquitination pathway and ERK/MAPK signaling. A stacked bar chart showing the percentage of genes positively or negatively affected by the interaction can be seen in Figure 3.

In the top canonical pathway, antigen presentation, we observed a negative estimate for multiple genes that code for MHC class II molecules involved in presentation of antigenic peptides (e.g. HLA-DRB1, HLA-DRA, HLA-DPB1, HLA-DQB1), as well as peptide loading and processing (HLA-DMA, CD74 (CLIP)). This pathway can be viewed in Figure 4.

Interestingly, genes involved in hepatic fibrosis/hepatic stellate cell activation were negatively affected by the interaction of HCV and alcohol. There was a negative interaction of genes associated with the extra-cellular matrix (MMP2, MMP7, TIMP3, COL1A2) as well as growth factors and receptors (FGFR1, FGFR2, PDGFRA, PDGFRB, CTGF). The analysis revealed toxicology lists with hepatic fibrosis as significant. A stacked bar chart showing hepatic fibrosis and two other lists (pro-apoptosis, positive acute phase response proteins) can be seen in Figure 5.

Genes involved in apoptosis were relevant in the analysis. AVEN, BAK1, BAD, and TRADD had a positive correlation and BCL2, BAX, CASP1, TNFSF21, DAP3K, BNIP3L, and TNFRSF21 had a negative correlation.

There was a negative estimate for genes involved in the immune response. These genes included chemokines (CXCL6, CXCL12, CCL19), chemokine receptors (CXCR4, CSF2RA, immune cell receptors (TRA@, TRBC1, TICAM2), immunoglobulins (IGP1, IGL, IGKC, IGJ, IGHG3). There were also negative estimates for genes present on the surface of immunotype cells (CD69 (CLEC2), CD24, CD69 and CD97).

Gene Expression Validation by QPCR

QPCR was used to confirm expression levels of mRNAs of CASP1, IL8, PDGFC, MX1, and TGFB1. There was significant differential expression of the genes between the different tissue types and the microarray results were reproduced ($r=0.82$, $P<0.001$; $r=0.71$, $P=0.002$; $r=0.65$, $P <0.001$; $r=0.7$, $P<0.001$; $r=0.73$, $P<0,001$; and $r=0.61$, $P <0.001$ respectively).

Figure 1- Heat Map generated from unsupervised cluster analysis

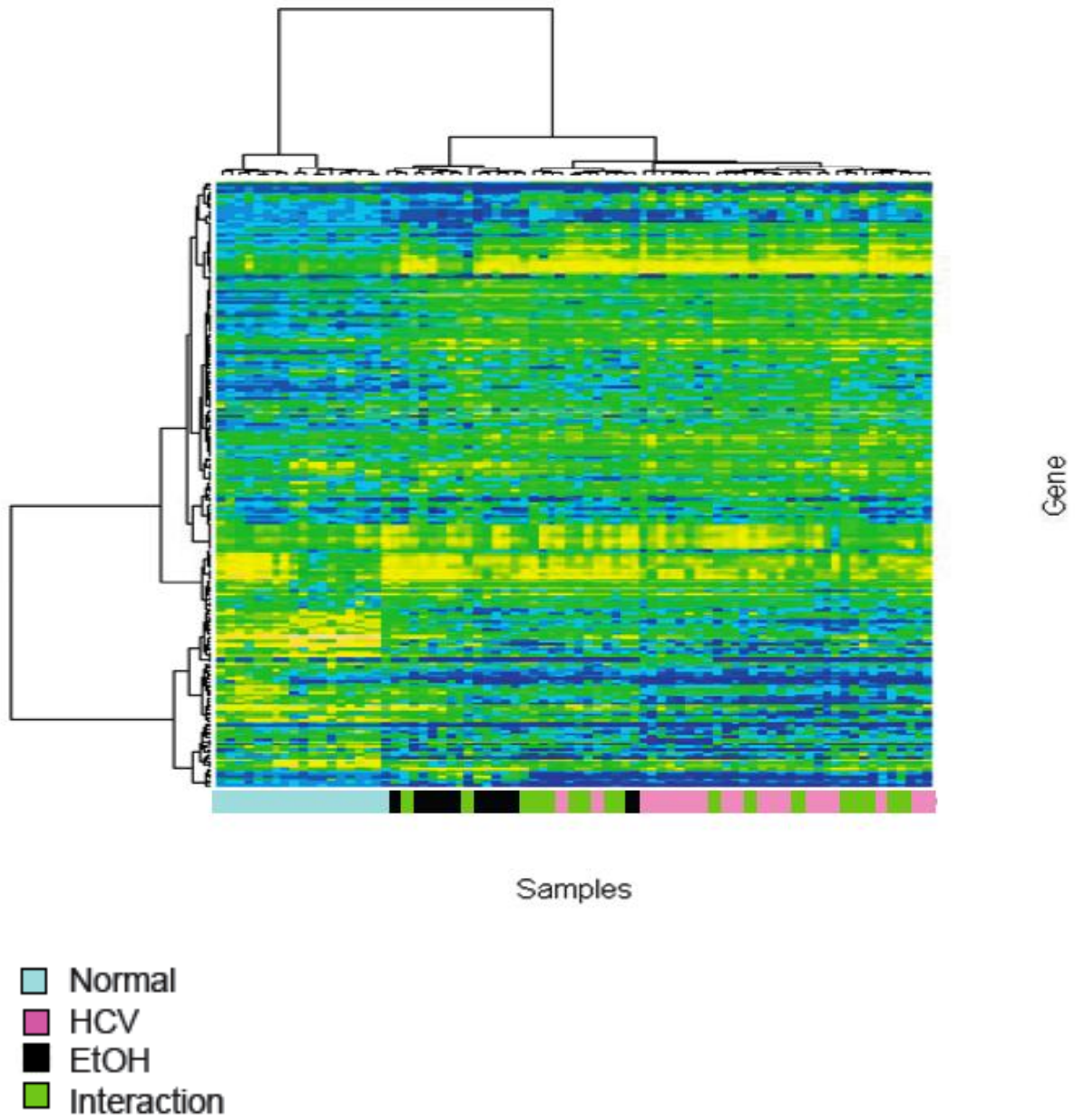
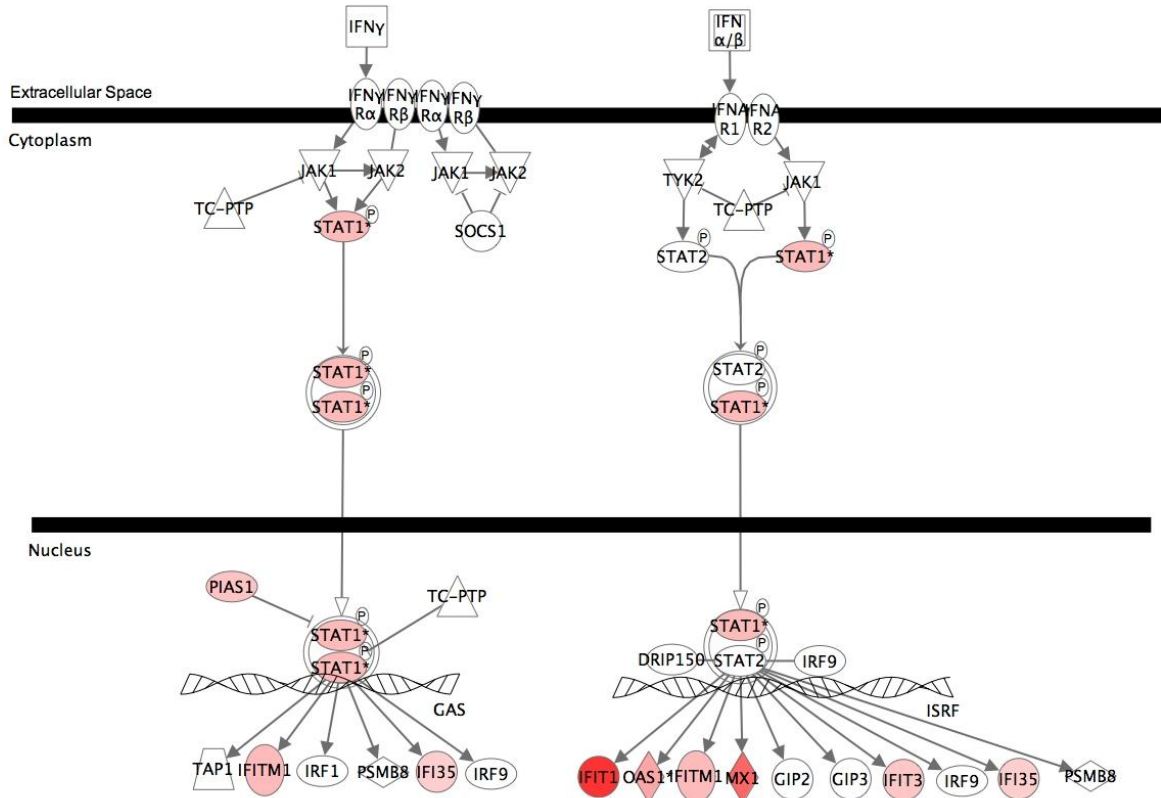


Figure 2- HCV Cirrhotic vs. Normal Tissue: Interferon Signaling

Interferon Signaling



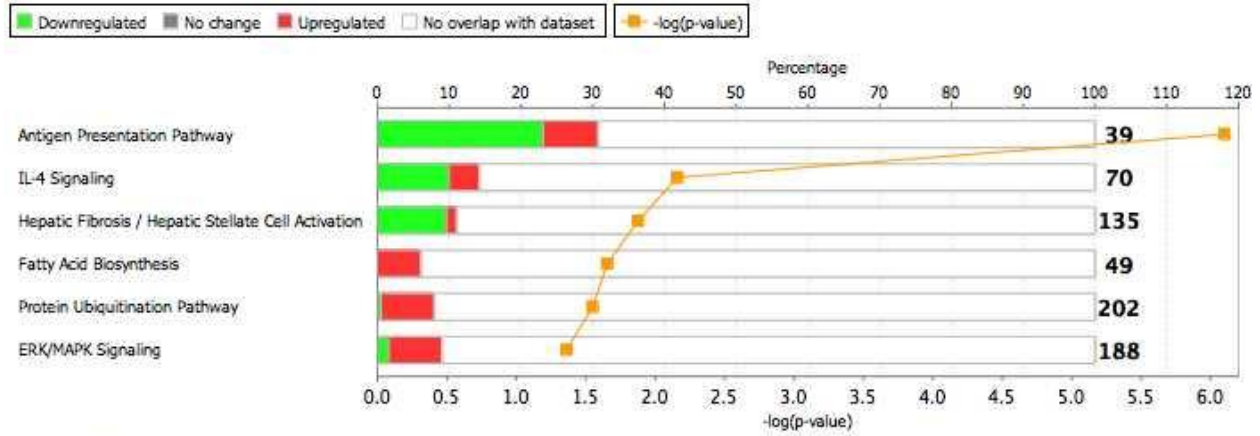
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Red- Up-regulated genes

Green-Down-regulated genes

Figure 3 – Top Canonical Pathways involved in the interaction of HCV*EtOH

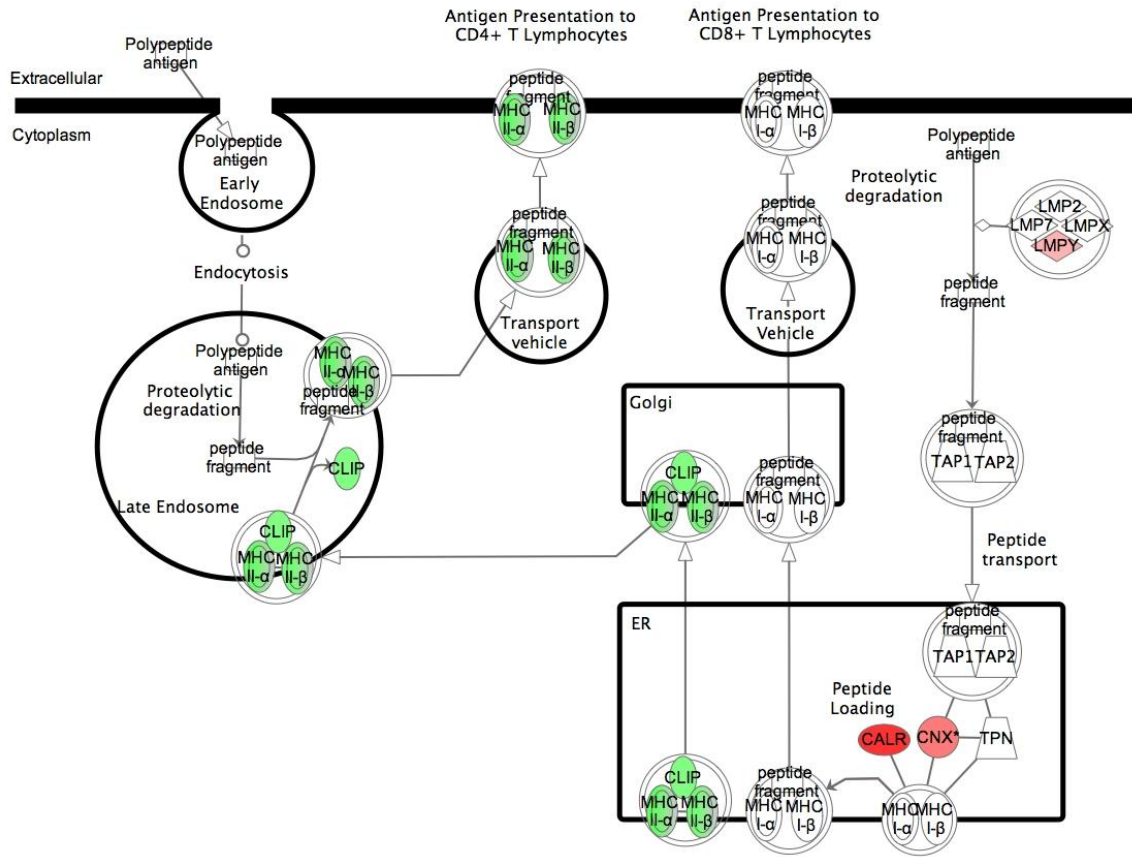
Analysis: significant interaction2 - 2009-02-13 10:40 AM



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Figure 4 - Significant interaction (HCV*EtOH): Antigen Presentation Pathway

Antigen Presentation Pathway



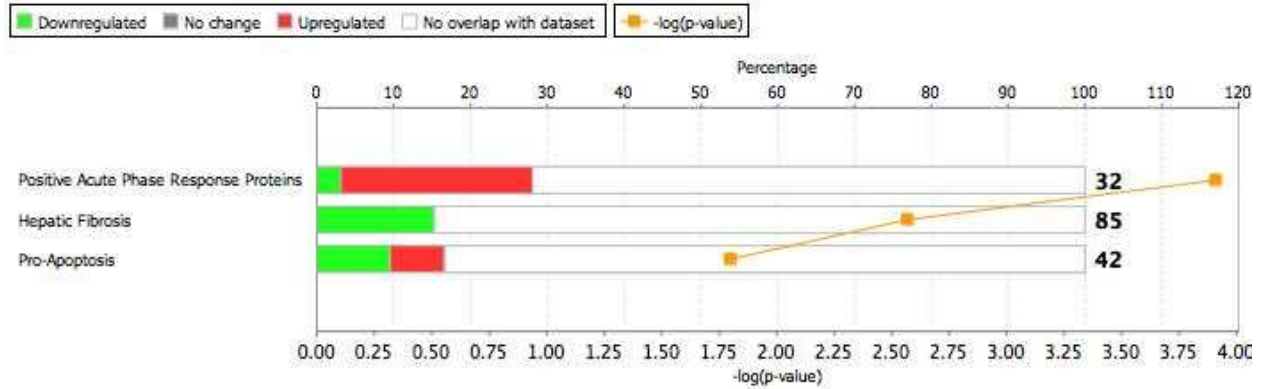
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Red- Genes with positive estimate term

Green- Genes with negative estimate term

Figure 5- Toxicology Lists for the Interaction of HCV*EtOH

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Table 1- Summary of More Important Findings in Each Analysis

	Alcohol cirrhotic tissues vs. Normal livers	HCV cirrhotic tissues vs. Normal livers	Significant Interaction analysis
Number of differentially expressed probe sets/genes	1,406 /1,272	2,222 /1,841	1,230 /1,051
Associated Network Functions (five top scored networks)	<p>1-Protein Degradation, Protein Synthesis, Immunologic al Disease (score 37)</p> <p>2- Gene Expression, Cancer, Infectious Disease (score 37)</p> <p>3- Cell Morphology, Tissue Morphology, RNA Damage and Repair (score 35)</p> <p>4- Cell Cycle, Cancer, Gastrointestinal Disease (score 35)</p>	<p>1-Molecular Transport, Connective Tissue Disorders, Dermatological Diseases and Conditions (score 43)</p> <p>2- Cell Death, Molecular Transport, Cellular Assembly and Organization (score 40)</p> <p>3- Lymphoid Tissue Structure and Development, Organ Development, Cellular Development (score 37)</p> <p>4- Gene Expression, Lipid Metabolism, Molecular Transport (score 37)</p>	<p>1-Genetic Disorder, Hematological Disease, Cell Cycle (score 45)</p> <p>2-Cancer, Cell Death, Reproductive System Disease (score 40)</p> <p>3-Lipid Metabolism, Small Molecule Biochemistry, Cellular Movement (score 38)</p> <p>4- Hematological Disease, Genetic Disorder, Cellular Assembly and Organization (score 38)</p>

	5- Cell Cycle, Cellular Development, Skeletal and Muscular System Development and Function (score 35)	5- Cancer, Immunological Disease, Organismal Development (score 35)	5- Protein Trafficking, Developmental Disorder, Genetic Disorder (score 38)
Top molecular and cellular functions	- Cellular Growth and Proliferation (P-value range=1.47E-04 - 4.24E-02), 314 genes	- Cellular Growth and Proliferation (P-value range=1.12E-13 - 4.03E-03) 402 genes	-Cell Death (P-value range=1.00E-08 - 2.19E-02) 228 genes
	- Gene Expression (P-value range=1.92E-04 - 3.81E-02), 236 genes	- Cell Death (P-value range=2.80E-13 - 3.90E-03) 361 genes	- Cellular Growth and Proliferation (P-value range=8.57E-08 - 2.12E-02) 267 genes
	- Cell Cycle (P-value ranges=4.81E-04 - 4.42E-02) 148 genes	- Cellular Movement (P-value range=2.88E-12 - 3.83E-03) 211 genes	- Cellular Compromise (P-value range=2.88E-05 - 1.17E-02) 14 genes
	- Amino Acid Metabolism (P-value range=7.68E-04 - 4.51E-02) 54 genes	- Cellular Development (P-value range=1.76E-09 - 3.76E-03) 260 genes	-Cell Morphology (P-value range=3.36E-05 -
	-Post-Translational Modification (P-value range=7.68E-04 - 4.38E-02) 135 genes	- Cell-To-Cell Signaling and Interaction (P-value range=6.38E-08 - 4.26E-03) 248 genes	-Cell-To-Cell Signaling and Interaction (P-value range=6.79E-05 - 1.63E-02) 96 genes

Top canonical pathways	- JAK/Stat Signaling (P=5.39E-04) - Protein Ubiquitination Pathway (P=8.22E-04) - VEGF Signaling (P=1.06E-03)	-Hepatic Fibrosis / Hepatic Stellate Cell Activation (P=9.17E-06) - Phospholipase C Signaling (P=1.62E-05) -G-Protein Coupled Receptor Signaling (P=3.46E-05) -Thrombin Signaling (P=4.21E-05)	- Antigen Presentation Pathway (P=7.92E-07) -IL-4 Signaling (P=6.92E-03) -Riboflavin Metabolism (P=1.27E-02) -Hepatic Fibrosis / Hepatic Stellate Cell Activation (P=1.32E-02)
Top over expressed genes (fold changes)	NTN3 (19.62) IGKC (11.95) IGL@ (10.56) HLA-C (7.08) IGHM (6.8) HBB (includes EG:3043) (6.65) ZCWPW2 (includes EG:152098) (5.73) MAFF (5.51) IL8 (5.4) HBA1(5.26)	IFI27 (21.72) NTN3 (19.62) IGKC (16.04) CXCL10 (10.89) IGL@ (10.56) HLA-DQB1 (9.98) IFIT1 (9.07) AKR1B10 (8.09) HBB (includes EG:3043) (8.01) IGHM (7.68)	N/A
Top under expressed genes	S100A8 (-5.57)	LPA (-4.5)	N/A

(fold changes)

FCN2 (-3.58)	ATF5 (-4.49)
RFC5 (-3.54)	STEAP1 (-3.8)
SAA2 (-3.47)	PZP (-3.63)
TFPI (-3.30)	SAA2 (-3.47)
ST6GAL1 (-3.1)	MT1M (-3.45)
KCNN2 (-3.1)	TFPI (-3.3)
ABCA1 (-2.99)	DHODH (-3.3)
TGM2 (-2.97)	SLCO4C1 (-3.2)
LMAN1 (-2.95)	KCNN2 (-3.1)

Discussion

Despite decades of directed research, the underlying molecular mechanisms involved in alcohol and HCV mediated liver disease are complex and not fully elucidated. The mechanisms in which alcohol worsens HCV infection outcome remain even more elusive. In the present study, we observed characteristic gene expression patterns in HCV cirrhotic tissue and alcoholic cirrhotic tissue. We were able to observe principle pathways of genes involved in molecular and cellular function by comparing each condition to normal liver tissue. Furthermore, we were able to identify genes synergistically or antagonistically involved in the direct interaction of alcohol and HCV.

Liver disease mediated by alcohol has been associated with modulated immune response, increased inflammation and oxidative stress, and hepatocyte apoptosis. Alcoholics have a diminished ability to clear bacterial and viral pathogenic challenges as infections are prolonged in the alcoholic patient. Additionally, both chronic and acute alcohol intake modulate host immunity differently. Hepatocyte apoptosis is marked with the appearance of Mallory hyaline bodies in alcoholic liver tissue (64). Inflammation results directly from the metabolism of ethanol and indirectly from subsequent leukocyte infiltration (65). However, the mechanisms involved in pathogenic damage from chronic alcohol and the events that lead to liver disease are still not understood very well. In the current study we identified gene expression patterns that may partially account for these characteristics of alcoholic liver disease.

A hallmark characteristic of alcoholic liver disease is leukocyte infiltration, particularly by neutrophils (66, 67). We observed an over abundance of genes that suggest the presence of

leukocytes: CD7 (T-cells, NK cells), CD8B (Cytotoxic T-cells), KLRB1 (NK cells), and CD72 (B-cells). B-cell presence is also suggested by the over abundance of immunoglobulins.

Importantly, one of our top up-regulated genes alcoholic cirrhotic tissue was CXC chemokine family member IL8, a very potent chemotactic attractant for neutrophils. Neutrophils release reactive oxygen species and are a major cellular contributor to inflammation and are characteristic of alcoholic hepatitis (67). IL8 is secreted by a wide variety of cell types and can be activated by transcription factors AP-1, NF- κ B, and C/EBP-B, which can be activated by a wide variety of stimuli including cytokines, oxidative stress and pathogens (68). Pertaining to our study, IL8 can be induced by oxidative stress via the AP-1 transcription factor. We found up-regulation of JUN, which encodes for a protein that is part of the AP-1 transcription factor complex.

Oxidative stress can lead to cell death via inactivation of the ubiquitin-proteasome pathway. We observed down-regulation of many genes involved in the protein ubiquitination canonical pathway. The genes involved encode for proteins of the 20S proteasome, the 26S proteasome and ubiquitin-conjugating enzymes. The ubiquitin-proteasome system is vital for protein catabolism in mammalian cells as it degrades damaged, oxidized or misfolded proteins, as well as short-lived regulatory proteins involved in intracellular signaling. The proteasome plays a role in ethanol-induced diseases (69,70). Oxidative stress has been shown to inhibit the proteasome in hepatic tissue as well as extra-hepatic tissue such as retinal epithelial cells and endothelial cells (71,72,73,74). Inhibition of the proteasome may provide the link between IL8 and oxidative stress (73). Proteasome inhibitors have been shown to activate IL8 in a NF- κ B independent manner via induction of AP-1 by enhanced JUN phosphorylation (71). In the current study, we found several genes under-expressed in NF- κ B signaling (MYD88, IRAK1, IKBKG, CHUK)

and up-regulation of JUN. Furthermore, the proteasome function is critical in trimming antigenic peptides for MHC-class-I antigen presentation and can be impaired by ethanol (53,54,75).

Our results provide, at a transcriptional level, a possible mechanism that ties together oxidative stress, apoptosis, inflammation and impaired MHC class-I restricted antigen presentation via proteasome malfunction in alcoholic patients. This may contribute to liver injury, fibrogenic stimuli and decreased resistance to pathogens affecting the liver such as HBV and HCV.

In HCV-induced cirrhotic liver tissue, we found gene expression patterns characteristic of chronic HCV infection. Studies have shown up-regulation of genes associated with the immune response, inflammation, apoptosis and hepatic fibrosis (76, 77, 78,79). Hepatic gene expression has been found to discriminate non-responders to responders of anti-viral therapy (80,81). HCV infection induces interferon signaling regardless of outcome. Patients with elevated expression of interferon-stimulated genes tend to respond poorly to antiviral treatment. Sarasin-Filipowicz theorized that pre-activation of interferon signaling could cause adaptive evasive mechanisms by the virus. In the current study, we found up-regulation of chemokines, cytokines and interferon-stimulated genes (82).

Plasma and intra-hepatic chemokine levels associated with poor outcome and liver damage in patients with HCV. CXCL9, CXCL10 and CXCL11 were elevated in both patients not currently on antiviral treatment and in comparing non-responders of treatment to responders (83). CXCL10 is a pro-inflammatory chemokine whose expression is up-regulated in HCV-infected liver tissue compared to normal liver tissue, HBV liver tissue and in non-viral cirrhotic

liver tissue (84). CXCL10 expression in hepatocytes was also found to be correlated with histological severity and lobular inflammation (85). IL-18, a pro-inflammatory IFN- γ inducing cytokine, has been found up-regulated in liver disease induced by HCV and also correlates with disease progression and hepatic damage (84,86). The over-expression of these cytokines is suggestive of an inflammatory state and may contribute to liver damage by the recruitment of non-specific T-cells that might result in non-specific inflammatory attack toward hepatocytes (87,88). The overabundance of inflammatory cytokines may lead to an unregulated cycle of inflammation as the immune response is activate but not resolved (89). The trafficking of T-cells to liver is intended to control the virus by destruction of infected cells, but may ultimately result in non-specific inflammation cell death in infected cells and uninfected cells (90).

Our results are in concordance with these studies. HCV mediated cirrhotic tissue showed a gene expression profile consistent of severe outcomes of HCV infection including genes that suggest pronounced inflammation, disease progression and probable failure to respond to anti-viral therapy.

The mechanisms in which alcohol worsens the outcome of HCV infection are still unclear but there has been evidence that alcohol and HCV together increase oxidative stress, cytotoxicity, steatosis, apoptosis and impairment of the immune response (91). Our results show positive estimates for genes involved in the acute phase and for fatty acid biosynthesis. Surprisingly genes related to hepatic fibrosis and apoptosis revealed a negative estimate. Most importantly, a negative interaction was observed for genes associated with the immune response, including several genes in the antigen presentation pathway.

The negative estimate of several genes encoding proteins involved in MHC class II restricted antigen presentation may partially account for the persistence of HCV. MHC Class II molecules are expressed by professional APCs, which are able to activate the cellular adaptive immune response. This step is critical in bridging the innate arm of the immune system for an effective adaptive response as it generates antigen specific T-helper cells which in turn promote the proliferation of antigen specific CTLs. Of the antigen presenting cells, (e.g. B-cells, sinusoidal endothelial cells, Kupffer Cells) the most potent APC in the liver are dendritic cells. Studies have suggested that both HCV infection and chronic alcohol intake individually impair the allostimulatory capacity of DCs and can have an additive effect of this inhibition in combination (58). HLA-DRB1, a gene we found to have a negative estimate in the interaction of HCV and ethanol, has been shown to target multiple epitopes of different HCV proteins and some alleles of HLA-DRB1 have been associated with patients that resolve HCV infection (92). Being that eradication of HCV from the host is dependent on a strong and coordinated response by the innate and adaptive immunity, it would be strategic for the virus to take advantage of this pathway for eluding the host defense response.

In conclusion, we have found characteristic gene expression signatures of both alcoholic cirrhotic tissue and HCV cirrhotic tissue compared to normal liver tissue. We also, for the first time, were able to exhibit genes that may be responsible for the synergistic/additive effect of the interaction of HCV and alcohol in human liver tissue. We observed that the addition of alcohol to HCV results in decreased immune response, especially in antigen presentation to T-cells by professional APCs.

Here we show that HCV induced cirrhosis shows an over-expression of inflammatory response genes, consistent with gene profile expressions that is associated with poor disease

progression, outcome and liver damage. The profile is also consistent to patients with reduced response to antiviral therapy. While certain aspects of the immune response are activated, such as IFN stimulated genes and leukocyte trafficking, the response is insufficient to eradicate the virus and may perpetuate a cycle of inflammation. Alcoholic cirrhotic tissue also exhibits a gene expression profile favoring an inflammatory state as well as immunomodulation by the differential expression of genes involved in signal transduction pathways and antigen presentation. Further more, our results may offer a pathway for reduced class I antigen presentation possibly induced by oxidative stress, allowing virally infected cells to escape surveillance by CTLs . While decrease in Class-I antigen presentation was not exhibited in the interaction of HCV and alcohol, we have found down regulation of genes involved in antigen loading and presentation in the context of class II restricted antigen presentation. This may account for may account for the reduced allostimulatory capacity of DCs observed in alcoholic patients with HCV which can result in increased viral persistence by possibly preventing the effective activation of the cellular immune response by DCs, resulting in inefficient effector action of T-cells.

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List of References

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Appendix 1

Supplemental Table 1- Genes Significantly Different Between ALD Cirrhotic Tissue Compared to Normal Liver Tissue

Entrez ID	Affy ID	Symbol	Gene Name	Fold
2342	1773_at	FNTB	farnesyltransferase, CAAX box, beta	-1.26
5690	200039_s_at	PSMB2	proteasome (prosome, macropain) subunit, beta type, 2	-1.81
8683	200044_at	SFRS9	splicing factor, arginine/serine-rich 9	-1.49
10899	200048_s_at	JTB	jumping translocation breakpoint	-1.99
375	200065_s_at	ARF1	ADP-ribosylation factor 1	-1.55
533	200078_s_at	ATP6V0B	ATPase, H ⁺ transporting, lysosomal 21kDa, V0 subunit b	-1.72
51433	200098_s_at	ANAPC5	anaphase promoting complex subunit 5	-1.6
7453	200628_s_at	WARS	tryptophanyl-tRNA synthetase	-1.81
4924	200646_s_at	NUCB1	nucleobindin 1	-2.43
3939	200650_s_at	LDHA	lactate dehydrogenase A	-1.67
7332	200683_s_at	UBE2L3	ubiquitin-conjugating enzyme E2L 3	-2.19
7332	200684_s_at	UBE2L3	ubiquitin-conjugating enzyme E2L 3	-1.25
2782	200744_s_at	GNB1	guanine nucleotide binding protein (G protein), beta polypeptide 1	-1.89
813	200756_x_at	CALU	calumenin	-1.59
5695	200786_at	PSMB7	proteasome (prosome, macropain) subunit, beta type, 7	-1.63
10960	200805_at	LMAN2	lectin, mannose-binding 2	-1.94
3329	200807_s_at	HSPD1	heat shock 60kDa protein 1 (chaperonin)	-1.67
10574	200812_at	CCT7	chaperonin containing TCP1, subunit 7 (eta)	-1.57

5351	200827_a_t	PLOD1	procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase 1	-1.61
5708	200830_a_t	PSMD2	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	-1.58
2058	200843_s_at	EPRS	glutamyl-prolyl-tRNA synthetase	-1.71
5499	200846_s_at	PPP1CA	protein phosphatase 1, catalytic subunit, alpha isoform	-1.77
11171	200870_a_t	STRAP	serine/threonine kinase receptor associated protein	-1.92
5689	200876_s_at	PSMB1	proteasome (prosome, macropain) subunit, beta type, 1	-1.65
6734	200918_s_at	SRPR	signal recognition particle receptor ('docking protein')	-2.44
51552	200927_s_at	RAB14	RAB14, member RAS oncogene family	-2.48
10972	200929_a_t	TMED10	transmembrane emp24-like trafficking protein 10 (yeast)	-1.76
7414	200931_s_at	VCL	vinculin	2.15
473	200938_s_at	RERE	arginine-glutamic acid dipeptide (RE) repeats	1.81
5479	200968_s_at	PPIB	peptidylprolyl isomerase B (cyclophilin B)	-1.89
10197	200987_x_at	PSME3	proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)	-2.13
6748	201004_a_t	SSR4	signal sequence receptor, delta (translocon-associated protein delta)	-1.77
10606	201013_s_at	PAICS	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase	-2.07
10606	201014_s_at	PAICS	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase	-1.86
1964	201017_a_t	EIF1AX	eukaryotic translation initiation factor 1A, X-linked	-1.97
7052	201042_a_t	TGM2	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)	-2.97
8125	201043_s_at	ANP32A	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	-1.48
9491	201052_s_at	PSMF1	proteasome (prosome, macropain) inhibitor subunit 1 (PI31)	-1.73
1537	201066_a_t	CYC1	cytochrome c-1	-1.89
5701	201068_s_at	PSMC2	proteasome (prosome, macropain) 26S subunit, ATPase, 2	-1.86
9144	201079_a_t	SYNGR2	synaptogyrin 2	-1.89
378	201097_s_at	ARF4	ADP-ribosylation factor 4	-1.87

9276	201098_a_t	COPB2	coatomer protein complex, subunit beta 2 (beta prime)	-2.31
1965	201144_s_at	EIF2S1	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa	-1.61
10456	201145_a_t	HAX1	HCLS1 associated protein X-1	-1.59
5878	201156_s_at	RAB5C	RAB5C, member RAS oncogene family	-1.61
4836	201157_s_at	NMT1	N-myristoyltransferase 1	-1.7
4836	201158_a_t	NMT1	N-myristoyltransferase 1	-1.78
51075	201175_a_t	TXNDC14	thioredoxin domain containing 14	-1.85
5707	201198_s_at	PSMD1	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1	-1.61
5510	201214_s_at	PPP1R7	protein phosphatase 1, regulatory (inhibitor) subunit 7	-1.54
10425	201229_s_at	ARIH2	ariadne homolog 2 (Drosophila)	-1.49
10425	201230_s_at	ARIH2	ariadne homolog 2 (Drosophila)	-1.43
9789	201239_s_at	SPCS2	signal peptidase complex subunit 2 homolog (S. cerevisiae)	-2.02
5894	201244_s_at	RAF1	v-raf-1 murine leukemia viral oncogene homolog 1	-1.59
7917	201255_x_at	BAT3	HLA-B associated transcript 3	-1.42
5869	201276_a_t	RAB5B	RAB5B, member RAS oncogene family	-1.35
11047	201281_a_t	ADRM1	adhesion regulating molecule 1	-1.9
10581	201315_x_at	IFITM2	interferon induced transmembrane protein 2 (I-8D)	-1.78
1315	201359_a_t	COPB1	coatomer protein complex, subunit beta 1	-1.84
5516	201374_x_at	PPP2CB	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	1.69
27101	201381_x_at	CACYBP	calcyclin binding protein	-2.02
5709	201388_a_t	PSMD3	proteasome (prosome, macropain) 26S subunit, non-ATPase, 3	-2.05
23471	201398_s_at	TRAM1	translocation associated membrane protein 1	-1.9
3295	201413_a_t	HSD17B4	hydroxysteroid (17-beta) dehydrogenase 4	-1.78
10856	201459_a_t	RUVBL2	RuvB-like 2 (E. coli)	-1.52
3725	201465_s_at	JUN	jun oncogene	2.43
3675	201474_s_at	ITGA3	integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor)	1.4
4141	201475_x_at	MARS	methionyl-tRNA synthetase	-1.98

10598	201491_a_t	AHSA1	AHA1, activator of heat shock 90kDa protein ATPase homolog 1 (yeast)	-1.84
4629	201495_x_at	MYH11	myosin, heavy chain 11, smooth muscle	1.42
6992	201500_s_at	PPP1R11	protein phosphatase 1, regulatory (inhibitor) subunit 11	-1.47
7247	201504_s_at	TSN	translin	-1.54
5684	201532_a_t	PSMA3	proteasome (prosome, macropain) subunit, alpha type, 3	-2.03
1845	201537_s_at	DUSP3	dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	-1.98
10765	201547_a_t	JARID1B	jumonji, AT rich interactive domain 1B	1.27
2720	201576_s_at	GLB1	galactosidase, beta 1	-1.72
4830	201577_a_t	NME1	non-metastatic cells 1, protein (NM23A) expressed in	-2.53
3654	201587_s_at	IRAK1	interleukin-1 receptor-associated kinase 1	-2.39
9352	201588_a_t	TXNL1	thioredoxin-like 1	-1.59
8243	201589_a_t	SMC1A	structural maintenance of chromosomes 1A	-2.02
8720	201620_a_t	MBTPS1	membrane-bound transcription factor peptidase, site 1	-1.48
1615	201624_a_t	DARS	aspartyl-tRNA synthetase	-1.88
1967	201632_a_t	EIF2B1	eukaryotic translation initiation factor 2B, subunit 1 alpha, 26kDa	-1.6
7264	201644_a_t	TSTA3	tissue specific transplantation antigen P35B	-2.28
400	201659_s_at	ARL1	ADP-ribosylation factor-like 1	-2.41
10051	201663_s_at	SMC4	structural maintenance of chromosomes 4	-1.45
5682	201676_x_at	PSMA1	proteasome (prosome, macropain) subunit, alpha type, 1	-1.5
7163	201690_s_at	TPD52	tumor protein D52	-2.18
7163	201691_s_at	TPD52	tumor protein D52	-1.4
1786	201697_s_at	DNMT1	DNA (cytosine-5-)-methyltransferase 1	-1.64
8683	201698_s_at	SFRS9	splicing factor, arginine/serine-rich 9	-1.95
6642	201716_a_t	SNX1	sorting nexin 1	-1.55
740	201717_a_t	MRPL49	mitochondrial ribosomal protein L49	-1.6
1994	201726_a_t	ELAVL1	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)	-1.73

6426	201741_x_at	SFRS1	splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor)	-1.16
7157	201746_a_t	TP53	tumor protein p53 (Li-Fraumeni syndrome)	-1.68
9813	201776_s_at	KIAA0494	KIAA0494	-2.09
9813	201777_s_at	KIAA0494	KIAA0494	-1.39
949	201819_a_t	SCARB1	scavenger receptor class B, member 1	-1.98
822	201850_a_t	CAPG	capping protein (actin filament), gelsolin-like	1.55
9208	201861_s_at	LRRFIP1	leucine rich repeat (in FLII) interacting protein 1	1.69
25820	201881_s_at	ARIH1	ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (Drosophila)	-1.63
1727	201885_s_at	CYB5R3	cytochrome b5 reductase 3	-1.88
1163	201897_s_at	CKS1B	CDC28 protein kinase regulatory subunit 1B	-2.12
7319	201898_s_at	UBE2A	ubiquitin-conjugating enzyme E2A (RAD6 homolog)	-1.52
10217	201906_s_at	CTDSPL	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like	1.76
23549	201937_s_at	DNPEP	aspartyl aminopeptidase	-1.52
8443	201956_s_at	GNPAT	glyceronephosphate O-acyltransferase	-1.38
221960	201973_s_at	C7orf28B	chromosome 7 open reading frame 28B	-1.84
9812	201977_s_at	KIAA0141	KIAA0141	-1.53
5536	201979_s_at	PPP5C	protein phosphatase 5, catalytic subunit	-1.62
9643	201994_a_t	MORF4L2	mortality factor 4 like 2	-1.54
2132	202012_s_at	EXT2	exostoses (multiple) 2	-1.95
2132	202013_s_at	EXT2	exostoses (multiple) 2	-1.8
439	202024_a_t	ASNA1	arsA arsenite transporter, ATP-binding, homolog 1 (bacterial)	-1.57
10295	202030_a_t	BCKDK	branched chain ketoacid dehydrogenase kinase	-1.55
3836	202058_s_at	KPNA1	karyopherin alpha 1 (importin alpha 5)	-2.39
3836	202059_s_at	KPNA1	karyopherin alpha 1 (importin alpha 5)	-1.93
6400	202061_s_at	SEL1L	sel-1 suppressor of lin-12-like (C. elegans)	-2.04
3419	202069_s	IDH3A	isocitrate dehydrogenase 3 (NAD+)	-2.18

	_at		alpha	
2802	202106_a_t	GOLGA3	golgi autoantigen, golgin subfamily a, 3	-1.67
9870	202128_a_t	KIAA0317	KIAA0317	-1.68
2071	202176_a_t	ERCC3	excision repair cross-complementing rodent repair deficiency, complementation group 3 (xeroderma pigmentosum group B complementing)	-1.54
8985	202185_a_t	PLOD3	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3	-2.02
5525	202186_x_at	PPP2R5A	protein phosphatase 2, regulatory subunit B', alpha isoform	1.91
5525	202187_s_at	PPP2R5A	protein phosphatase 2, regulatory subunit B', alpha isoform	-1.61
8522	202191_s_at	GAS7	growth arrest-specific 7	1.69
8522	202192_s_at	GAS7	growth arrest-specific 7	1.39
50999	202194_a_t	TMED5	transmembrane emp24 protein transport domain containing 5	-2.44
6732	202200_s_at	SRPK1	SFRS protein kinase 1	-1.85
267	202204_s_at	AMFR	autocrine motility factor receptor	-2.14
4802	202216_x_at	NFYC	nuclear transcription factor Y, gamma	-1.5
1674	202222_s_at	DES	desmin	1.57
10523	202229_s_at	CHERP	calcium homeostasis endoplasmic reticulum protein	-1.31
7102	202242_a_t	TSPAN7	tetraspanin 7	-1.81
5692	202243_s_at	PSMB4	proteasome (prosome, macropain) subunit, beta type, 4	-1.73
5692	202244_a_t	PSMB4	proteasome (prosome, macropain) subunit, beta type, 4	-1.48
1019	202246_s_at	CDK4	cyclin-dependent kinase 4	-1.52
6944	202261_a_t	VPS72	vacuolar protein sorting 72 homolog (S. cerevisiae)	-1.6
4070	202285_s_at	TACSTD2	tumor-associated calcium signal transducer 2	1.36
593	202331_a_t	BCKDHA	branched chain keto acid dehydrogenase E1, alpha polypeptide	-1.56
3093	202346_a_t	HIP2	huntingtin interacting protein 2	-1.82
5718	202352_s_at	PSMD12	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12	-2.01
5718	202353_s_at	PSMD12	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12	-2.55
25782	202374_s_at	RAB3GAP2	RAB3 GTPase activating protein subunit 2 (non-catalytic)	-1.51

6949	202384_s_at	TCOF1	Treacher Collins-Franceschetti syndrome 1	1.57
55324	202394_s_at	ABCF3	ATP-binding cassette, sub-family F (GCN20), member 3	-1.31
10204	202397_a_t	NUTF2	nuclear transport factor 2	-1.64
10239	202398_a_t	AP3S2	adaptor-related protein complex 3, sigma 2 subunit	-1.25
3481	202409_a_t	IGF2	insulin-like growth factor 2 (somatomedin A)	-1.62
9817	202417_a_t	KEAP1	kelch-like ECH-associated protein 1	-1.39
3421	202471_s_at	IDH3G	isocitrate dehydrogenase 3 (NAD+) gamma	-1.48
5902	202482_x_at	RANBP1	RAN binding protein 1	1.53
6903	202495_a_t	TBCC	tubulin folding cofactor C	-1.6
1739	202514_a_t	DLG1	discs, large homolog 1 (Drosophila)	-1.73
4292	202520_s_at	MLH1	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)	-2.14
5635	202529_a_t	PRPSAP1	phosphoribosyl pyrophosphate synthetase-associated protein 1	-1.82
1432	202530_a_t	MAPK14	mitogen-activated protein kinase 14	-1.4
2764	202543_s_at	GMFB	glia maturation factor, beta	-2.47
26097	202560_s_at	C1orf77	chromosome 1 open reading frame 77	-1.81
11161	202563_a_t	C14orf1	chromosome 14 open reading frame 1	1.47
10048	202583_s_at	RANBP9	RAN binding protein 9	-1.49
4799	202584_a_t	NFX1	nuclear transcription factor, X-box binding 1	-1.35
203	202587_s_at	AK1	adenylate kinase 1	-1.85
4893	202647_s_at	NRAS	neuroblastoma RAS viral (v-ras) oncogene homolog	-1.59
790	202715_a_t	CAD	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase	-1.63
8881	202717_s_at	CDC16	cell division cycle 16 homolog (S. cerevisiae)	-1.86
23518	202754_a_t	R3HDM1	R3H domain containing 1	-1.76
2817	202755_s_at	GPC1	glypican 1	1.38
53	202767_a_t	ACP2	acid phosphatase 2, lysosomal	-1.49
1725	202802_a_t	DHPS	deoxyhypusine synthase	-1.57
10907	202836_s	TXNL4A	thioredoxin-like 4A	-2.11

	_at			
11054	202841_x_at	OGFR	opioid growth factor receptor	-1.88
10928	202845_s_at	RALBP1	ralA binding protein 1	-1.38
10775	202868_s_at	POP4	processing of precursor 4, ribonuclease P/MRP subunit (<i>S. cerevisiae</i>)	-1.61
528	202873_at	ATP6V1C1	ATPase, H ⁺ transporting, lysosomal 42kDa, V1 subunit C1	-1.22
5519	202886_s_at	PPP2R1B	protein phosphatase 2 (formerly 2A), regulatory subunit A, beta isoform	-2.85
140885	202896_s_at	SIRPA	signal-regulatory protein alpha	-1.78
4927	202900_s_at	NUP88	nucleoporin 88kDa	-2.23
6279	202917_s_at	S100A8	S100 calcium binding protein A8	-5.57
10269	202939_at	ZMPSTE24	zinc metallopeptidase (STE24 homolog, <i>S. cerevisiae</i>)	-2.12
10565	202955_s_at	ARFGEF1	ADP-ribosylation factor guanine nucleotide-exchange factor 1 (brefeldin A-inhibited)	-1.38
58487	202977_s_at	CREBZF	CREB/ATF bZIP transcription factor	1.82
9915	202986_at	ARNT2	aryl-hydrocarbon receptor nuclear translocator 2	1.2
4017	202997_s_at	LOXL2	lysyl oxidase-like 2	1.26
2271	203032_s_at	FH	fumarate hydratase	-2.34
717	203052_at	C2	complement component 2	-1.66
9060	203059_s_at	PAPSS2	3'-phosphoadenosine 5'-phosphosulfate synthase 2	-2.44
9060	203060_s_at	PAPSS2	3'-phosphoadenosine 5'-phosphosulfate synthase 2	-2.07
27429	203089_s_at	HTRA2	HtrA serine peptidase 2	-1.65
2235	203116_s_at	FECH	ferrochelatase (protoporphyrin)	-1.83
9159	203118_at	PCSK7	proprotein convertase subtilisin/kexin type 7	-1.36
51112	203122_at	TTC15	tetratricopeptide repeat domain 15	-1.69
10244	203150_at	RABEPK	Rab9 effector protein with kelch motifs	-1.86
4728	203189_s_at	NDUFS8	NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase)	-1.82
4728	203190_at	NDUFS8	NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase)	-1.84
10058	203191_at	ABCB6	ATP-binding cassette, sub-family B (MDR/TAP), member 6	1.62

4928	203194_s _at	NUP98	nucleoporin 98kDa	-1.42
4552	203199_s _at	MTRR	5-methyltetrahydrofolate-homocysteine methyltransferase reductase	-1.75
5373	203201_a _t	PMM2	phosphomannomutase 2	-1.69
5601	203218_a _t	MAPK9	mitogen-activated protein kinase 9	-1.71
55312	203225_s _at	RFK	riboflavin kinase	-2.32
6302	203226_s _at	TSPAN31	tetraspanin 31	-1.51
10641	203246_s _at	TUSC4	tumor suppressor candidate 4	-1.67
23262	203253_s _at	HISPPD1	histidine acid phosphatase domain containing 1	-1.83
8263	203274_a _t	F8A1	coagulation factor VIII-associated (intronic transcript) 1	-1.61
3998	203293_s _at	LMAN1	lectin, mannose-binding, 1	-2.95
2794	203307_a _t	GNL1	guanine nucleotide binding protein-like 1	1.95
10245	203342_a _t	TIMM17B	translocase of inner mitochondrial membrane 17 homolog B (yeast)	-1.5
164	203350_a _t	APIG1	adaptor-related protein complex 1, gamma 1 subunit	-1.63
5000	203351_s _at	ORC4L	origin recognition complex, subunit 4- like (yeast)	-1.61
5000	203352_a _t	ORC4L	origin recognition complex, subunit 4- like (yeast)	-1.21
23362	203355_s _at	PSD3	pleckstrin and Sec7 domain containing 3	3.04
7174	203374_s _at	TPP2	tripeptidyl peptidase II	-1.72
8624	203405_a _t	DSCR2	Down syndrome critical region gene 2	-1.99
3488	203426_s _at	IGFBP5	insulin-like growth factor binding protein 5	1.31
8834	203437_a _t	TMEM11	transmembrane protein 11	-1.35
1000	203440_a _t	CDH2	cadherin 2, type 1, N-cadherin (neuronal)	1.41
5711	203447_a _t	PSMD5	proteasome (prosome, macropain) 26S subunit, non-ATPase, 5	-1.87
669	203502_a _t	BPGM	2,3-bisphosphoglycerate mutase	-1.57
19	203504_s _at	ABCA1	ATP-binding cassette, sub-family A (ABC1), member 1	-2.99
10651	203517_a _t	MTX2	metaxin 2	-1.56
27257	203534_a _t	LSM1	LSM1 homolog, U6 small nuclear RNA associated (<i>S. cerevisiae</i>)	-1.55
7739	203585_a _t	ZNF185	zinc finger protein 185 (LIM domain)	1.5

8634	203594_a_t	RTCD1	RNA terminal phosphate cyclase domain 1	-1.88
24138	203595_s_at	IFIT5	interferon-induced protein with tetratricopeptide repeats 5	-1.6
9724	203614_a_t	UTP14C	UTP14, U3 small nucleolar ribonucleoprotein, homolog C (yeast)	-2.32
6502	203625_x_at	SKP2	S-phase kinase-associated protein 2 (p45)	-2.33
9797	203648_a_t	TATDN2	TatD DNase domain containing 2	-1.33
8694	203669_s_at	DGAT1	diacylglycerol O-acyltransferase homolog 1 (mouse)	-1.92
26140	203670_a_t	TTL3	tubulin tyrosine ligase-like family, member 3	1.7
2799	203676_a_t	GNS	glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID)	-1.67
4350	203686_a_t	MPG	N-methylpurine-DNA glycosylase	-1.38
2067	203720_s_at	ERCC1	excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence)	-1.54
5914	203749_s_at	RARA	retinoic acid receptor, alpha	-1.94
5442	203782_s_at	POLRMT	polymerase (RNA) mitochondrial (DNA directed)	-1.83
55794	203785_s_at	DDX28	DEAD (Asp-Glu-Ala-Asp) box polypeptide 28	-1.59
7164	203786_s_at	TPD52L1	tumor protein D52-like 1	-2.04
9936	203799_a_t	CD302	CD302 molecule	-1.81
63931	203800_s_at	MRPS14	mitochondrial ribosomal protein S14	-1.89
1716	203816_a_t	DGUOK	deoxyguanosine kinase	-1.63
10188	203838_s_at	TNK2	tyrosine kinase, non-receptor, 2	1.5
57149	203897_a_t	LYRM1	LYR motif containing 1	-2.07
9111	203964_a_t	NMI	N-myc (and STAT) interactor	-1.76
8504	203970_s_at	PEX3	peroxisomal biogenesis factor 3	-2.23
8504	203972_s_at	PEX3	peroxisomal biogenesis factor 3	-2.53
8226	203974_a_t	HDHD1A	haloacid dehalogenase-like hydrolase domain containing 1A	-1.5
10036	203976_s_at	CHAF1A	chromatin assembly factor 1, subunit A (p150)	1.4
4682	203978_a_t	NUBP1	nucleotide binding protein 1 (MinD homolog, E. coli)	-1.61
23395	204016_a_t	LARS2	leucyl-tRNA synthetase 2, mitochondrial	-1.49

5984	204023_a_t	RFC4	replication factor C (activator 1) 4, 37kDa	-1.64
5134	204025_s_at	PDCD2	programmed cell death 2	-1.77
4234	204027_s_at	METTL1	methyltransferase like 1	-1.82
1050	204039_a_t	CEBPA	CCAAT/enhancer binding protein (C/EBP), alpha	-2.35
5090	204082_a_t	PBX3	pre-B-cell leukemia homeobox 3	-1.69
8884	204087_s_at	SLC5A6	solute carrier family 5 (sodium-dependent vitamin transporter), member 6	-3.03
5147	204091_a_t	PDE6D	phosphodiesterase 6D, cGMP-specific, rod, delta	-1.45
132	204119_s_at	ADK	adenosine kinase	-2.28
55556	204143_s_at	ENOSF1	enolase superfamily member 1	-2.09
7027	204147_s_at	TFDP1	transcription factor Dp-1	-1.26
5481	204185_x_at	PPID	peptidylprolyl isomerase D (cyclophilin D)	-2.28
5916	204189_a_t	RARG	retinoic acid receptor, gamma	-1.41
8732	204208_a_t	RNGTT	RNA guanylyltransferase and 5'-phosphatase	-1.27
2643	204224_s_at	GCH1	GTP cyclohydrolase 1 (dopa-responsive dystonia)	-2.12
10591	204238_s_at	C6orf108	chromosome 6 open reading frame 108	-2
10592	204240_s_at	SMC2	structural maintenance of chromosomes 2	-1.29
10926	204244_s_at	DBF4	DBF4 homolog (S. cerevisiae)	-1.32
11258	204246_s_at	DCTN3	dynactin 3 (p22)	-1.62
1020	204247_s_at	CDK5	cyclin-dependent kinase 5	-1.45
2767	204248_a_t	GNA11	guanine nucleotide binding protein (G protein), alpha 11 (Gq class)	-2.21
7084	204276_a_t	TK2	thymidine kinase 2, mitochondrial	-1.65
9166	204278_s_at	EBAG9	estrogen receptor binding site associated, antigen, 9	-1.79
6794	204292_x_at	STK11	serine/threonine kinase 11	1.76
10772	204299_a_t	FUSIP1	FUS interacting protein (serine/arginine-rich) 1	-1.98
11322	204328_a_t	TMC6	transmembrane channel-like 6	1.58
6183	204331_s_at	MRPS12	mitochondrial ribosomal protein S12	-2.81
10484	204344_s	SEC23A	Sec23 homolog A (S. cerevisiae)	-1.94

	_at			
25913	204354_a_t	POT1	POT1 protection of telomeres 1 homolog (S. pombe)	-1.6
22907	204355_a_t	DHX30	DEAH (Asp-Glu-Ala-His) box polypeptide 30	-1.8
2976	204366_s_at	GTF3C2	general transcription factor IIIC, polypeptide 2, beta 110kDa	-1.48
9730	204376_a_t	VPRBP	Vpr (HIV-1) binding protein	-1.15
8805	204390_a_t	TRIM24	tripartite motif-containing 24	1.55
8501	204394_a_t	SLC43A1	solute carrier family 43, member 1	-1.82
4289	204423_a_t	MKLN1	muskelin 1, intracellular mediator containing kelch motifs	-1.33
10959	204426_a_t	TMED2	transmembrane emp24 domain trafficking protein 2	-2.86
9825	204433_s_at	SPATA2	spermatogenesis associated 2	-1.33
8425	204442_x_at	LTBP4	latent transforming growth factor beta binding protein 4	1.54
9640	204473_s_at	ZNF592	zinc finger protein 592	-1.49
79095	204480_s_at	C9orf16	chromosome 9 open reading frame 16	-1.79
3784	204486_a_t	KCNQ1	potassium voltage-gated channel, KQT-like subfamily, member 1	1.74
22845	204488_a_t	DOLK	dolichol kinase	-1.49
637	204493_a_t	BID	BH3 interacting domain death agonist	-1.87
5534	204507_s_at	PPP3R1	protein phosphatase 3 (formerly 2B), regulatory subunit B, alpha isoform	-1.43
5978	204535_s_at	REST	RE1-silencing transcription factor	1.87
65082	204590_x_at	VPS33A	vacuolar protein sorting 33 homolog A (S. cerevisiae)	-1.27
54471	204593_s_at	SMCR7L	Smith-Magenis syndrome chromosome region, candidate 7-like	-1.72
10573	204599_s_at	MRPL28	mitochondrial ribosomal protein L28	1.81
80143	204666_s_at	SIKE	suppressor of IKK epsilon	-1.13
25880	204676_a_t	TMEM186	transmembrane protein 186	-1.44
27042	204699_s_at	C1orf107	chromosome 1 open reading frame 107	-1.67
27042	204700_x_at	C1orf107	chromosome 1 open reading frame 107	-2.67
2051	204718_a_t	EPHB6	EPH receptor B6	1.71
4690	204725_s_at	NCK1	NCK adaptor protein 1	-1.57

1464	204736_s _at	CSPG4	chondroitin sulfate proteoglycan 4	1.27
3376	204744_s _at	IARS	isoleucyl-tRNA synthetase	-1.95
10038	204752_x _at	PARP2	poly (ADP-ribose) polymerase family, member 2	-1.54
9742	204792_s _at	IFT140	intraflagellar transport 140 homolog (Chlamydomonas)	1.27
10732	204849_a _t	TCFL5	transcription factor-like 5 (basic helix- loop-helix)	-1.93
10536	204854_a _t	LEPREL2	leprecan-like 2	1.64
9767	204866_a _t	PHF16	PHD finger protein 16	-1.67
3396	204868_a _t	ICT1	immature colon carcinoma transcript 1	-1.52
9344	204877_s _at	TAOK2	TAO kinase 2	1.3
10232	204885_s _at	MSLN	mesothelin	1.49
8819	204899_s _at	SAP30	Sin3A-associated protein, 30kDa	1.47
9521	204905_s _at	EEF1E1	eukaryotic translation elongation factor 1 epsilon 1	-2.13
79703	204922_a _t	C11orf80	chromosome 11 open reading frame 80	1.44
5871	204936_a _t	MAP4K2	mitogen-activated protein kinase kinase kinase kinase 2	1.28
9149	204954_s _at	DYRK1B	dual-specificity tyrosine-(Y)- phosphorylation regulated kinase 1B	1.5
5001	204957_a _t	ORC5L	origin recognition complex, subunit 5- like (yeast)	-1.77
79090	204985_s _at	TRAPPC6 A	trafficking protein particle complex 6A	-1.31
7216	205028_a _t	TRO	trophinin	1.41
9150	205035_a _t	CTDP1	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1	-1.41
23542	205050_s _at	MAPK8IP2	mitogen-activated protein kinase 8 interacting protein 2	1.82
5557	205053_a _t	PRIM1	primase, DNA, polypeptide 1 (49kDa)	-1.23
3425	205058_a _t	IDUA	iduronidase, alpha-L-	1.7
8790	205140_a _t	FPGT	fucose-1-phosphate guanylyltransferase	-1.67
215	205142_x _at	ABCD1	ATP-binding cassette, sub-family D (ALD), member 1	-1.45
4921	205168_a _t	DDR2	discoidin domain receptor family, member 2	1.75
6773	205170_a _t	STAT2	signal transducer and activator of transcription 2, 113kDa	-1.3

3184	205183_a_t	HNRPD	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)	1.53
9585	205235_s_at	MPHOSPH1	M-phase phosphoprotein 1	-1.18
9997	205241_a_t	SCO2	SCO cytochrome oxidase deficient homolog 2 (yeast)	-1.7
10849	205264_a_t	CD3EAP	CD3e molecule, epsilon associated protein	-1.37
9567	205275_a_t	GTPBP1	GTP binding protein 1	1.32
9567	205276_s_at	GTPBP1	GTP binding protein 1	1.47
2533	205285_s_at	FYB	FYN binding protein (FYB-120/130)	1.53
2267	205305_a_t	FGL1	fibrinogen-like 1	-1.59
24140	205324_s_at	FTSJ1	FtsJ homolog 1 (E. coli)	-2.86
9986	205332_a_t	RCE1	RCE1 homolog, prenyl protein peptidase (S. cerevisiae)	1.37
6728	205335_s_at	SRP19	signal recognition particle 19kDa	-2.25
2355	205409_a_t	FOSL2	FOS-like antigen 2	1.57
493	205410_s_at	ATP2B4	ATPase, Ca ⁺⁺ transporting, plasma membrane 4	-1.23
2953	205439_a_t	GSTT2	glutathione S-transferase theta 2	-1.75
3241	205462_s_at	HPCAL1	hippocalcin-like 1	-1.47
7410	205537_s_at	VAV2	vav 2 guanine nucleotide exchange factor	1.96
7297	205546_s_at	TYK2	tyrosine kinase 2	-1.5
7425	205586_x_at	VGF	VGF nerve growth factor inducible	1.35
11116	205588_s_at	FGFR1OP	FGFR1 oncogene partner	-1.43
57147	205607_s_at	SCYL3	SCY1-like 3 (S. cerevisiae)	-1.52
284	205608_s_at	ANGPT1	angiopoietin 1	1.59
284	205609_a_t	ANGPT1	angiopoietin 1	1.73
8846	205621_a_t	ALKBH1	alkB, alkylation repair homolog 1 (E. coli)	-1.34
7140	205693_a_t	TNNT3	troponin T type 3 (skeletal, fast)	1.43
23545	205704_s_at	ATP6V0A2	ATPase, H ⁺ transporting, lysosomal V0 subunit a2	-1.46
22852	205706_s_at	ANKRD26	ankyrin repeat domain 26	1.21
23765	205707_a_t	IL17RA	interleukin 17 receptor A	-1.72

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5098	205717_x_at	PCDHGC3	protocadherin gamma subfamily C, 3	-1.38
3899	205734_s_at	AFF3	AF4/FMR2 family, member 3	1.44
79171	205740_s_at	RBM42	RNA binding motif protein 42	-1.46
2157	205756_s_at	F8	coagulation factor VIII, procoagulant component (hemophilia A)	-1.97
8557	205766_at	TCAP	titin-cap (telethonin)	1.88
2936	205770_at	GSR	glutathione reductase	-1.78
9605	205781_at	C16orf7	chromosome 16 open reading frame 7	1.5
3316	205824_at	HSPB2	heat shock 27kDa protein 2	1.41
8941	205852_at	CDK5R2	cyclin-dependent kinase 5, regulatory subunit 2 (p39)	1.75
10168	205855_at	ZNF197	zinc finger protein 197	1.24
2902	205914_s_at	GRIN1	glutamate receptor, ionotropic, N-methyl D-aspartate 1	2.25
3046	205919_at	HBE1	hemoglobin, epsilon 1	1.37
9466	205926_at	IL27RA	interleukin 27 receptor, alpha	1.31
9093	205963_s_at	DNAJA3	DnaJ (Hsp40) homolog, subfamily A, member 3	-1.79
1457	206075_s_at	CSNK2A1	casein kinase 2, alpha 1 polypeptide	-1.43
575	206083_at	BAI1	brain-specific angiogenesis inhibitor 1	1.45
10772	206095_s_at	FUSIP1	FUS interacting protein (serine/arginine-rich) 1	-1.92
5881	206103_at	RAC3	ras-related C3 botulinum toxin substrate 3 (rho family, small GTP binding protein Rac3)	1.48
152	206128_at	ADRA2C	adrenergic, alpha-2C-, receptor	1.9
7855	206136_at	FZD5	frizzled homolog 5 (Drosophila)	1.56
10389	206147_x_at	SCML2	sex comb on midleg-like 2 (Drosophila)	-1.51
23264	206169_x_at	ZC3H7B	zinc finger CCCH-type containing 7B	2.24
10198	206205_at	MPHOSPH9	M-phase phosphoprotein 9	-1.66
762	206208_at	CA4	carbonic anhydrase IV	1.6
762	206209_s_at	CA4	carbonic anhydrase IV	1.48
10138	206238_s_at	YAF2	YY1 associated factor 2	-1.33

5210	206246_a_t	PFKFB4	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4	1.33
1212	206284_x_at	CLTB	clathrin, light chain (Lcb)	-1.5
11163	206302_s_at	NUDT4	nudix (nucleoside diphosphate linked moiety X)-type motif 4	-2.08
9244	206315_a_t	CRLF1	cytokine receptor-like factor 1	1.57
4440	206333_a_t	MSI1	musashi homolog 1 (Drosophila)	1.49
1995	206338_a_t	ELAVL3	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 3 (Hu antigen C)	2.18
9971	206340_a_t	NR1H4	nuclear receptor subfamily 1, group H, member 4	-2.35
5165	206347_a_t	PDK3	pyruvate dehydrogenase kinase, isozyme 3	-1.23
5165	206348_s_at	PDK3	pyruvate dehydrogenase kinase, isozyme 3	-1.25
5196	206390_x_at	PF4	platelet factor 4 (chemokine (C-X-C motif) ligand 4)	-1.29
2657	206397_x_at	GDF1	growth differentiation factor 1	1.38
773	206399_x_at	CACNA1A	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	2.53
23061	206431_x_at	TBC1D9B	TBC1 domain family, member 9B (with GRAM domain)	-1.35
8775	206491_s_at	NAPA	N-ethylmaleimide-sensitive factor attachment protein, alpha	-2.59
7310	206512_a_t	ZRSR1	zinc finger (CCCH type), RNA-binding motif and serine/arginine rich 1	1.3
4987	206564_a_t	OPRL1	opiate receptor-like 1	1.42
7141	206568_a_t	TNP1	transition protein 1 (during histone to protamine replacement)	1.31
7458	206621_s_at	EIF4H	eukaryotic translation initiation factor 4H	-1.41
55721	206650_a_t	IQCC	IQ motif containing C	1.74
2812	206655_s_at	GP1BB	glycoprotein Ib (platelet), beta polypeptide	1.52
2745	206662_a_t	GLRX	glutaredoxin (thioltransferase)	-1.65
598	206665_s_at	BCL2L1	BCL2-like 1	1.54
359	206672_a_t	AQP2	aquaporin 2 (collecting duct)	1.41
10524	206689_x_at	HTATIP	HIV-1 Tat interacting protein, 60kDa	-1.46
4861	206699_x_at	NPAS1	neuronal PAS domain protein 1	1.44
631	206746_a_t	BFSP1	beaded filament structural protein 1, filensin	1.43

2208	206760_s_at	FCER2	Fc fragment of IgE, low affinity II, receptor for (CD23)	1.27
10225	206761_a_t	CD96	CD96 molecule	1.26
9087	206769_a_t	TMSB4Y	thymosin, beta 4, Y-linked	1.31
3338	206781_a_t	DNAJC4	DnaJ (Hsp40) homolog, subfamily C, member 4	2
26206	206815_a_t	SPAG8	sperm associated antigen 8	1.98
26206	206816_s_at	SPAG8	sperm associated antigen 8	1.68
98	206833_s_at	ACYP2	acylphosphatase 2, muscle type	-1.87
8545	206861_s_at	CGGBP1	CGG triplet repeat binding protein 1	-1.81
8712	206897_a_t	PAGE1	P antigen family, member 1 (prostate associated)	1.32
9941	206902_s_at	ENDOGL1	endonuclease G-like 1	1.25
	206903_a_t		NA	1.28
2323	206980_s_at	FLT3LG	fms-related tyrosine kinase 3 ligand	1.33
8817	206986_a_t	FGF18	fibroblast growth factor 18	1.44
596	207004_a_t	BCL2	B-cell CLL/lymphoma 2	1.58
3858	207023_x_at	KRT10	keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris)	-2.21
492	207026_s_at	ATP2B3	ATPase, Ca ⁺⁺ transporting, plasma membrane 3	-1.3
9120	207038_a_t	SLC16A6	solute carrier family 16, member 6 (monocarboxylic acid transporter 7)	1.35
5297	207081_s_at	PI4KA	phosphatidylinositol 4-kinase, catalytic, alpha	-1.69
8402	207088_s_at	SLC25A11	solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11	-1.99
207	207163_s_at	AKT1	v-akt murine thymoma viral oncogene homolog 1	-1.73
55018	207259_a_t	C17orf73	chromosome 17 open reading frame 73	1.22
64386	207289_a_t	MMP25	matrix metalloproteinase 25	1.52
23457	207321_s_at	ABCB9	ATP-binding cassette, sub-family B (MDR/TAP), member 9	1.3
4155	207323_s_at	MBP	myelin basic protein	1.54
30848	207337_a_t	CTAG2	cancer/testis antigen 2	1.51
8674	207350_s_at	VAMP4	vesicle-associated membrane protein 4	-1.26

2561	207352_s_at	GABRB2	gamma-aminobutyric acid (GABA) A receptor, beta 2	1.3
6247	207363_a_t	RS1	retinoschisis (X-linked, juvenile) 1	1.18
10195	207396_s_at	ALG3	asparagine-linked glycosylation 3 homolog (S. cerevisiae, alpha-1,3-mannosyltransferase)	-2.08
10073	207438_s_at	SNUPN	snurportin 1	-1.62
7355	207439_s_at	SLC35A2	solute carrier family 35 (UDP-galactose transporter), member A2	-1.52
26257	207451_a_t	NKX2-8	NK2 homeobox 8	1.75
50618	207476_a_t	ITSN2	intersectin 2	1.52
6953	207503_a_t	TCP10	t-complex 10 (mouse)	1.36
27013	207511_s_at	C2orf24	chromosome 2 open reading frame 24	1.52
2779	207514_s_at	GNAT1	guanine nucleotide binding protein (G protein), alpha transducing activity polypeptide 1	1.14
3918	207517_a_t	LAMC2	laminin, gamma 2	1.33
6915	207555_s_at	TBXA2R	thromboxane A2 receptor	1.89
5020	207576_x_at	OXT	oxytocin, prepro- (neurophysin I)	1.96
8340	207611_a_t	HIST1H2BL	histone cluster 1, H2bl	-1.16
617	207618_s_at	BCS1L	BCS1-like (yeast)	-1.4
7024	207627_s_at	TFCP2	transcription factor CP2	-1.39
4917	207640_x_at	NTN2L	netrin 2-like (chicken)	1.48
7132	207643_s_at	TNFRSF1A	tumor necrosis factor receptor superfamily, member 1A	-1.6
4868	207673_a_t	NPHS1	nephrosis 1, congenital, Finnish type (nephrin)	1.26
6396	207707_s_at	SEC13	SEC13 homolog (S. cerevisiae)	-1.73
54900	207734_a_t	LAX1	lymphocyte transmembrane adaptor 1	1.24
9647	207758_a_t	PPM1F	protein phosphatase 1F (PP2C domain containing)	2.09
10114	207764_s_at	HIPK3	homeodomain interacting protein kinase 3	-1.25
11273	207798_s_at	ATXN2L	ataxin 2-like	1.44
9921	207801_s_at	RNF10	ring finger protein 10	-1.57
2220	207804_s_at	FCN2	ficolin (collagen/fibrinogen domain containing lectin) 2 (hucolin)	-3.58

5715	207805_s_at	PSMD9	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	-1.55
4150	207824_s_at	MAZ	MYC-associated zinc finger protein (purine-binding transcription factor)	-1.27
10458	207832_at	BAIAP2	BAI1-associated protein 2	1.47
55559	207891_s_at	UCHL5IP	UCHL5 interacting protein	-1.18
2128	207914_x_at	EVX1	even-skipped homeobox 1	3.03
3363	207927_at	HTR7	5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-coupled)	1.48
3933	207930_at	LCN1	lipocalin 1 (tear prealbumin)	1.46
3382	207949_s_at	ICA1	islet cell autoantigen 1, 69kDa	1.57
1770	207959_s_at	DNAH9	dynein, axonemal, heavy chain 9	1.49
2741	207972_at	GLRA1	glycine receptor, alpha 1 (startle disease/hyperekplexia)	1.25
8174	208037_s_at	MADCAM1	mucosal vascular addressin cell adhesion molecule 1	1.51
1175	208074_s_at	AP2S1	adaptor-related protein complex 2, sigma 1 subunit	-1.54
326	208090_s_at	AIRE	autoimmune regulator	1.49
81605	208101_s_at	URM1	ubiquitin related modifier 1 homolog (S. cerevisiae)	-1.31
5662	208102_s_at	PSD	pleckstrin and Sec7 domain containing	1.35
554	208111_at	AVPR2	arginine vasopressin receptor 2 (nephrogenic diabetes insipidus)	1.92
6928	208135_at	TCF2	transcription factor 2, hepatic; LF-B3; variant hepatic nuclear factor	1.43
83475	208141_s_at	DOHH	deoxyhypusine hydroxylase/monooxygenase	2.14
22947	208201_at	DUX4	double homeobox, 4	1.47
8735	208208_at	MYH13	myosin, heavy chain 13, skeletal muscle	1.55
3084	208232_x_at	NRG1	neuregulin 1	1.87
30062	208242_at	RAX	retina and anterior neural fold homeobox	-1.38
10634	208258_s_at	GAS2L1	growth arrest-specific 2 like 1	1.89
8669	208264_s_at	EIF3J	eukaryotic translation initiation factor 3, subunit J	-2.64
10863	208269_s_at	ADAM28	ADAM metallopeptidase domain 28	1.59
8911	208299_at	CACNAII	calcium channel, voltage-dependent, T type, alpha II subunit	1.41
2821	208308_s	GPI	glucose phosphate isomerase	-1.94

	_at			
11167	208310_s_at	FSTL1	folliculin-like 1	-1.9
4952	208316_s_at	OCRL	oculocerebrorenal syndrome of Lowe	-1.34
9524	208336_s_at	GPSN2	glycoprotein, synaptic 2	-1.94
5594	208351_s_at	MAPK1	mitogen-activated protein kinase 1	-1.29
6015	208371_s_at	RING1	ring finger protein 1	-1.51
8879	208381_s_at	SGPL1	sphingosine-1-phosphate lyase 1	-1.21
10111	208393_s_at	RAD50	RAD50 homolog (S. cerevisiae)	-1.7
720	208451_s_at	C4A	complement component 4A (Rodgers blood group)	-1.94
7511	208453_s_at	XPNPEP1	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	-1.59
22800	208456_s_at	RRAS2	related RAS viral (r-ras) oncogene homolog 2	-1.53
26251	208550_x_at	KCNG2	potassium voltage-gated channel, subfamily G, member 2	1.82
2900	208552_a_t	GRIK4	glutamate receptor, ionotropic, kainate 4	1.29
5459	208554_a_t	POU4F3	POU class 4 homeobox 3	1.27
6623	208584_a_t	SNCG	synuclein, gamma (breast cancer-specific protein 1)	1.81
2923	208612_a_t	PDIA3	protein disulfide isomerase family A, member 3	-2.03
1642	208619_a_t	DDB1	damage-specific DNA binding protein 1, 127kDa	-1.56
5093	208620_a_t	PCBP1	poly(rC) binding protein 1	-1.69
1650	208675_s_at	DDOST	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	-2.19
7086	208699_x_at	TKT	transketolase (Wernicke-Korsakoff syndrome)	-2.4
4898	208709_s_at	NRD1	nardilysin (N-arginine dibasic convertase)	-1.63
5861	208724_s_at	RAB1A	RAB1A, member RAS oncogene family	-1.84
5862	208730_x_at	RAB2A	RAB2A, member RAS oncogene family	1.68
5862	208731_a_t	RAB2A	RAB2A, member RAS oncogene family	-1.7
5717	208777_s_at	PSMD11	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	-1.74
11222	208787_a_t	MRPL3	mitochondrial ribosomal protein L3	-2
6731	208801_a_t	SRP72	signal recognition particle 72kDa	-1.97

6731	208802_a _t	SRP72	signal recognition particle 72kDa	-2.13
3308	208814_a _t	HSPA4	heat shock 70kDa protein 4	-1.7
5127	208824_x _at	PCTK1	PCTAIRE protein kinase 1	-1.47
26003	208842_s _at	GORASP2	golgi reassembly stacking protein 2, 55kDa	-1.93
26003	208843_s _at	GORASP2	golgi reassembly stacking protein 2, 55kDa	-2.03
7070	208851_s _at	THY1	Thy-1 cell surface antigen	2.22
821	208852_s _at	CANX	calnexin	-1.99
5110	208857_s _at	PCMT1	protein-L-isoaspartate (D-aspartate) O- methyltransferase	-2.43
7905	208872_s _at	REEP5	receptor accessory protein 5	-1.94
6234	208902_s _at	RPS28	ribosomal protein S28	1.28
28973	208907_s _at	MRPS18B	mitochondrial ribosomal protein S18B	-1.93
4758	208926_a _t	NEU1	sialidase 1 (lysosomal sialidase)	-2
5531	208932_a _t	PPP4C	protein phosphatase 4 (formerly X), catalytic subunit	-1.58
22929	208939_a _t	SEPHS1	selenophosphate synthetase 1	-1.52
22929	208941_s _at	SEPHS1	selenophosphate synthetase 1	-1.67
5976	208947_s _at	UPF1	UPF1 regulator of nonsense transcripts homolog (yeast)	-1.41
23185	208952_s _at	LARP5	La ribonucleoprotein domain family, member 5	-1.41
23071	208959_s _at	TXNDC4	thioredoxin domain containing 4 (endoplasmic reticulum)	-2.05
204	208967_s _at	AK2	adenylate kinase 2	-1.47
8669	208985_s _at	EIF3J	eukaryotic translation initiation factor 3, subunit J	-2.83
5432	208996_s _at	POLR2C	polymerase (RNA) II (DNA directed) polypeptide C, 33kDa	-1.68
10492	209025_s _at	SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein	-2.04
50813	209029_a _t	COPS7A	COP9 constitutive photomorphogenic homolog subunit 7A (Arabidopsis)	-1.44
10938	209038_s _at	EHD1	EH-domain containing 1	1.31
7381	209065_a _t	UQCRB	ubiquinol-cytochrome c reductase binding protein	-1.82
10539	209080_x _at	GLRX3	glutaredoxin 3	-1.98
182	209097_s _at	JAG1	jagged 1 (Alagille syndrome)	1.17

55651	209104_s_at	NOLA2	nucleolar protein family A, member 2 (H/ACA small nucleolar RNPs)	-2.05
4615	209124_a_t	MYD88	myeloid differentiation primary response gene (88)	-1.99
7326	209141_a_t	UBE2G1	ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, yeast)	-1.81
7326	209142_s_at	UBE2G1	ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, yeast)	-2.16
10548	209149_s_at	TM9SF1	transmembrane 9 superfamily member 1	-2.4
10548	209150_s_at	TM9SF1	transmembrane 9 superfamily member 1	-1.83
8644	209160_a_t	AKR1C3	aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II)	-2.39
11196	209175_a_t	SEC23IP	SEC23 interacting protein	-1.83
10524	209192_x_at	HTATIP	HIV-1 Tat interacting protein, 60kDa	-1.42
9554	209206_a_t	SEC22B	SEC22 vesicle trafficking protein homolog B (<i>S. cerevisiae</i>)	-2.31
9526	209208_a_t	MPDU1	mannose-P-dolichol utilization defect 1	-1.94
10227	209215_a_t	TETRAN	tetracycline transporter-like protein	1.48
11152	209217_s_at	WDR45	WD repeat domain 45	-1.95
10061	209247_s_at	ABCF2	ATP-binding cassette, sub-family F (GCN20), member 2	-1.54
2063	209262_s_at	NR2F6	nuclear receptor subfamily 2, group F, member 6	-1.9
1201	209275_s_at	CLN3	ceroid-lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease)	-1.69
2745	209276_s_at	GLRX	glutaredoxin (thioltransferase)	-2.54
4781	209290_s_at	NFIB	nuclear factor I/B	1.83
5437	209302_a_t	POLR2H	polymerase (RNA) II (DNA directed) polypeptide H	-1.45
10767	209316_s_at	HBS1L	HBS1-like (<i>S. cerevisiae</i>)	-2.32
10111	209349_a_t	RAD50	RAD50 homolog (<i>S. cerevisiae</i>)	-1.33
8764	209354_a_t	TNFRSF14	tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator)	1.71
11212	209384_a_t	PROSC	proline synthetase co-transcribed homolog (bacterial)	-2.03
51014	209404_s_at	TMED7	transmembrane emp24 protein transport domain containing 7	-1.85
4436	209421_a_t	MSH2	mutS homolog 2, colon cancer, nonpolyposis type 1 (<i>E. coli</i>)	-1.42

5471	209434_s _at	PPAT	phosphoribosyl pyrophosphate amidotransferase	-1.34
5256	209439_s _at	PHKA2	phosphorylase kinase, alpha 2 (liver)	-1.74
55744	209445_x _at	C7orf44	chromosome 7 open reading frame 44	-1.6
57418	209461_x _at	WDR18	WD repeat domain 18	-1.74
4041	209468_a _t	LRP5	low density lipoprotein receptor-related protein 5	-2
201254	209478_a _t	STRA13	stimulated by retinoic acid 13 homolog (mouse)	-1.71
10248	209482_a _t	POP7	processing of precursor 7, ribonuclease P/MRP subunit (<i>S. cerevisiae</i>)	-2.49
7025	209506_s _at	NR2F1	nuclear receptor subfamily 2, group F, member 1	1.63
5435	209511_a _t	POLR2F	polymerase (RNA) II (DNA directed) polypeptide F	-1.6
	209535_s _at		NA	-1.41
7849	209552_a _t	PAX8	paired box 8	1.49
7737	209565_a _t	RNF113A	ring finger protein 113A	-1.77
27348	209593_s _at	TOR1B	torsin family 1, member B (torsin B)	-1.83
64087	209623_a _t	MCCC2	methycrotonoyl-Coenzyme A carboxylase 2 (beta)	-2.39
55916	209628_a _t	NXT2	nuclear transport factor 2-like export factor 2	-1.92
55916	209629_s _at	NXT2	nuclear transport factor 2-like export factor 2	-1.37
26190	209630_s _at	FBXW2	F-box and WD repeat domain containing 2	-2.01
1147	209666_s _at	CHUK	conserved helix-loop-helix ubiquitous kinase	-2.36
5805	209694_a _t	PTS	6-pyruvoyltetrahydropterin synthase	-1.99
10026	209707_a _t	PIGK	phosphatidylinositol glycan anchor biosynthesis, class K	-2
2624	209710_a _t	GATA2	GATA binding protein 2	1.36
23169	209713_s _at	SLC35D1	solute carrier family 35 (UDP- glucuronic acid/UDP-N- acetylgalactosamine dual transporter), member D1	-1.94
7541	209724_s _at	ZFP161	zinc finger protein 161 homolog (mouse)	-1.3
83737	209744_x _at	ITCH	itchy homolog E3 ubiquitin protein ligase (mouse)	-1.6
4613	209756_s _at	MYCN	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	1.47
5413	209767_s	5-Sep	septin 5	1.8

	_at			
1628	209783_a_t	DBP	D site of albumin promoter (albumin D-box) binding protein	2.64
10197	209853_s_at	PSME3	proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)	-1.84
3817	209855_s_at	KLK2	kallikrein-related peptidase 2	1.64
310	209860_s_at	ANXA7	annexin A7	-1.88
4091	209886_s_at	SMAD6	SMAD family member 6	1.67
25956	209889_a_t	SEC31B	SEC31 homolog B (S. cerevisiae)	-1.45
22827	209899_s_at	PUF60	poly-U binding splicing factor 60KDa	-1.74
26097	209927_s_at	C1orf77	chromosome 1 open reading frame 77	1.49
8517	209929_s_at	IKBKG	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma	-1.79
4133	210015_s_at	MAP2	microtubule-associated protein 2	1.41
3910	210089_s_at	LAMA4	laminin, alpha 4	2.02
8498	210120_s_at	RANBP3	RAN binding protein 3	-1.59
5678	210126_a_t	PSG9	pregnancy specific beta-1-glycoprotein 9	1.72
1241	210128_s_at	LTB4R	leukotriene B4 receptor	1.43
11074	210159_s_at	TRIM31	tripartite motif-containing 31	1.29
4772	210161_a_t	NFATC1	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1	1.64
10772	210178_x_at	FUSIP1	FUS interacting protein (serine/arginine-rich) 1	-2.21
1325	210182_a_t	CORT	cortistatin	1.83
10745	210191_s_at	PHTF1	putative homeodomain transcription factor 1	-1.4
7917	210208_x_at	BAT3	HLA-B associated transcript 3	-1.49
5810	210216_x_at	RAD1	RAD1 homolog (S. pombe)	-1.78
3140	210223_s_at	MR1	major histocompatibility complex, class I-related	1.87
3164	210226_a_t	NR4A1	nuclear receptor subfamily 4, group A, member 1	1.51
8500	210235_s_at	PPFIA1	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liptin), alpha 1	-1.36
7476	210248_a_t	WNT7A	wingless-type MMTV integration site family, member 7A	1.26
8450	210257_x	CUL4B	cullin 4B	-1.34

	_at			
3754	210263_a_t	KCNF1	potassium voltage-gated channel, subfamily F, member 1	1.93
51592	210266_s_at	TRIM33	tripartite motif-containing 33	1.86
4477	210297_s_at	MSMB	microseminoprotein, beta-	1.21
90410	210312_s_at	IFT20	intraflagellar transport 20 homolog (Chlamydomonas)	-1.67
6854	210315_a_t	SYN2	synapsin II	1.14
2324	210316_a_t	FLT4	fms-related tyrosine kinase 4	1.28
7531	210317_s_at	YWHAE	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	-2.68
5949	210318_a_t	RBP3	retinol binding protein 3, interstitial	1.53
6444	210329_s_at	SGCD	sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)	1.57
9536	210367_s_at	PTGES	prostaglandin E synthase	1.46
7164	210372_s_at	TPD52L1	tumor protein D52-like 1	-2.34
84084	210406_s_at	RAB6C	RAB6C, member RAS oncogene family	-1.79
5298	210417_s_at	PI4KB	phosphatidylinositol 4-kinase, catalytic, beta	-1.4
251	210431_a_t	ALPPL2	alkaline phosphatase, placental-like 2	1.57
9468	210456_a_t	PCYT1B	phosphate cytidyltransferase 1, choline, beta	1.59
5710	210459_a_t	PSMD4	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4	1.47
5710	210460_s_at	PSMD4	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4	-1.57
10332	210481_s_at	CLEC4M	C-type lectin domain family 4, member M	-2.32
10677	210507_s_at	AVIL	advillin	1.49
2637	210560_a_t	GBX2	gastrulation brain homeobox 2	1.47
3189	210588_x_at	HNRPH3	heterogeneous nuclear ribonucleoprotein H3 (2H9)	1.81
9019	210594_x_at	MPZL1	myelin protein zero-like 1	-1.28
84061	210596_a_t	RP11-217H1.1	implantation-associated protein	-1.94
51035	210623_a_t	LOC51035	SAPK substrate protein 1	1.39
8165	210625_s_at	AKAP1	A kinase (PRKA) anchor protein 1	-2.04

8425	210628_x_at	LTBP4	latent transforming growth factor beta binding protein 4	1.44
26268	210638_s_at	FBXO9	F-box protein 9	-2.36
7267	210645_s_at	TTC3	tetratricopeptide repeat domain 3	-1.77
10555	210678_s_at	AGPAT2	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta)	-1.58
85363	210705_s_at	TRIM5	tripartite motif-containing 5	-2.14
6249	210716_s_at	CLIP1	CAP-GLY domain containing linker protein 1	-1.73
10362	210719_s_at	HMG20B	high-mobility group 20B	-2.1
5682	210759_s_at	PSMA1	proteasome (prosome, macropain) subunit, alpha type, 1	-1.76
4771	210767_a_t	NF2	neurofibromin 2 (bilateral acoustic neuroma)	1.6
1258	210769_a_t	CNGB1	cyclic nucleotide gated channel beta 1	1.47
2902	210782_x_at	GRIN1	glutamate receptor, ionotropic, N-methyl D-aspartate 1	1.48
10747	210798_x_at	MASP2	mannan-binding lectin serine peptidase 2	-2.58
1201	210859_x_at	CLN3	ceroid-lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease)	-1.67
4850	210867_a_t	CNOT4	CCR4-NOT transcription complex, subunit 4	1.85
10899	210927_x_at	JTB	jumping translocation breakpoint	-1.7
6049	210932_s_at	RNF6	ring finger protein (C3H2C3 type) 6	1.21
4176	210983_s_at	MCM7	minichromosome maintenance complex component 7	-1.31
221	211004_s_at	ALDH3B1	aldehyde dehydrogenase 3 family, member B1	1.61
2651	211020_a_t	GCNT2	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme (I blood group)	-1.21
10636	211021_s_at	RGS14	regulator of G-protein signaling 14	1.85
51433	211036_x_at	ANAPC5	anaphase promoting complex subunit 5	-1.49
51512	211040_x_at	GTSE1	G-2 and S-phase expressed 1	1.56
4162	211042_x_at	MCAM	melanoma cell adhesion molecule	-1.66
81033	211045_s_at	KCNH6	potassium voltage-gated channel, subfamily H (eag-related), member 6	1.44
4763	211094_s_at	NF1	neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease)	-1.26
5089	211096_a_t	PBX2	pre-B-cell leukemia homeobox 2	1.51

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6560	211112_a _t	SLC12A4	solute carrier family 12 (potassium/chloride transporters), member 4	1.61
9127	211147_s _at	P2RXL1	purinergic receptor P2X-like 1, orphan receptor	1.4
9001	211222_s _at	HAP1	huntingtin-associated protein 1 (neuroan 1)	1.44
8756	211239_s _at	ADAM7	ADAM metalloproteinase domain 7	1.11
5046	211263_s _at	PCSK6	proprotein convertase subtilisin/kexin type 6	1.42
6899	211274_a _t	TBX1	T-box 1	1.4
4899	211280_s _at	NRF1	nuclear respiratory factor 1	1.22
7157	211300_s _at	TP53	tumor protein p53 (Li-Fraumeni syndrome)	-1.2
2204	211306_s _at	FCAR	Fc fragment of IgA, receptor for	1.24
9031	211313_s _at	BAZ1B	bromodomain adjacent to zinc finger domain, 1B	1.44
8913	211315_s _at	CACNA1G	calcium channel, voltage-dependent, T type, alpha 1G subunit	1.33
	211319_a _t		NA	1.28
27229	211337_s _at	76P	gamma tubulin ring complex protein (76p gene)	-1.45
25792	211358_s _at	CIZ1	CDKN1A interacting zinc finger protein 1	1.75
3761	211451_s _at	KCNJ4	potassium inwardly-rectifying channel, subfamily J, member 4	1.27
	211459_a _t		NA	1.11
5600	211499_s _at	MAPK11	mitogen-activated protein kinase 11	-1.24
652	211518_s _at	BMP4	bone morphogenetic protein 4	-1.4
6622	211546_x _at	SNCA	synuclein, alpha (non A4 component of amyloid precursor)	1.48
8725	211563_s _at	C19orf2	chromosome 19 open reading frame 2	-1.39
7337	211575_s _at	UBE3A	ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome)	-1.35
775	211592_s _at	CACNA1C	calcium channel, voltage-dependent, L type, alpha 1C subunit	1.15
64963	211595_s _at	MRPS11	mitochondrial ribosomal protein S11	-1.51
26018	211596_s _at	LRIG1	leucine-rich repeats and immunoglobulin-like domains 1	-2.37
3597	211612_s _at	IL13RA1	interleukin 13 receptor, alpha 1	-2.47

228	211617_a_t	ALDOAP2	aldolase A, fructose-bisphosphate pseudogene 2	1.53
250	211619_s_at	ALPP	alkaline phosphatase, placental (Regan isozyme)	1.75
3493	211693_a_t	IGHA1	immunoglobulin heavy constant alpha 1	1.98
10580	211705_s_at	SORBS1	sorbin and SH3 domain containing 1	1.62
203068	211714_x_at	TUBB	tubulin, beta	-1.71
637	211725_s_at	BID	BH3 interacting domain death agonist	-1.66
2327	211726_s_at	FMO2	flavin containing monooxygenase 2 (non-functional)	2.75
5682	211746_x_at	PSMA1	proteasome (prosome, macropain) subunit, alpha type, 1	-1.5
8674	211760_s_at	VAMP4	vesicle-associated membrane protein 4	-1.41
5452	211771_s_at	POU2F2	POU class 2 homeobox 2	1.96
161	211779_x_at	AP2A2	adaptor-related protein complex 2, alpha 2 subunit	-1.53
4802	211797_s_at	NFYC	nuclear transcription factor Y, gamma	-1.37
5818	211845_a_t	PVRL1	poliovirus receptor-related 1 (herpesvirus entry mediator C)	1.42
56107	211873_s_at	PCDHGA9	protocadherin gamma subfamily A, 9	-1.3
634	211889_x_at	CEACAM1	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	-1.42
2047	211898_s_at	EPHB1	EPH receptor B1	-1.24
4352	211903_s_at	MPL	myeloproliferative leukemia virus oncogene	1.36
5893	211904_x_at	RAD52	RAD52 homolog (S. cerevisiae)	1.81
5733	211909_x_at	PTGER3	prostaglandin E receptor 3 (subtype EP3)	2.61
56604	211915_s_at	TUBB4Q	tubulin, beta polypeptide 4, member Q	1.47
3843	211953_s_at	RANBP5	RAN binding protein 5	-2.22
84364	211975_a_t	ZNF289	zinc finger protein 289, ID1 regulated	-1.57
23214	211982_x_at	XPO6	exportin 6	-1.49
26099	212005_a_t	C1orf144	chromosome 1 open reading frame 144	-1.93
23190	212008_a_t	UBXD2	UBX domain containing 2	-2.8
23199	212056_a_t	KIAA0182	KIAA0182	-1.41
23197	212108_a_t	UBXD8	UBX domain containing 8	-1.64

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5987	212116_a_t	TRIM27	tripartite motif-containing 27	-1.73
81614	212129_a_t	NIPA2	non imprinted in Prader-Willi/Angelman syndrome 2	-1.63
81614	212133_a_t	NIPA2	non imprinted in Prader-Willi/Angelman syndrome 2	-1.35
161	212159_x_at	AP2A2	adaptor-related protein complex 2, alpha 2 subunit	-1.53
92703	212164_a_t	TMEM183A	transmembrane protein 183A	-1.53
204	212175_s_at	AK2	adenylate kinase 2	-1.96
5270	212190_a_t	SERPINE2	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2	2.34
9777	212194_s_at	TM9SF4	transmembrane 9 superfamily protein member 4	-1.94
10410	212203_x_at	IFITM3	interferon induced transmembrane protein 3 (1-8U)	-1.88
26173	212210_a_t	INTS1	integrator complex subunit 1	1.48
26057	212211_a_t	ANKRD17	ankyrin repeat domain 17	-1.75
4976	212214_a_t	OPA1	optic atrophy 1 (autosomal dominant)	-1.9
9581	212216_a_t	PREPL	prolyl endopeptidase-like	-1.79
23198	212219_a_t	PSME4	proteasome (prosome, macropain) activator subunit 4	-1.6
57017	212228_s_at	COQ9	coenzyme Q9 homolog (S. cerevisiae)	-1.55
171023	212237_a_t	ASXL1	additional sex combs like 1 (Drosophila)	-1.53
27032	212255_s_at	ATP2C1	ATPase, Ca ⁺⁺ transporting, type 2C, member 1	-1.62
5594	212271_a_t	MAPK1	mitogen-activated protein kinase 1	-1.78
27346	212279_a_t	TMEM97	transmembrane protein 97	-2.76
375790	212285_s_at	AGRN	agrin	1.71
10213	212296_a_t	PSMD14	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	-2.27
23168	212302_a_t	RTF1	Rtf1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	-1.34
375056	212305_s_at	MIA3	melanoma inhibitory activity family, member 3	-2.25
23122	212309_a_t	CLASP2	cytoplasmic linker associated protein 2	1.53
8879	212322_a_t	SGPL1	sphingosine-1-phosphate lyase 1	-1.79
22937	212329_a_t	SCAP	SREBF chaperone	-1.99

25940	212333_a_t	FAM98A	family with sequence similarity 98, member A	-1.95
2618	212378_a_t	GART	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase	-2
23358	212381_a_t	USP24	ubiquitin specific peptidase 24	-1.39
23065	212396_s_at	KIAA0090	KIAA0090	-1.51
5962	212398_a_t	RDX	radixin	-2.13
89910	212403_a_t	UBE3B	ubiquitin protein ligase E3B	-1.33
92856	212411_a_t	IMP4	IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)	-2.24
80273	212432_a_t	GRPEL1	GrpE-like 1, mitochondrial (E. coli)	-2.16
23218	212443_a_t	NBEAL2	neurobeachin-like 2	1.35
23625	212484_a_t	FAM89B	family with sequence similarity 89, member B	-1.25
23513	212556_a_t	SCRIB	scribbled homolog (Drosophila)	-1.74
91304	212575_a_t	C19orf6	chromosome 19 open reading frame 6	1.87
9716	212584_a_t	AQR	aquarius homolog (mouse)	-1.53
23140	212601_a_t	ZZEF1	zinc finger, ZZ-type with EF-hand domain 1	-1.65
440026	212622_a_t	TMEM41B	transmembrane protein 41B	-2.24
23376	212633_a_t	KIAA0776	KIAA0776	-1.93
54505	212648_a_t	DHX29	DEAH (Asp-Glu-Ala-His) box polypeptide 29	-1.88
23174	212655_a_t	ZCCHC14	zinc finger, CCHC domain containing 14	-2.56
4763	212676_a_t	NF1	neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease)	-1.57
644879	212680_x_at	LOC644879	hypothetical LOC644879	-1.71
26608	212685_s_at	TBL2	transducin (beta)-like 2	-1.73
23511	212691_a_t	NUP188	nucleoporin 188kDa	-1.34
1741	212728_a_t	DLG3	discs, large homolog 3 (neuroendocrine-dlg, Drosophila)	1.46
23041	212754_s_at	MON2	MON2 homolog (S. cerevisiae)	-1.47
818	212757_s_at	CAMK2G	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma	-1.41

23241	212778_a t	PACS2	phosphofurin acidic cluster sorting protein 2	-1.32
5930	212783_a t	RBBP6	retinoblastoma binding protein 6	1.44
26130	212804_s at	GAPVD1	GTPase activating protein and VPS9 domains 1	-1.33
23382	212814_a t	KIAA0828	adenosylhomocysteinase 3	-1.41
22976	212825_a t	PAXIP1	PAX interacting (with transcription-activation domain) protein 1	-1.49
1955	212830_a t	MEGF9	multiple EGF-like-domains 9	-2.53
91137	212833_a t	SLC25A46	solute carrier family 25, member 46	-2.53
23142	212851_a t	DCUN1D4	DCN1, defective in cullin neddylation 1, domain containing 4 (<i>S. cerevisiae</i>)	-1.4
203069	212866_a t	R3HCC1	R3H domain and coiled-coil containing 1	-1.44
51588	212881_a t	PIAS4	protein inhibitor of activated STAT, 4	-1.51
23517	212896_a t	SKIV2L2	superkiller viralicidic activity 2-like 2 (<i>S. cerevisiae</i>)	-1.77
23097	212897_a t	CDC2L6	cell division cycle 2-like 6 (CDK8-like)	1.61
10802	212900_a t	SEC24A	SEC24 related gene family, member A (<i>S. cerevisiae</i>)	-1.92
10802	212902_a t	SEC24A	SEC24 related gene family, member A (<i>S. cerevisiae</i>)	-2.51
57470	212904_a t	LRRC47	leucine rich repeat containing 47	-1.66
23283	212905_a t	CSTF2T	cleavage stimulation factor, 3' pre-RNA, subunit 2, 64kDa, tau variant	-1.81
23341	212908_a t	DNAJC16	DnaJ (Hsp40) homolog, subfamily C, member 16	-1.8
1291	212938_a t	COL6A1	collagen, type VI, alpha 1	1.45
23125	212948_a t	CAMTA2	calmodulin binding transcription activator 2	-1.41
5438	212955_s at	POLR2I	polymerase (RNA) II (DNA directed) polypeptide I, 14.5kDa	-1.95
541578	212961_x at	CXorf40B	chromosome X open reading frame 40B	-1.61
23119	212964_a t	HIC2	hypermethylated in cancer 2	-1.3
11011	212986_s at	TLK2	tousled-like kinase 2	-1.44
26268	212987_a t	FBXO9	F-box protein 9	-2.05
80097	212995_x at	FAM128B	family with sequence similarity 128, member B	-1.4
4591	213009_s at	TRIM37	tripartite motif-containing 37	-1.54
9479	213013_a t	MAPK8IP1	mitogen-activated protein kinase 8 interacting protein 1	1.58

23503	213073_a_t	ZFYVE26	zinc finger, FYVE domain containing 26	-1.33
9911	213096_a_t	TMCC2	transmembrane and coiled-coil domain family 2	1.42
9125	213098_a_t	RQCD1	RCD1 required for cell differentiation1 homolog (S. pombe)	-1.25
	213100_a_t		NA	1.33
29015	213113_s_at	SLC43A3	solute carrier family 43, member 3	-2.2
6625	213121_a_t	SNRP70	small nuclear ribonucleoprotein 70kDa polypeptide (RNP antigen)	1.66
27349	213132_s_at	MCAT	malonyl CoA:ACP acyltransferase (mitochondrial)	-1.34
23302	213155_a_t	WSCD1	WSC domain containing 1	1.44
	213156_a_t		NA	2.39
653784	213166_x_at	FAM128A	family with sequence similarity 128, member A	-1.49
23162	213177_a_t	MAPK8IP3	mitogen-activated protein kinase 8 interacting protein 3	1.6
4337	213181_s_at	MOCS1	molybdenum cofactor synthesis 1	-1.48
91	213198_a_t	ACVR1B	activin A receptor, type IB	-1.58
6855	213200_a_t	SYP	synaptophysin	1.64
92482	213224_s_at	LOC92482	hypothetical protein LOC92482	-1.62
3858	213287_s_at	KRT10	keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris)	-2.52
340562	213289_a_t	SATL1	spermidine/spermine N1-acetyl transferase-like 1	-2.11
23161	213292_s_at	SNX13	sorting nexin 13	-1.68
5198	213302_a_t	PFAS	phosphoribosylformylglycinamide synthase (FGAR amidotransferase)	-1.47
57150	213312_a_t	C6orf162	chromosome 6 open reading frame 162	-1.37
91966	213315_x_at	CXorf40A	chromosome X open reading frame 40A	-1.86
57608	213316_a_t	KIAA1462	KIAA1462	1.27
7917	213318_s_at	BAT3	HLA-B associated transcript 3	-1.67
10196	213320_a_t	PRMT3	protein arginine methyltransferase 3	-1.66
152559	213372_a_t	PAQR3	progesterone and adipoQ receptor family member III	-1.46
9640	213389_a_t	ZNF592	zinc finger protein 592	1.34
10799	213427_a_t	RPP40	ribonuclease P/MRP 40kDa subunit	-1.53

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317662	213463_s_at	KIAA0974	KIAA0974	-1.41
5510	213465_s_at	PPP1R7	protein phosphatase 1, regulatory (inhibitor) subunit 7	-2.05
2068	213468_a_t	ERCC2	excision repair cross-complementing rodent repair deficiency, complementation group 2 (xeroderma pigmentosum D)	-1.3
5605	213490_s_at	MAP2K2	mitogen-activated protein kinase kinase 2	-1.51
7528	213494_s_at	YY1	YY1 transcription factor	-1.26
9276	213500_a_t	COPB2	coatamer protein complex, subunit beta 2 (beta prime)	-1.27
26469	213521_a_t	PTPN18	protein tyrosine phosphatase, non-receptor type 18 (brain-derived)	1.27
	213525_a_t		NA	1.4
146542	213527_s_at	ZNF688	zinc finger protein 688	-1.49
92342	213528_a_t	C1orf156	chromosome 1 open reading frame 156	-1.67
146542	213529_a_t	ZNF688	zinc finger protein 688	2.09
55573	213548_s_at	CDV3	CDV3 homolog (mouse)	-1.58
8476	213595_s_at	CDC42BP A	CDC42 binding protein kinase alpha (DMPK-like)	1.32
2987	213621_s_at	GUK1	guanylate kinase 1	1.3
23155	213628_a_t	CLCC1	chloride channel CLIC-like 1	-1.82
	213637_a_t		NA	-1.61
221692	213638_a_t	PHACTR1	phosphatase and actin regulator 1	1.35
	213642_a_t		NA	-2.33
1763	213647_a_t	DNA2L	DNA2 DNA replication helicase 2-like (yeast)	-1.26
7626	213659_a_t	ZNF75	zinc finger protein 75 (D8C6)	-1.35
23149	213669_a_t	FCHO1	FCH domain only 1	1.74
112950	213696_s_at	MED8	mediator complex subunit 8	-1.62
6945	213708_s_at	MLX	MAX-like protein X	-1.46
3887	213711_a_t	KRT81	keratin 81	1.6
256949	213715_s_at	ANKRD47	ankyrin repeat domain 47	1.28
5985	213734_a_t	RFC5	replication factor C (activator 1) 5,	-3.54

	t		36.5kDa	
3836	213741_s_at	KPNA1	karyopherin alpha 1 (importin alpha 5)	-1.77
6497	213755_s_at	SKI	v-ski sarcoma viral oncogene homolog (avian)	1.56
8844	213770_a_t	KSR1	kinase suppressor of ras 1	-1.26
58509	213815_x_at	C19orf29	chromosome 19 open reading frame 29	-1.26
51406	213838_a_t	NOL7	nucleolar protein 7, 27kDa	-1.62
120526	213853_a_t	DPH4	DPH4, JJJ3 homolog (S. cerevisiae)	-2.2
81688	213875_x_at	C6orf62	chromosome 6 open reading frame 62	-1.93
79912	213878_a_t	PYROXD1	pyridine nucleotide-disulphide oxidoreductase domain 1	-2.42
353	213892_s_at	APRT	adenine phosphoribosyltransferase	-1.95
339005	213908_a_t	WHDC1L1	WAS protein homology region 2 domain containing 1-like 1	-1.53
23225	213945_s_at	NUP210	nucleoporin 210kDa	-1.26
83475	213949_s_at	DOHH	deoxyhypusine hydroxylase/monooxygenase	1.34
4637	214002_a_t	MYL6	myosin, light chain 6, alkali, smooth muscle and non-muscle	1.5
3693	214021_x_at	ITGB5	integrin, beta 5	-1.21
7535	214032_a_t	ZAP70	zeta-chain (TCR) associated protein kinase 70kDa	1.5
9046	214054_a_t	DOK2	docking protein 2, 56kDa	1.57
81577	214076_a_t	GFOD2	glucose-fructose oxidoreductase domain containing 2	-1.45
9260	214122_a_t	PDLIM7	PDZ and LIM domain 7 (enigma)	1.7
9659	214130_s_at	PDE4DIP	phosphodiesterase 4D interacting protein (myomegalin)	-2.11
343990	214134_a_t	C2orf55	chromosome 2 open reading frame 55	1.23
8034	214140_a_t	SLC25A16	solute carrier family 25 (mitochondrial carrier; Graves disease autoantigen), member 16	-2.32
5433	214144_a_t	POLR2D	polymerase (RNA) II (DNA directed) polypeptide D	-1.44
6710	214145_s_at	SPTB	spectrin, beta, erythrocytic (includes spherocytosis, clinical type I)	1.43
9236	214151_s_at	CCPG1	cell cycle progression 1	-1.65
284244	214162_a_t	LOC284244	hypothetical protein LOC284244	-1.16
8572	214174_s	PDLIM4	PDZ and LIM domain 4	2.17

	_at			
27042	214193_s_at	C1orf107	chromosome 1 open reading frame 107	-2.31
10539	214205_x_at	GLRX3	glutaredoxin 3	-1.7
10478	214210_at	SLC25A17	solute carrier family 25 (mitochondrial carrier; peroxisomal membrane protein, 34kDa), member 17	-1.29
23078	214231_s_at	RP11-125A7.3	KIAA0564 protein	-1.31
5074	214237_x_at	PAWR	PRKC, apoptosis, WT1, regulator	1.59
57194	214255_at	ATP10A	ATPase, Class V, type 10A	1.37
9554	214257_s_at	SEC22B	SEC22 vesicle trafficking protein homolog B (<i>S. cerevisiae</i>)	-1.99
3691	214292_at	ITGB4	integrin, beta 4	1.38
10570	214301_s_at	DPYSL4	dihydropyrimidinase-like 4	1.44
4586	214303_x_at	MUC5AC	mucin 5AC, oligomeric mucus/gel-forming	1.5
23336	214304_x_at	DMN	desmuslin	1.47
130916	214364_at	MTERFD2	MTERF domain containing 2	-1.27
10595	214372_x_at	ERN2	endoplasmic reticulum to nucleus signaling 2	1.5
116138	214383_x_at	KLHDC3	kelch domain containing 3	-1.56
4586	214385_s_at	MUC5AC	mucin 5AC, oligomeric mucus/gel-forming	1.35
25803	214403_x_at	SPDEF	SAM pointed domain containing ets transcription factor	1.53
9063	214442_s_at	PIAS2	protein inhibitor of activated STAT, 2	-1.44
9306	214462_at	SOCS6	suppressor of cytokine signaling 6	-1.4
10280	214484_s_at	OPRS1	opioid receptor, sigma 1	-2.11
2488	214489_at	FSHB	follicle stimulating hormone, beta polypeptide	-1.25
10207	214493_s_at	INADL	InaD-like (<i>Drosophila</i>)	1.64
23404	214507_s_at	EXOSC2	exosome component 2	-1.47
1053	214523_at	CEBPE	CCAAT/enhancer binding protein (C/EBP), epsilon	1.64
10084	214527_s_at	PQBPI	polyglutamine binding protein 1	-1.65
57152	214536_at	SLURP1	secreted LY6/PLAUR domain containing 1	1.47
9444	214541_s_at	QKI	quaking homolog, KH domain RNA binding (mouse)	-1.17

924	214551_s _at	CD7	CD7 molecule	1.42
8368	214562_a _t	HIST1H4L	histone cluster 1, H4l	1.32
25812	214570_x _at	POM121L1	POM121 membrane glycoprotein-like 1 (rat)	1.42
5205	214594_x _at	ATP8B1	ATPase, Class I, type 8B, member 1	3.41
3755	214595_a _t	KCNQ1	potassium voltage-gated channel, subfamily G, member 1	1.53
26100	214699_x _at	WIP12	WD repeat domain, phosphoinositide interacting 2	1.42
91373	214755_a _t	UAP1L1	UDP-N-acetylglucosamine pyrophosphorylase 1-like 1	1.19
1954	214778_a _t	MEGF8	multiple EGF-like-domains 8	1.35
91442	214816_x _at	C19orf40	chromosome 19 open reading frame 40	1.59
23096	214819_a _t	IQSEC2	IQ motif and Sec7 domain 2	1.53
80306	214831_a _t	MED28	mediator complex subunit 28	-1.3
157627	214839_a _t	LOC157627	hypothetical protein LOC157627	1.49
	214871_x _at		NA	1.58
7067	214883_a _t	THRA	thyroid hormone receptor, alpha (erythroblastic leukemia viral (v-erb-a) oncogene homolog, avian)	1.4
610	214893_x _at	HCN2	hyperpolarization activated cyclic nucleotide-gated potassium channel 2	1.67
6709	214925_s _at	SPTAN1	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)	1.42
374868	214934_a _t	ATP9B	ATPase, Class II, type 9B	-1.4
23636	214935_a _t	NUP62	nucleoporin 62kDa	1.53
8539	214959_s _at	API5	apoptosis inhibitor 5	-1.62
8539	214960_a _t	API5	apoptosis inhibitor 5	-1.49
2901	214966_a _t	GRIK5	glutamate receptor, ionotropic, kainate 5	1.38
6480	214971_s _at	ST6GAL1	ST6 beta-galactosamide alpha-2,6- sialyltransferase 1	-3.1
84720	214990_a _t	PIGO	phosphatidylinositol glycan anchor biosynthesis, class O	1.65
9736	215013_s _at	USP34	ubiquitin specific peptidase 34	1.38
2926	215030_a _t	GRSF1	G-rich RNA sequence binding factor 1	-1.38
79625	215059_a _t	C4orf31	chromosome 4 open reading frame 31	1.24
399818	215061_a	LOC399818	similar to CG9643-PA	1.5

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9191	215158_s_at	DEDD	death effector domain containing	-1.36
7372	215165_x_at	UMPS	uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase)	-1.53
10440	215171_s_at	TIMM17A	translocase of inner mitochondrial membrane 17 homolog A (yeast)	-2.16
55338	215187_a_t	FLJ11292	hypothetical protein FLJ11292	1.23
9612	215205_x_at	NCOR2	nuclear receptor co-repressor 2	1.47
2707	215243_s_at	GJB3	gap junction protein, beta 3, 31kDa	1.33
92106	215262_a_t	OXNAD1	oxidoreductase NAD-binding domain containing 1	-1.14
2016	215265_a_t	EMX1	empty spiracles homeobox 1	1.38
107	215348_a_t	ADCY1	adenylate cyclase 1 (brain)	1.31
27043	215354_s_at	PELP1	proline, glutamic acid and leucine rich protein 1	1.82
4130	215384_s_at	MAP1A	microtubule-associated protein 1A	1.93
5380	215410_a_t	PMS2L2	postmeiotic segregation increased 2-like 2	1.72
84263	215436_a_t	HSDL2	hydroxysteroid dehydrogenase like 2	-1.5
200205	215490_a_t	C1orf69	chromosome 1 open reading frame 69	1.28
	215502_a_t		NA	1.62
202559	215527_a_t	KHDRBS2	KH domain containing, RNA binding, signal transduction associated 2	1.26
9215	215538_a_t	LARGE	like-glycosyltransferase	1.67
23256	215548_s_at	SCFD1	sec1 family domain containing 1	-1.87
54516	215560_x_at	MTRF1L	mitochondrial translational release factor 1-like	1.52
	215594_a_t		NA	1.49
56910	215609_a_t	STARD7	StAR-related lipid transfer (START) domain containing 7	1.54
63973	215632_a_t	NEUROG2	neurogenin 2	1.21
2972	215677_s_at	BRF1	BRF1 homolog, subunit of RNA polymerase III transcription initiation factor IIIB (<i>S. cerevisiae</i>)	1.36
1746	215685_s_at	DLX2	distal-less homeobox 2	1.65
23469	215718_s_at	PHF3	PHD finger protein 3	1.83

2521	215744_a_t	FUS	fusion (involved in t(12;16) in malignant liposarcoma)	1.21
79998	215759_a_t	ANKRD53	ankyrin repeat domain 53	1.75
55547	215778_x_at	HAB1	B1 for mucin	1.81
114819	215827_x_at	CROCCL2	ciliary rootlet coiled-coil, rootletin-like 2	1.53
7316	215834_x_at	UBC	ubiquitin C	-1.35
19	215869_a_t	ABCA1	ATP-binding cassette, sub-family A (ABC1), member 1	1.46
126070	215892_a_t	ZNF440	zinc finger protein 440	1.19
23550	215923_s_at	PSD4	pleckstrin and Sec7 domain containing 4	-1.71
727830	215935_a_t	FAM75A3	family with sequence similarity 75, member A3	1.22
51512	215942_s_at	GTSE1	G-2 and S-phase expressed 1	1.42
4946	215952_s_at	OAZ1	ornithine decarboxylase antizyme 1	-1.99
25859	215972_a_t	PART1	prostate androgen-regulated transcript 1	1.48
23187	216019_x_at	PHLDB1	pleckstrin homology-like domain, family B, member 1	1.39
23030	216023_a_t	JMJD2B	jumonji domain containing 2B	1.35
23162	216137_s_at	MAPK8IP3	mitogen-activated protein kinase 8 interacting protein 3	1.44
23162	216139_s_at	MAPK8IP3	mitogen-activated protein kinase 8 interacting protein 3	1.34
	216151_a_t		NA	1.1
5609	216206_x_at	MAP2K7	mitogen-activated protein kinase kinase 7	2.42
134	216220_s_at	ADORA1	adenosine A1 receptor	1.83
5566	216234_s_at	PRKACA	protein kinase, cAMP-dependent, catalytic, alpha	-1.18
29780	216253_s_at	PARVB	parvin, beta	1.92
10565	216266_s_at	ARFGEF1	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited)	-1.56
1804	216290_x_at	DPP6	dipeptidyl-peptidase 6	1.46
84162	216294_s_at	KIAA1109	KIAA1109	-1.2
51750	216325_x_at	RTEL1	regulator of telomere elongation helicase 1	1.54
1550	216334_s_at	CYP2A7P1	cytochrome P450, family 2, subfamily A, polypeptide 7 pseudogene 1	1.61

25844	216338_s _at	YIPF3	Yip1 domain family, member 3	-1.58
442233	216358_a _t	LOC442233	similar to SWI/SNF-related matrix-associated actin-dependent regulator of chromatin e1	1.89
80028	216395_a _t	FBXL18	F-box and leucine-rich repeat protein 18	1.59
7184	216450_x _at	HSP90B1	heat shock protein 90kDa beta (Grp94), member 1	-2.47
79184	216521_s _at	BRCC3	BRCA1/BRCA2-containing complex, subunit 3	-1.3
120364	216559_x _at	LOC120364	similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-strand binding protein) (hnRNP core protein A1) (HDP-1) (Topoisomerase-inhibitor suppressed)	1.68
79962	216595_a _t	FLJ13236	hypothetical protein FLJ13236	-1.26
2193	216602_s _at	FARSA	phenylalanyl-tRNA synthetase, alpha subunit	-1.49
4099	216617_s _at	MAG	myelin associated glycoprotein	1.6
6929	216645_a _t	TCF3	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	1.4
1810	216652_s _at	DR1	down-regulator of transcription 1, TBP-binding (negative cofactor 2)	-1.68
	216656_a _t		NA	1.46
5101	216707_a _t	PCDH9	protocadherin 9	1.46
28	216716_a _t	ABO	ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltransferase)	1.38
166614	216724_a _t	DCLK2	doublecortin-like kinase 2	1.22
323	216747_a _t	APBB2	amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like)	1.71
	216789_a _t		NA	1.85
	216797_a _t		NA	1.2
390418	216808_a _t	KRT18P27	keratin 27 pseudogene 27	1.41
862	216831_s _at	RUNX1T1	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	1.59
1796	216835_s _at	DOK1	docking protein 1, 62kDa (downstream of tyrosine kinase 1)	1.7
2044	216837_a _t	EPHA5	EPH receptor A5	-1.14
5379	216843_x	PMS2L1	postmeiotic segregation increased 2-like	-1.54

	_at		1	
3192	216855_s_at	HNRNPU	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	1.56
57198	216873_s_at	ATP8B2	ATPase, Class I, type 8B, member 2	1.42
55547	216875_x_at	HAB1	B1 for mucin	1.95
11155	216888_at	LDB3	LIM domain binding 3	1.37
23119	216911_s_at	HIC2	hypermethylated in cancer 2	1.45
388699	216935_at	C1orf46	chromosome 1 open reading frame 46	1.34
4861	216975_x_at	NPAS1	neuronal PAS domain protein 1	1.5
177	217046_s_at	AGER	advanced glycosylation end product-specific receptor	1.46
4584	217054_at	MUC3A	mucin 3A, cell surface associated	1.58
	217055_x_at		NA	1.75
1760	217062_at	DMPK	dystrophia myotonica-protein kinase	1.54
1758	217067_s_at	DMP1	dentin matrix acidic phosphoprotein	1.23
4524	217071_s_at	MTHFR	5,10-methylenetetrahydrofolate reductase (NADPH)	1.61
9568	217077_s_at	GABBR2	gamma-aminobutyric acid (GABA) B receptor, 2	1.43
7932	217081_at	OR2H2	olfactory receptor, family 2, subfamily H, member 2	1.3
22996	217101_at	C1orf34	chromosome 1 open reading frame 34	1.59
55727	217141_at	BTBD7	BTB (POZ) domain containing 7	1.36
2099	217163_at	ESR1	estrogen receptor 1	1.22
4586	217182_at	MUC5AC	mucin 5AC, oligomeric mucus/gel-forming	1.85
2099	217190_x_at	ESR1	estrogen receptor 1	2.51
8935	217217_at	SKAP2	src kinase associated phosphoprotein 2	1.37
283820	217225_x_at	NOMO2	NODAL modulator 2	-1.9
6337	217264_s_at	SCNN1A	sodium channel, nonvoltage-gated 1 alpha	1.71
6474	217278_x_at	SHOX2	short stature homeobox 2	1.44
6474	217283_at	SHOX2	short stature homeobox 2	1.51
	217314_at		NA	1.41

	217322_x _at		NA	2.12
3850	217325_a _t	KRT3	keratin 3	2.09
22809	217389_s _at	ATF5	activating transcription factor 5	1.6
	217401_a _t		NA	1.41
7290	217427_s _at	HIRA	HIR histone cell cycle regulation defective homolog A (<i>S. cerevisiae</i>)	-2.29
	217446_x _at		NA	2.01
689	217461_x _at	BTF3	basic transcription factor 3	1.31
745	217462_a _t	C11orf9	chromosome 11 open reading frame 9	1.32
400963	217466_x _at	LOC400963	hypothetical gene supported by AB082925; BC019021; NM_002952	-1.28
7067	217476_a _t	THRA	thyroid hormone receptor, alpha (erythroblastic leukemia viral (v-erb-a) oncogene homolog, avian)	1.18
388336	217481_x _at	FLJ45455	FLJ45455 protein	-1.14
1890	217497_a _t	ECGF1	endothelial cell growth factor 1 (platelet-derived)	1.53
3433	217502_a _t	IFIT2	interferon-induced protein with tetratricopeptide repeats 2	-1.26
400642	217506_a _t	LOC400642	hypothetical gene supported by BC041875; BX648984	-1.99
1406	217510_a _t	CRX	cone-rod homeobox	1.47
2905	217573_a _t	GRIN2C	glutamate receptor, ionotropic, N-methyl D-aspartate 2C	1.54
90204	217592_a _t	ZSWIM1	zinc finger, SWIM-type containing 1	-1.25
65110	217596_a _t	UPF3A	UPF3 regulator of nonsense transcripts homolog A (yeast)	1.21
10966	217597_x _at	RAB40B	RAB40B, member RAS oncogene family	2
	217625_x _at		NA	-1.87
25950	217648_a _t	RWDD3	RWD domain containing 3	-1.18
79784	217660_a _t	MYH14	myosin, heavy chain 14	1.85
9123	217685_a _t	SLC16A3	solute carrier family 16, member 3 (monocarboxylic acid transporter 4)	2.24
9466	217702_a _t	IL27RA	interleukin 27 receptor, alpha	2.05
26135	217725_x _at	SERBP1	SERPINE1 mRNA binding protein 1	-2.2
22818	217726_a _t	COPZ1	coatamer protein complex, subunit zeta 1	-1.65

27102	217735_s_at	EIF2AK1	eukaryotic translation initiation factor 2-alpha kinase 1	-1.3
54606	217754_a_t	DDX56	DEAD (Asp-Glu-Ala-Asp) box polypeptide 56	-1.57
51155	217755_a_t	HN1	hematological and neurological expressed 1	-1.66
6747	217790_s_at	SSR3	signal sequence receptor, gamma (translocon-associated protein gamma)	-2.64
80762	217800_s_at	NDFIP1	Nedd4 family interacting protein 1	-1.63
51714	217811_a_t	SELT	selenoprotein T	-2.24
10492	217832_a_t	SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein	-2.2
55969	217835_x_at	C20orf24	chromosome 20 open reading frame 24	-1.91
51428	217840_a_t	DDX41	DEAD (Asp-Glu-Ala-Asp) box polypeptide 41	-1.57
9939	217856_a_t	RBM8A	RNA binding motif protein 8A	-1.45
55334	217859_s_at	SLC39A9	solute carrier family 39 (zinc transporter), member 9	-1.3
10113	217861_s_at	PREB	prolactin regulatory element binding	-2.57
9328	217876_a_t	GTF3C5	general transcription factor IIIC, polypeptide 5, 63kDa	-1.34
996	217879_a_t	CDC27	cell division cycle 27 homolog (S. cerevisiae)	-1.95
56851	217898_a_t	C15orf24	chromosome 15 open reading frame 24	-1.71
29074	217907_a_t	MRPL18	mitochondrial ribosomal protein L18	-1.83
6945	217910_x_at	MLX	MAX-like protein X	-1.48
28977	217919_s_at	MRPL42	mitochondrial ribosomal protein L42	-2.27
10905	217920_a_t	MAN1A2	mannosidase, alpha, class 1A, member 2	-1.61
553115	217923_a_t	PEF1	penta-EF-hand domain containing 1	-1.47
28972	217927_a_t	SPCS1	signal peptidase complex subunit 1 homolog (S. cerevisiae)	-1.69
10273	217934_x_at	STUB1	STIP1 homology and U-box containing protein 1	-1.31
54977	217961_a_t	SLC25A38	solute carrier family 25, member 38	-1.6
7260	217968_a_t	TSSC1	tumor suppressing subtransferable candidate 1	-1.37
55585	217978_s_at	UBE2Q1	ubiquitin-conjugating enzyme E2Q (putative) 1	-1.94
51116	218001_a_t	MRPS2	mitochondrial ribosomal protein S2	-1.49
55069	218008_a_t	C7orf42	chromosome 7 open reading frame 42	-1.89

79902	218014_a_t	NUP85	nucleoporin 85kDa	-1.47
55718	218016_s_at	POLR3E	polymerase (RNA) III (DNA directed) polypeptide E (80kD)	-1.87
60685	218020_s_at	ZFAND3	zinc finger, AN1-type domain 3	-1.62
64834	218028_a_t	ELOVL1	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1	-1.51
51569	218050_a_t	UFM1	ubiquitin-fold modifier 1	-1.66
57130	218052_s_at	ATP13A1	ATPase type 13A1	-1.6
10328	218057_x_at	COX4NB	COX4 neighbor	-1.95
51123	218059_a_t	ZNF706	zinc finger protein 706	-1.55
51647	218074_a_t	FAM96B	family with sequence similarity 96, member B	-1.87
11124	218080_x_at	FAF1	Fas (TNFRSF6) associated factor 1	-1.42
79004	218097_s_at	CUEDC2	CUE domain containing 2	-1.81
	218098_a_t		NA	-2.02
55148	218108_a_t	C14orf130	chromosome 14 open reading frame 130	-1.81
65993	218112_a_t	MRPS34	mitochondrial ribosomal protein S34	-1.45
60491	218133_s_at	NIF3L1	NIF3 NGG1 interacting factor 3-like 1 (S. pombe)	-1.73
60682	218137_s_at	SMAP1	stromal membrane-associated protein 1	-1.57
8195	218138_a_t	MKKS	McKusick-Kaufman syndrome	-1.75
55745	218139_s_at	C14orf108	chromosome 14 open reading frame 108	-2.08
10066	218143_s_at	SCAMP2	secretory carrier membrane protein 2	-1.4
28985	218163_a_t	MCTS1	malignant T cell amplified sequence 1	-2.18
55697	218169_a_t	VAC14	Vac14 homolog (S. cerevisiae)	-1.72
60684	218179_s_at	FLJ12716	FLJ12716 protein	-1.67
51026	218193_s_at	GOLT1B	golgi transport 1 homolog B (S. cerevisiae)	-2.8
29880	218203_a_t	ALG5	asparagine-linked glycosylation 5 homolog (S. cerevisiae, dolichyl-phosphate beta-glucosyltransferase)	-1.91
55197	218209_s_at	P15RS	hypothetical protein FLJ10656	-1.84
79083	218211_s_at	MLPH	melanophilin	-1.78

60314	218220_a_t	C12orf10	chromosome 12 open reading frame 10	-1.64
10101	218227_a_t	NUBP2	nucleotide binding protein 2 (MinD homolog, E. coli)	-1.83
64429	218249_a_t	ZDHHC6	zinc finger, DHHC-type containing 6	-1.48
79016	218260_a_t	C19orf58	chromosome 19 open reading frame 58	-2.01
56647	218264_a_t	BCCIP	BRCA2 and CDKN1A interacting protein	-1.98
79590	218270_a_t	MRPL24	mitochondrial ribosomal protein L24	-1.67
54663	218278_a_t	WDR74	WD repeat domain 74	1.64
51642	218281_a_t	MRPL48	mitochondrial ribosomal protein L48	-1.67
10762	218295_s_at	NUP50	nucleoporin 50kDa	-1.36
80013	218297_a_t	C10orf97	chromosome 10 open reading frame 97	-1.51
55851	218302_a_t	PSENE1	presenilin enhancer 2 homolog (C. elegans)	-1.7
26520	218316_a_t	TIMM9	translocase of inner mitochondrial membrane 9 homolog (yeast)	-1.47
79008	218317_x_at	GIYD2	GIY-YIG domain containing 2	-1.71
9342	218327_s_at	SNAP29	synaptosomal-associated protein, 29kDa	-1.82
51117	218328_a_t	COQ4	coenzyme Q4 homolog (S. cerevisiae)	-1.36
11108	218329_a_t	PRDM4	PR domain containing 4	1.3
51009	218333_a_t	DERL2	Der1-like domain family, member 2	-2.06
29093	218339_a_t	MRPL22	mitochondrial ribosomal protein L22	-1.76
9330	218343_s_at	GTF3C3	general transcription factor IIIC, polypeptide 3, 102kDa	-1.6
55213	218352_a_t	RCBTB1	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 1	-2
80023	218359_a_t	NRSN2	neurensin 2	-1.28
53343	218375_a_t	NUDT9	nudix (nucleoside diphosphate linked moiety X)-type motif 9	-1.82
25796	218388_a_t	PGLS	6-phosphogluconolactonase	-1.56
10884	218398_a_t	MRPS30	mitochondrial ribosomal protein S30	-2.43
26519	218408_a_t	TIMM10	translocase of inner mitochondrial membrane 10 homolog (yeast)	-1.49
26276	218415_a_t	VPS33B	vacuolar protein sorting 33 homolog B (yeast)	-1.34
51542	218423_x	VPS54	vacuolar protein sorting 54 homolog (S.	-1.89

	_at		cerevisiae)	
51397	218439_s_at	COMMD10	COMM domain containing 10	-1.63
9054	218455_a_t	NFS1	NFS1 nitrogen fixation 1 homolog (S. cerevisiae)	-1.52
64395	218458_a_t	GMCL1	germ cell-less homolog 1 (Drosophila)	-1.72
54919	218460_a_t	HEATR2	HEAT repeat containing 2	-1.52
54442	218474_s_at	KCTD5	potassium channel tetramerisation domain containing 5	-1.68
79622	218493_a_t	C16orf33	chromosome 16 open reading frame 33	-1.65
246243	218496_a_t	RNASEH1	ribonuclease H1	-1.87
246243	218497_s_at	RNASEH1	ribonuclease H1	-1.61
55759	218512_a_t	WDR12	WD repeat domain 12	-1.81
55032	218519_a_t	SLC35A5	solute carrier family 35, member A5	-1.83
29098	218526_s_at	RANGRF	RAN guanine nucleotide release factor	-1.34
54840	218527_a_t	APTX	aprataxin	-1.43
55109	218534_s_at	AGGF1	angiogenic factor with G patch and FHA domains 1	-1.86
57380	218536_a_t	MRS2L	MRS2-like, magnesium homeostasis factor (S. cerevisiae)	-1.47
57380	218538_s_at	MRS2L	MRS2-like, magnesium homeostasis factor (S. cerevisiae)	-1.42
60672	218551_a_t	RP5-1077B9.4	invasion inhibitory protein 45	1.69
54148	218558_s_at	MRPL39	mitochondrial ribosomal protein L39	-1.87
55219	218562_s_at	TMEM57	transmembrane protein 57	-1.67
10072	218567_x_at	DPP3	dipeptidyl-peptidase 3	-1.6
54998	218580_x_at	AURKAIP1	aurora kinase A interacting protein 1	-1.61
55131	218593_a_t	RBM28	RNA binding motif protein 28	-1.4
55127	218594_a_t	HEATR1	HEAT repeat containing 1	-1.83
80774	218600_a_t	LIMD2	LIM domain containing 2	1.48
64216	218605_a_t	TFB2M	transcription factor B2, mitochondrial	-2.31
55153	218607_s_at	SDAD1	SDA1 domain containing 1	-1.52
55254	218615_s_at	TMEM39A	transmembrane protein 39A	-1.79
79903	218661_a	FLJ14154	hypothetical protein FLJ14154	-1.72

	t			
10533	218673_s_at	ATG7	ATG7 autophagy related 7 homolog (S. cerevisiae)	-1.44
80006	218674_a_t	FLJ13611	hypothetical protein FLJ13611	-2.07
55813	218715_a_t	UTP6	UTP6, small subunit (SSU) processome component, homolog (yeast)	-1.61
79714	218722_s_at	CCDC51	coiled-coil domain containing 51	-1.72
55294	218751_s_at	FBXW7	F-box and WD repeat domain containing 7	1.57
79707	218754_a_t	NOL9	nucleolar protein 9	-1.37
51004	218760_a_t	COQ6	coenzyme Q6 homolog, monooxygenase (S. cerevisiae)	-1.57
57109	218767_a_t	REXO4	REX4, RNA exonuclease 4 homolog (S. cerevisiae)	-1.4
54494	218789_s_at	C11orf71	chromosome 11 open reading frame 71	-2.23
54957	218794_s_at	TXNL4B	thioredoxin-like 4B	-1.55
7145	218863_s_at	TNS1	tensin 1	2.13
57180	218868_a_t	ACTR3B	ARP3 actin-related protein 3 homolog B (yeast)	-1.34
60487	218877_s_at	TRMT11	tRNA methyltransferase 11 homolog (S. cerevisiae)	-2.44
55110	218894_s_at	FLJ10292	mago-nashi homolog 2	-1.69
79724	218916_a_t	ZNF768	zinc finger protein 768	1.72
1486	218924_s_at	CTBS	chitobiase, di-N-acetyl-	-2.44
79176	218938_a_t	FBXL15	F-box and leucine-rich repeat protein 15	-1.36
64852	218965_s_at	TUT1	terminal uridylyl transferase 1, U6 snRNA-specific	1.7
80010	218979_a_t	RMI1	RMI1, RecQ mediated genome instability 1, homolog (S. cerevisiae)	-1.41
54517	218984_a_t	PUS7	pseudouridylate synthase 7 homolog (S. cerevisiae)	-2.04
55178	218993_a_t	RNMTL1	RNA methyltransferase like 1	-1.37
60526	219008_a_t	C2orf43	chromosome 2 open reading frame 43	-1.6
55849	219015_s_at	ALG13	asparagine-linked glycosylation 13 homolog (S. cerevisiae)	-2.17
51002	219030_a_t	TPRKB	TP53RK binding protein	-2.21
54956	219034_a_t	PARP16	poly (ADP-ribose) polymerase family, member 16	-1.43
29803	219041_s_at	REPIN1	replication initiator 1	-1.62

741	219050_s_at	ZNHIT2	zinc finger, HIT type 2	-1.38
55133	219055_a_t	SRBD1	S1 RNA binding domain 1	-1.45
8270	219061_s_at	LAGE3	L antigen family, member 3	-1.61
51072	219065_s_at	MEMO1	mediator of cell motility 1	-1.93
55751	219074_a_t	TMEM34	transmembrane protein 34	-1.62
55105	219078_a_t	GPATCH2	G patch domain containing 2	-1.3
51167	219079_a_t	CYB5R4	cytochrome b5 reductase 4	-1.46
51005	219082_a_t	AMDHD2	amidohydrolase domain containing 2	1.62
55164	219083_a_t	SHQ1	SHQ1 homolog (S. cerevisiae)	-1.48
79177	219088_s_at	ZNF576	zinc finger protein 576	-1.43
51735	219112_a_t	RAPGEF6	Rap guanine nucleotide exchange factor (GEF) 6	1.33
51303	219117_s_at	FKBP11	FK506 binding protein 11, 19 kDa	-2.37
51303	219118_a_t	FKBP11	FK506 binding protein 11, 19 kDa	-2.32
7775	219123_a_t	ZNF232	zinc finger protein 232	-1.44
80185	219124_a_t	C8orf41	chromosome 8 open reading frame 41	-1.37
54482	219130_a_t	CCDC76	coiled-coil domain containing 76	-1.87
54995	219133_a_t	OXSM	3-oxoacyl-ACP synthase, mitochondrial	-1.92
51163	219149_x_at	DBR1	debranching enzyme homolog 1 (S. cerevisiae)	-1.46
11158	219151_s_at	RABL2B	RAB, member of RAS oncogene family-like 2B	-1.35
55102	219164_s_at	ATG2B	ATG2 autophagy related 2 homolog B (S. cerevisiae)	-2.28
51182	219212_a_t	HSPA14	heat shock 70kDa protein 14	-1.64
64080	219222_a_t	RBKS	ribokinase	-1.52
79634	219234_x_at	SCRN3	secernin 3	-1.18
80007	219240_s_at	C10orf88	chromosome 10 open reading frame 88	-1.22
80254	219242_a_t	CEP63	centrosomal protein 63kDa	-1.53
55112	219251_s_at	WDR60	WD repeat domain 60	1.47
55027	219289_a_t	HEATR3	HEAT repeat containing 3	-1.83

79959	219311_a t	CEP76	centrosomal protein 76kDa	-1.36
64860	219335_a t	ARMCX5	armadillo repeat containing, X-linked 5	-1.84
79414	219346_a t	LRFN3	leucine rich repeat and fibronectin type III domain containing 3	-1.29
56616	219350_s at	DIABLO	diablo homolog (Drosophila)	-1.38
55086	219355_a t	CXorf57	chromosome X open reading frame 57	-1.2
79796	219374_s at	ALG9	asparagine-linked glycosylation 9 homolog (S. cerevisiae, alpha-1,2-mannosyltransferase)	-1.47
79139	219402_s at	DERL1	Der1-like domain family, member 1	-2.05
79078	219406_a t	C1orf50	chromosome 1 open reading frame 50	-1.61
25830	219425_a t	SULT4A1	sulfotransferase family 4A, member 1	1.39
51006	219447_s at	SLC35C2	solute carrier family 35, member C2	-1.32
55703	219459_a t	POLR3B	polymerase (RNA) III (DNA directed) polypeptide B	-1.73
54826	219467_a t	GIN1	gypsy retrotransposon integrase 1	-1.43
79070	219479_a t	KDELC1	KDEL (Lys-Asp-Glu-Leu) containing 1	-1.89
7733	219495_s at	ZNF180	zinc finger protein 180	-1.26
23529	219500_a t	CLCF1	cardiotrophin-like cytokine factor 1	1.39
10045	219513_s at	SH2D3A	SH2 domain containing 3A	1.25
59341	219516_a t	TRPV4	transient receptor potential cation channel, subfamily V, member 4	1.65
79833	219539_a t	GEMIN6	gem (nuclear organelle) associated protein 6	-1.5
7564	219548_a t	ZNF16	zinc finger protein 16	1.4
55812	219583_s at	SPATA7	spermatogenesis associated 7	1.32
51134	219644_a t	CCDC41	coiled-coil domain containing 41	-1.28
29929	219649_a t	ALG6	asparagine-linked glycosylation 6 homolog (S. cerevisiae, alpha-1,3-glucosyltransferase)	-1.48
26063	219664_s at	DECR2	2,4-dienoyl CoA reductase 2, peroxisomal	-1.8
54844	219673_a t		NA	-1.48
56920	219689_a t	SEMA3G	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3G	1.42
27132	219707_a	CPNE7	copine VII	1.52

	t			
8110	219746_a_t	DPF3	D4, zinc and double PHD fingers, family 3	-1.2
80776	219766_a_t	MGC4093	hypothetical protein MGC4093	1.76
594855	219775_s_at	CPLX3	complexin 3	1.43
79791	219785_s_at	FBXO31	F-box protein 31	-1.49
55796	219814_a_t	MBNL3	muscleblind-like 3 (Drosophila)	-2.21
55147	219816_s_at	RBM23	RNA binding motif protein 23	-1.38
9617	219822_a_t	MTRF1	mitochondrial translational release factor 1	-1.25
26548	219829_a_t	ITGB1BP2	integrin beta 1 binding protein (melusin) 2	-1.27
11123	219864_s_at	RCAN3	RCAN family member 3	1.11
64116	219869_s_at	SLC39A8	solute carrier family 39 (zinc transporter), member 8	-1.77
51340	219913_s_at	CRNKL1	crooked neck pre-mRNA splicing factor-like 1 (Drosophila)	-1.64
59349	219931_s_at	KLHL12	kelch-like 12 (Drosophila)	-1.23
51022	219933_a_t	GLRX2	glutaredoxin 2	-1.61
79442	219949_a_t	LRRC2	leucine rich repeat containing 2	-1.97
26230	219950_s_at	TIAM2	T-cell lymphoma invasion and metastasis 2	-1.16
51501	219979_s_at	C11orf73	chromosome 11 open reading frame 73	-2.03
26277	220052_s_at	TINF2	TERF1 (TRF1)-interacting nuclear factor 2	1.47
9503	220057_a_t	XAGE1D	X antigen family, member 1D	1.67
79807	220063_a_t	GSTCD	glutathione S-transferase, C-terminal domain containing	-1.12
51377	220083_x_at	UCHL5	ubiquitin carboxyl-terminal hydrolase L5	-1.25
79750	220117_a_t	ZNF659	zinc finger protein 659	1.42
54850	220127_s_at	FBXL12	F-box and leucine-rich repeat protein 12	-1.69
65980	220155_s_at	BRD9	bromodomain containing 9	1.48
80067	220172_a_t	C2orf37	chromosome 2 open reading frame 37	-1.12
25803	220192_x_at	SPDEF	SAM pointed domain containing ets transcription factor	1.4
374819	220219_s_at	LRRC37A3	leucine rich repeat containing 37, member A3	1.38

55968	220248_x _at	NSFL1C	NSFL1 (p97) cofactor (p47)	-1.67
80231	220252_x _at	CXorf21	chromosome X open reading frame 21	1.73
9597	220263_a _t	SMAD5OS	SMAD family member 5 opposite strand	-1.28
27190	220273_a _t	IL17B	interleukin 17B	1.58
58157	220337_a _t	NGB	neuroglobin	1.81
80267	220342_x _at	EDEM3	ER degradation enhancer, mannosidase alpha-like 3	-2.26
79595	220367_s _at	SAP130	Sin3A-associated protein, 130kDa	-1.46
11147	220387_s _at	HHLA3	HERV-H LTR-associating 3	-1.58
22992	220410_s _at	FBXL11	F-box and leucine-rich repeat protein 11	1.15
79444	220451_s _at	BIRC7	baculoviral IAP repeat-containing 7 (livin)	1.53
23539	220455_a _t	SLC16A8	solute carrier family 16, member 8 (monocarboxylic acid transporter 3)	1.44
11316	220469_a _t	COPE	coatamer protein complex, subunit epsilon	1.46
9464	220480_a _t	HAND2	heart and neural crest derivatives expressed 2	1.69
54828	220488_s _at	BCAS3	breast carcinoma amplified sequence 3	1.43
2974	220506_a _t	GUCY1B2	guanylate cyclase 1, soluble, beta 2	1.25
550	220525_s _at	AUP1	ancient ubiquitous protein 1	-1.72
55237	220536_a _t	C14orf115	chromosome 14 open reading frame 115	1.58
55690	220557_s _at	PACS1	phosphofurin acidic cluster sorting protein 1	1.53
51214	220561_a _t	IGF2AS	insulin-like growth factor 2 antisense	1.74
54905	220562_a _t	CYP2W1	cytochrome P450, family 2, subfamily W, polypeptide 1	2.06
80129	220581_a _t	C6orf97	chromosome 6 open reading frame 97	1.13
79092	220598_a _t	CARD14	caspase recruitment domain family, member 14	1.25
22933	220605_s _at	SIRT2	sirtuin (silent mating type information regulation 2 homolog) 2 (S. cerevisiae)	-1.51
51497	220607_x _at	TH1L	TH1-like (Drosophila)	-1.56
53944	220640_a _t	CSNK1G1	casein kinase 1, gamma 1	1.34
51088	220682_s _at	KLHL5	kelch-like 5 (Drosophila)	-1.15
11173	220705_s _at	ADAMTS7	ADAM metalloproteinase with thrombospondin type 1 motif, 7	1.49

11173	220706_a_t	ADAMTS7	ADAM metallopeptidase with thrombospondin type 1 motif, 7	1.3
	220726_a_t		NA	1.16
55768	220742_s_at	NGLY1	N-glycanase 1	-1.51
55065	220756_s_at	GPR172B	G protein-coupled receptor 172B	1.4
55293	220775_s_at	UEVLD	UEV and lactate/malate dehydrogenase domains	-1.7
9238	220789_s_at	TBRG4	transforming growth factor beta regulator 4	-1.35
79948	220798_x_at	PRG2	plasticity-related gene 2	2.57
	220837_a_t		NA	1.09
23590	220865_s_at	PDSS1	prenyl (decaprenyl) diphosphate synthase, subunit 1	-1.67
57728	220917_s_at	WDR19	WD repeat domain 19	-1.86
80267	220926_s_at	EDEM3	ER degradation enhancer, mannosidase alpha-like 3	-2.87
27090	220937_s_at	ST6GALNAC4	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 4	1.49
29072	220946_s_at	SETD2	SET domain containing 2	1.42
81624	220997_s_at	DIAPH3	diaphanous homolog 3 (Drosophila)	-1.12
81033	221023_s_at	KCNH6	potassium voltage-gated channel, subfamily H (eag-related), member 6	1.56
11022	221053_s_at	TDRKH	tudor and KH domain containing	-1.15
55239	221090_s_at	OGFOD1	2-oxoglutarate and iron-dependent oxygenase domain containing 1	-1.67
55140	221094_s_at	ELP3	elongation protein 3 homolog (S. cerevisiae)	-1.31
54979	221122_a_t	HRASLS2	HRAS-like suppressor 2	1.29
29919	221190_s_at	C18orf8	chromosome 18 open reading frame 8	-1.92
51136	221194_s_at	LOC51136	PTD016 protein	-1.59
79184	221196_x_at	BRCC3	BRCA1/BRCA2-containing complex, subunit 3	-1.45
6343	221198_a_t	SCT	secretin	1.66
55118	221204_s_at	CRTAC1	cartilage acidic protein 1	1.29
54964	221222_s_at	C1orf56	chromosome 1 open reading frame 56	-1.31
1154	221223_x_at	CISH	cytokine inducible SH2-containing protein	-2.1

79877	221224_s _at	DCAKD	dephospho-CoA kinase domain containing	1.21
51805	221227_x _at	COQ3	coenzyme Q3 homolog, methyltransferase (<i>S. cerevisiae</i>)	-1.59
55006	221229_s _at	FLJ20628	hypothetical protein FLJ20628	-1.66
81567	221253_s _at	TXNDC5	thioredoxin domain containing 5	-1.91
83460	221255_s _at	TMEM93	transmembrane protein 93	-1.89
81926	221267_s _at	FAM108A1	family with sequence similarity 108, member A1	-1.53
6714	221284_s _at	SRC	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	1.25
80328	221291_a _t	ULBP2	UL16 binding protein 2	1.25
50943	221333_a _t	FOXP3	forkhead box P3	1.51
2848	221363_x _at	GPR25	G protein-coupled receptor 25	1.25
10316	221383_a _t	NMUR1	neuromedin U receptor 1	1.67
64106	221387_a _t	NPFPR1	neuropeptide FF receptor 1	1.5
27179	221404_a _t	IL1F6	interleukin 1 family, member 6 (epsilon)	1.26
56124	221408_x _at	PCDHB12	protocadherin beta 12	1.42
56132	221410_x _at	PCDHB3	protocadherin beta 3	1.39
56123	221450_x _at	PCDHB13	protocadherin beta 13	1.51
51271	221490_a _t	UBAP1	ubiquitin associated protein 1	-1.42
54471	221516_s _at	SMCR7L	Smith-Magenis syndrome chromosome region, candidate 7-like	-1.84
8559	221547_a _t	PRPF18	PRP18 pre-mRNA processing factor 18 homolog (<i>S. cerevisiae</i>)	-1.69
1355	221550_a _t	COX15	COX15 homolog, cytochrome c oxidase assembly protein (yeast)	-1.34
8555	221556_a _t	CDC14B	CDC14 cell division cycle 14 homolog B (<i>S. cerevisiae</i>)	-2.64
29100	221597_s _at	HSPC171	HSPC171 protein	-1.5
60626	221647_s _at	RIC8A	resistance to inhibitors of cholinesterase 8 homolog A (<i>C. elegans</i>)	-1.31
54797	221650_s _at	MED18	mediator complex subunit 18	-1.39
55726	221652_s _at	C12orf11	chromosome 12 open reading frame 11	-1.55
27034	221669_s _at	ACAD8	acyl-Coenzyme A dehydrogenase family, member 8	-1.79
29980	221677_s	DONSON	downstream neighbor of SON	-1.83

	_at			
57406	221679_s_at	ABHD6	abhydrolase domain containing 6	-2.54
1290	221730_at	COL5A2	collagen, type V, alpha 2	1.69
56005	221739_at	C19orf10	chromosome 19 open reading frame 10	-2.51
54915	221741_s_at	YTHDF1	YTH domain family, member 1	-1.55
93436	221758_at	ARMC6	armadillo repeat containing 6	-1.49
54431	221782_at	DNAJC10	DnaJ (Hsp40) homolog, subfamily C, member 10	-2.47
387263	221786_at	C6orf120	chromosome 6 open reading frame 120	-2.74
5238	221788_at	PGM3	phosphoglucomutase 3	-2.39
11021	221819_at	RAB35	RAB35, member RAS oncogene family	-1.45
10616	221827_at	RBCK1	RanBP-type and C3HC4-type zinc finger containing 1	-2.06
	221844_x_at		NA	-1.78
23232	221858_at	TBC1D12	TBC1 domain family, member 12	-1.36
27147	221885_at	DENND2A	DENN/MADD domain containing 2A	1.41
57863	221921_s_at	CADM3	cell adhesion molecule 3	1.47
51526	221954_at	C20orf111	chromosome 20 open reading frame 111	-1.46
90133	222060_at	KRT8P12	keratin 8 pseudogene 12	1.71
80755	222064_s_at	AARSD1	alanyl-tRNA synthetase domain containing 1	-1.3
	222080_s_at		NA	1.57
64419	222143_s_at	MTMR14	myotubularin related protein 14	-1.35
55288	222148_s_at	RHOT1	ras homolog gene family, member T1	-1.47
79029	222163_s_at	SPATA5L1	spermatogenesis associated 5-like 1	-1.76
4848	222182_s_at	CNOT2	CCR4-NOT transcription complex, subunit 2	1.84
389517	222207_x_at	LOC389517	Williams Beuren syndrome chromosome region 19 pseudogene	1.8
63875	222216_s_at	MRPL17	mitochondrial ribosomal protein L17	-1.56
55500	222262_s_at	ETNK1	ethanolamine kinase 1	-2.38
6141	222297_x_at	RPL18	ribosomal protein L18	1.62
	222323_a		NA	1.43

	t			
643224	222361_a_t	LOC643224	similar to tubulin, beta 8	1.14
347853	222377_a_t	TBX10	T-box 10	1.46
9684	32062_at	LRRC14	leucine rich repeat containing 14	1.26
10555	32837_at	AGPAT2	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta)	-1.97
5939	34187_at	RBMS2	RNA binding motif, single stranded interacting protein 2	1.22
23395	34764_at	LARS2	leucyl-tRNA synthetase 2, mitochondrial	-1.62
203069	35156_at	R3HCC1	R3H domain and coiled-coil containing 1	-1.43
26229	35179_at	B3GAT3	beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase I)	1.51
7067	35846_at	THRA	thyroid hormone receptor, alpha (erythroblastic leukemia viral (v-erb-a) oncogene homolog, avian)	1.29
1497	36566_at	CTNS	cystinosis, nephropathic	-1.59
4285	36830_at	MIPEP	mitochondrial intermediate peptidase	-1.47
7264	36936_at	TSTA3	tissue specific transplantation antigen P35B	-2.03
527	36994_at	ATP6V0C	ATPase, H ⁺ transporting, lysosomal 16kDa, V0 subunit c	-1.64
23349	37566_at	KIAA1045	KIAA1045	1.17
8629	37872_at	JRK	jerky homolog (mouse)	1.4
360	39248_at	AQP3	aquaporin 3 (Gill blood group)	-2.39
80003	39650_s_at	PCNXL2	pecanex-like 2 (Drosophila)	1.56
9416	40465_at	DDX23	DEAD (Asp-Glu-Ala-Asp) box polypeptide 23	-1.63
254531	40472_at	AGPAT7	1-acylglycerol-3-phosphate O-acyltransferase 7 (lysophosphatidic acid acyltransferase, eta)	1.6
55101	45828_at	FLJ10241	hypothetical protein FLJ10241	-1.46
11108	49485_at	PRDM4	PR domain containing 4	1.28
54976	50314_i_at	C20orf27	chromosome 20 open reading frame 27	1.26
79959	52285_f_at	CEP76	centrosomal protein 76kDa	-1.62
55337	53720_at	FLJ11286	hypothetical protein FLJ11286	-1.95
57787	55065_at	MARK4	MAP/microtubule affinity-regulating kinase 4	-2.26
85377	55081_at	MICALL1	MICAL-like 1	-1.5
63916	55692_at	ELMO2	engulfment and cell motility 2	-1.45
2767	564_at	GNA11	guanine nucleotide binding protein (G protein), alpha 11 (Gq class)	-1.54
63897	65493_at	HEATR6	HEAT repeat containing 6	1.17
63935	89948_at	C20orf67	chromosome 20 open reading frame 67	1.23

Appendix 2

Supplemental Table 2- Genes Significantly Different Between HCV Cirrhotic Tissue Compared to Normal Liver Tissue

Entrez ID	Affy ID	Symbol	Gene Name	Fold
7318	1294_at	UBE1L	ubiquitin-activating enzyme E1-like	1.36

7067	1316_at	THRA	thyroid hormone receptor, alpha (erythroblastic leukemia viral (v-erb-a) oncogene homolog, avian)	-1.31
6352	1405_i_at	CCL5	chemokine (C-C motif) ligand 5	4.71
4323	160020_a_t	MMP14	matrix metalloproteinase 14 (membrane- inserted)	-1.37
8664	200005_a_t	EIF3D	eukaryotic translation initiation factor 3, subunit D	1.93
377	200011_s_at	ARF3	ADP-ribosylation factor 3	1.48
3178	200016_x_at	HNRNPA1	heterogeneous nuclear ribonucleoprotein A1	1.53
6141	200022_a_t	RPL18	ribosomal protein L18	1.38
1655	200033_a_t	DDX5	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	1.42
1327	200086_s_at	COX4I1	cytochrome c oxidase subunit IV isoform 1	1.26
9948	200609_s_at	WDR1	WD repeat domain 1	1.45
9782	200624_s_at	MATR3	matrin 3	1.46
5792	200635_s_at	PTPRF	protein tyrosine phosphatase, receptor type, F	-1.69
7534	200640_a_t	YWHAZ	tyrosine 3-monooxygenase/tryptophan 5- monooxygenase activation protein, zeta polypeptide	1.93
3069	200643_a_t	HDLBP	high density lipoprotein binding protein (vigilin)	-1.56
5476	200661_a_t	CTSA	cathepsin A	1.49
9804	200662_s_at	TOMM20	translocase of outer mitochondrial membrane 20 homolog (yeast)	1.43
7494	200670_a_t	XBP1	X-box binding protein 1	-1.54
2896	200678_x_at	GRN	granulin	1.58
5518	200695_a_t	PPP2R1A	protein phosphatase 2 (formerly 2A), regulatory subunit A , alpha isoform	1.42
3098	200697_a_t	HK1	hexokinase 1	1.89
10577	200701_a_t	NPC2	Niemann-Pick disease, type C2	1.83
6500	200711_s_at	SKP1A	S-phase kinase-associated protein 1A (p19A)	1.47
22919	200712_s_at	MAPRE1	microtubule-associated protein, RP/EB family, member 1	2.06
22919	200713_s_at	MAPRE1	microtubule-associated protein, RP/EB family, member 1	1.57
10121	200721_s_at	ACTR1A	ARP1 actin-related protein 1 homolog A, cetractin alpha (yeast)	-1.35
6134	200724_a_t	RPL10	ribosomal protein L10	-1.25
6134	200725_x	RPL10	ribosomal protein L10	1.31

	_at			
5501	200726_a_t	PPP1CC	protein phosphatase 1, catalytic subunit, gamma isoform	1.87
6232	200741_s_at	RPS27	ribosomal protein S27 (metallopanstimulin 1)	1.29
1200	200743_s_at	TPP1	tripeptidyl peptidase I	1.44
2782	200746_s_at	GNB1	guanine nucleotide binding protein (G protein), beta polypeptide 1	1.54
6427	200754_x_at	SFRS2	splicing factor, arginine/serine-rich 2	1.67
813	200757_s_at	CALU	calumenin	-1.54
10550	200760_s_at	ARL6IP5	ADP-ribosylation-like factor 6 interacting protein 5	2.26
10550	200761_s_at	ARL6IP5	ADP-ribosylation-like factor 6 interacting protein 5	2.12
4735	200778_s_at	2-Sep	septin 2	1.82
2778	200780_x_at	GNAS	GNAS complex locus	1.46
4035	200785_s_at	LRP1	low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)	-1.42
8682	200787_s_at	PEA15	phosphoprotein enriched in astrocytes 15	2.38
6136	200809_x_at	RPL12	ribosomal protein L12	1.56
1153	200811_a_t	CIRBP	cold inducible RNA binding protein	2.01
6209	200819_s_at	RPS15	ribosomal protein S15	1.48
6159	200823_x_at	RPL29	ribosomal protein L29	1.43
6633	200826_a_t	SNRPD2	small nuclear ribonucleoprotein D2 polypeptide 16.5kDa	1.7
9798	200851_s_at	KIAA0174	KIAA0174	1.68
9611	200854_a_t	NCOR1	nuclear receptor co-repressor 1	-1.71
1718	200862_a_t	DHCR24	24-dehydrocholesterol reductase	-2.18
8766	200863_s_at	RAB11A	RAB11A, member RAS oncogene family	1.51
6281	200872_a_t	S100A10	S100 calcium binding protein A10	2.5
7385	200883_a_t	UQCRC2	ubiquinol-cytochrome c reductase core protein II	1.53
6772	200887_s_at	STAT1	signal transducer and activator of transcription 1, 91kDa	2.6
10724	200898_s_at	MGEA5	meningioma expressed antigen 5 (hyaluronidase)	1.6
10724	200899_s_at	MGEA5	meningioma expressed antigen 5 (hyaluronidase)	1.79

191	200903_s _at	AHCY	S-adenosylhomocysteine hydrolase	-1.57
3133	200904_a _t	HLA-E	major histocompatibility complex, class I, E	2.12
1974	200912_s _at	EIF4A2	eukaryotic translation initiation factor 4A, isoform 2	1.65
3959	200923_a _t	LGALS3 BP	lectin, galactoside-binding, soluble, 3 binding protein	5.9
10540	200932_s _at	DCTN2	dynactin 2 (p50)	1.3
6191	200933_x _at	RPS4X	ribosomal protein S4, X-linked	1.28
473	200940_s _at	RERE	arginine-glutamic acid dipeptide (RE) repeats	1.72
2746	200947_s _at	GLUD1	glutamate dehydrogenase 1	-2.2
6224	200949_x _at	RPS20	ribosomal protein S20	1.45
894	200953_s _at	CCND2	cyclin D2	2.09
6386	200958_s _at	SDCBP	syndecan binding protein (syntenin)	1.63
22928	200961_a _t	SEPHS2	selenophosphate synthetase 2	-1.65
6160	200962_a _t	RPL31	ribosomal protein L31	2.38
6160	200963_x _at	RPL31	ribosomal protein L31	1.43
5538	200975_a _t	PPT1	palmitoyl-protein thioesterase 1 (ceroid-lipofuscinosis, neuronal 1, infantile)	2.8
8887	200977_s _at	TAX1BP 1	Tax1 (human T-cell leukemia virus type I) binding protein 1	1.46
4190	200978_a _t	MDH1	malate dehydrogenase 1, NAD (soluble)	1.49
2778	200981_x _at	GNAS	GNAS complex locus	1.51
966	200983_x _at	CD59	CD59 molecule, complement regulatory protein	2.28
966	200984_s _at	CD59	CD59 molecule, complement regulatory protein	2.2
966	200985_s _at	CD59	CD59 molecule, complement regulatory protein	1.95
3032	201007_a _t	HADHB	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit	1.63
6184	201011_a _t	RPN1	ribophorin I	-2.12
3187	201031_s _at	HNRPH1	heterogeneous nuclear ribonucleoprotein H1 (H)	1.46
1843	201044_x _at	DUSP1	dual specificity phosphatase 1	3.11
10949	201054_a _t	HNRNPA 0	heterogeneous nuclear ribonucleoprotein A0	1.65

2804	201057_s_at	GOLGB1	golgin B1, golgi integral membrane protein	1.42
10398	201058_s_at	MYL9	myosin, light chain 9, regulatory	3.9
23451	201070_x_at	SF3B1	splicing factor 3b, subunit 1, 155kDa	1.8
23451	201071_x_at	SF3B1	splicing factor 3b, subunit 1, 155kDa	1.72
5931	201092_a_t	RBBP7	retinoblastoma binding protein 7	1.39
7057	201108_s_at	THBS1	thrombospondin 1	2.52
7057	201109_s_at	THBS1	thrombospondin 1	4
1363	201116_s_at	CPE	carboxypeptidase E	2.26
3693	201125_s_at	ITGB5	integrin, beta 5	1.65
7078	201147_s_at	TIMP3	TIMP metalloproteinase inhibitor 3 (Sorsby fundus dystrophy, pseudoinflammatory)	2.57
4154	201152_s_at	MBNL1	muscleblind-like (Drosophila)	1.64
4836	201159_s_at	NMT1	N-myristoyltransferase 1	-1.33
9698	201164_s_at	PUM1	pumilio homolog 1 (Drosophila)	1.41
25793	201178_a_t	FBXO7	F-box protein 7	1.6
1108	201182_s_at	CHD4	chromodomain helicase DNA binding protein 4	-1.34
4043	201186_a_t	LRPAP1	low density lipoprotein receptor-related protein associated protein 1	1.4
6122	201217_x_at	RPL3	ribosomal protein L3	1.37
1488	201218_a_t	CTBP2	C-terminal binding protein 2	3.1
7832	201235_s_at	BTG2	BTG family, member 2	1.74
7832	201236_s_at	BTG2	BTG family, member 2	2.37
6513	201249_a_t	SLC2A1	solute carrier family 2 (facilitated glucose transporter), member 1	-1.23
633	201262_s_at	BGN	biglycan	2.23
	201265_a_t		NA	-1.25
231	201272_a_t	AKR1B1	aldo-keto reductase family 1, member B1 (aldose reductase)	2.37
1601	201279_s_at	DAB2	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	2.2
397	201288_a_t	ARHGDI B	Rho GDP dissociation inhibitor (GDI) beta	3.1
26118	201295_s	WSB1	WD repeat and SOCS box-containing 1	2.07

	_at			
9775	201303_a_t	EIF4A3	eukaryotic translation initiation factor 4A, isoform 3	1.32
10541	201306_s_at	ANP32B	acidic (leucine-rich) nuclear phosphoprotein 32 family, member B	1.41
6451	201311_s_at	SH3BGR_L	SH3 domain binding glutamic acid-rich protein like	3.69
10494	201314_a_t	STK25	serine/threonine kinase 25 (STE20 homolog, yeast)	-1.33
6601	201321_s_at	SMARCC2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2	1.93
2012	201325_s_at	EMP1	epithelial membrane protein 1	5.16
23365	201334_s_at	ARHGEF12	Rho guanine nucleotide exchange factor (GEF) 12	-1.55
9341	201337_s_at	VAMP3	vesicle-associated membrane protein 3 (cellubrevin)	2.35
7322	201345_s_at	UBE2D2	ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog, yeast)	1.73
9368	201349_a_t	SLC9A3R1	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1	-1.39
678	201368_a_t	ZFP36L2	zinc finger protein 36, C3H type-like 2	2.01
1665	201386_s_at	DHX15	DEAH (Asp-Glu-Ala-His) box polypeptide 15	1.72
10181	201394_s_at	RBM5	RNA binding motif protein 5	1.6
10181	201395_a_t	RBM5	RNA binding motif protein 5	1.41
4259	201403_s_at	MGST3	microsomal glutathione S-transferase 3	1.44
6173	201406_a_t	RPL36A	ribosomal protein L36a	1.57
4676	201414_s_at	NAP1L4	nucleosome assembly protein 1-like 4	1.5
6659	201416_a_t	SOX4	SRY (sex determining region Y)-box 4	1.86
6659	201417_a_t	SOX4	SRY (sex determining region Y)-box 4	7.29
1809	201431_s_at	DPYSL3	dihydropyrimidinase-like 3	2.09
8729	201439_a_t	GBF1	golgi-specific brefeldin A resistance factor 1	-1.41
9184	201457_x_at	BUB3	BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast)	1.54
3725	201466_s_at	JUN	jun oncogene	3.77
6829	201480_s_at	SUPT5H	suppressor of Ty 5 homolog (S. cerevisiae)	-1.41
1075	201487_a_t	CTSC	cathepsin C	2.08
4629	201497_x_at	MYH11	myosin, heavy chain 11, smooth muscle	1.9

5201	201507_a_t	PFDN1	prefoldin subunit 1	1.6
10146	201514_s_at	G3BP1	GTPase activating protein (SH3 domain) binding protein 1	-1.39
10951	201518_a_t	CBX1	chromobox homolog 1 (HP1 beta homolog Drosophila)	1.98
6638	201522_x_at	SNRPN	small nuclear ribonucleoprotein polypeptide N	2
7334	201524_x_at	UBE2N	ubiquitin-conjugating enzyme E2N (UBC13 homolog, yeast)	1.43
9296	201527_a_t	ATP6V1F	ATPase, H ⁺ transporting, lysosomal 14kDa, V1 subunit F	1.43
7538	201531_a_t	ZFP36	zinc finger protein 36, C3H type, homolog (mouse)	2.42
2273	201539_s_at	FHL1	four and a half LIM domains 1	1.87
2273	201540_a_t	FHL1	four and a half LIM domains 1	2.08
3916	201553_s_at	LAMP1	lysosomal-associated membrane protein 1	1.34
5420	201578_a_t	PODXL	podocalyxin-like	2.13
2195	201579_a_t	FAT	FAT tumor suppressor homolog 1 (Drosophila)	2.17
8667	201592_a_t	EIF3H	eukaryotic translation initiation factor 3, subunit H	1.75
8519	201601_x_at	IFITM1	interferon induced transmembrane protein 1 (9-27)	2.67
4659	201602_s_at	PPP1R12A	protein phosphatase 1, regulatory (inhibitor) subunit 12A	1.82
4659	201603_a_t	PPP1R12A	protein phosphatase 1, regulatory (inhibitor) subunit 12A	1.84
4659	201604_s_at	PPP1R12A	protein phosphatase 1, regulatory (inhibitor) subunit 12A	2.01
8906	201613_s_at	APIG2	adaptor-related protein complex 1, gamma 2 subunit	1.42
800	201616_s_at	CALD1	caldesmon 1	2.12
1209	201640_x_at	CLPTM1	cleft lip and palate associated transmembrane protein 1	-1.41
684	201641_a_t	BST2	bone marrow stromal cell antigen 2	2.55
3880	201650_a_t	KRT19	keratin 19	3.23
4082	201669_s_at	MARCKS	myristoylated alanine-rich protein kinase C substrate	3.99
4082	201670_s_at	MARCKS	myristoylated alanine-rich protein kinase C substrate	2.37
9878	201684_s_at	TOX4	TOX high mobility group box family member 4	-1.28
896	201700_a_t	CCND3	cyclin D3	1.93
10424	201701_s	PGRMC2	progesterone receptor membrane	-1.67

	_at		component 2	
2037	201718_s_at	EPB41L2	erythrocyte membrane protein band 4.1-like 2	2.14
7805	201720_s_at	LAPTM5	lysosomal associated multispinning membrane protein 5	2.42
7805	201721_s_at	LAPTM5	lysosomal associated multispinning membrane protein 5	3.16
10289	201738_a_t	EIF1B	eukaryotic translation initiation factor 1B	1.43
1889	201749_a_t	ECE1	endothelin converting enzyme 1	-1.58
3073	201765_s_at	HEXA	hexosaminidase A (alpha polypeptide)	1.45
23394	201773_a_t	ADNP	activity-dependent neuroprotector homeobox	1.6
9049	201781_s_at	AIP	aryl hydrocarbon receptor interacting protein	1.52
6035	201785_a_t	RNASE1	ribonuclease, RNase A family, 1 (pancreatic)	3.12
7407	201796_s_at	VAR5	valyl-tRNA synthetase	-1.37
7407	201797_s_at	VAR5	valyl-tRNA synthetase	-1.86
26509	201798_s_at	FER1L3	fer-1-like 3, myoferlin (C. elegans)	3.51
2022	201809_s_at	ENG	endoglin (Osler-Rendu-Weber syndrome 1)	2.44
54543	201812_s_at	TOMM7	translocase of outer mitochondrial membrane 7 homolog (yeast)	1.47
2631	201816_s_at	GBAS	glioblastoma amplified sequence	1.66
3852	201820_a_t	KRT5	keratin 5 (epidermolysis bullosa simplex, Dowling-Meara/Kobner/Weber-Cockayne types)	-1.37
8933	201828_x_at	FAM127A	family with sequence similarity 127, member A	1.4
23429	201844_s_at	RYBP	RING1 and YY1 binding protein	1.62
23429	201846_s_at	RYBP	RING1 and YY1 binding protein	1.67
1281	201852_x_at	COL3A1	collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant)	2.86
10953	201870_a_t	TOMM34	translocase of outer mitochondrial membrane 34	-1.33
6059	201873_s_at	ABCE1	ATP-binding cassette, sub-family E (OABP), member 1	-1.8
25820	201880_a_t	ARIH1	ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (Drosophila)	1.45
80344	201886_a_t	WDR23	WD repeat domain 23	-1.69
55186	201917_s_at	SLC25A36	solute carrier family 25, member 36	2.27

10412	201922_a _t	TINP1	TGF beta-inducible nuclear protein 1	1.56
3074	201944_a _t	HEXB	hexosaminidase B (beta polypeptide)	1.46
9987	201993_x _at	HNRPDL	heterogeneous nuclear ribonucleoprotein D-like	1.84
6993	201999_s _at	DYNLT1	dynein, light chain, Tctex-type 1	1.78
7082	202011_a _t	TJP1	tight junction protein 1 (zona occludens 1)	1.75
10209	202021_x _at	EIF1	eukaryotic translation initiation factor 1	1.78
23466	202048_s _at	CBX6	chromobox homolog 6	-1.54
8500	202065_s _at	PPFIA1	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1	-1.38
6397	202083_s _at	SEC14L1	SEC14-like 1 (S. cerevisiae)	1.91
6397	202084_s _at	SEC14L1	SEC14-like 1 (S. cerevisiae)	1.83
4599	202086_a _t	MX1	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	5.97
25800	202088_a _t	SLC39A6	solute carrier family 39 (zinc transporter), member 6	1.81
25800	202089_s _at	SLC39A6	solute carrier family 39 (zinc transporter), member 6	1.45
9993	202099_s _at	DGCR2	DiGeorge syndrome critical region gene 2	-1.47
5977	202116_a _t	DPF2	D4, zinc and double PHD fingers family 2	1.53
10920	202141_s _at	COPS8	COP9 constitutive photomorphogenic homolog subunit 8 (Arabidopsis)	1.56
3475	202147_s _at	IFRD1	interferon-related developmental regulator 1	1.66
4739	202150_s _at	NEDD9	neural precursor cell expressed, developmentally down-regulated 9	2.55
10422	202151_s _at	UBAC1	UBA domain containing 1	-1.37
7392	202152_x _at	USF2	upstream transcription factor 2, c-fos interacting	-1.58
10659	202156_s _at	CUGBP2	CUG triplet repeat, RNA binding protein 2	2.43
10659	202158_s _at	CUGBP2	CUG triplet repeat, RNA binding protein 2	1.99
2193	202159_a _t	FARSA	phenylalanyl-tRNA synthetase, alpha subunit	-1.45
5504	202165_a _t	PPP1R2	protein phosphatase 1, regulatory (inhibitor) subunit 2	1.63
7716	202171_a _t	VEZF1	vascular endothelial zinc finger 1	1.94
7716	202172_a _t	VEZF1	vascular endothelial zinc finger 1	1.47
9766	202181_a	KIAA024	KIAA0247	2.09

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27122	202196_s_at	DKK3	dickkopf homolog 3 (<i>Xenopus laevis</i>)	2.52
10123	202206_at	ARL4C	ADP-ribosylation factor-like 4C	2.61
3703	202223_at	STT3A	STT3, subunit of the oligosaccharyltransferase complex, homolog A (<i>S. cerevisiae</i>)	-2.48
4837	202237_at	NNMT	nicotinamide N-methyltransferase	-1.51
9129	202251_at	PRPF3	PRP3 pre-mRNA processing factor 3 homolog (<i>S. cerevisiae</i>)	1.41
10421	202257_s_at	CD2BP2	CD2 (cytoplasmic tail) binding protein 2	1.27
23219	202271_at	FBXO28	F-box protein 28	-1.95
11313	202292_x_at	LYPLA2	lysophospholipase II	-1.5
65117	202302_s_at	RSRC2	arginine/serine-rich coiled-coil 2	1.65
1277	202310_s_at	COL1A1	collagen, type I, alpha 1	4.09
10277	202317_s_at	UBE4B	ubiquitination factor E4B (UFD2 homolog, yeast)	-1.51
9453	202322_s_at	GGPS1	geranylgeranyl diphosphate synthase 1	1.45
10919	202326_at	EHMT2	euchromatic histone-lysine N-methyltransferase 2	1.3
2171	202345_s_at	FABP5	fatty acid binding protein 5 (psoriasis-associated)	3.9
399979	202359_s_at	SNX19	sorting nexin 19	-1.48
35	202366_at	ACADS	acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain	-1.83
865	202370_s_at	CBFB	core-binding factor, beta subunit	1.99
79921	202371_at	TCEAL4	transcription elongation factor A (SII)-like 4	1.52
3064	202390_s_at	HD	huntingtin (Huntington disease)	-1.41
10409	202391_at	BASP1	brain abundant, membrane attached signal protein 1	1.86
1278	202404_s_at	COL1A2	collagen, type I, alpha 2	3.42
3429	202411_at	IFI27	interferon, alpha-inducible protein 27	21.72
2531	202419_at	FVT1	follicular lymphoma variant translocation 1	-1.9
3321	202421_at	IGSF3	immunoglobulin superfamily, member 3	1.43
1545	202436_s_at	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	3.02
1513	202450_s_at	CTSK	cathepsin K	2.52

10844	202476_s_at	TUBGCP2	tubulin, gamma complex associated protein 2	-1.2
10844	202477_s_at	TUBGCP2	tubulin, gamma complex associated protein 2	-1.27
8932	202485_s_at	MBD2	methyl-CpG binding domain protein 2	-1.28
79065	202492_at	ATG9A	ATG9 autophagy related 9 homolog A (S. cerevisiae)	-1.35
6515	202499_s_at	SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3	3.48
6616	202508_s_at	SNAP25	synaptosomal-associated protein, 25kDa	1.64
7127	202510_s_at	TNFAIP2	tumor necrosis factor, alpha-induced protein 2	2.5
9806	202524_s_at	SPOCK2	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 2	1.84
25949	202553_s_at	SYF2	SYF2 homolog, RNA splicing factor (S. cerevisiae)	1.49
10445	202556_s_at	MCRS1	microspherule protein 1	-1.44
4140	202568_s_at	MARK3	MAP/microtubule affinity-regulating kinase 3	1.5
23484	202594_at	LEPROT L1	leptin receptor overlapping transcript-like 1	1.81
6284	202598_at	S100A13	S100 calcium binding protein A13	2.12
2776	202615_at	GNAQ	guanine nucleotide binding protein (G protein), q polypeptide	1.35
7128	202643_s_at	TNFAIP3	tumor necrosis factor, alpha-induced protein 3	3.71
7128	202644_s_at	TNFAIP3	tumor necrosis factor, alpha-induced protein 3	3.58
9792	202656_s_at	SERTAD2	SERTA domain containing 2	2.07
5699	202659_at	PSMB10	proteasome (prosome, macropain) subunit, beta type, 10	1.82
7922	202667_s_at	SLC39A7	solute carrier family 39 (zinc transporter), member 7	-1.63
5921	202677_at	RASA1	RAS p21 protein activator (GTPase activating protein) 1	1.63
558	202686_s_at	AXL	AXL receptor tyrosine kinase	2.75
1327	202698_x_at	COX4I1	cytochrome c oxidase subunit IV isoform 1	1.25
2331	202709_at	FMOD	fibromodulin	2.48
11142	202732_at	PKIG	protein kinase (cAMP-dependent, catalytic) inhibitor gamma	1.47
8503	202743_at	PIK3R3	phosphoinositide-3-kinase, regulatory subunit 3 (p55, gamma)	2.06
6575	202744_at	SLC20A2	solute carrier family 20 (phosphate transporter), member 2	-1.35
9452	202746_a	ITM2A	integral membrane protein 2A	4.3

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9452	202747_s_at	ITM2A	integral membrane protein 2A	1.84
7485	202749_at	WRB	tryptophan rich basic protein	-1.64
2200	202765_s_at	FBN1	fibrillin 1	1.73
2200	202766_s_at	FBN1	fibrillin 1	2.72
901	202769_at	CCNG2	cyclin G2	2.21
901	202770_s_at	CCNG2	cyclin G2	1.66
5019	202780_at	OXCT1	3-oxoacid CoA transferase 1	1.61
4701	202785_at	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7, 14.5kDa	1.35
27347	202786_at	STK39	serine threonine kinase 39 (STE20/SPS1 homolog, yeast)	2.39
11078	202795_x_at	TRIOBP	TRIO and F-actin binding protein	1.62
3689	202803_s_at	ITGB2	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)	2.2
54838	202808_at	C10orf26	chromosome 10 open reading frame 26	-1.78
5265	202833_s_at	SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	-1.25
2517	202838_at	FUCA1	fucosidase, alpha-L- 1, tissue	1.68
5279	202846_s_at	PIGC	phosphatidylinositol glycan anchor biosynthesis, class C	1.39
2870	202849_x_at	GRK6	G protein-coupled receptor kinase 6	-1.64
3576	202859_x_at	IL8	interleukin 8	6.26
5187	202861_at	PER1	period homolog 1 (Drosophila)	1.86
6672	202864_s_at	SP100	SP100 nuclear antigen	1.62
4938	202869_at	OAS1	2',5'-oligoadenylate synthetase 1, 40/46kDa	3.44
5519	202885_s_at	PPP2R1B	protein phosphatase 2 (formerly 2A), regulatory subunit A, beta isoform	-1.21
54541	202887_s_at	DDIT4	DNA-damage-inducible transcript 4	2.9
1869	2028_s_at	E2F1	E2F transcription factor 1	-1.36
1520	202902_s_at	CTSS	cathepsin S	2.96
7466	202908_at	WFS1	Wolfram syndrome 1 (wolframin)	-1.6
133	202912_at	ADM	adrenomedullin	3.21

25843	202918_s_at	MOBK13	MOB1, Mps One Binder kinase activator-like 3 (yeast)	1.71
5326	202924_s_at	PLAGL2	pleiomorphic adenoma gene-like 2	-1.36
3099	202934_a_t	HK2	hexokinase 2	1.54
713	202953_a_t	C1QB	complement component 1, q subcomponent, B chain	3.03
3059	202957_a_t	HCLS1	hematopoietic cell-specific Lyn substrate 1	2.51
827	202965_s_at	CAPN6	calpain 6	1.38
2192	202995_s_at	FBLN1	fibulin 1	1.89
11075	203000_a_t	STMN2	stathmin-like 2	2.77
11075	203001_s_at	STMN2	stathmin-like 2	3.23
6776	203010_a_t	STAT5A	signal transducer and activator of transcription 5A	-1.28
6147	203012_x_at	RPL23A	ribosomal protein L23a	1.47
11319	203013_a_t	ECD	ecdysoneless homolog (Drosophila)	1.33
9910	203020_a_t	RABGAP1L	RAB GTPase activating protein 1-like	1.8
56951	203024_s_at	C5orf15	chromosome 5 open reading frame 15	1.44
1535	203028_s_at	CYBA	cytochrome b-245, alpha polypeptide	2.65
5796	203038_a_t	PTPRK	protein tyrosine phosphatase, receptor type, K	1.55
22856	203044_a_t	CHSY1	carbohydrate (chondroitin) synthase 1	2.34
11270	203061_s_at	NRM	nurim (nuclear envelope membrane protein)	-1.33
857	203065_s_at	CAV1	caveolin 1, caveolae protein, 22kDa	3.4
244	203074_a_t	ANXA8L2	annexin A8-like 2	1.78
4087	203075_a_t	SMAD2	SMAD family member 2	1.7
7058	203083_a_t	THBS2	thrombospondin 2	2.4
7040	203085_s_at	TGFB1	transforming growth factor, beta 1	2.27
10469	203093_s_at	TIMM44	translocase of inner mitochondrial membrane 44 homolog (yeast)	-1.49
1436	203104_a_t	CSF1R	colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog	2.38
4891	203124_s_at	SLC11A2	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	-2.09

4891	203125_x_at	SLC11A2	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	-1.56
1612	203139_a_t	DAPK1	death-associated protein kinase 1	1.86
3434	203153_a_t	IFIT1	interferon-induced protein with tetratricopeptide repeats 1	9.07
9025	203161_s_at	RNF8	ring finger protein 8	-1.2
10428	203166_a_t	CFDP1	craniofacial development protein 1	1.86
7019	203177_x_at	TFAM	transcription factor A, mitochondrial	-1.74
9770	203185_a_t	RASSF2	Ras association (RalGDS/AF-6) domain family 2	2.01
54987	203197_s_at	C1orf123	chromosome 1 open reading frame 123	1.28
8898	203211_s_at	MTMR2	myotubularin related protein 2	1.76
7088	203221_a_t	TLE1	transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)	1.84
7064	203235_a_t	THOP1	thimet oligopeptidase 1	-1.77
3965	203236_s_at	LGALS9	lectin, galactoside-binding, soluble, 9 (galectin 9)	1.62
4854	203237_s_at	NOTCH3	Notch homolog 3 (Drosophila)	-1.29
7405	203241_a_t	UVRAG	UV radiation resistance associated gene	1.43
2145	203249_a_t	EZH1	enhancer of zeste homolog 1 (Drosophila)	1.69
10263	203252_a_t	CDK2AP2	CDK2-associated protein 2	-1.89
1819	203267_s_at	DRG2	developmentally regulated GTP binding protein 2	-1.34
8439	203269_a_t	NSMAF	neutral sphingomyelinase (N-SMase) activation associated factor	1.61
2632	203282_a_t	GBE1	glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV)	-1.64
9988	203301_s_at	DMTF1	cyclin D binding myb-like transcription factor 1	1.9
1633	203302_a_t	DCK	deoxycytidine kinase	2.63
25805	203304_a_t	BAMBI	BMP and activin membrane-bound inhibitor homolog (Xenopus laevis)	2.55
3257	203309_s_at	HPS1	Hermansky-Pudlak syndrome 1	-1.26
7050	203313_s_at	TGIF1	TGFB-induced factor homeobox 1	2.16
858	203324_s_at	CAV2	caveolin 2	2.28
5797	203329_a_t	PTPRM	protein tyrosine phosphatase, receptor	1.73

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22920	203333_a_t	KIFAP3	kinesin-associated protein 3	1.73
6195	203379_a_t	RPS6KA1	ribosomal protein S6 kinase, 90kDa, polypeptide 1	1.34
6430	203380_x_at	SFRS5	splicing factor, arginine/serine-rich 5	1.57
1606	203385_a_t	DGKA	diacylglycerol kinase, alpha 80kDa	1.59
9882	203386_a_t	TBC1D4	TBC1 domain family, member 4	1.56
2591	203397_s_at	GALNT3	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 3 (GalNAc-T3)	1.88
9823	203404_a_t	ARMCX2	armadillo repeat containing, X-linked 2	1.57
963	203416_a_t	CD53	CD53 molecule	3.71
5947	203423_a_t	RBP1	retinol binding protein 1, cellular	4.11
4311	203435_s_at	MME	membrane metallo-endopeptidase	-2.22
10556	203436_a_t	RPP30	ribonuclease P/MRP 30kDa subunit	1.45
8417	203457_a_t	STX7	syntaxin 7	1.4
1106	203461_a_t	CHD2	chromodomain helicase DNA binding protein 2	-1.22
7162	203476_a_t	TPBG	trophoblast glycoprotein	1.77
6252	203485_a_t	RTN1	reticulon 1	1.53
19	203505_a_t	ABCA1	ATP-binding cassette, sub-family A (ABC1), member 1	-1.94
7133	203508_a_t	TNFRSF1B	tumor necrosis factor receptor superfamily, member 1B	1.83
9973	203522_a_t	CCS	copper chaperone for superoxide dismutase	-1.44
4046	203523_a_t	LSP1	lymphocyte-specific protein 1	1.42
10507	203528_a_t	SEMA4D	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D	1.58
9670	203546_a_t	IPO13	importin 13	-1.32
10712	203550_s_at	C1orf2	chromosome 1 open reading frame 2	-1.39
2212	203561_a_t	FCGR2A	Fc fragment of IgG, low affinity IIa, receptor (CD32)	2.41
60312	203563_a_t	AFAP1	actin filament associated protein 1	1.13

178	203566_s_at	AGL	amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III)	-2.31
8481	203569_s_at	OFD1	oral-facial-digital syndrome 1	2.07
4016	203570_a_t	LOXL1	lysyl oxidase-like 1	2.2
7709	203602_s_at	ZBTB17	zinc finger and BTB domain containing 17	-1.54
9873	203620_s_at	FCHSD2	FCH and double SH3 domains 2	1.78
1374	203633_a_t	CPT1A	carnitine palmitoyltransferase 1A (liver)	2.96
4281	203636_a_t	MID1	midline 1 (Opitz/BBB syndrome)	1.96
2077	203643_a_t	ERF	Ets2 repressor factor	1.67
10544	203650_a_t	PROCR	protein C receptor, endothelial (EPCR)	1.97
9896	203656_a_t	FIG4	FIG4 homolog (S. cerevisiae)	1.41
5577	203680_a_t	PRKAR2B	protein kinase, cAMP-dependent, regulatory, type II, beta	2.17
5311	203688_a_t	PKD2	polycystic kidney disease 2 (autosomal dominant)	1.94
2487	203697_a_t	FRZB	frizzled-related protein	3.17
2487	203698_s_at	FRZB	frizzled-related protein	2.12
9654	203703_s_at	TTLL4	tubulin tyrosine ligase-like family, member 4	-1.33
8324	203705_s_at	FZD7	frizzled homolog 7 (Drosophila)	1.83
5142	203708_a_t	PDE4B	phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila)	2.73
10908	203718_a_t	PNPLA6	patatin-like phospholipase domain containing 6	-1.43
1647	203725_a_t	GADD45A	growth arrest and DNA-damage-inducible, alpha	2.62
3909	203726_s_at	LAMA3	laminin, alpha 3	1.38
2014	203729_a_t	EMP3	epithelial membrane protein 3	2.27
6503	203760_s_at	SLA	Src-like-adaptor	1.94
25802	203766_s_at	LMOD1	leiomodulin 1 (smooth muscle)	1.49
23635	203787_a_t	SSBP2	single-stranded DNA binding protein 2	1.68
3489	203851_a_t	IGFBP6	insulin-like growth factor binding protein 6	2.73
88	203864_s	ACTN2	actinin, alpha 2	-1.26

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54475	203867_s_at	NLE1	notchless homolog 1 (Drosophila)	-1.3
5293	203879_a_t	PIK3CD	phosphoinositide-3-kinase, catalytic, delta polypeptide	1.4
7056	203887_s_at	THBD	thrombomodulin	3.03
27297	203898_a_t	RCP9	calcitonin gene-related peptide-receptor component protein	-1.59
9843	203903_s_at	HEPH	hephaestin	2.09
8671	203908_a_t	SLC4A4	solute carrier family 4, sodium bicarbonate cotransporter, member 4	2.66
4283	203915_a_t	CXCL9	chemokine (C-X-C motif) ligand 9	6.7
6919	203919_a_t	TCEA2	transcription elongation factor A (SII), 2	3.07
9371	203943_a_t	KIF3B	kinesin family member 3B	-1.57
11120	203944_x_at	BTN2A1	butyrophilin, subfamily 2, member A1	1.5
10529	203962_s_at	NEBL	nebulette	1.66
1317	203971_a_t	SLC31A1	solute carrier family 31 (copper transporters), member 1	-2.12
2530	203988_s_at	FUT8	fucosyltransferase 8 (alpha (1,6) fucosyltransferase)	1.45
10681	204000_a_t	GNB5	guanine nucleotide binding protein (G protein), beta 5	1.73
5074	204005_s_at	PAWR	PRKC, apoptosis, WT1, regulator	1.63
1846	204014_a_t	DUSP4	dual specificity phosphatase 4	1.74
1846	204015_s_at	DUSP4	dual specificity phosphatase 4	1.58
3039	204018_x_at	HBA1	hemoglobin, alpha 1	5.55
1902	204036_a_t	EDG2	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2	1.83
9338	204045_a_t	TCEAL1	transcription elongation factor A (SII)-like 1	1.9
5728	204053_x_at	PTEN	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	1.8
4598	204056_s_at	MVK	mevalonate kinase (mevalonic aciduria)	-1.49
3394	204057_a_t	IRF8	interferon regulatory factor 8	2.13
5613	204061_a_t	PRKX	protein kinase, X-linked	1.6
9583	204077_x_at	ENTPD4	ectonucleoside triphosphate diphosphohydrolase 4	-1.41
6351	204103_a	CCL4	chemokine (C-C motif) ligand 4	2.73

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962	204118_a_t	CD48	CD48 molecule	2.97
132	204120_s_at	ADK	adenosine kinase	-2.56
7305	204122_a_t	TYROBP	TYRO protein tyrosine kinase binding protein	3.82
3980	204123_a_t	LIG3	ligase III, DNA, ATP-dependent	-1.27
2309	204132_s_at	FOXO3	forkhead box O3	2.24
10403	204162_a_t	NDC80	NDC80 homolog, kinetochore complex component (<i>S. cerevisiae</i>)	1.34
11117	204163_a_t	EMILIN1	elastin microfibril interfacier 1	2.04
241	204174_a_t	ALOX5A P	arachidonate 5-lipoxygenase-activating protein	2.75
4151	204179_a_t	MB	myoglobin	-1.4
2766	204187_a_t	GMPR	guanosine monophosphate reductase	1.56
951	204192_a_t	CD37	CD37 molecule	2.58
864	204197_s_at	RUNX3	runt-related transcription factor 3	1.77
864	204198_s_at	RUNX3	runt-related transcription factor 3	1.98
5783	204201_s_at	PTPN13	protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase)	2.24
60489	204205_a_t	APOBEC 3G	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3G	3
5130	204209_a_t	PCYT1A	phosphate cytidylyltransferase 1, choline, alpha	-1.42
79161	204215_a_t	C7orf23	chromosome 7 open reading frame 23	2.57
11010	204221_x_at	GLIPR1	GLI pathogenesis-related 1 (glioma)	1.78
11010	204222_s_at	GLIPR1	GLI pathogenesis-related 1 (glioma)	2.58
5549	204223_a_t	PRELP	proline/arginine-rich end leucine-rich repeat protein	2.5
10465	204228_a_t	PPIH	peptidylprolyl isomerase H (cyclophilin H)	1.46
7748	204234_s_at	ZNF195	zinc finger protein 195	1.5
2313	204236_a_t	FLI1	Friend leukemia virus integration 1	1.98
4005	204249_s_at	LMO2	LIM domain only 2 (rhombotin-like 1)	1.65
1017	204252_a_t	CDK2	cyclin-dependent kinase 2	-1.32
9088	204267_x_at	PKMYT1	protein kinase, membrane associated tyrosine/threonine 1	-1.42

11040	204269_a_t	PIM2	pim-2 oncogene	1.33
1910	204271_s_at	EDNRB	endothelin receptor type B	2.69
1910	204273_a_t	EDNRB	endothelin receptor type B	2.52
5698	204279_a_t	PSMB9	proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional peptidase 2)	2.08
5366	204285_s_at	PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1	1.29
5366	204286_s_at	PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1	1.28
9920	204301_a_t	KBTBD1 1	kelch repeat and BTB (POZ) domain containing 11	-1.5
8842	204304_s_at	PROM1	prominin 1	3.95
1385	204312_x_at	CREB1	cAMP responsive element binding protein 1	1.44
1385	204313_s_at	CREB1	cAMP responsive element binding protein 1	1.43
6001	204316_a_t	RGS10	regulator of G-protein signaling 10	1.22
6001	204319_s_at	RGS10	regulator of G-protein signaling 10	3.18
4763	204325_s_at	NF1	neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease)	-1.19
4501	204326_x_at	MT1X	metallothionein IX	-1.99
29957	204342_a_t	SLC25A2 4	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 24	1.9
7188	204352_a_t	TRAF5	TNF receptor-associated factor 5	2.05
6578	204368_a_t	SLCO2A 1	solute carrier organic anion transporter family, member 2A1	1.64
8942	204385_a_t	KYNU	kynureninase (L-kynurenine hydrolase)	-1.6
4128	204388_s_at	MAOA	monoamine oxidase A	-2.38
4128	204389_a_t	MAOA	monoamine oxidase A	-1.98
55	204393_s_at	ACPP	acid phosphatase, prostate	-1.14
2869	204396_s_at	GRK5	G protein-coupled receptor kinase 5	1.89
25807	204402_a_t	RHBDD3	rhomboid domain containing 3	-1.4
6558	204404_a_t	SLC12A2	solute carrier family 12 (sodium/potassium/chloride transporters), member 2	1.71
6518	204429_s_at	SLC2A5	solute carrier family 2 (facilitated glucose/fructose transporter), member 5	-1.4
10964	204439_a	IFI44L	interferon-induced protein 44-like	7.49

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8321	204451_a_t	FZD1	frizzled homolog 1 (Drosophila)	2.59
23641	204454_a_t	LDOC1	leucine zipper, down-regulated in cancer 1	1.51
2619	204457_s_at	GAS1	growth arrest-specific 1	5.63
960	204490_s_at	CD44	CD44 molecule (Indian blood group)	1.89
5144	204491_a_t	PDE4D	phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila)	2.09
115	204498_s_at	ADCY9	adenylate cyclase 9	-1.35
6314	204516_a_t	ATXN7	ataxin 7	2.01
51090	204519_s_at	PLLP	plasma membrane proteolipid (plasmolipin)	1.74
11138	204526_s_at	TBC1D8	TBC1 domain family, member 8 (with GRAM domain)	1.82
3627	204533_a_t	CXCL10	chemokine (C-X-C motif) ligand 10	10.89
2564	204537_s_at	GABRE	gamma-aminobutyric acid (GABA) A receptor, epsilon	1.67
9284	204538_x_at	NPIP	nuclear pore complex interacting protein	1.41
	204552_a_t		NA	1.69
5509	204554_a_t	PPP1R3D	protein phosphatase 1, regulatory (inhibitor) subunit 3D	1.24
22873	204557_s_at	DZIP1	DAZ interacting protein 1	1.32
8438	204558_a_t	RAD54L	RAD54-like (S. cerevisiae)	-1.28
51690	204559_s_at	LSM7	LSM7 homolog, U6 small nuclear RNA associated (S. cerevisiae)	1.49
354	204583_x_at	KLK3	kallikrein-related peptidase 3	-1.22
8927	204586_a_t	BSN	bassoon (presynaptic cytomatrix protein)	-1.19
6781	204595_s_at	STC1	stanniocalcin 1	2.37
6781	204597_x_at	STC1	stanniocalcin 1	2.26
6366	204606_a_t	CCL21	chemokine (C-C motif) ligand 21	5.35
5336	204613_a_t	PLCG2	phospholipase C, gamma 2 (phosphatidylinositol-specific)	1.95
1462	204619_s_at	VCAN	versican	2.26
10495	204643_s_at	ENOX2	ecto-NOX disulfide-thiol exchanger 2	-1.54
6352	204655_a_t	CCL5	chemokine (C-C motif) ligand 5	4.02

1043	204661_a_t	CD52	CD52 molecule	3.71
4053	204682_a_t	LTPB2	latent transforming growth factor beta binding protein 2	1.75
3384	204683_a_t	ICAM2	intercellular adhesion molecule 2	1.59
8910	204688_a_t	SGCE	sarcoglycan, epsilon	2.53
3669	204698_a_t	ISG20	interferon stimulated exonuclease gene 20kDa	3.33
9399	204701_s_at	STOML1	stomatin (EPB72)-like 1	-1.43
9603	204702_s_at	NFE2L3	nuclear factor (erythroid-derived 2)-like 3	1.3
55800	204723_a_t	SCN3B	sodium channel, voltage-gated, type III, beta	-1.19
5141	204735_a_t	PDE4A	phosphodiesterase 4A, cAMP-specific (phosphodiesterase E2 dunce homolog, Drosophila)	1.31
29114	204743_a_t	TAGLN3	transgelin 3	-1.4
4495	204745_x_at	MT1G	metallothionein 1G	-2.67
3437	204747_a_t	IFIT3	interferon-induced protein with tetratricopeptide repeats 3	2.16
9854	204757_s_at	TMEM24	transmembrane protein 24	-1.39
1102	204759_a_t	RCBTB2	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 2	1.97
7984	204765_a_t	ARHGEF5	Rho guanine nucleotide exchange factor (GEF) 5	-1.47
2123	204774_a_t	EVI2A	ecotropic viral integration site 2A	4.66
355	204780_s_at	FAS	Fas (TNF receptor superfamily, member 6)	2.19
355	204781_s_at	FAS	Fas (TNF receptor superfamily, member 6)	1.67
4092	204790_a_t	SMAD7	SMAD family member 7	2.39
1844	204794_a_t	DUSP2	dual specificity phosphatase 2	1.64
3134	204806_x_at	HLA-F	major histocompatibility complex, class I, F	2.13
10384	204820_s_at	BTN3A3	butyrophilin, subfamily 3, member A3	2.52
10384	204821_a_t	BTN3A3	butyrophilin, subfamily 3, member A3	1.88
89795	204823_a_t	NAV3	neuron navigator 3	2.02
2350	204829_s_at	FOLR2	folate receptor 2 (fetal)	1.66
10875	204834_a_t	FGL2	fibrinogen-like 2	4.07

27030	204838_s _at	MLH3	mutL homolog 3 (E. coli)	1.62
10331	204856_a _t	B3GNT3	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3	1.41
8379	204857_a _t	MAD1L1	MAD1 mitotic arrest deficient-like 1 (yeast)	1.75
7357	204881_s _at	UGCG	UDP-glucose ceramide glucosyltransferase	3.16
9938	204882_a _t	ARHGAP25	Rho GTPase activating protein 25	1.72
3932	204891_s _at	LCK	lymphocyte-specific protein tyrosine kinase	1.83
8639	204894_s _at	AOC3	amine oxidase, copper containing 3 (vascular adhesion protein 1)	2.12
5734	204897_a _t	PTGER4	prostaglandin E receptor 4 (subtype EP4)	5.43
8819	204900_x _at	SAP30	Sin3A-associated protein, 30kDa	2
3587	204912_a _t	IL10RA	interleukin 10 receptor, alpha	2.16
662	204930_s _at	BNIP1	BCL2/adenovirus E1B 19kDa interacting protein 1	-1.37
6943	204931_a _t	TCF21	transcription factor 21	1.93
27076	204952_a _t	LYPD3	LY6/PLAUR domain containing 3	-1.3
8406	204955_a _t	SRPX	sushi-repeat-containing protein, X-linked	3.01
5790	204960_a _t	PTPRCA P	protein tyrosine phosphatase, receptor type, C-associated protein	1.42
4939	204972_a _t	OAS2	2'-5'-oligoadenylate synthetase 2, 69/71kDa	2.87
2239	204984_a _t	GPC4	glypican 4	2.46
2244	204988_a _t	FGB	fibrinogen beta chain	-1.34
4600	204994_a _t	MX2	myxovirus (influenza virus) resistance 2 (mouse)	1.85
22809	204998_s _at	ATF5	activating transcription factor 5	-3.4
22809	204999_s _at	ATF5	activating transcription factor 5	-4.49
55922	205004_a _t	NKRF	NF-kappaB repressing factor	-1.28
10124	205020_s _at	ARL4A	ADP-ribosylation factor-like 4A	1.44
1080	205043_a _t	CFTR	cystic fibrosis transmembrane conductance regulator (ATP-binding cassette sub-family C, member 7)	3.82
2568	205044_a _t	GABRP	gamma-aminobutyric acid (GABA) A receptor, pi	2.62
5167	205065_a _t	ENPP1	ectonucleotide pyrophosphatase/phosphodiesterase 1	-1.13
5167	205066_s	ENPP1	ectonucleotide	-2.14

	_at		pyrophosphatase/phosphodiesterase 1	
5345	205075_a_t	SERPINF2	serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 2	-1.93
316	205083_a_t	AOX1	aldehyde oxidase 1	-2.29
5193	205094_a_t	PEX12	peroxisomal biogenesis factor 12	-1.51
2258	205110_s_at	FGF13	fibroblast growth factor 13	1.37
51196	205111_s_at	PLCE1	phospholipase C, epsilon 1	1.24
6348	205114_s_at	CCL3	chemokine (C-C motif) ligand 3	2.14
6443	205120_s_at	SGCB	sarcoglycan, beta (43kDa dystrophin-associated glycoprotein)	2.1
1183	205149_s_at	CLCN4	chloride channel 4	-1.21
958	205153_s_at	CD40	CD40 molecule, TNF receptor superfamily member 5	1.38
965	205173_x_at	CD58	CD58 molecule	2.03
25797	205174_s_at	QPCT	glutaminyl-peptide cyclotransferase (glutaminyl cyclase)	1.29
3795	205175_s_at	KHK	ketohehexokinase (fructokinase)	-1.88
2176	205189_s_at	FANCC	Fanconi anemia, complementation group C	-2.33
9262	205214_a_t	STK17B	serine/threonine kinase 17b	1.93
3556	205227_a_t	IL1RAP	interleukin 1 receptor accessory protein	-2.02
79979	205238_a_t	CXorf34	chromosome X open reading frame 34	-1.48
374	205239_a_t	AREG	amphiregulin (schwannoma-derived growth factor)	3.96
9880	205256_a_t	ZBTB39	zinc finger and BTB domain containing 39	-1.27
97	205260_s_at	ACYP1	acylphosphatase 1, erythrocyte (common) type	1.53
5225	205261_a_t	PGC	progastricsin (pepsinogen C)	-1.41
5450	205267_a_t	POU2AF1	POU class 2 associating factor 1	3.65
3937	205269_a_t	LCP2	lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa)	3.94
3937	205270_s_at	LCP2	lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa)	2.25
8556	205288_a_t	CDC14A	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	1.24
650	205290_s_at	BMP2	bone morphogenetic protein 2	1.52

10458	205293_x _at	BAIAP2	BAI1-associated protein 2	-1.48
6645	205315_s _at	SNTB2	syntrophin, beta 2 (dystrophin-associated protein A1, 59kDa, basic component 2)	1.46
3798	205318_a _t	KIF5A	kinesin family member 5A	-1.43
5816	205336_a _t	PVALB	parvalbumin	-1.23
2593	205354_a _t	GAMT	guanidinoacetate N-methyltransferase	-1.96
9472	205359_a _t	AKAP6	A kinase (PRKA) anchor protein 6	-1.33
10234	205381_a _t	LRRC17	leucine rich repeat containing 17	2.52
26137	205383_s _at	ZBTB20	zinc finger and BTB domain containing 20	1.8
9201	205399_a _t	DCLK1	doublecortin-like kinase 1	1.26
8434	205407_a _t	RECK	reversion-inducing-cysteine-rich protein with kazal motifs	2.44
653	205431_s _at	BMP5	bone morphogenetic protein 5	1.38
22848	205434_s _at	AAK1	AP2 associated kinase 1	1.56
5617	205445_a _t	PRL	prolactin	-1.27
29901	205449_a _t	SAC3D1	SAC3 domain containing 1	-1.74
9957	205466_s _at	HS3ST1	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	1.93
259	205477_s _at	AMBP	alpha-1-microglobulin/bikunin precursor	-1.32
9636	205483_s _at	ISG15	ISG15 ubiquitin-like modifier	7.65
3001	205488_a _t	GZMA	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3)	3.58
2707	205491_s _at	GJB3	gap junction protein, beta 3, 31kDa	-1.18
10570	205492_s _at	DPYSL4	dihydropyrimidinase-like 4	-1.27
55786	205514_a _t	ZNF415	zinc finger protein 415	1.15
8418	205518_s _at	CMAH	cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N-acetylneuraminic acid monooxygenase)	3.06
1404	205524_s _at	HAPLN1	hyaluronan and proteoglycan link protein 1	-1.25
800	205525_a _t	CALD1	caldesmon 1	1.97
862	205528_s _at	RUNX1T1	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	1.24
1004	205532_s _at	CDH6	cadherin 6, type 2, K-cadherin (fetal kidney)	1.4

26872	205542_a_t	STEAP1	six transmembrane epithelial antigen of the prostate 1	-3.8
10950	205548_s_at	BTG3	BTG family, member 3	2.2
4938	205552_s_at	OAS1	2',5'-oligoadenylate synthetase 1, 40/46kDa	2.48
5125	205559_s_at	PCSK5	proprotein convertase subtilisin/kexin type 5	1.29
2687	205582_s_at	GGTLA1	gamma-glutamyltransferase-like activity 1	1.76
79868	205584_a_t	CXorf45	chromosome X open reading frame 45	1.59
6521	205592_a_t	SLC4A1	solute carrier family 4, anion exchanger, member 1 (erythrocyte membrane protein band 3, Diego blood group)	-1.33
64750	205596_s_at	SMURF2	SMAD specific E3 ubiquitin protein ligase 2	2.62
3215	205600_x_at	HOXB5	homeobox B5	-1.51
51760	205613_a_t	SYT17	synaptotagmin XVII	-1.71
79143	205634_x_at	LENG4	leukocyte receptor cluster (LRC) member 4	-1.36
6457	205637_s_at	SH3GL3	SH3-domain GRB2-like 3	-1.43
577	205638_a_t	BAI3	brain-specific angiogenesis inhibitor 3	1.34
221	205640_a_t	ALDH3B1	aldehyde dehydrogenase 3 family, member B1	1.35
11064	205642_a_t	CEP110	centrosomal protein 110kDa	1.27
5521	205643_s_at	PPP2R2B	protein phosphatase 2 (formerly 2A), regulatory subunit B, beta isoform	-1.27
9185	205645_a_t	REPS2	RALBP1 associated Eps domain containing 2	-1.29
2243	205649_s_at	FGA	fibrinogen alpha chain	-1.5
722	205654_a_t	C4BPA	complement component 4 binding protein, alpha	-1.66
8638	205660_a_t	OASL	2'-5'-oligoadenylate synthetase-like	3.18
54039	205663_a_t	PCBP3	poly(rC) binding protein 3	-1.46
4065	205668_a_t	LY75	lymphocyte antigen 75	2.55
55667	205684_s_at	DENND4C	DENN/MADD domain containing 4C	1.66
1271	205723_a_t	CNTFR	ciliary neurotrophic factor receptor	-1.43
5317	205724_a_t	PKP1	plakophilin 1 (ectodermal dysplasia/skin fragility syndrome)	-1.28
2147	205754_a_t	F2	coagulation factor II (thrombin)	-1.67
925	205758_a_t	CD8A	CD8a molecule	2.71

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26085	205783_a_t	KLK13	kallikrein-related peptidase 13	-1.41
3684	205785_a_t	ITGAM	integrin, alpha M (complement component 3 receptor 3 subunit)	-1.24
9877	205788_s_at	ZC3H11A	zinc finger CCCH-type containing 11A	1.46
7220	205802_a_t	TRPC1	transient receptor potential cation channel, subfamily C, member 1	1.42
7220	205803_s_at	TRPC1	transient receptor potential cation channel, subfamily C, member 1	1.44
6002	205823_a_t	RGS12	regulator of G-protein signaling 12	-1.65
25859	205834_s_at	PART1	prostate androgen-regulated transcript 1	-1.29
2688	205840_x_at	GH1	growth hormone 1	-1.23
1384	205843_x_at	CRAT	carnitine acetyltransferase	-1.7
8912	205845_a_t	CACNA1H	calcium channel, voltage-dependent, T type, alpha 1H subunit	-1.38
7381	205849_s_at	UQCRB	ubiquinol-cytochrome c reductase binding protein	1.46
624	205870_a_t	BDKRB2	bradykinin receptor B2	1.88
5342	205871_a_t	PLGLB2	plasminogen-like B2	-1.67
5463	205878_a_t	POU6F1	POU class 6 homeobox 1	1.43
5979	205879_x_at	RET	ret proto-oncogene	-1.56
4958	205907_s_at	OMD	osteomodulin	1.7
10223	205929_a_t	GPA33	glycoprotein A33 (transmembrane)	-1.31
2294	205935_a_t	FOXF1	forkhead box F1	1.36
5166	205960_a_t	PDK4	pyruvate dehydrogenase kinase, isozyme 4	4.87
10538	205965_a_t	BATF	basic leucine zipper transcription factor, ATF-like	1.61
4504	205970_a_t	MT3	metallothionein 3	-1.55
3231	205975_s_at	HOXD1	homeobox D1	-1.24
3600	205992_s_at	IL15	interleukin 15	1.57
10863	205997_a_t	ADAM28	ADAM metallopeptidase domain 28	1.55
3680	206009_a_t	ITGA9	integrin, alpha 9	1.42
834	206011_a_t	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	2.24

7044	206012_a_t	LEFTY2	left-right determination factor 2	-1.25
10461	206028_s_at	MERTK	c-mer proto-oncogene tyrosine kinase	2.42
8926	206042_x_at	SNURF	SNRPN upstream reading frame	2.55
26191	206060_s_at	PTPN22	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)	1.36
5889	206066_s_at	RAD51C	RAD51 homolog C (<i>S. cerevisiae</i>)	1.35
2042	206071_s_at	EPHA3	EPH receptor A3	1.63
1368	206100_a_t	CPM	carboxypeptidase M	2.26
3996	206123_a_t	LLGL1	lethal giant larvae homolog 1 (<i>Drosophila</i>)	-2.26
4163	206132_a_t	MCC	mutated in colorectal cancers	-1.7
5322	206178_a_t	PLA2G5	phospholipase A2, group V	1.54
2689	206195_x_at	GH2	growth hormone 2	-1.3
8382	206197_a_t	NME5	non-metastatic cells 5, protein expressed in (nucleoside-diphosphate kinase)	1.37
311	206200_s_at	ANXA11	annexin A11	1.92
1358	206212_a_t	CPA2	carboxypeptidase A2 (pancreatic)	-1.3
7941	206214_a_t	PLA2G7	phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)	2.33
3780	206231_a_t	KCNN1	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 1	-1.31
9331	206232_s_at	B4GALT6	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6	-1.11
552	206250_x_at	AVPR1A	arginine vasopressin receptor 1A	-1.68
552	206252_s_at	AVPR1A	arginine vasopressin receptor 1A	-1.56
4922	206291_a_t	NTS	neurotensin	2.01
3606	206295_a_t	IL18	interleukin 18 (interferon-gamma-inducing factor)	2.43
11194	206317_s_at	ABCB8	ATP-binding cassette, sub-family B (MDR/TAP), member 8	-1.29
325	206350_a_t	APCS	amyloid P component, serum	-1.69
28234	206354_a_t	SLCO1B3	solute carrier organic anion transporter family, member 1B3	-3.06
6375	206366_x_at	XCL1	chemokine (C motif) ligand 1	1.93
5294	206370_a_t	PIK3CG	phosphoinositide-3-kinase, catalytic, gamma polypeptide	1.15

5918	206392_s _at	RARRES 1	retinoic acid receptor responder (tazarotene induced) 1	2.18
1608	206395_a _t	DGKG	diacylglycerol kinase, gamma 90kDa	-1.14
9623	206413_s _at	TCL1B	T-cell leukemia/lymphoma 1B	-1.29
1044	206430_a _t	CDX1	caudal type homeobox 1	-1.39
6010	206454_s _at	RHO	rhodopsin (opsin 2, rod pigment) (retinitis pigmentosa 4, autosomal dominant)	-1.3
4496	206461_x _at	MT1H	metallothionein 1H	-1.78
4948	206498_a _t	OCA2	oculocutaneous albinism II (pink-eye dilution homolog, mouse)	-1.31
5304	206509_a _t	PIP	prolactin-induced protein	-1.4
946	206520_x _at	SIGLEC6	sialic acid binding Ig-like lectin 6	-1.33
6862	206524_a _t	T	T, brachyury homolog (mouse)	-1.32
57016	206561_s _at	AKR1B1 0	aldo-keto reductase family 1, member B10 (aldose reductase)	8.09
51230	206567_s _at	PHF20	PHD finger protein 20	1.32
23643	206584_a _t	LY96	lymphocyte antigen 96	2.94
1269	206586_a _t	CNR2	cannabinoid receptor 2 (macrophage)	-1.51
23178	206594_a _t	PASK	PAS domain containing serine/threonine kinase	-1.3
9121	206599_a _t	SLC16A5	solute carrier family 16, member 5 (monocarboxylic acid transporter 6)	-1.2
8200	206614_a _t	GDF5	growth differentiation factor 5	-1.35
5961	206625_a _t	PRPH2	peripherin 2 (retinal degeneration, slow)	-1.2
9719	206629_a _t	ADAMT SL2	ADAMTS-like 2	1.87
7299	206630_a _t	TYR	tyrosinase (oculocutaneous albinism IA)	-1.28
5732	206631_a _t	PTGER2	prostaglandin E receptor 2 (subtype EP2), 53kDa	1.55
9934	206637_a _t	P2RY14	purinergic receptor P2Y, G-protein coupled, 14	1.4
3357	206638_a _t	HTR2B	5-hydroxytryptamine (serotonin) receptor 2B	2.18
9522	206668_s _at	SCAMP1	secretory carrier membrane protein 1	1.63
40	206690_a _t	ACCN1	amiloride-sensitive cation channel 1, neuronal (degenerin)	-1.24
5407	206694_a _t	PNLIPRP 1	pancreatic lipase-related protein 1	-1.29
3240	206697_s	HP	haptoglobin	-1.6

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1910	206701_x_at	EDNRB	endothelin receptor type B	2.68
1140	206703_a_t	CHRNA1	cholinergic receptor, nicotinic, beta 1 (muscle)	-1.22
9750	206707_x_at	C6orf32	chromosome 6 open reading frame 32	1.24
23546	206719_a_t	SYNGR4	synaptogyrin 4	-1.21
9170	206723_s_at	EDG4	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 4	1.31
735	206727_a_t	C9	complement component 9	-1.87
432	206743_s_at	ASGR1	asialoglycoprotein receptor 1	-2.01
2572	206780_a_t	GAD2	glutamate decarboxylase 2 (pancreatic islets and brain, 65kDa)	-1.29
2249	206783_a_t	FGF4	fibroblast growth factor 4 (heparin secretory transforming protein 1, Kaposi sarcoma oncogene)	-1.3
9940	206798_x_at	DLEC1	deleted in lung and esophageal cancer 1	-1.41
917	206804_a_t	CD3G	CD3g molecule, gamma (CD3-TCR complex)	1.39
119	206807_s_at	ADD2	adducin 2 (beta)	-1.5
3268	206821_x_at	HRBL	HIV-1 Rev binding protein-like	-1.37
2566	206849_a_t	GABRG2	gamma-aminobutyric acid (GABA) A receptor, gamma 2	-1.2
2788	206896_s_at	GNG7	guanine nucleotide binding protein (G protein), gamma 7	1.39
28513	206898_a_t	CDH19	cadherin 19, type 2	4.91
9023	206932_a_t	CH25H	cholesterol 25-hydroxylase	2.78
8499	206973_a_t	PPFIA2	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2	-1.31
27109	206993_a_t	ATP5S	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit s (factor B)	-1.24
1831	207001_x_at	TSC22D3	TSC22 domain family, member 3	2.54
5325	207002_s_at	PLAGL1	pleiomorphic adenoma gene-like 1	2.16
1144	207024_a_t	CHRNA1	cholinergic receptor, nicotinic, delta	-1.28
10408	207028_a_t	MYCN	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian) opposite strand	-1.19
2694	207033_a_t	GIF	gastric intrinsic factor (vitamin B synthesis)	-1.18

7781	207035_a_t	SLC30A3	solute carrier family 30 (zinc transporter), member 3	-1.35
7068	207044_a_t	THRB	thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian)	-1.3
9119	207065_a_t	KRT75	keratin 75	-1.38
10001	207079_s_at	MED6	mediator complex subunit 6	1.81
1438	207085_x_at	CSF2RA	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)	1.32
5204	207132_x_at	PFDN5	prefoldin subunit 5	1.96
5253	207138_a_t	PHF2	PHD finger protein 2	-1.33
9555	207168_s_at	H2AFY	H2A histone family, member Y	1.53
780	207169_x_at	DDR1	discoidin domain receptor family, member 1	1.59
25875	207170_s_at	LETMD1	LETM1 domain containing 1	1.52
1009	207173_x_at	CDH11	cadherin 11, type 2, OB-cadherin (osteoblast)	2.9
3718	207187_a_t	JAK3	Janus kinase 3 (a protein tyrosine kinase, leukocyte)	-1.42
3671	207191_s_at	ISLR	immunoglobulin superfamily containing leucine-rich repeat	1.5
1089	207205_a_t	CEACAM4	carcinoembryonic antigen-related cell adhesion molecule 4	-1.13
27290	207214_a_t	SPINK4	serine peptidase inhibitor, Kazal type 4	-1.26
2158	207218_a_t	F9	coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B)	-1.55
9002	207221_a_t	F2RL3	coagulation factor II (thrombin) receptor-like 3	-1.17
8399	207222_a_t	PLA2G10	phospholipase A2, group X	-1.26
5788	207238_s_at	PTPRC	protein tyrosine phosphatase, receptor type, C	4.88
3953	207255_a_t	LEPR	leptin receptor	3.07
319	207262_a_t	APOF	apolipoprotein F	-2.59
5937	207266_x_at	RBMS1	RNA binding motif, single stranded interacting protein 1	3.15
6340	207295_a_t	SCNN1G	sodium channel, nonvoltage-gated 1, gamma	-1.14
845	207317_s_at	CASQ2	calsequestrin 2 (cardiac muscle)	-1.51
5858	207330_a_t	PZP	pregnancy-zone protein	-3.63
4923	207360_s	NTSR1	neurotensin receptor 1 (high affinity)	-1.27

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479	207367_a_t	ATP12A	ATPase, H+/K+ transporting, nongastric, alpha polypeptide	-1.35
2811	207389_a_t	GP1BA	glycoprotein Ib (platelet), alpha polypeptide	-1.44
8748	207423_s_at	ADAM20	ADAM metallopeptidase domain 20	-1.27
7101	207443_a_t	NR2E1	nuclear receptor subfamily 2, group E, member 1	-1.18
2994	207459_x_at	GYPB	glycophorin B (MNS blood group)	-1.32
4295	207473_a_t	MLN	motilin	-1.32
11119	207485_x_at	BTN3A1	butyrophilin, subfamily 3, member A1	1.39
7743	207513_s_at	ZNF189	zinc finger protein 189	1.72
7982	207524_a_t	ST7	suppression of tumorigenicity 7	-1.56
3565	207538_a_t	IL4	interleukin 4	-1.32
5394	207541_s_at	EXOSC10	exosome component 10	1.61
11170	207547_s_at	FAM107A	family with sequence similarity 107, member A	1.57
1609	207562_a_t	DGKQ	diacylglycerol kinase, theta 110kDa	-1.26
9473	207571_x_at	C1orf38	chromosome 1 open reading frame 38	1.87
4018	207584_a_t	LPA	lipoprotein, Lp(a)	-4.5
147	207589_a_t	ADRA1B	adrenergic, alpha-1B-, receptor	-1.41
649	207595_s_at	BMP1	bone morphogenetic protein 1	-1.31
9407	207602_a_t	TMPRSS11D	transmembrane protease, serine 11D	-1.45
1390	207630_s_at	CREM	cAMP responsive element modulator	2.52
8928	207644_a_t	FOXH1	forkhead box H1	-1.45
9085	207646_s_at	CDY1	chromodomain protein, Y-linked, 1	-1.3
1821	207648_a_t	DRP2	dystrophin related protein 2	-1.47
3891	207670_a_t	KRT85	keratin 85	-1.35
953	207691_x_at	ENTPD1	ectonucleoside triphosphate diphosphohydrolase 1	1.62
8202	207700_s_at	NCOA3	nuclear receptor coactivator 3	1.96
59344	207708_a_t	ALOXE3	arachidonate lipoxygenase 3	-1.48
5318	207717_s	PKP2	plakophilin 2	-1.93

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4014	207720_a_t	LOR	loricrin	-1.18
1741	207732_s_at	DLG3	discs, large homolog 3 (neuroendocrine-dlg, Drosophila)	1.15
5678	207733_x_at	PSG9	pregnancy specific beta-1-glycoprotein 9	-1.31
10721	207746_a_t	POLQ	polymerase (DNA directed), theta	-1.16
	207748_a_t		NA	-1.39
57343	207753_a_t	ZNF304	zinc finger protein 304	1.43
6524	207771_a_t	SLC5A2	solute carrier family 5 (sodium/glucose cotransporter), member 2	-1.22
1539	207780_a_t	CYLC2	cylicin, basic protein of sperm head cytoskeleton 2	-1.1
5627	207808_s_at	PROS1	protein S (alpha)	-1.58
3399	207826_s_at	ID3	inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	2.33
662	207829_s_at	BNIP1	BCL2/adenovirus E1B 19kDa interacting protein 1	1.43
2192	207834_a_t	FBLN1	fibulin 1	-1.44
22794	207842_s_at	CASC3	cancer susceptibility candidate 3	1.42
1142	207859_s_at	CHRN3	cholinergic receptor, nicotinic, beta 3	-1.18
8913	207869_s_at	CACNA1G	calcium channel, voltage-dependent, T type, alpha 1G subunit	1.08
51350	207878_a_t	KRT76	keratin 76	-1.29
3000	207884_a_t	GUCY2D	guanylate cyclase 2D, membrane (retina-specific)	-1.2
9333	207911_s_at	TGM5	transglutaminase 5	-1.44
417	207919_a_t	ART1	ADP-ribosyltransferase 1	-1.59
1473	207925_a_t	CST5	cystatin D	-1.24
2925	207929_a_t	GRPR	gastrin-releasing peptide receptor	-1.35
7783	207933_a_t	ZP2	zona pellucida glycoprotein 2 (sperm receptor)	-1.23
9584	207941_s_at	RBM39	RNA binding motif protein 39	1.53
1453	207945_s_at	CSNK1D	casein kinase 1, delta	1.73
288	207950_s_at	ANK3	ankyrin 3, node of Ranvier (ankyrin G)	1.41
5579	207957_s_at	PRKCB1	protein kinase C, beta 1	1.52

3441	207964_x _at	IFNA4	interferon, alpha 4	-1.17
23177	207971_s _at	CEP68	centrosomal protein 68kDa	1.25
8013	207978_s _at	NR4A3	nuclear receptor subfamily 4, group A, member 3	1.85
56	207991_x _at	ACRV1	acrosomal vesicle protein 1	-1.15
272	207992_s _at	AMPD3	adenosine monophosphate deaminase (isoform E)	1.44
104	207999_s _at	ADARB1	adenosine deaminase, RNA-specific, B1 (RED1 homolog rat)	-1.33
	208007_a _t		NA	-1.34
3431	208012_x _at	SP110	SP110 nuclear body protein	1.66
56	208013_s _at	ACRV1	acrosomal vesicle protein 1	-1.16
118	208030_s _at	ADD1	adducin 1 (alpha)	1.8
5990	208031_s _at	RFX2	regulatory factor X, 2 (influences HLA class II expression)	-1.44
2916	208035_a _t	GRM6	glutamate receptor, metabotropic 6	-1.26
4607	208040_s _at	MYBPC3	myosin binding protein C, cardiac	-1.42
835	208050_s _at	CASP2	caspase 2, apoptosis-related cysteine peptidase (neural precursor cell expressed, developmentally down- regulated 2)	-1.22
5675	208106_x _at	PSG6	pregnancy specific beta-1-glycoprotein 6	-1.47
554	208108_s _at	AVPR2	arginine vasopressin receptor 2 (nephrogenic diabetes insipidus)	-1.26
5740	208131_s _at	PTGIS	prostaglandin I2 (prostacyclin) synthase	3.38
54504	208146_s _at	CPVL	carboxypeptidase, vitellogenic-like	3.16
4622	208148_a _t	MYH4	myosin, heavy chain 4, skeletal muscle	4.02
11487 6	208158_s _at	OSBPL1 A	oxysterol binding protein-like 1A	1.68
3804	208179_x _at	KIR2DL3	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 3	-1.29
3448	208182_x _at	IFNA14	interferon, alpha 14	-1.2
	208187_s _at		NA	-1.19
3857	208188_a _t	KRT9	keratin 9 (epidermolytic palmoplantar keratoderma)	-1.42
51599	208190_s _at	LSR	lipolysis stimulated lipoprotein receptor	-1.5
859	208204_s _at	CAV3	caveolin 3	-1.31

238	208211_s _at	ALK	anaplastic lymphoma kinase (Ki-1)	-1.14
3211	208224_a _t	HOXB1	homeobox B1	-1.54
53616	208226_x _at	ADAM22	ADAM metallopeptidase domain 22	-1.21
53616	208227_x _at	ADAM22	ADAM metallopeptidase domain 22	-1.29
53616	208237_x _at	ADAM22	ADAM metallopeptidase domain 22	-1.26
3444	208259_x _at	IFNA7	interferon, alpha 7	-1.16
37428 6	208279_s _at	CDRT1	CMT1A duplicated region transcript 1	-1.39
26659	208285_a _t	OR7A5	olfactory receptor, family 7, subfamily A, member 5	-1.45
27302	208292_a _t	BMP10	bone morphogenetic protein 10	-1.2
25816	208296_x _at	TNFAIP8	tumor necrosis factor, alpha-induced protein 8	3.08
9942	208318_s _at	XYLB	xylulokinase homolog (H. influenzae)	-1.41
312	208323_s _at	ANXA13	annexin A13	2.49
11214	208325_s _at	AKAP13	A kinase (PRKA) anchor protein 13	1.68
64579	208334_a _t	NDST4	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4	-1.17
11043	208384_s _at	MID2	midline 2	-1.39
2740	208391_s _at	GLP1R	glucagon-like peptide 1 receptor	-1.15
5136	208396_s _at	PDE1A	phosphodiesterase 1A, calmodulin- dependent	2.04
1500	208407_s _at	CTNND1	catenin (cadherin-associated protein), delta 1	1.72
7275	208431_s _at	TUB	tubby homolog (mouse)	-1.22
3957	208450_a _t	LGALS2	lectin, galactoside-binding, soluble, 2	2.18
10052	208460_a _t	GJA7	gap junction protein, alpha 7, 45kDa	-1.34
3250	208471_a _t	HPR	haptoglobin-related protein	-3.01
3736	208479_a _t	KCNA1	potassium voltage-gated channel, shaker-related subfamily, member 1 (episodic ataxia with myokymia)	-1.24
1816	208486_a _t	DRD5	dopamine receptor D5	-1.35
26532	208520_a _t	OR10H3	olfactory receptor, family 10, subfamily H, member 3	-1.27
2838	208524_a _t	GPR15	G protein-coupled receptor 15	-1.32

390502	208531_a_t	SERPINA2	serpin peptidase inhibitor, clade A (alpha-1 antitrypsin), member 2	-1.37
57830	208532_x_at	KRTAP5-8	keratin associated protein 5-8	-1.55
729659	208540_x_at	LOC729659	similar to Putative S100 calcium-binding protein A11 pseudogene	1.78
3008	208553_a_t	HIST1H1E	histone cluster 1, H1e	-1.14
4161	208565_a_t	MC5R	melanocortin 5 receptor	-1.33
6336	208578_a_t	SCN10A	sodium channel, voltage-gated, type X, alpha subunit	-1.35
59347	208588_a_t	FKSG2	apoptosis inhibitor	-1.2
1270	208597_a_t	CNTF	ciliary neurotrophic factor	-1.32
7148	208609_s_at	TNXB	tenascin XB	1.44
7430	208621_s_at	VIL2	villin 2 (ezrin)	2.29
7430	208622_s_at	VIL2	villin 2 (ezrin)	2.25
23499	208634_s_at	MACF1	microtubule-actin crosslinking factor 1	1.68
5879	208640_a_t	RAC1	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	1.34
5879	208641_s_at	RAC1	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	1.59
6208	208646_a_t	RPS14	ribosomal protein S14	1.41
934	208651_x_at	CD24	CD24 molecule	3.74
3151	208668_x_at	HMG2	high-mobility group nucleosomal binding domain 2	1.79
529	208678_a_t	ATP6V1E1	ATPase, H ⁺ transporting, lysosomal 31kDa, V1 subunit E1	1.55
10109	208679_s_at	ARPC2	actin related protein 2/3 complex, subunit 2, 34kDa	1.73
10916	208682_s_at	MAGED2	melanoma antigen family D, 2	1.69
6046	208686_s_at	BRD2	bromodomain containing 2	1.35
9124	208690_s_at	PDLIM1	PDZ and LIM domain 1 (elfin)	1.69
3646	208697_s_at	EIF3E	eukaryotic translation initiation factor 3, subunit E	1.65
10521	208718_a_t	DDX17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	1.83
8894	208725_a_t	EIF2S2	eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa	-1.45
998	208728_s	CDC42	cell division cycle 42 (GTP binding)	1.47

	_at		protein, 25kDa)	
3106	208729_x_at	HLA-B	major histocompatibility complex, class I, B	2.75
10106	208735_s_at	CTDSP2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2	-1.48
10284	208742_s_at	SAP18	Sin3A-associated protein, 18kDa	1.55
1979	208769_a_t	EIF4EBP2	eukaryotic translation initiation factor 4E binding protein 2	-1.42
11167	208782_a_t	FSTL1	follistatin-like 1	2.92
23015	208798_x_at	GOLGA8A	golgi autoantigen, golgin subfamily a, 8A	2.35
3148	208808_s_at	HMGB2	high-mobility group box 2	3.07
3107	208812_x_at	HLA-C	major histocompatibility complex, class I, C	1.87
304	208816_x_at	ANXA2P2	annexin A2 pseudogene 2	1.63
6147	208825_x_at	RPL23A	ribosomal protein L23a	1.47
6147	208834_x_at	RPL23A	ribosomal protein L23a	1.37
8428	208854_s_at	STK24	serine/threonine kinase 24 (STE20 homolog, yeast)	1.77
8428	208855_s_at	STK24	serine/threonine kinase 24 (STE20 homolog, yeast)	2.13
546	208861_s_at	ATRX	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)	1.52
5062	208876_s_at	PAK2	p21 (CDKN1A)-activated kinase 2	-1.34
5062	208877_a_t	PAK2	p21 (CDKN1A)-activated kinase 2	-1.77
23062	208915_s_at	GGA2	golgi associated, gamma adaptin ear containing, ARF binding protein 2	-1.38
10482	208922_s_at	NXF1	nuclear RNA export factor 1	2.11
56650	208925_a_t	CLDND1	claudin domain containing 1	2.06
7048	208944_a_t	TGFBR2	transforming growth factor, beta receptor II (70/80kDa)	2.03
1397	208978_a_t	CRIP2	cysteine-rich protein 2	1.78
7316	208980_s_at	UBC	ubiquitin C	1.34
5175	208981_a_t	PECAM1	platelet/endothelial cell adhesion molecule (CD31 antigen)	2.61
5175	208982_a_t	PECAM1	platelet/endothelial cell adhesion molecule (CD31 antigen)	2.79
5175	208983_s_at	PECAM1	platelet/endothelial cell adhesion molecule (CD31 antigen)	3.25

7351	208998_a_t	UCP2	uncoupling protein 2 (mitochondrial, proton carrier)	2.52
23176	208999_a_t	8-Sep	septin 8	1.58
57035	209006_s_at	C1orf63	chromosome 1 open reading frame 63	2.9
57035	209007_s_at	C1orf63	chromosome 1 open reading frame 63	2.91
3856	209008_x_at	KRT8	keratin 8	1.55
51526	209020_a_t	C20orf111	chromosome 20 open reading frame 111	1.64
10735	209022_a_t	STAG2	stromal antigen 2	1.55
23705	209030_s_at	CADM1	cell adhesion molecule 1	1.71
9061	209043_a_t	PAPSS1	3'-phosphoadenosine 5'-phosphosulfate synthase 1	1.62
23613	209048_s_at	ZMYND8	zinc finger, MYND-type containing 8	1.94
7381	209066_x_at	UQCRB	ubiquinol-cytochrome c reductase binding protein	1.46
8490	209070_s_at	RGS5	regulator of G-protein signaling 5	2.37
8490	209071_s_at	RGS5	regulator of G-protein signaling 5	2.49
11170	209074_s_at	FAM107A	family with sequence similarity 107, member A	2.12
23479	209075_s_at	ISCU	iron-sulfur cluster scaffold homolog (E. coli)	1.43
11151	209083_a_t	CORO1A	coronin, actin binding protein, 1A	2.26
26959	209102_s_at	HBP1	HMG-box transcription factor 1	1.51
5863	209110_s_at	RGL2	ral guanine nucleotide dissociation stimulator-like 2	1.68
10103	209114_a_t	TSPAN1	tetraspanin 1	-1.41
3043	209116_x_at	HBB	hemoglobin, beta	8.01
54939	209133_s_at	COMMD4	COMM domain containing 4	-1.23
8575	209139_s_at	PRKRA	protein kinase, interferon-inducible double stranded RNA dependent activator	1.46
3106	209140_x_at	HLA-B	major histocompatibility complex, class I, B	2.25
9139	209145_s_at	CBFA2T2	core-binding factor, runt domain, alpha subunit 2; translocated to, 2	-1.18
30851	209154_a_t	TAX1BP3	Tax1 (human T-cell leukemia virus type I) binding protein 3	2.32
1292	209156_s_at	COL6A2	collagen, type VI, alpha 2	2.93
11067	209182_s	C10orf10	chromosome 10 open reading frame 10	3.21

	_at			
8660	209184_s_at	IRS2	insulin receptor substrate 2	1.66
84617	209191_at	TUBB6	tubulin, beta 6	3.14
5292	209193_at	PIM1	pim-1 oncogene	-1.81
4208	209199_s_at	MEF2C	myocyte enhancer factor 2C	2.45
4208	209200_at	MEF2C	myocyte enhancer factor 2C	1.87
688	209211_at	KLF5	Kruppel-like factor 5 (intestinal)	1.6
688	209212_s_at	KLF5	Kruppel-like factor 5 (intestinal)	1.71
7991	209228_x_at	TUSC3	tumor suppressor candidate 3	1.81
8473	209240_at	OGT	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	1.99
2810	209260_at	SFN	stratifin	-1.32
7106	209263_x_at	TSPAN4	tetraspanin 4	1.88
56339	209265_s_at	METTL3	methyltransferase like 3	1.59
81689	209273_s_at	ISCA1	iron-sulfur cluster assembly 1 homolog (S. cerevisiae)	1.48
10602	209288_s_at	CDC42EP3	CDC42 effector protein (Rho GTPase binding) 3	3.13
3400	209292_at	ID4	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	4
23075	209306_s_at	SWAP70	SWAP-70 protein	2.82
23075	209307_at	SWAP70	SWAP-70 protein	1.91
5325	209318_x_at	PLAGL1	pleiomorphic adenoma gene-like 1	2.1
109	209320_at	ADCY3	adenylate cyclase 3	1.23
109	209321_s_at	ADCY3	adenylate cyclase 3	1.23
7171	209344_at	TPM4	tropomyosin 4	2.43
30008	209356_x_at	EFEMP2	EGF-containing fibulin-like extracellular matrix protein 2	2.2
57060	209361_s_at	PCBP4	poly(rC) binding protein 4	1.36
1893	209365_s_at	ECM1	extracellular matrix protein 1	1.7
306	209369_at	ANXA3	annexin A3	5.32
3507	209374_s	IGHM	immunoglobulin heavy constant mu	7.68

	_at			
4071	209386_a_t	TM4SF1	transmembrane 4 L six family member 1	2.91
4071	209387_s_at	TM4SF1	transmembrane 4 L six family member 1	2.99
1622	209389_x_at	DBI	diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein)	-1.66
51343	209415_a_t	FZR1	fizzy/cell division cycle 20 related 1 (Drosophila)	-1.4
3430	209417_s_at	IFI35	interferon-induced protein 35	1.87
51230	209422_a_t	PHF20	PHD finger protein 20	2.03
7542	209428_s_at	ZFPL1	zinc finger protein-like 1	-1.52
10418	209436_a_t	SPON1	spondin 1, extracellular matrix protein	2.15
3039	209458_x_at	HBA1	hemoglobin, alpha 1	6.16
18	209459_s_at	ABAT	4-aminobutyrate aminotransferase	-1.86
18	209460_a_t	ABAT	4-aminobutyrate aminotransferase	-2.03
5764	209465_x_at	PTN	pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1)	2.06
5764	209466_x_at	PTN	pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1)	1.38
2823	209469_a_t	GPM6A	glycoprotein M6A	3.75
2823	209470_s_at	GPM6A	glycoprotein M6A	2.87
	209473_a_t		NA	1.44
953	209474_s_at	ENTPD1	ectonucleoside triphosphate diphosphohydrolase 1	1.83
54861	209481_a_t	SNRK	SNF related kinase	2.04
58473	209504_s_at	PLEKHB1	pleckstrin homology domain containing, family B (evectins) member 1	1.44
7025	209505_a_t	NR2F1	nuclear receptor subfamily 2, group F, member 1	2.21
50810	209524_a_t	HDGFRP3	hepatoma-derived growth factor, related protein 3	2.37
50810	209526_s_at	HDGFRP3	hepatoma-derived growth factor, related protein 3	1.36
8612	209529_a_t	PPAP2C	phosphatidic acid phosphatase type 2C	1.68
11214	209534_x_at	AKAP13	A kinase (PRKA) anchor protein 13	1.91
30844	209536_s_at	EHD4	EH-domain containing 4	1.59

9459	209539_a_t	ARHGEF6	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	2.1
8767	209545_s_at	RIPK2	receptor-interacting serine-threonine kinase 2	1.65
4692	209550_a_t	NDN	neccin homolog (mouse)	1.98
23179	209568_s_at	RGL1	ral guanine nucleotide dissociation stimulator-like 1	1.7
27350	209584_x_at	APOBEC3C	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3C	1.34
5678	209594_x_at	PSG9	pregnancy specific beta-1-glycoprotein 9	-1.37
10687	209598_a_t	PNMA2	paraneoplastic antigen MA2	1.45
2625	209604_s_at	GATA3	GATA binding protein 3	1.32
1501	209617_s_at	CTNND2	catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein)	1.17
26031	209626_s_at	OSBPL3	oxysterol binding protein-like 3	1.5
6002	209639_s_at	RGS12	regulator of G-protein signaling 12	-1.33
7041	209651_a_t	TGFB1I1	transforming growth factor beta 1 induced transcript 1	2.45
83604	209656_s_at	TMEM47	transmembrane protein 47	1.76
28755	209670_a_t	TRAC	T cell receptor alpha constant	2.74
868	209682_a_t	CBLB	Cas-Br-M (murine) ecotropic retroviral transforming sequence b	3.01
81553	209683_a_t	FAM49A	family with sequence similarity 49, member A	1.51
5579	209685_s_at	PRKCB1	protein kinase C, beta 1	2.04
27340	209725_a_t	UTP20	UTP20, small subunit (SSU) processome component, homolog (yeast)	-1.42
9976	209732_a_t	CLEC2B	C-type lectin domain family 2, member B	3.05
9975	209750_a_t	NR1D2	nuclear receptor subfamily 1, group D, member 2	2.77
10597	209751_s_at	SEDLP	spondyloepiphyseal dysplasia, late, pseudogene	2
3431	209761_s_at	SP110	SP110 nuclear body protein	2.33
3431	209762_x_at	SP110	SP110 nuclear body protein	1.92
91851	209763_a_t	CHRDL1	chordin-like 1	1.84
11119	209770_a_t	BTN3A1	butyrophilin, subfamily 3, member A1	2.03
6573	209777_s_at	SLC19A1	solute carrier family 19 (folate transporter), member 1	-1.65
10473	209787_s	HMGNA4	high mobility group nucleosomal	1.98

	_at		binding domain 4	
9937	209804_a_t	DCLRE1A	DNA cross-link repair 1A (PSO2 homolog, <i>S. cerevisiae</i>)	-1.37
6983	209813_x_at	TRGV9	T cell receptor gamma variable 9	1.53
5727	209815_a_t	PTCH1	patched homolog 1 (<i>Drosophila</i>)	1.6
3119	209823_x_at	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1	3.64
960	209835_x_at	CD44	CD44 molecule (Indian blood group)	1.8
11118	209846_s_at	BTN3A2	butyrophilin, subfamily 3, member A2	2.47
5937	209868_s_at	RBMS1	RNA binding motif, single stranded interacting protein 1	3.29
150	209869_a_t	ADRA2A	adrenergic, alpha-2A-, receptor	1.75
54805	209874_x_at	CNNM2	cyclin M2	-1.32
6404	209879_a_t	SELPLG	selectin P ligand	1.38
6016	209882_a_t	RIT1	Ras-like without CAAX 1	1.49
2526	209892_a_t	FUT4	fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)	1.64
9353	209897_s_at	SLIT2	slit homolog 2 (<i>Drosophila</i>)	1.81
199	209901_x_at	AIF1	allograft inflammatory factor 1	2.29
719	209906_a_t	C3AR1	complement component 3a receptor 1	1.86
11314	209933_s_at	CD300A	CD300a molecule	1.68
7424	209946_a_t	VEGFC	vascular endothelial growth factor C	1.84
9898	209947_a_t	UBAP2L	ubiquitin associated protein 2-like	-1.3
2191	209955_s_at	FAP	fibroblast activation protein, alpha	1.97
6772	209969_s_at	STAT1	signal transducer and activator of transcription 1, 91kDa	2.68
834	209970_x_at	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	2.26
5243	209993_a_t	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP), member 1	1.56
5243	209994_s_at	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP), member 1	1.97
3263	210013_a_t	HPX	hemopexin	-1.68
9576	210033_s_at	SPAG6	sperm associated antigen 6	-1.14

7881	210079_x_at	KCNAB1	potassium voltage-gated channel, shaker-related subfamily, beta member 1	-1.28
10136	210080_x_at	ELA3A	elastase 3A, pancreatic	-1.4
7177	210084_x_at	TPSAB1	tryptase alpha/beta 1	2.46
4635	210088_x_at	MYL4	myosin, light chain 4, alkali; atrial, embryonic	-1.27
3486	210095_s_at	IGFBP3	insulin-like growth factor binding protein 3	2.19
2534	210105_s_at	FYN	FYN oncogene related to SRC, FGR, YES	2.38
27099	210109_a_t	C7orf54	chromosome 7 open reading frame 54	-1.52
26140	210129_s_at	TTL3	tubulin tyrosine ligase-like family, member 3	1.43
6474	210134_x_at	SHOX2	short stature homeobox 2	-1.27
8530	210140_a_t	CST7	cystatin F (leukocystatin)	1.88
5321	210145_a_t	PLA2G4A	phospholipase A2, group IVA (cytosolic, calcium-dependent)	1.66
4653	210155_a_t	MYOC	myocilin, trabecular meshwork inducible glucocorticoid response	-1.29
4772	210162_s_at	NFATC1	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1	1.55
3002	210164_a_t	GZMB	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)	1.35
9717	210169_a_t	SEC14L5	SEC14-like 5 (S. cerevisiae)	-1.17
27295	210170_a_t	PDLIM3	PDZ and LIM domain 3	1.75
2494	210174_a_t	NR5A2	nuclear receptor subfamily 5, group A, member 2	-1.93
4850	210203_a_t	CNOT4	CCR4-NOT transcription complex, subunit 4	1.14
7036	210215_a_t	TFR2	transferrin receptor 2	-1.91
6672	210218_s_at	SP100	SP100 nuclear antigen	2.02
25816	210260_s_at	TNFAIP8	tumor necrosis factor, alpha-induced protein 8	2.83
11078	210276_s_at	TRIOBP	TRIO and F-actin binding protein	1.75
10605	210283_x_at	PAIP1	poly(A) binding protein interacting protein 1	-1.48
2273	210298_x_at	FHL1	four and a half LIM domains 1	1.82
2273	210299_s_at	FHL1	four and a half LIM domains 1	2.48
2250	210311_a_t	FGF5	fibroblast growth factor 5	-1.23
3817	210339_s_at	KLK2	kallikrein-related peptidase 2	-1.55

1438	210340_s_at	CSF2RA	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)	1.39
1770	210345_s_at	DNAH9	dynein, axonemal, heavy chain 9	-1.25
2002	210376_x_at	ELK1	ELK1, member of ETS oncogene family	-1.41
8549	210393_a_t	LGR5	leucine-rich repeat-containing G protein-coupled receptor 5	-1.16
4635	210395_x_at	MYL4	myosin, light chain 4, alkali; atrial, embryonic	-1.27
2528	210399_x_at	FUT6	fucosyltransferase 6 (alpha (1,3) fucosyltransferase)	-1.42
2905	210400_a_t	GRIN2C	glutamate receptor, ionotropic, N-methyl D-aspartate 2C	-1.19
440270	210425_x_at	GOLGA8B	golgi autoantigen, golgin subfamily a, 8B	2.06
6007	210430_x_at	RHD	Rh blood group, D antigen	-1.39
6738	210438_x_at	TROVE2	TROVE domain family, member 2	1.46
4111	210467_x_at	MAGEA12	melanoma antigen family A, 12	-1.15
166647	210473_s_at	GPR125	G protein-coupled receptor 125	-2.67
5618	210476_s_at	PRLR	prolactin receptor	-1.33
3135	210514_x_at	HLA-G	HLA-G histocompatibility antigen, class I, G	1.76
	210524_x_at		NA	-2.4
7278	210527_x_at	TUBA3C	tubulin, alpha 3c	-1.53
1488	210554_s_at	CTBP2	C-terminal binding protein 2	1.94
26118	210561_s_at	WSB1	WD repeat and SOCS box-containing 1	2.02
2642	210565_a_t	GCGR	glucagon receptor	-1.58
6007	210586_x_at	RHD	Rh blood group, D antigen	-1.32
1837	210611_s_at	DTNA	dystrobrevin, alpha	1.12
5251	210617_a_t	PHEX	phosphate regulating endopeptidase homolog, X-linked (hypophosphatemia, vitamin D resistant rickets)	-1.26
27252	210635_s_at	KLHL20	kelch-like 20 (Drosophila)	1.45
2852	210640_s_at	GPER	G protein-coupled estrogen receptor 1	-2.11
5414	210657_s_at	4-Sep	septin 4	1.83
8302	210690_a_t	KLRC4	killer cell lectin-like receptor subfamily C, member 4	1.06

51741	210695_s _at	WWOX	WW domain containing oxidoreductase	-1.4
	210717_a _t		NA	1.44
4149	210734_x _at	MAX	MYC associated factor X	1.42
8671	210738_s _at	SLC4A4	solute carrier family 4, sodium bicarbonate cotransporter, member 4	1.56
9321	210760_x _at	TRIP11	thyroid hormone receptor interactor 11	-1.27
9473	210785_s _at	C1orf38	chromosome 1 open reading frame 38	2.54
946	210796_x _at	SIGLEC6	sialic acid binding Ig-like lectin 6	-1.28
10587	210803_a _t	TXNRD2	thioredoxin reductase 2	-1.27
6546	210804_x _at	SLC8A1	solute carrier family 8 (sodium/calcium exchanger), member 1	-1.18
10241	210817_s _at	CALCOCO2	calcium binding and coiled-coil domain 2	1.37
5733	210832_x _at	PTGER3	prostaglandin E receptor 3 (subtype EP3)	-1.25
8826	210840_s _at	IQGAP1	IQ motif containing GTPase activating protein 1	1.95
27072	210849_s _at	VPS41	vacuolar protein sorting 41 homolog (S. cerevisiae)	1.44
3077	210864_x _at	HFE	hemochromatosis	-1.35
1949	210883_x _at	EFNB3	ephrin-B3	-1.4
3697	210888_s _at	ITIH1	inter-alpha (globulin) inhibitor H1	-2.03
960	210916_s _at	CD44	CD44 molecule (Indian blood group)	1.32
10439	210924_a _t	OLFM1	olfactomedin 1	-1.48
25998	210970_s _at	IBTK	inhibitor of Bruton agammaglobulinemia tyrosine kinase	-2.38
5213	210976_s _at	PFKM	phosphofructokinase, muscle	1.75
427	210980_s _at	ASAH1	N-acylsphingosine amidohydrolase (acid ceramidase) 1	1.54
7168	210987_x _at	TPM1	tropomyosin 1 (alpha)	2.56
9783	210991_s _at	RIMS3	regulating synaptic membrane exocytosis 3	-1.29
5162	211023_a _t	PDHB	pyruvate dehydrogenase (lipoamide) beta	-1.41
2137	211051_s _at	EXTL3	exostosin (multiple)-like 3	-1.42
253725	211068_x _at	FAM21C	family with sequence similarity 21, member C	2.1
6122	211073_x _at	RPL3	ribosomal protein L3	1.37

11183	211081_s_at	MAP4K5	mitogen-activated protein kinase kinase kinase kinase 5	1.22
6789	211085_s_at	STK4	serine/threonine kinase 4	1.63
6528	211123_a_t	SLC5A5	solute carrier family 5 (sodium iodide symporter), member 5	-1.71
7066	211154_a_t	THPO	thrombopoietin (myeloproliferative leukemia virus oncogene ligand, megakaryocyte growth and development factor)	-1.24
1281	211161_s_at	COL3A1	collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant)	2.74
84641	211185_s_at	HIATL1	hippocampus abundant transcript-like 1	1.63
2492	211201_a_t	FSHR	follicle stimulating hormone receptor	-1.19
8756	211238_a_t	ADAM7	ADAM metallopeptidase domain 7	-1.2
6005	211254_x_at	RHAG	Rh-associated glycoprotein	-1.28
8021	211261_a_t	NUP214	nucleoporin 214kDa	-1.42
5046	211262_a_t	PCSK6	proprotein convertase subtilisin/kexin type 6	-1.64
2896	211284_s_at	GRN	granulin	1.61
7316	211296_x_at	UBC	ubiquitin C	1.31
10076	211320_s_at	PTPRU	protein tyrosine phosphatase, receptor type, U	-1.33
3077	211328_x_at	HFE	hemochromatosis	-1.28
3702	211339_s_at	ITK	IL2-inducible T-cell kinase	3.9
4162	211340_s_at	MCAM	melanoma cell adhesion molecule	2.16
3953	211354_s_at	LEPR	leptin receptor	4.08
3953	211355_x_at	LEPR	leptin receptor	3.72
3953	211356_x_at	LEPR	leptin receptor	3.92
834	211366_x_at	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	2.46
834	211367_s_at	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	2.87
10407	211381_x_at	SPAG11B	sperm associated antigen 11B	-1.29
	211388_s_at		NA	-1.18

2263	211401_s_at	FGFR2	fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer syndrome, Jackson-Weiss syndrome)	2.24
3451	211405_x_at	IFNA17	interferon, alpha 17	-1.33
5265	211429_s_at	SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	-1.19
80256	211433_x_at	KIAA1539	KIAA1539	-1.33
7201	211438_at	TRHR	thyrotropin-releasing hormone receptor	-1.53
84227	211446_at	RGSL2	regulator of G-protein signaling like 2	-1.25
645745	211456_x_at	MT1P2	metallothionein 1 pseudogene 2	-1.48
23654	211472_at	PLXNB2	plexin B2	-1.26
5269	211474_s_at	SERPINB6	serpin peptidase inhibitor, clade B (ovalbumin), member 6	1.41
4824	211497_x_at	NKX3-1	NK3 homeobox 1	-1.31
9475	211504_x_at	ROCK2	Rho-associated, coiled-coil containing protein kinase 2	-1.34
3576	211506_s_at	IL8	interleukin 8	3.82
3135	211528_x_at	HLA-G	HLA-G histocompatibility antigen, class I, G	1.82
3135	211529_x_at	HLA-G	HLA-G histocompatibility antigen, class I, G	1.94
3135	211530_x_at	HLA-G	HLA-G histocompatibility antigen, class I, G	1.43
2260	211535_s_at	FGFR1	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome)	1.59
2692	211544_s_at	GHRHR	growth hormone releasing hormone receptor	-1.41
2983	211555_s_at	GUCY1B3	guanylate cyclase 1, soluble, beta 3	1.72
901	211559_s_at	CCNG2	cyclin G2	1.6
1462	211571_s_at	VCAN	versican	2.6
1136	211587_x_at	CHRNA3	cholinergic receptor, nicotinic, alpha 3	-1.37
84525	211597_s_at	HOP	homeodomain-only protein	1.75
367	211621_at	AR	androgen receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease)	-1.89

2683	211631_x_at	B4GALT1	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 1	-1.45
3500	211633_x_at	IGHG1	immunoglobulin heavy constant gamma 1 (G1m marker)	3.47
28461	211634_x_at	IGHV1-69	immunoglobulin heavy variable 1-69	4.77
28461	211635_x_at	IGHV1-69	immunoglobulin heavy variable 1-69	3.03
652128	211637_x_at	LOC652128	similar to Ig heavy chain V-II region ARH-77 precursor	5.07
8935	211639_x_at	SKAP2	src kinase associated phosphoprotein 2	3.02
28461	211640_x_at	IGHV1-69	immunoglobulin heavy variable 1-69	2.69
	211641_x_at		NA	1.65
3514	211643_x_at	IGKC	immunoglobulin kappa constant	5.3
3514	211644_x_at	IGKC	immunoglobulin kappa constant	16.04
3500	211647_x_at	IGHG1	immunoglobulin heavy constant gamma 1 (G1m marker)	1.31
3500	211649_x_at	IGHG1	immunoglobulin heavy constant gamma 1 (G1m marker)	2.22
3576	211650_x_at	IL8	interleukin 8	2.99
7001	211658_a_t	PRDX2	peroxiredoxin 2	-1.31
7417	211662_s_at	VDAC2	voltage-dependent anion channel 2	1.72
5730	211663_x_at	PTGDS	prostaglandin D2 synthase 21kDa (brain)	3.35
2908	211671_s_at	NR3C1	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	1.55
1781	211684_s_at	DYNC1I2	dynein, cytoplasmic 1, intermediate chain 2	1.87
3043	211696_x_at	HBB	hemoglobin, beta	6.06
3039	211699_x_at	HBA1	hemoglobin, alpha 1	5.78
83941	211703_s_at	TM2D1	TM2 domain containing 1	1.6
474343	211704_s_at	SPIN2B	spindlin family, member 2B	1.24
644	211729_x_at	BLVRA	biliverdin reductase A	2.39
2205	211734_s_at	FCER1A	Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide	2.24
5764	211737_x_at	PTN	pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1)	1.93
10136	211738_x_at	ELA3A	elastase 3A, pancreatic	-1.3

2124	211742_s_at	EVI2B	ecotropic viral integration site 2B	2.98
3040	211745_x_at	HBA2	hemoglobin, alpha 2	5.33
9341	211749_s_at	VAMP3	vesicle-associated membrane protein 3 (cellubrevin)	2.07
23136	211776_s_at	EPB41L3	erythrocyte membrane protein band 4.1-like 3	1.64
28831	211798_x_at	IGLJ3	immunoglobulin lambda joining 3	5.5
3107	211799_x_at	HLA-C	major histocompatibility complex, class I, C	1.99
7375	211800_s_at	USP4	ubiquitin specific peptidase 4 (proto-oncogene)	1.53
6546	211805_s_at	SLC8A1	solute carrier family 8 (sodium/calcium exchanger), member 1	-1.24
28396	211835_a_t	IGHV4-31	immunoglobulin heavy variable 4-31	1.36
2778	211858_x_at	GNAS	GNAS complex locus	1.84
26509	211864_s_at	FER1L3	fer-1-like 3, myoferlin (C. elegans)	1.62
2537	211868_x_at	IFI6	interferon, alpha-inducible protein 6	2.92
56145	211870_s_at	PCDHA3	protocadherin alpha 3	-1.37
6955	211902_x_at	TRA@	T cell receptor alpha locus	1.39
3576	211908_x_at	IL8	interleukin 8	2.17
3106	211911_x_at	HLA-B	major histocompatibility complex, class I, B	2.68
4627	211926_s_at	MYH9	myosin, heavy chain 9, non-muscle	1.86
220988	211929_a_t	HNRPA3	heterogeneous nuclear ribonucleoprotein A3	1.9
1975	211938_a_t	EIF4B	eukaryotic translation initiation factor 4B	1.46
3020	211940_x_at	H3F3A	H3 histone, family 3A	1.51
23215	211944_a_t	BAT2D1	BAT2 domain containing 1	1.94
10092	211963_s_at	ARPC5	actin related protein 2/3 complex, subunit 5, 16kDa	1.62
1284	211966_a_t	COL4A2	collagen, type IV, alpha 2	2.64
	211973_a_t		NA	-1.42
57720	211977_a_t	GPR107	G protein-coupled receptor 107	-1.53
1282	211981_a_t	COL4A1	collagen, type IV, alpha 1	4.28
6605	211989_a_t	SMARCE1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin,	1.42

			subfamily e, member 1	
3021	211997_x _at	H3F3B	H3 histone, family 3B (H3.3B)	1.86
3021	211998_a _t	H3F3B	H3 histone, family 3B (H3.3B)	1.66
3021	211999_a _t	H3F3B	H3 histone, family 3B (H3.3B)	2.07
4288	212021_s _at	MKI67	antigen identified by monoclonal antibody Ki-67	-1.25
6122	212039_x _at	RPL3	ribosomal protein L3	1.33
6157	212044_s _at	RPL27A	ribosomal protein L27a	1.69
960	212063_a _t	CD44	CD44 molecule (Indian blood group)	4.61
715	212067_s _at	C1R	complement component 1, r subcomponent	-1.44
23353	212074_a _t	UNC84A	unc-84 homolog A (C. elegans)	1.65
800	212077_a _t	CALD1	caldesmon 1	1.41
4297	212080_a _t	MLL	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	1.49
293	212085_a _t	SLC25A6	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6	2.3
4000	212086_x _at	LMNA	lamin A/C	1.78
26284	212087_s _at	ERAL1	Era G-protein-like 1 (E. coli)	-1.39
857	212097_a _t	CAV1	caveolin 1, caveolae protein, 22kDa	3.12
23633	212102_s _at	KPNA6	karyopherin alpha 6 (importin alpha 7)	-1.22
23673	212111_a _t	STX12	syntaxin 12	1.47
10209	212130_x _at	EIF1	eukaryotic translation initiation factor 1	1.65
23244	212140_a _t	PDS5A	PDS5, regulator of cohesion maintenance, homolog A (S. cerevisiae)	-1.56
3486	212143_s _at	IGFBP3	insulin-like growth factor binding protein 3	2.69
5087	212148_a _t	PBX1	pre-B-cell leukemia homeobox 1	2.92
23126	212153_a _t	POGZ	pogo transposable element with ZNF domain	1.39
149603	212155_a _t	RNF187	ring finger protein 187	-1.58
161	212161_a _t	AP2A2	adaptor-related protein complex 2, alpha 2 subunit	-1.33
10137	212168_a _t	RBM12	RNA binding motif protein 12	2.04

11328	212169_a_t	FKBP9	FK506 binding protein 9, 63 kDa	1.63
204	212172_a_t	AK2	adenylate kinase 2	-1.3
204	212173_a_t	AK2	adenylate kinase 2	-1.29
1399	212180_a_t	CRKL	v-crk sarcoma virus CT10 oncogene homolog (avian)-like	-1.45
23164	212197_x_at	M-RIP	myosin phosphatase-Rho interacting protein	1.66
23141	212201_a_t	KIAA0692	KIAA0692	1.33
26173	212212_s_at	INTS1	integrator complex subunit 1	-1.42
10209	212227_x_at	EIF1	eukaryotic translation initiation factor 1	1.9
23014	212231_a_t	FBXO21	F-box protein 21	1.6
23360	212232_a_t	FNBP4	formin binding protein 4	1.85
	212233_a_t		NA	1.94
57326	212259_s_at	PBXIP1	pre-B-cell leukemia homeobox interacting protein 1	1.36
6430	212266_s_at	SFRS5	splicing factor, arginine/serine-rich 5	1.72
2778	212273_x_at	GNAS	GNAS complex locus	1.52
375790	212283_a_t	AGRN	agrin	-1.41
23048	212288_a_t	FNBP1	formin binding protein 1	1.53
23231	212311_a_t	KIAA0746	KIAA0746 protein	3.49
23534	212318_a_t	TNPO3	transportin 3	1.45
55000	212337_a_t	TUG1	taurine upregulated gene 1	1.66
23036	212366_a_t	ZNF292	zinc finger protein 292	1.51
387680	212370_x_at	FAM21A	family with sequence similarity 21, member A	1.85
6925	212385_a_t	TCF4	transcription factor 4	2.22
9686	212399_s_at	VGLL4	vestigial like 4 (Drosophila)	1.75
23157	212415_a_t	6-Sep	septin 6	1.67
1997	212418_a_t	ELF1	E74-like factor 1 (ets domain transcription factor)	1.99
1997	212420_a_t	ELF1	E74-like factor 1 (ets domain transcription factor)	2.01
23327	212445_s_at	NEDD4L	neural precursor cell expressed, developmentally down-regulated 4-like	1.97

25948	212447_a_t	KBTBD2	kelch repeat and BTB (POZ) domain containing 2	1.52
26128	212453_a_t	KIAA1279	KIAA1279	1.85
171546	212460_a_t	C14orf147	chromosome 14 open reading frame 147	1.96
966	212463_a_t	CD59	CD59 molecule, complement regulatory protein	1.53
7171	212481_s_at	TPM4	tropomyosin 4	1.95
1289	212488_a_t	COL5A1	collagen, type V, alpha 1	2.42
1289	212489_a_t	COL5A1	collagen, type V, alpha 1	1.49
23171	212510_a_t	GPD1L	glycerol-3-phosphate dehydrogenase 1-like	1.65
23012	212572_a_t	STK38L	serine/threonine kinase 38 like	1.62
23347	212579_a_t	SMCHD1	structural maintenance of chromosomes flexible hinge domain containing 1	2.54
114882	212582_a_t	OSBPL8	oxysterol binding protein-like 8	2.05
831	212586_a_t	CAST	calpastatin	1.66
5788	212587_s_at	PTPRC	protein tyrosine phosphatase, receptor type, C	4.88
10042	212596_s_at	HMG2L1	high-mobility group protein 2-like 1	1.62
11118	212613_a_t	BTN3A2	butyrophilin, subfamily 3, member A2	1.7
84159	212614_a_t	ARID5B	AT rich interactive domain 5B (MRF1-like)	3.3
23060	212617_a_t	ZNF609	zinc finger protein 609	-1.31
8417	212632_a_t	STX7	syntaxin 7	1.81
11059	212637_s_at	WWP1	WW domain containing E3 ubiquitin protein ligase 1	-2.77
3097	212641_a_t	HIVEP2	human immunodeficiency virus type 1 enhancer binding protein 2	1.55
6237	212647_a_t	RRAS	related RAS viral (r-ras) oncogene homolog	1.43
23177	212675_s_at	CEP68	centrosomal protein 68kDa	2.21
23177	212677_s_at	CEP68	centrosomal protein 68kDa	2.08
3987	212687_a_t	LIMS1	LIM and senescent cell antigen-like domains 1	1.7
55818	212689_s_at	JMJD1A	jumonji domain containing 1A	2.18
339287	212708_a_t	MSL-1	male-specific lethal-1 homolog	1.41

9842	212717_a_t	PLEKHM1	pleckstrin homology domain containing, family M (with RUN domain) member 1	-1.34
23210	212723_a_t	JMJD6	jumonji domain containing 6	1.65
55000	212725_s_at	TUG1	taurine upregulated gene 1	1.83
23294	212747_a_t	ANKS1A	ankyrin repeat and sterile alpha motif domain containing 1A	1.71
10336	212753_a_t	PCGF3	polycomb group ring finger 3	1.38
6935	212764_a_t	ZEB1	zinc finger E-box binding homeobox 1	1.72
51574	212785_s_at	LARP7	La ribonucleoprotein domain family, member 7	1.47
23310	212789_a_t	NCAPD3	non-SMC condensin II complex, subunit D3	-1.29
23325	212795_a_t	KIAA1033	KIAA1033	1.39
83700	212813_a_t	JAM3	junctional adhesion molecule 3	1.75
26030	212821_a_t	PLEKHG3	pleckstrin homology domain containing, family G (with RhoGef domain) member 3	-1.41
57493	212822_a_t	HEG1	HEG homolog 1 (zebrafish)	1.28
8939	212824_a_t	FUBP3	far upstream element (FUSE) binding protein 3	-2.12
293	212826_s_at	SLC25A6	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6	1.95
3507	212827_a_t	IGHM	immunoglobulin heavy constant mu	1.89
8871	212828_a_t	SYNJ2	synaptojanin 2	1.67
23526	212873_a_t	HMHA1	histocompatibility (minor) HA-1	1.55
3831	212878_s_at	KLC1	kinesin light chain 1	1.72
29	212895_s_at	ABR	active BCR-related gene	1.3
56950	212922_s_at	SMYD2	SET and MYND domain containing 2	1.91
23158	212956_a_t	TBC1D9	TBC1 domain family, member 9 (with GRAM domain)	3.18
9736	212980_a_t	USP34	ubiquitin specific peptidase 34	1.89
	212985_a_t		NA	1.91
3119	212998_x_at	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1	9.98
23452	213001_a_t	ANGPTL2	angiopoietin-like 2	1.61
4798	213028_a_t	NFRKB	nuclear factor related to kappaB binding protein	-1.3

4781	213033_s _at	NFIB	nuclear factor I/B	1.31
23370	213039_a _t	ARHGEF 18	rho/rac guanine nucleotide exchange factor (GEF) 18	1.76
6093	213044_a _t	ROCK1	Rho-associated, coiled-coil containing protein kinase 1	1.53
6418	213047_x _at	SET	SET translocation (myeloid leukemia- associated)	1.6
19644 1	213065_a _t	CCDC13 1	coiled-coil domain containing 131	1.76
1805	213068_a _t	DPT	dermatopontin	7.54
57493	213069_a _t	HEG1	HEG homolog 1 (zebrafish)	2.01
6147	213084_x _at	RPL23A	ribosomal protein L23a	1.51
57211	213094_a _t	GPR126	G protein-coupled receptor 126	-1.68
199	213095_x _at	AIF1	allograft inflammatory factor 1	2.15
23357	213099_a _t	ANGEL1	angel homolog 1 (Drosophila)	-1.38
25903	213125_a _t	OLFML2 B	olfactomedin-like 2B	1.29
10950	213134_x _at	BTG3	BTG family, member 3	2.15
6591	213139_a _t	SNAI2	snail homolog 2 (Drosophila)	5.62
54103	213142_x _at	tcag7.131 4	hypothetical protein LOC54103	2.36
25740 7	213143_a _t	LOC2574 07	hypothetical protein LOC257407	-1.83
989	213151_s _at	7-Sep	septin 7	2.02
9037	213169_a _t	SEMA5A	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A	1.91
23162	213178_s _at	MAPK8I P3	mitogen-activated protein kinase 8 interacting protein 3	1.25
1028	213182_x _at	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	1.73
1028	213183_s _at	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	1.73
28639	213193_x _at	TRBC1	T cell receptor beta constant 1	3.15
6091	213194_a _t	ROBO1	roundabout, axon guidance receptor, homolog 1 (Drosophila)	2.76
10629	213209_a _t	TAF6L	TAF6-like RNA polymerase II, p300/CBP-associated factor (PCAF)- associated factor, 65kDa	-1.27
57613	213232_a _t	KIAA146 7	KIAA1467	-1.32
23328	213236_a	SASH1	SAM and SH3 domain containing 1	1.51

	t			
10154	213241_a_t	PLXNC1	plexin C1	2.01
283638	213242_x_at	KIAA0284	KIAA0284	-1.45
3725	213281_a_t	JUN	jun oncogene	1.49
161291	213285_a_t	TMEM30B	transmembrane protein 30B	3.04
1292	213290_a_t	COL6A2	collagen, type VI, alpha 2	1.52
	213294_a_t		NA	1.93
53405	213317_a_t	CLIC5	chloride intracellular channel 5	1.32
6843	213326_a_t	VAMP1	vesicle-associated membrane protein 1 (synaptobrevin 1)	1.63
56929	213341_a_t	FEM1C	fem-1 homolog c (C. elegans)	1.72
3014	213344_s_at	H2AFX	H2A histone family, member X	-1.39
1028	213348_a_t	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	3.03
340591	213363_a_t	CA5BL	carbonic anhydrase VB-like	-1.34
6642	213364_s_at	SNX1	sorting nexin 1	1.62
124152	213392_a_t	IQCK	IQ motif containing K	1.67
283	213397_x_at	ANG	angiogenin, ribonuclease, RNase A family, 5	-1.6
	213403_a_t		NA	-1.65
6009	213404_s_at	RHEB	Ras homolog enriched in brain	-1.39
11037	213413_a_t	STON1	stonin 1	2.72
1193	213415_a_t	CLIC2	chloride intracellular channel 2	2.07
375298	213416_a_t	CERKL	ceramide kinase-like	3.32
54587	213422_s_at	MXRA8	matrix-remodelling associated 8	1.47
7991	213423_x_at	TUSC3	tumor suppressor candidate 3	3.29
1291	213428_s_at	COL6A1	collagen, type VI, alpha 1	2.87
23114	213438_a_t	NFASC	neurofascin homolog (chicken)	2.55
4580	213448_a_t	MTX1	metaxin 1	-1.31
7148	213451_x_at	TNXB	tenascin XB	2.14

260294	213460_x_at	NSUN5C	NOL1/NOP2/Sun domain family, member 5C	1.36
3187	213470_s_at	HNRPH1	heterogeneous nuclear ribonucleoprotein H1 (H)	1.6
3683	213475_s_at	ITGAL	integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide)	1.34
23398	213483_a_t	PPWD1	peptidylprolyl isomerase domain and WD repeat containing 1	1.79
1280	213492_a_t	COL2A1	collagen, type II, alpha 1 (primary osteoarthritis, spondyloepiphyseal dysplasia, congenital)	-1.18
10147	213505_s_at	SFRS14	splicing factor, arginine/serine-rich 14	1.39
7329	213535_s_at	UBE2I	ubiquitin-conjugating enzyme E2I (UBC9 homolog, yeast)	1.41
3113	213537_a_t	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	1.96
915	213539_a_t	CD3D	CD3d molecule, delta (CD3-TCR complex)	1.87
222161	213546_a_t	DKFZp586I1420	hypothetical protein DKFZp586I1420	1.71
9470	213570_a_t	EIF4E2	eukaryotic translation initiation factor 4E family member 2	-1.26
5134	213581_a_t	PDCD2	programmed cell death 2	1.45
6585	213601_a_t	SLIT1	slit homolog 1 (Drosophila)	-1.23
5880	213603_s_at	RAC2	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)	2.3
	213604_a_t		NA	-1.54
3187	213619_a_t	HNRPH1	heterogeneous nuclear ribonucleoprotein H1 (H)	1.83
10916	213627_a_t	MAGED2	melanoma antigen family D, 2	1.61
4498	213629_x_at	MT1JP	metallothionein 1J (pseudogene)	-2.6
1723	213631_x_at	DHODH	dihydroorotate dehydrogenase	-3.3
23016	213648_a_t	EXOSC7	exosome component 7	-1.23
6432	213649_a_t	SFRS7	splicing factor, arginine/serine-rich 7, 35kDa	1.98
5125	213652_a_t	PCSK5	proprotein convertase subtilisin/kexin type 5	1.28
155400	213670_x_at	NSUN5B	NOL1/NOP2/Sun domain family, member 5B	1.45
54665	213694_a_t	RSBN1	round spermatid basic protein 1	1.7
9204	213698_a_t	ZMYM6	zinc finger, MYM-type 6	2.48

427	213702_x _at	ASAHI	N-acylsphingosine amidohydrolase (acid ceramidase) 1	1.7
150759	213703_a _t	LOC150759	hypothetical protein LOC150759	1.68
54898	213712_a _t	ELOVL2	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2	2.24
89944	213713_s _at	LOC89944	hypothetical protein BC008326	-1.34
6398	213716_s _at	SECTM1	secreted and transmembrane 1	1.5
2316	213746_s _at	FLNA	filamin A, alpha (actin binding protein 280)	1.73
6698	213796_a _t	SPRR1A	small proline-rich protein 1A	-1.19
	213813_x _at		NA	1.77
3207	213823_a _t	HOXA11	homeobox A11	-1.47
3020	213828_x _at	H3F3A	H3 histone, family 3A	1.5
6183	213840_s _at	MRPS12	mitochondrial ribosomal protein S12	-1.21
1350	213846_a _t	COX7C	cytochrome c oxidase subunit VIIc	1.78
1302	213870_a _t	COL11A2	collagen, type XI, alpha 2	-1.4
83941	213882_a _t	TM2D1	TM2 domain containing 1	1.51
80342	213888_s _at	TRAF3IP3	TRAF3 interacting protein 3	1.37
221981	213894_a _t	THSD7A	thrombospondin, type I, domain containing 7A	2.01
3490	213910_a _t	IGFBP7	insulin-like growth factor binding protein 7	1.63
5912	213923_a _t	RAP2B	RAP2B, member of RAS oncogene family	1.78
3105	213932_x _at	HLA-A	major histocompatibility complex, class I, A	1.8
57863	213948_x _at	CADM3	cell adhesion molecule 3	-1.19
240	213952_s _at	ALOX5	arachidonate 5-lipoxygenase	-1.16
6159	213969_x _at	RPL29	ribosomal protein L29	1.35
9910	213982_s _at	RABGAP1L	RAB GTPase activating protein 1-like	1.73
6303	213988_s _at	SAT1	spermidine/spermine N1-acetyltransferase 1	2.11
9957	213991_s _at	HS3ST1	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	-1.23
10418	213994_s _at	SPON1	spondin 1, extracellular matrix protein	2.62
10581	214022_s _at	IFITM2	interferon induced transmembrane protein 2 (1-8D)	2.68

131544	214030_a_t	DKFZp667G2110	hypothetical protein DKFZp667G2110	1.43
4882	214066_x_at	NPR2	natriuretic peptide receptor B/guanylate cyclase B (atriuretic peptide receptor B)	-1.18
29937	214072_x_at	NENF	neuron derived neurotrophic factor	-1.26
11103	214085_x_at	KRR1	KRR1, small subunit (SSU) processome component, homolog (yeast)	3.26
2878	214091_s_at	GPX3	glutathione peroxidase 3 (plasma)	1.66
10147	214092_x_at	SFRS14	splicing factor, arginine/serine-rich 14	1.64
9659	214099_s_at	PDE4DIP	phosphodiesterase 4D interacting protein (myomegalin)	-1.32
155400	214100_x_at	NSUN5B	NOL1/NOP2/Sun domain family, member 5B	1.45
509	214132_a_t	ATP5C1	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, gamma polypeptide 1	1.91
57326	214176_s_at	PBXIP1	pre-B-cell leukemia homeobox interacting protein 1	1.49
57326	214177_s_at	PBXIP1	pre-B-cell leukemia homeobox interacting protein 1	1.64
382	214182_a_t	ARF6	ADP-ribosylation factor 6	1.9
2495	214211_a_t	FTH1	ferritin, heavy polypeptide 1	1.85
23185	214215_s_at	LARP5	La ribonucleoprotein domain family, member 5	-1.2
57194	214256_a_t	ATP10A	ATPase, Class V, type 10A	-1.32
6136	214271_x_at	RPL12	ribosomal protein L12	1.46
1540	214272_a_t	CYLD	cylindromatosis (turban tumor syndrome)	-1.21
57447	214279_s_at	NDRG2	NDRG family member 2	2.7
3178	214280_x_at	HNRNPA1	heterogeneous nuclear ribonucleoprotein A1	1.74
23157	214298_x_at	6-Sep	septin 6	1.73
23451	214305_s_at	SF3B1	splicing factor 3b, subunit 1, 155kDa	1.81
6203	214317_x_at	RPS9	ribosomal protein S9	1.46
818	214322_a_t	CAMK2G	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma	-1.22
31	214358_a_t	ACACA	acetyl-Coenzyme A carboxylase alpha	-1.59
9782	214363_s_at	MATR3	matrin 3	1.35
54346	214382_a_t	UNC93A	unc-93 homolog A (C. elegans)	2.26

586	214390_s _at	BCAT1	branched chain aminotransferase 1, cytosolic	-1.35
10659	214405_a _t	CUGBP2	CUG triplet repeat, RNA binding protein 2	1.39
2994	214407_x _at	GYPB	glycophorin B (MNS blood group)	-1.23
1504	214411_x _at	CTRB1	chymotrypsinogen B1	-1.31
3039	214414_x _at	HBA1	hemoglobin, alpha 1	3.76
1559	214419_s _at	CYP2C9	cytochrome P450, family 2, subfamily C, polypeptide 9	2.25
1559	214420_s _at	CYP2C9	cytochrome P450, family 2, subfamily C, polypeptide 9	2.54
229	214423_x _at	ALDOB	aldolase B, fructose-bisphosphate	1.56
720	214428_x _at	C4A	complement component 4A (Rodgers blood group)	-1.88
10561	214453_s _at	IFI44	interferon-induced protein 44	4.86
6289	214456_x _at	SAA2	serum amyloid A2	-3.47
3107	214459_x _at	HLA-C	major histocompatibility complex, class I, C	1.82
8477	214467_a _t	GPR65	G protein-coupled receptor 65	1.77
3820	214470_a _t	KLRB1	killer cell lectin-like receptor subfamily B, member 1	3.77
6694	214478_a _t	SPP2	secreted phosphoprotein 2, 24kDa	4.12
4956	214485_a _t	ODF1	outer dense fiber of sperm tails 1	-1.49
9555	214500_a _t	H2AFY	H2A histone family, member Y	1.77
2273	214505_s _at	FHL1	four and a half LIM domains 1	1.97
10923	214512_s _at	SUB1	SUB1 homolog (S. cerevisiae)	1.84
1385	214513_s _at	CREB1	cAMP responsive element binding protein 1	1.47
10776	214553_s _at	ARPP-19	cyclic AMP phosphoprotein, 19 kD	1.52
6846	214567_s _at	XCL2	chemokine (C motif) ligand 2	2.13
4131	214577_a _t	MAP1B	microtubule-associated protein 1B	1.27
6093	214578_s _at	ROCK1	Rho-associated, coiled-coil containing protein kinase 1	1.44
27242	214581_x _at	TNFRSF2 1	tumor necrosis factor receptor superfamily, member 21	1.85
27334	214615_a _t	P2RY10	purinergic receptor P2Y, G-protein coupled, 10	1.17
8353	214616_a _t	HIST1H3 E	histone cluster 1, H3e	-1.36

5551	214617_a _t	PRF1	perforin 1 (pore forming protein)	1.64
50488	214625_s _at	MINK1	misshapen-like kinase 1 (zebrafish)	-1.29
8898	214649_s _at	MTMR2	myotubularin related protein 2	1.42
1195	214683_s _at	CLK1	CDC-like kinase 1	2.2
10781	214686_a _t	ZNF266	zinc finger protein 266	2.11
57730	214723_x _at	KIAA164 1	KIAA1641	1.83
23086	214734_a _t	EXPH5	exophilin 5	-2.26
118	214736_s _at	ADD1	adducin 1 (alpha)	1.62
9349	214744_s _at	RPL23	ribosomal protein L23	-1.31
19158 5	214750_a _t	PLAC4	placenta-specific 4	-1.29
2316	214752_x _at	FLNA	filamin A, alpha (actin binding protein 280)	1.84
10443	214753_a _t	PFAAP5	phosphonoformate immuno-associated protein 5	1.8
26094	214758_a _t	WDR21A	WD repeat domain 21A	-1.29
3514	214768_x _at	IGKC	immunoglobulin kappa constant	11.95
23164	214771_x _at	M-RIP	myosin phosphatase-Rho interacting protein	1.5
	214777_a _t		NA	12.24
26054	214790_a _t	SEN6	SUMO1/sentrin specific peptidase 6	1.48
23114	214799_a _t	NFASC	neurofascin homolog (chicken)	1.21
	214807_a _t		NA	2.02
55233	214812_s _at	MOBKL1 B	MOB1, Mps One Binder kinase activator-like 1B (yeast)	1.45
	214824_a _t		NA	-1.38
8801	214835_s _at	SUCLG2	succinate-CoA ligase, GDP-forming, beta subunit	-1.79
37503 5	214838_a _t	SFT2D2	SFT2 domain containing 2	-1.46
14669 1	214840_a _t	TOM1L2	target of myb1-like 2 (chicken)	-1.36
	214848_a _t		NA	1.16
23105	214859_a _t	FSTL4	follistatin-like 4	-1.26
84444	214865_a _t	DOT1L	DOT1-like, histone H3 methyltransferase (<i>S. cerevisiae</i>)	-1.17

339047	214870_x_at	LOC339047	hypothetical protein LOC339047	1.52
7392	214879_x_at	USF2	upstream transcription factor 2, c-fos interacting	-1.39
800	214880_x_at	CALD1	caldesmon 1	1.83
6427	214882_s_at	SFRS2	splicing factor, arginine/serine-rich 2	1.56
90273	214907_a_t	CEACAM21	carcinoembryonic antigen-related cell adhesion molecule 21	-1.39
3576	214916_x_at	IL8	interleukin 8	4.23
221981	214920_a_t	THSD7A	thrombospondin, type I, domain containing 7A	2.49
57498	214932_a_t	KIDINS220	kinase D-interacting substrate of 220 kDa	-1.18
387680	214946_x_at	FAM21A	family with sequence similarity 21, member A	1.65
317781	214968_a_t	DDX51	DEAD (Asp-Glu-Ala-Asp) box polypeptide 51	-1.38
4293	214969_a_t	MAP3K9	mitogen-activated protein kinase kinase 9	-1.22
3495	214973_x_at	IGHD	immunoglobulin heavy constant delta	3.82
25787	215003_a_t	DGCR9	DiGeorge syndrome critical region gene 9	-1.23
4071	215034_s_at	TM4SF1	transmembrane 4 L six family member 1	4.95
199	215051_x_at	AIF1	allograft inflammatory factor 1	1.95
114793	215062_a_t	FMNL2	formin-like 2	1.24
1281	215076_s_at	COL3A1	collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant)	3.21
9940	215085_x_at	DLEC1	deleted in lung and esophageal cancer 1	-1.35
23117	215123_a_t	LOC23117	KIAA0220-like protein	2.5
57244	215137_a_t	KIAA0508	KIAA0508 protein	-1.28
55619	215151_a_t	DOCK10	dedicator of cytokinesis 10	1.17
6925	215164_a_t	TCF4	transcription factor 4	1.19
53371	215213_a_t	NUP54	nucleoporin 54kDa	-1.13
3535	215214_a_t	IGL@	immunoglobulin lambda locus	3.1
7266	215252_a_t	DNAJC7	DnaJ (Hsp40) homolog, subfamily C, member 7	1.73
6929	215260_s_at	TCF3	transcription factor 3 (E2A immunoglobulin enhancer binding	-1.29

			factors E12/E47)	
27315	215293_s_at	FRAG1	FGF receptor activating protein 1	-1.37
3105	215313_x_at	HLA-A	major histocompatibility complex, class I, A	2.07
91694	215322_a_t	LONRF1	LON peptidase N-terminal domain and ring finger 1	1.57
926	215332_s_at	CD8B	CD8b molecule	1.17
107	215340_a_t	ADCY1	adenylate cyclase 1 (brain)	-1.32
	215344_a_t		NA	-1.15
8634	215351_a_t	RTCD1	RNA terminal phosphate cyclase domain 1	1.18
23334	215364_s_at	KIAA0467	KIAA0467	-1.42
23233	215417_a_t	EXOC6B	exocyst complex component 6B	1.11
	215421_a_t		NA	-1.26
22938	215424_s_at	SNW1	SNW domain containing 1	1.49
23333	215433_a_t	DPY19L1	dpy-19-like 1 (C. elegans)	-1.23
56271	215440_s_at	BEXL1	brain expressed X-linked-like 1	2.75
4015	215446_s_at	LOX	lysyl oxidase	1.49
7035	215447_a_t	TFPI	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	-3.3
22264 2	215449_a_t	BZRPL1	benzodiazapine receptor (peripheral)-like 1	-1.49
	215476_a_t		NA	-1.26
	215477_a_t		NA	-1.14
10612	215484_a_t	TRIM3	tripartite motif-containing 3	-1.56
4610	215491_a_t	MYCL1	v-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma derived (avian)	-1.26
11120	215493_x_at	BTN2A1	butyrophilin, subfamily 2, member A1	1.4
6942	215511_a_t	TCF20	transcription factor 20 (AR1)	-1.32
55243	215515_a_t	KIRREL	kin of IRRE like (Drosophila)	-1.41
1729	215541_s_at	DIAPH1	diaphanous homolog 1 (Drosophila)	-1.42
11313	215568_x_at	LYPLA2	lysophospholipase II	-1.39

	215590_x _at		NA	-1.21
51533	215622_x _at	PHF7	PHD finger protein 7	-1.34
23348	215626_a _t	DOCK9	dedicator of cytokinesis 9	1.2
9849	215644_a _t	ZNF518	zinc finger protein 518	-1.21
1462	215646_s _at	VCAN	versican	3.67
5364	215668_s _at	PLXNB1	plexin B1	-1.37
85368	215681_a _t	KIAA165 4	KIAA1654 protein	-1.22
8733	215690_x _at	GPAA1	glycosylphosphatidylinositol anchor attachment protein 1 homolog (yeast)	-1.45
1080	215702_s _at	CFTR	cystic fibrosis transmembrane conductance regulator (ATP-binding cassette sub-family C, member 7)	1.66
3483	215712_s _at	IGFALS	insulin-like growth factor binding protein, acid labile subunit	-1.76
6530	215715_a _t	SLC6A2	solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2	-1.18
355	215719_x _at	FAS	Fas (TNF receptor superfamily, member 6)	2.59
7392	215737_x _at	USF2	upstream transcription factor 2, c-fos interacting	-1.59
55735	215792_s _at	DNAJC1 1	DnaJ (Hsp40) homolog, subfamily C, member 11	-1.41
10840	215798_a _t	ALDH1L 1	aldehyde dehydrogenase 1 family, member L1	-1.42
1565	215809_a _t	CYP2D6	cytochrome P450, family 2, subfamily D, polypeptide 6	-1.71
6006	215819_s _at	RHCE	Rh blood group, CcEe antigens	-1.29
28392 7	215824_a _t	NUDT7	nudix (nucleoside diphosphate linked moiety X)-type motif 7	-1.19
91683	215865_a _t	SYT12	synaptotagmin XII	-1.27
5322	215870_s _at	PLA2G5	phospholipase A2, group V	2.97
	215906_a _t		NA	-1.37
971	215925_s _at	CD72	CD72 molecule	1.51
10564	215927_a _t	ARFGEF 2	ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibited)	-1.37
9205	215948_x _at	ZMYM5	zinc finger, MYM-type 5	1.17
3507	215949_x _at	IGHM	immunoglobulin heavy constant mu	2.07
8495	215959_a _t	PPFIBP2	PTPRF interacting protein, binding protein 2 (liprin beta 2)	-1.22

64274_1	215963_x_at	LOC642741	similar to ribosomal protein L3 isoform a	1.36
80868	215974_a_t	HCG4P6	HLA complex group 4 pseudogene 6	-1.22
37428_6	215999_a_t	CDRT1	CMT1A duplicated region transcript 1	-1.23
37428_6	216003_a_t	CDRT1	CMT1A duplicated region transcript 1	-1.2
55334	216011_a_t	SLC39A9	solute carrier family 39 (zinc transporter), member 9	-1.47
2534	216033_s_at	FYN	FYN oncogene related to SRC, FGR, YES	2.67
23038	216036_x_at	WDTC1	WD and tetratricopeptide repeats 1	-1.49
2896	216041_x_at	GRN	granulin	1.77
4635	216054_x_at	MYL4	myosin, light chain 4, alkali; atrial, embryonic	-1.27
23002	216060_s_at	DAAM1	dishevelled associated activator of morphogenesis 1	1.88
23428	216092_s_at	SLC7A8	solute carrier family 7 (cationic amino acid transporter, y+ system), member 8	-1.37
23187	216102_a_t	PHLDB1	pleckstrin homology-like domain, family B, member 1	-1.46
	216126_a_t		NA	-1.4
399	216166_a_t	RHOH	ras homolog gene family, member H	1.17
5425	216175_a_t	POLD2	polymerase (DNA directed), delta 2, regulatory subunit 50kDa	-1.24
11649_2	216186_a_t	C1orf20	chromosome 1 open reading frame 20	-1.4
2173	216192_a_t	FABP7	fatty acid binding protein 7, brain	-1.27
1312	216204_a_t	COMT	catechol-O-methyltransferase	-1.32
28902	216207_x_at	IGKV1D-13	immunoglobulin kappa variable 1D-13	11.42
40008_4	216209_a_t	LOC400084	hypothetical gene supported by AK057632; AL137270; BC057846	-1.27
11078	216210_x_at	TRIOBP	TRIO and F-actin binding protein	1.49
23369	216221_s_at	PUM2	pumilio homolog 2 (Drosophila)	1.35
9332	216233_a_t	CD163	CD163 molecule	1.82
2244	216238_s_at	FGB	fibrinogen beta chain	-1.47
355	216252_x_at	FAS	Fas (TNF receptor superfamily, member 6)	2.2
85360	216271_x_at	SYDE1	synapse defective 1, Rho GTPase, homolog 1 (C. elegans)	-1.5

699	216275_a _t	BUB1	BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast)	-1.3
8776	216303_s _at	MTMR1	myotubularin related protein 1	-1.24
8629	216309_x _at	JRK	jerky homolog (mouse)	-1.49
113457	216323_x _at	TUBA3D	tubulin, alpha 3d	-1.52
7148	216333_x _at	TNXB	tenascin XB	2.21
54661	216355_a _t	PCDHB1 7	protocadherin beta 17 pseudogene	-1.37
	216366_x _at		NA	-1.45
27318	216382_s _at	TNRC21	trinucleotide repeat containing 21	-1.46
220077	216385_a _t	LOC2200 77	docking protein 1-like protein	-1.58
3712	216412_x _at	IVD	isovaleryl Coenzyme A dehydrogenase	2.46
90011	216428_x _at	KIR3DX1	killer cell immunoglobulin-like receptor, three domains, X1	-1.36
3535	216430_x _at	IGL@	immunoglobulin lambda locus	2.33
80314	216437_a _t	EPC1	enhancer of polycomb homolog 1 (Drosophila)	-1.17
3507	216491_x _at	IGHM	immunoglobulin heavy constant mu	6.8
	216500_a _t		NA	-1.33
152098	216510_x _at	ZCWPW 2	zinc finger, CW type with PWWP domain 2	5.73
1638	216512_s _at	DCT	dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2)	-1.17
28299	216517_a _t	IGKV1-5	immunoglobulin kappa variable 1-5	2.36
3107	216526_x _at	HLA-C	major histocompatibility complex, class I, C	1.67
	216530_a _t		NA	-1.22
57863	216535_a _t	CADM3	cell adhesion molecule 3	-1.91
28461	216541_x _at	IGHV1- 69	immunoglobulin heavy variable 1-69	1.72
3493	216542_x _at	IGHA1	immunoglobulin heavy constant alpha 1	2.08
127406	216547_a _t	LOC1274 06	similar to laminin receptor 1 (ribosomal protein SA)	-1.67
2537	216557_x _at	IFI6	interferon, alpha-inducible protein 6	3.82
	216558_x _at		NA	1.46

3535	216560_x _at	IGL@	immunoglobulin lambda locus	5.06
	216573_a _t		NA	1.43
4917	216576_x _at	NTN2L	netrin 2-like (chicken)	19.62
12753 4	216579_a _t	GJB4	gap junction protein, beta 4	-1.48
	216582_a _t		NA	-1.26
1645	216594_x _at	AKR1C1	aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)	-1.97
65363 9	216606_x _at	LYPLA2 P1	lysophospholipase II pseudogene 1	-1.24
6093	216621_a _t	ROCK1	Rho-associated, coiled-coil containing protein kinase 1	1.23
65030 3	216650_a _t	LOC6503 03	similar to 60S ribosomal protein L29 (Cell surface heparin binding protein HIP)	-1.43
41431 8	216675_a _t	C9orf106	chromosome 9 open reading frame 106	-1.42
55764	216678_a _t	IFT122	intraflagellar transport 122 homolog (Chlamydomonas)	-1.62
64578 4	216686_a _t	FLJ40330	similar to protein immuno-reactive with anti-PTH polyclonal antibodies	1.11
50810	216693_x _at	HDGFRP 3	hepatoma-derived growth factor, related protein 3	1.41
26628	216698_x _at	OR7E47P	olfactory receptor, family 7, subfamily E, member 47 pseudogene	-1.93
	216730_a _t		NA	-1.42
38976 8	216732_a _t	LOC3897 68	similar to potassium channel tetramerisation domain containing 1	-1.45
3269	216738_a _t	HRH1	histamine receptor H1	-1.28
	216757_a _t		NA	-1.3
23189	216763_a _t	ANKRD1 5	ankyrin repeat domain 15	-1.17
	216774_a _t		NA	-1.32
85452	216781_a _t	KIAA175 1	KIAA1751	-1.21
	216800_a _t		NA	-1.28
85452	216807_a _t	KIAA175 1	KIAA1751	-1.2
	216815_a _t		NA	-1.16
26707	216818_s _at	OR2J2	olfactory receptor, family 2, subfamily J, member 2	-1.19

	216824_a_t		NA	-1.26
862	216832_a_t	RUNX1T1	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	-1.46
2994	216833_x_at	GYPB	glycophorin B (MNS blood group)	-1.22
2064	216836_s_at	ERBB2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	1.71
3908	216840_s_at	LAMA2	laminin, alpha 2 (merosin, congenital muscular dystrophy)	3.92
3535	216846_a_t	IGL@	immunoglobulin lambda locus	1.33
85374	216848_a_t	KIAA1660	KIAA1660 protein	-1.36
3535	216852_x_at	IGL@	immunoglobulin lambda locus	-1.27
27251	216879_a_t	HR44	Hr44 antigen	-1.35
6768	216905_s_at	ST14	suppression of tumorigenicity 14 (colon carcinoma)	1.78
5782	216915_s_at	PTPN12	protein tyrosine phosphatase, non-receptor type 12	1.63
9537	216919_a_t	TP53I11	tumor protein p53 inducible protein 11	-1.28
445347	216920_s_at	TARP	TCR gamma alternate reading frame protein	1.86
6886	216925_s_at	TAL1	T-cell acute lymphocytic leukemia 1	-1.35
6927	216930_a_t	TCF1	transcription factor 1, hepatic; LF-B1, hepatic nuclear factor (HNF1), albumin proximal factor	-1.42
	216943_a_t		NA	-1.34
51412	216978_x_at	ACTL6B	actin-like 6B	-1.11
7767	216983_s_at	ZNF224	zinc finger protein 224	1.39
3535	216984_x_at	IGL@	immunoglobulin lambda locus	7.09
2918	216992_s_at	GRM8	glutamate receptor, metabotropic 8	-1.28
	217018_a_t		NA	-1.26
	217030_a_t		NA	-1.44
3500	217039_x_at	IGHG1	immunoglobulin heavy constant gamma 1 (G1m marker)	-1.51
9436	217045_x_at	NCR2	natural cytotoxicity triggering receptor 2	-1.49
6760	217051_s_at	SS18	synovial sarcoma translocation, chromosome 18	-1.26

8550	217084_a_t	MAPKAP K5	mitogen-activated protein kinase-activated protein kinase 5	1.18
9437	217095_x_at	NCR1	natural cytotoxicity triggering receptor 1	-1.29
27445	217096_a_t	PCLO	piccolo (presynaptic cytomatrix protein)	-1.23
4507	217134_a_t	MTAP	methylthioadenosine phosphorylase	-1.24
648390	217144_a_t	LOC648390	similar to ubiquitin B precursor	-2.15
3514	217145_a_t	IGKC	immunoglobulin kappa constant	1.34
50852	217147_s_at	TRAT1	T cell receptor associated transmembrane adaptor 1	2.16
3535	217148_x_at	IGL@	immunoglobulin lambda locus	10.56
	217152_a_t		NA	1.57
	217157_x_at		NA	6.46
728683	217158_a_t	LOC728683	similar to Prostaglandin E2 receptor, EP4 subtype (Prostanoid EP4 receptor) (PGE receptor, EP4 subtype)	-1.38
4494	217165_x_at	MT1F	metallothionein 1F	-1.71
10297	217174_s_at	APC2	adenomatosis polyposis coli 2	-1.37
7366	217175_a_t	UGT2B15	UDP glucuronosyltransferase 2 family, polypeptide B15	1.29
96610	217179_x_at	LOC96610	hypothetical gene LOC96610	5.34
1534	217200_x_at	CYB561	cytochrome b-561	-1.41
390861	217211_a_t	LOC390861	similar to cytoplasmic beta-actin	-1.76
27030	217216_x_at	MLH3	mutL homolog 3 (E. coli)	1.26
	217224_a_t		NA	-1.21
3576	217227_x_at	IL8	interleukin 8	5.4
3043	217232_x_at	HBB	hemoglobin, beta	6.65
7430	217234_s_at	VIL2	villin 2 (ezrin)	1.96
	217235_x_at		NA	4.06
3500	217236_x_at	IGHG1	immunoglobulin heavy constant gamma 1 (G1m marker)	1.68
54504	217239_x_at	CPVL	carboxypeptidase, vitellogenic-like	1.74
	217249_x_at		NA	-1.57

3712	217258_x _at	IVD	isovaleryl Coenzyme A dehydrogenase	4.46
8220	217275_a _t	DGCR14	DiGeorge syndrome critical region gene 14	-1.33
4323	217279_x _at	MMP14	matrix metalloproteinase 14 (membrane-inserted)	-1.37
57446	217286_s _at	NDRG3	NDRG family member 3	1.6
27185	217330_a _t	DISC1	disrupted in schizophrenia 1	-1.2
12819 2	217346_a _t	LOC128192	similar to peptidylprolyl isomerase A isoform 1	-1.24
3493	217360_x _at	IGHA1	immunoglobulin heavy constant alpha 1	2.04
3128	217362_x _at	HLA-DRB6	major histocompatibility complex, class II, DR beta 6 (pseudogene)	2.14
23051	217367_s _at	ZHX3	zinc fingers and homeoboxes 3	-1.48
2521	217370_x _at	FUS	fusion (involved in t(12;16) in malignant liposarcoma)	1.39
44193 8	217376_a _t	LOC441938	similar to Signal-regulatory protein gamma precursor (Signal-regulatory protein beta-2) (SIRP-beta-2) (SIRP-b2) (CD172g antigen)	-1.46
	217378_x _at		NA	12.89
3576	217384_x _at	IL8	interleukin 8	1.58
84560	217395_a _t	MT4	metallothionein 4	-1.54
2309	217399_s _at	FOXO3	forkhead box O3	1.34
28973	217408_a _t	MRPS18B	mitochondrial ribosomal protein S18B	-1.84
3039	217414_x _at	HBA1	hemoglobin, alpha 1	5.26
1277	217430_x _at	COL1A1	collagen, type I, alpha 1	-1.45
4158	217434_a _t	MC2R	melanocortin 2 receptor (adrenocorticotrophic hormone)	-1.11
73039 9	217436_x _at	LOC730399	hypothetical protein LOC730399	2.04
6867	217437_s _at	TACC1	transforming, acidic coiled-coil containing protein 1	1.73
57863	217442_a _t	CADM3	cell adhesion molecule 3	-1.54
5910	217457_s _at	RAP1GDS1	RAP1, GTP-GDP dissociation stimulator 1	-1.5
3107	217480_x _at	HLA-C	major histocompatibility complex, class I, C	7.08
11191	217492_s _at	PTENP1	phosphatase and tensin homolog (mutated in multiple advanced cancers 1), pseudogene 1	1.62
9436	217493_x	NCR2	natural cytotoxicity triggering receptor 2	-1.44

	_at			
283298	217525_a_t	OLFML1	olfactomedin-like 1	2.03
4499	217546_a_t	MT1M	metallothionein 1M	-3.45
142684	217589_a_t	RAB40A	RAB40A, member RAS oncogene family	-1.24
9875	217633_a_t	URB1	URB1 ribosome biogenesis 1 homolog (S. cerevisiae)	-1.21
5428	217636_a_t	POLG	polymerase (DNA directed), gamma	-1.21
6834	217646_a_t	SURF1	surfeit 1	-1.3
2778	217673_x_at	GNAS	GNAS complex locus	1.33
	217676_a_t		NA	-1.26
5770	217686_a_t	PTPN1	protein tyrosine phosphatase, non-receptor type 1	-1.22
108	217687_a_t	ADCY2	adenylate cyclase 2 (brain)	-1.28
7763	217741_s_at	ZFAND5	zinc finger, AN1-type domain 5	3.24
373156	217751_a_t	GSTK1	glutathione S-transferase kappa 1	1.65
718	217767_a_t	C3	complement component 3	-1.26
51280	217771_a_t	GOLM1	golgi membrane protein 1	3.52
51109	217776_a_t	RDH11	retinol dehydrogenase 11 (all-trans/9-cis/11-cis)	-1.82
51398	217780_a_t	C19orf56	chromosome 19 open reading frame 56	1.34
58533	217789_a_t	SNX6	sorting nexin 6	1.33
4848	217798_a_t	CNOT2	CCR4-NOT transcription complex, subunit 2	1.39
26073	217806_s_at	POLDIP2	polymerase (DNA-directed), delta interacting protein 2	-1.61
29997	217807_s_at	GLTSCR2	glioma tumor suppressor candidate region gene 2	2.05
10093	217818_s_at	ARPC4	actin related protein 2/3 complex, subunit 4, 20kDa	-1.58
51465	217824_a_t	UBE2J1	ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)	-1.56
55249	217836_s_at	YY1AP1	YY1 associated protein 1	1.45
55207	217852_s_at	ARL8B	ADP-ribosylation factor-like 8B	1.42
25825	217867_x_at	BACE2	beta-site APP-cleaving enzyme 2	3.16
51108	217868_s_at	METTL9	methyltransferase like 9	2.11

55011	217872_a _t	PIH1D1	PIH1 domain containing 1	-1.36
2060	217886_a _t	EPS15	epidermal growth factor receptor pathway substrate 15	1.7
79901	217889_s _at	CYBRD1	cytochrome b reductase 1	1.81
55742	217890_s _at	PARVA	parvin, alpha	1.73
51474	217892_s _at	LIMA1	LIM domain and actin binding 1	1.99
54867	217899_a _t	FLJ20254	hypothetical protein FLJ20254	-1.42
23621	217904_s _at	BACE1	beta-site APP-cleaving enzyme 1	-1.54
55827	217908_s _at	IQWD1	IQ motif and WD repeats 1	-1.59
83658	217917_s _at	DYNLRB 1	dynein, light chain, roadblock-type 1	2.08
83658	217918_a _t	DYNLRB 1	dynein, light chain, roadblock-type 1	1.79
64771	217925_s _at	C6orf106	chromosome 6 open reading frame 106	-1.52
29115	217965_s _at	SAP30BP	SAP30 binding protein	1.55
11649 6	217967_s _at	FAM129 A	family with sequence similarity 129, member A	3.49
51186	217975_a _t	WBP5	WW domain binding protein 5	2.65
8635	217983_s _at	RNASET 2	ribonuclease T2	3.93
57820	217988_a _t	CCNB1IP 1	cyclin B1 interacting protein 1	2.36
51292	217990_a _t	GMPR2	guanosine monophosphate reductase 2	1.49
27430	217993_s _at	MAT2B	methionine adenosyltransferase II, beta	1.5
79144	218010_x _at	C20orf14 9	chromosome 20 open reading frame 149	1.54
8303	218032_a _t	SNN	stannin	1.68
79650	218060_s _at	C16orf57	chromosome 16 open reading frame 57	-1.45
56674	218065_s _at	TMEM9B	TMEM9 domain family, member B	1.38
55082	218067_s _at	FLJ10154	hypothetical protein FLJ10154	2.05
53827	218084_x _at	FXVD5	FXVD domain containing ion transport regulator 5	2.09
55861	218094_s _at	DBNDD2	dysbindin (dystrobrevin binding protein 1) domain containing 2	1.74
55081	218100_s _at	IFT57	intraflagellar transport 57 homolog (Chlamydomonas)	2.41
4801	218128_a _t	NFYB	nuclear transcription factor Y, beta	1.64

56882	218157_x _at	CDC42S E1	CDC42 small effector 1	1.84
64769	218165_a _t	C1orf149	chromosome 1 open reading frame 149	1.79
57111	218186_a _t	RAB25	RAB25, member RAS oncogene family	1.94
29796	218190_s _at	UCRC	ubiquinol-cytochrome c reductase complex (7.2 kD)	1.35
51447	218192_a _t	IHPK2	inositol hexaphosphate kinase 2	1.54
55760	218198_a _t	DHX32	DEAH (Asp-Glu-Ala-His) box polypeptide 32	-1.32
59342	218217_a _t	SCPEP1	serine carboxypeptidase 1	1.53
55198	218218_a _t	APPL2	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 2	1.49
405	218222_x _at	ARNT	aryl hydrocarbon receptor nuclear translocator	-1.38
51177	218223_s _at	PLEKHO 1	pleckstrin homology domain containing, family O member 1	1.44
55577	218231_a _t	NAGK	N-acetylglucosamine kinase	1.35
51082	218258_a _t	POLR1D	polymerase (RNA) I polypeptide D, 16kDa	1.98
64777	218262_a _t	RMND5B	required for meiotic nuclear division 5 homolog B (<i>S. cerevisiae</i>)	-1.39
58486	218263_s _at	ZBED5	zinc finger, BED-type containing 5	2.11
1468	218275_a _t	SLC25A1 0	solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter), member 10	-1.59
79665	218277_s _at	DHX40	DEAH (Asp-Glu-Ala-His) box polypeptide 40	1.73
80017	218298_s _at	C14orf15 9	chromosome 14 open reading frame 159	2.23
79711	218305_a _t	IPO4	importin 4	-1.53
55316	218307_a _t	RSAD1	radical S-adenosyl methionine domain containing 1	-1.5
65982	218312_s _at	ZSCAN1 8	zinc finger and SCAN domain containing 18	1.89
55758	218344_s _at	RCOR3	REST corepressor 3	1.7
27244	218346_s _at	SESN1	sestrin 1	2.07
51053	218350_s _at	GMNN	geminin, DNA replication inhibitor	3.46
8490	218353_a _t	RGS5	regulator of G-protein signaling 5	2.02
51330	218368_s _at	TNFRSF1 2A	tumor necrosis factor receptor superfamily, member 12A	2.27
64766	218370_s _at	S100PBP	S100P binding protein	1.58

64780	218376_s_at	MICAL1	microtubule associated monooxygenase, calponin and LIM domain containing 1	1.49
79706	218378_s_at	PRKRIP1	PRKR interacting protein 1 (IL11 inducible)	1.43
22861	218380_at	NLRP1	NLR family, pyrin domain containing 1	1.31
94081	218392_x_at	SFXN1	sideroflexin 1	-1.71
55038	218399_s_at	CDCA4	cell division cycle associated 4	-1.25
55240	218424_s_at	STEAP3	STEAP family member 3	-2.13
56984	218467_at	TNFSF5IP1	tumor necrosis factor superfamily, member 5-induced protein 1	1.57
582	218471_s_at	BBS1	Bardet-Biedl syndrome 1	1.43
50650	218501_at	ARHGEF3	Rho guanine nucleotide exchange factor (GEF) 3	2.48
7227	218502_s_at	TRPS1	trichorhinophalangeal syndrome 1	1.71
55030	218539_at	FBXO34	F-box protein 34	1.36
79762	218546_at	C1orf115	chromosome 1 open reading frame 115	-1.68
9935	218559_s_at	MAFB	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	3.2
29995	218574_s_at	LMCD1	LIM and cysteine-rich domains 1	1.65
11266	218576_s_at	DUSP12	dual specificity phosphatase 12	1.44
10161	218589_at	P2RY5	purinergic receptor P2Y, G-protein coupled, 5	2.97
55625	218606_at	ZDHHC7	zinc finger, DHHC-type containing 7	1.43
51278	218611_at	IER5	immediate early response 5	2.6
10078	218612_s_at	TSSC4	tumor suppressing subtransferable candidate 4	-1.29
6839	218619_s_at	SUV39H1	suppressor of variegation 3-9 homolog 1 (Drosophila)	-1.44
54903	218630_at	MKS1	Meckel syndrome, type 1	-1.27
79364	218639_s_at	ZXDC	ZXD family zinc finger C	-1.35
64285	218686_s_at	RHBDF1	rhomboid 5 homolog 1 (Drosophila)	1.68
56667	218687_s_at	MUC13	mucin 13, cell surface associated	2.55
51309	218694_at	ARMCX1	armadillo repeat containing, X-linked 1	2.26
8436	218711_s_at	SDPR	serum deprivation response (phosphatidylserine binding protein)	2.53
56034	218718_at	PDGFC	platelet derived growth factor C	1.97

56925	218729_a_t	LXN	latexin	5.11
29763	218744_s_at	PACSIN3	protein kinase C and casein kinase substrate in neurons 3	-1.65
55080	218746_a_t	TAPBPL	TAP binding protein-like	1.8
5583	218764_a_t	PRKCH	protein kinase C, eta	3
80021	218776_s_at	TMEM62	transmembrane protein 62	-1.26
55013	218802_a_t	CCDC109B	coiled-coil domain containing 109B	1.93
80228	218811_a_t	ORAI2	ORAI calcium release-activated calcium modulator 2	-1.33
51619	218837_s_at	UBE2D4	ubiquitin-conjugating enzyme E2D 4 (putative)	-1.42
64798	218858_a_t	DEPDC6	DEP domain containing 6	1.86
79050	218860_a_t	NOC4L	nucleolar complex associated 4 homolog (S. cerevisiae)	-1.39
79754	218862_a_t	ASB13	ankyrin repeat and SOCS box-containing 13	-2.35
79794	218867_s_at	C12orf49	chromosome 12 open reading frame 49	-1.58
79695	218885_s_at	GALNT12	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 12 (GalNAc-T12)	1.21
79591	218891_a_t	C10orf76	chromosome 10 open reading frame 76	-1.45
63906	218895_a_t	GPATCH3	G patch domain containing 3	-1.35
23586	218943_s_at	DDX58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	1.57
55601	218986_s_at	FLJ20035	hypothetical protein FLJ20035	3.9
63897	218991_a_t	HEATR6	HEAT repeat containing 6	1.23
1906	218995_s_at	EDN1	endothelin 1	1.74
55281	218999_a_t	TMEM140	transmembrane protein 140	1.96
31776_2	219018_s_at	C14orf65	chromosome 14 open reading frame 65	-1.26
79668	219033_a_t	PARP8	poly (ADP-ribose) polymerase family, member 8	2.51
80196	219035_s_at	RNF34	ring finger protein 34	1.73
55790	219049_a_t	ChGn	chondroitin beta1,4 N-acetylgalactosaminyltransferase	2.76
11488_4	219073_s_at	OSBPL10	oxysterol binding protein-like 10	1.87
55022	219093_a_t	PID1	phosphotyrosine interaction domain containing 1	-2.94

79575	219101_x _at	ABHD8	abhydrolase domain containing 8	-1.42
55616	219103_a _t	DDEFL1	development and differentiation enhancing factor-like 1	-1.36
53832	219115_s _at	IL20RA	interleukin 20 receptor, alpha	1.27
51192	219161_s _at	CKLF	chemokine-like factor	1.84
79187	219170_a _t	FSD1	fibronectin type III and SPRY domain containing 1	-1.53
51339	219179_a _t	DACT1	dapper, antagonist of beta-catenin, homolog 1 (<i>Xenopus laevis</i>)	2.05
55670	219180_s _at	PEX26	peroxisome biogenesis factor 26	-1.41
63943	219187_a _t	FKBPL	FK506 binding protein like	-1.5
55833	219192_a _t	UBAP2	ubiquitin associated protein 2	1.84
64135	219209_a _t	IFIH1	interferon induced with helicase C domain 1	2.25
11094	219223_a _t	C9orf7	chromosome 9 open reading frame 7	-1.42
55422	219228_a _t	ZNF331	zinc finger protein 331	4.11
28232	219229_a _t	SLCO3A 1	solute carrier organic anion transporter family, member 3A1	1.39
55273	219230_a _t	TMEM10 0	transmembrane protein 100	2.89
55303	219243_a _t	GIMAP4	GTPase, IMAP family member 4	1.84
79676	219245_s _at	OGFOD2	2-oxoglutarate and iron-dependent oxygenase domain containing 2	-1.43
79886	219276_x _at	C9orf82	chromosome 9 open reading frame 82	-1.63
55619	219279_a _t	DOCK10	dedicator of cytokinesis 10	1.73
79652	219315_s _at	C16orf30	chromosome 16 open reading frame 30	2.46
51003	219318_x _at	MED31	mediator complex subunit 31	-1.35
80179	219320_a _t	MYOHD 1	myosin head domain containing 1	-1.34
51374	219329_s _at	C2orf28	chromosome 2 open reading frame 28	1.5
79778	219332_a _t	MICALL 2	MICAL-like 2	1.55
55008	219352_a _t	HERC6	hect domain and RLD 6	2.18
10365	219371_s _at	KLF2	Kruppel-like factor 2 (lung)	2.01
28981	219372_a _t	IFT81	intraflagellar transport 81 homolog (<i>Chlamydomonas</i>)	1.45
10319	219407_s _at	LAMC3	laminin, gamma 3	2.19

79863	219419_a_t	C18orf22	chromosome 18 open reading frame 22	-1.4
10742	219440_a_t	RAI2	retinoic acid induced 2	2.17
79705	219441_s_at	LRRK1	leucine-rich repeat kinase 1	1.25
79659	219469_a_t	DYNC2H1	dynein, cytoplasmic 2, heavy chain 1	1.35
54920	219486_a_t	DUS2L	dihydrouridine synthase 2-like, SMM1 homolog (<i>S. cerevisiae</i>)	-1.48
51816	219505_a_t	CECR1	cat eye syndrome chromosome region, candidate 1	3.76
79630	219506_a_t	C1orf54	chromosome 1 open reading frame 54	1.73
54996	219527_a_t	MOSC2	MOCO sulphurase C-terminal domain containing 2	-1.63
64919	219528_s_at	BCL11B	B-cell CLL/lymphoma 11B (zinc finger protein)	1.62
1028	219534_x_at	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	1.81
10308	219540_a_t	ZNF267	zinc finger protein 267	1.79
79987	219552_a_t	SVEP1	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	1.3
55604	219573_a_t	LRRC16	leucine rich repeat containing 16	1.62
55378	219599_a_t		NA	2.52
7551	219605_a_t	ZNF3	zinc finger protein 3	-1.3
64793	219611_s_at	CCDC21	coiled-coil domain containing 21	-1.35
51548	219613_s_at	SIRT6	sirtuin (silent mating type information regulation 2 homolog) 6 (<i>S. cerevisiae</i>)	-1.55
51322	219679_s_at	WAC	WW domain containing adaptor with coiled-coil	2.07
80223	219681_s_at	RAB11FIP1	RAB11 family interacting protein 1 (class I)	1.87
64108	219684_a_t	RTP4	receptor (chemosensory) transporter protein 4	1.97
54809	219691_a_t	SAMD9	sterile alpha motif domain containing 9	1.41
54491	219694_a_t	FAM105A	family with sequence similarity 105, member A	1.53
65990	219709_x_at	C16orf24	chromosome 16 open reading frame 24	-1.44
23729	219712_s_at	CARKL	carbohydrate kinase-like	-1.5
56894	219723_x_at	AGPAT3	1-acylglycerol-3-phosphate O-acyltransferase 3	-1.43
5101	219738_s_at	PCDH9	protocadherin 9	1.27
9946	219767_s_at	CRYZL1	crystallin, zeta (quinone reductase)-like 1	2.24

3619	219769_a_t	INCENP	inner centromere protein antigens 135/155kDa	-1.24
23414	219778_a_t	ZFPM2	zinc finger protein, multitype 2	2.76
54978	219783_a_t	C2orf18	chromosome 2 open reading frame 18	-1.31
80778	219801_a_t	ZNF34	zinc finger protein 34	1.24
54853	219809_a_t	WDR55	WD repeat domain 55	-1.44
79037	219812_a_t	PVRIG	poliovirus receptor related immunoglobulin domain containing	1.27
55684	219828_a_t	C9orf86	chromosome 9 open reading frame 86	-1.46
79885	219847_a_t	HDAC11	histone deacetylase 11	-1.47
80741	219860_a_t	LY6G5C	lymphocyte antigen 6 complex, locus G5C	-1.18
51191	219863_a_t	HERC5	hect domain and RLD 5	2.47
29092	219865_a_t	HSPC157	HSPC157 protein	-1.55
79667	219871_a_t	FLJ13197	hypothetical FLJ13197	1.42
79698	219877_a_t	ZMAT4	zinc finger, matrin type 4	-1.2
55106	219885_a_t	SLFN12	schlafen family member 12	1.38
9204	219924_s_at	ZMYM6	zinc finger, MYM-type 6	1.38
4122	219999_a_t	MAN2A2	mannosidase, alpha, class 2A, member 2	-1.49
79836	220009_a_t	LONRF3	LON peptidase N-terminal domain and ring finger 3	-1.76
51334	220014_a_t	PRR16	proline rich 16	1.45
54897	220015_a_t	CASZ1	castor zinc finger 1	-1.48
63929	220020_a_t	XPNPEP3	X-prolyl aminopeptidase (aminopeptidase P) 3, putative	-1.47
23678	220038_a_t	SGK3	serum/glucocorticoid regulated kinase family, member 3	-2.17
57018	220046_s_at	CCNL1	cyclin L1	2.06
10913	220048_a_t	EDAR	ectodysplasin A receptor	-1.22
9573	220053_a_t	GDF3	growth differentiation factor 3	-1.23
55200	220073_s_at	PLEKHG6	pleckstrin homology domain containing, family G (with RhoGef domain) member 6	-1.29
54866	220082_a_t	PPP1R14D	protein phosphatase 1, regulatory (inhibitor) subunit 14D	-1.33
728	220088_a	C5AR1	complement component 5a receptor 1	3

	t			
27156	220105_a_t	RTDR1	rhabdoid tumor deletion region gene 1	-1.18
29881	220106_a_t	NPC1L1	NPC1 (Niemann-Pick disease, type C1, gene)-like 1	-1.98
3781	220116_a_t	KCNN2	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 2	-3.1
29121	220132_s_at	CLEC2D	C-type lectin domain family 2, member D	1.3
9421	220138_a_t	HAND1	heart and neural crest derivatives expressed 1	-1.4
58516	220147_s_at	FAM60A	family with sequence similarity 60, member A	2.19
79645	220156_a_t	EFCAB1	EF-hand calcium binding domain 1	-1.27
56891	220158_a_t	LGALS14	lectin, galactoside-binding, soluble, 14	-1.15
11133	220160_s_at	KPTN	kaptin (actin binding protein)	-1.28
24150	220167_s_at	TP53TG3	TP53TG3 protein	-1.27
64699	220177_s_at	TMPRSS3	transmembrane protease, serine 3	1.99
54542	220201_a_t	RC3H2	ring finger and CCCH-type zinc finger domains 2	-1.5
353500	220203_a_t	BMP8A	bone morphogenetic protein 8a	-1.41
51700	220230_s_at	CYB5R2	cytochrome b5 reductase 2	1.39
55066	220236_a_t	PDPR	pyruvate dehydrogenase phosphatase regulatory subunit	-1.2
51151	220245_a_t	SLC45A2	solute carrier family 45, member 2	-1.36
65989	220262_s_at	DLK2	delta-like 2 homolog (Drosophila)	-1.4
79781	220274_a_t	IQCA	IQ motif containing with AAA domain	-1.18
55693	220278_a_t	JMJD2D	jumonji domain containing 2D	-1.12
79802	220283_a_t	KIAA1822L	KIAA1822-like	-1.35
54857	220291_a_t	GDPD2	glycerophosphodiester phosphodiesterase domain containing 2	-1.3
54925	220292_a_t	ZNF434	zinc finger protein 434	-1.32
79839	220301_a_t	CCDC102B	coiled-coil domain containing 102B	1.55
55001	220309_a_t	TTC22	tetratricopeptide repeat domain 22	-1.23
64092	220330_s_at	SAMSN1	SAM domain, SH3 domain and nuclear localization signals 1	3.4
25823	220339_s_at	TPSG1	tryptase gamma 1	-1.3

80000	220340_a_t	KIAA1772	KIAA1772	-1.48
54798	220373_a_t	DCHS2	dachsous 2 (Drosophila)	-1.22
55466	220395_a_t	DNAJA4	DnaJ (Hsp40) homolog, subfamily A, member 4	-1.51
79158	220398_a_t	GNPTAB	N-acetylglucosamine-1-phosphate transferase, alpha and beta subunits	-1.27
50613	220422_a_t	UBQLN3	ubiquilin 3	-1.22
7827	220424_a_t	NPHS2	nephrosis 2, idiopathic, steroid-resistant (podocin)	-1.43
79890	220439_a_t	RIN3	Ras and Rab interactor 3	-1.26
23418	220522_a_t	CRB1	crumbs homolog 1 (Drosophila)	-1.32
79907	220531_a_t	FLJ14126	hypothetical protein FLJ14126	-1.21
55138	220535_a_t	FAM90A1	family with sequence similarity 90, member A1	-1.27
51297	220542_s_at	PLUNC	palate, lung and nasal epithelium carcinoma associated	-1.53
38775_1	220577_a_t	GVIN1	GTPase, very large interferon inducible 1	1.46
80114	220580_a_t	BICC1	bicaudal C homolog 1 (Drosophila)	1.56
56985	220606_s_at	C17orf48	chromosome 17 open reading frame 48	1.78
55205	220617_s_at	ZNF532	zinc finger protein 532	1.41
54827	220645_a_t	FAM55D	family with sequence similarity 55, member D	-1.23
25979	220690_s_at	DHRS7B	dehydrogenase/reductase (SDR family) member 7B	1.37
10320	220704_a_t	IKZF1	IKAROS family zinc finger 1 (Ikaros)	1.25
	220708_a_t		NA	-1.35
60482	220722_s_at	SLC5A7	solute carrier family 5 (choline transporter), member 7	-1.51
29949	220745_a_t	IL19	interleukin 19	-1.45
79741	220749_a_t	C10orf68	chromosome 10 open reading frame 68	-1.41
3770	220776_a_t	KCNJ14	potassium inwardly-rectifying channel, subfamily J, member 14	-1.24
51702	220779_a_t	PADI3	peptidyl arginine deiminase, type III	-1.3
10394	220811_a_t	PRG3	proteoglycan 3	-1.18
29119	220815_a_t	CTNNA3	catenin (cadherin-associated protein), alpha 3	-1.34
5590	220846_s_at	PRKCZ	protein kinase C, zeta	-1.27

79712	220853_a_t	GTDC1	glycosyltransferase-like domain containing 1	-1.38
	220857_a_t		NA	-1.25
29968	220892_s_at	PSAT1	phosphoserine aminotransferase 1	-2.62
54878	220939_s_at	DPP8	dipeptidyl-peptidase 8	2.11
57730	220940_a_t	KIAA1641	KIAA1641	2.43
57115	220944_a_t	PGLYRP4	peptidoglycan recognition protein 4	-1.81
26000	220947_s_at	TBC1D10B	TBC1 domain family, member 10B	-1.4
29943	220962_s_at	PADI1	peptidyl arginine deiminase, type I	-1.47
29091	220995_a_t	STXBP6	syntaxin binding protein 6 (amisyn)	-1.2
81622	220998_s_at	UNC93B1	unc-93 homolog B1 (C. elegans)	1.64
63969	221001_a_t	C15orf49	chromosome 15 open reading frame 49	-1.22
81618	221004_s_at	ITM2C	integral membrane protein 2C	1.36
83448	221025_x_at	PUS7L	pseudouridylate synthase 7 homolog (S. cerevisiae)-like	-1.27
80975	221032_s_at	TMPRSS5	transmembrane protease, serine 5 (spinesin)	-1.34
56156	221034_s_at	TEX13B	testis expressed 13B	-1.45
50807	221039_s_at	DDEF1	development and differentiation enhancing factor 1	1.89
11022	221052_a_t	TDRKH	tudor and KH domain containing	-1.22
51192	221058_s_at	CKLF	chemokine-like factor	1.68
80833	221087_s_at	APOL3	apolipoprotein L, 3	2.56
10242	221097_s_at	KCNMB2	potassium large conductance calcium-activated channel, subfamily M, beta member 2	-1.25
51310	221106_a_t	SLC22A17	solute carrier family 22 (organic cation transporter), member 17	-1.21
51384	221113_s_at	WNT16	wingless-type MMTV integration site family, member 16	-1.3
55891	221115_s_at	LENEP	lens epithelial protein	-1.26
51741	221147_x_at	WWOX	WW domain containing oxidoreductase	-1.49
56344	221160_s_at	CABP5	calcium binding protein 5	-1.19
10086	221162_a_t	HHLA1	HERV-H LTR-associating 1	-1.39
1103	221197_s	CHAT	choline acetyltransferase	-1.32

	_at			
64096	221199_a_t	GFRA4	GDNF family receptor alpha 4	-1.45
26960	221207_s_at	NBEA	neurobeachin	1.53
26012	221214_s_at	NELF	nasal embryonic LHRH factor	-1.41
79366	221238_a_t	NSBP1	nucleosomal binding protein 1	-1.19
79369	221240_s_at	B3GNT4	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 4	-1.36
	221242_a_t		NA	-1.47
7145	221246_x_at	TNS1	tensin 1	1.47
81566	221260_s_at	FAM130A1	family with sequence similarity 130, member A1	1.65
83442	221269_s_at	SH3BGR L3	SH3 domain binding glutamic acid-rich protein like 3	1.76
727800	221273_s_at	RNF208	ring finger protein 208	-1.39
51237	221286_s_at	MGC29506	hypothetical protein MGC29506	3.11
6041	221287_a_t	RNASEL	ribonuclease L (2',5'-oligoadenylate synthetase-dependent)	-1.37
54328	221299_a_t	GPR173	G protein-coupled receptor 173	-1.29
9293	221313_a_t	GPR52	G protein-coupled receptor 52	-1.43
2661	221314_a_t	GDF9	growth differentiation factor 9	-1.4
58158	221318_a_t	NEUROD4	neurogenic differentiation 4	-1.27
1132	221357_a_t	CHRM4	cholinergic receptor, muscarinic 4	-1.27
	221382_a_t		NA	-1.38
30814	221389_a_t	PLA2G2E	phospholipase A2, group IIE	-1.23
50832	221392_a_t	TAS2R4	taste receptor, type 2, member 4	-1.22
60401	221399_a_t	EDA2R	ectodysplasin A2 receptor	-1.42
56656	221409_a_t	OR2S2	olfactory receptor, family 2, subfamily S, member 2	-1.41
81623	221414_s_at	DEFB126	defensin, beta 126	-1.14
53637	221417_x_at	EDG8	endothelial differentiation, sphingolipid G-protein-coupled receptor, 8	-1.2
81669	221427_s_at	CCNL2	cyclin L2	1.97
81847	221430_s_at	RNF146	ring finger protein 146	1.46

81797	221431_s _at	OR12D3	olfactory receptor, family 12, subfamily D, member 3	-1.24
64960	221437_s _at	MRPS15	mitochondrial ribosomal protein S15	-1.42
50833	221444_a _t	TAS2R16	taste receptor, type 2, member 16	-1.15
83468	221447_s _at	GLT8D2	glycosyltransferase 8 domain containing 2	1.39
56154	221448_s _at	TEX15	testis expressed 15	-1.17
57818	221453_a _t	G6PC2	glucose-6-phosphatase, catalytic, 2	-1.33
4993	221460_a _t	OR2C1	olfactory receptor, family 2, subfamily C, member 1	-1.27
55554	221462_x _at	KLK15	kallikrein-related peptidase 15	-1.24
103910	221474_a _t	MRLC2	myosin regulatory light chain MRLC2	1.39
6138	221475_s _at	RPL15	ribosomal protein L15	1.55
6138	221476_s _at	RPL15	ribosomal protein L15	1.38
665	221479_s _at	BNIP3L	BCL2/adenovirus E1B 19kDa interacting protein 3-like	1.97
339047	221501_x _at	LOC339047	hypothetical protein LOC339047	1.5
2744	221510_s _at	GLS	glutaminase	2.36
9440	221517_s _at	MED17	mediator complex subunit 17	1.76
55143	221520_s _at	CDCA8	cell division cycle associated 8	-1.29
83483	221529_s _at	PLVAP	plasmalemma vesicle associated protein	2.73
79365	221530_s _at	BHLHB3	basic helix-loop-helix domain containing, class B, 3	1.55
10025	221545_x _at	MED16	mediator complex subunit 16	-1.38
84061	221553_a _t	RP11-217H1.1	implantation-associated protein	-1.92
6160	221593_s _at	RPL31	ribosomal protein L31	1.96
57408	221612_a _t	LRTM1	leucine-rich repeats and transmembrane domains 1	-1.16
11277	221642_a _t	TREX1	three prime repair exonuclease 1	-1.19
8022	221670_s _at	LHX3	LIM homeobox 3	-1.53
64581	221698_s _at	CLEC7A	C-type lectin domain family 7, member A	2.58
64220	221701_s _at	STRA6	stimulated by retinoic acid gene 6 homolog (mouse)	-1.28
6146	221726_a _t	RPL22	ribosomal protein L22	1.51

1290	221729_a_t	COL5A2	collagen, type V, alpha 2	2.07
8266	221746_a_t	UBL4A	ubiquitin-like 4A	-1.36
7145	221747_a_t	TNS1	tensin 1	1.91
7145	221748_s_at	TNS1	tensin 1	1.89
11379 1	221756_a_t	PIK3IP1	phosphoinositide-3-kinase interacting protein 1	2.6
4121	221760_a_t	MAN1A1	mannosidase, alpha, class 1A, member 1	-2.15
7357	221765_a_t	UGCG	UDP-glucose ceramide glucosyltransferase	2.59
6421	221768_a_t	SFPQ	splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated)	2.11
2004	221773_a_t	ELK3	ELK3, ETS-domain protein (SRF accessory protein 2)	2.36
55661	221780_s_at	DDX27	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27	1.34
9367	221808_a_t	RAB9A	RAB9A, member RAS oncogene family	1.75
51131	221816_s_at	PHF11	PHD finger protein 11	2.18
57171	221817_a_t	DOLPP1	dolichyl pyrophosphate phosphatase 1	-1.79
54934	221821_s_at	C12orf41	chromosome 12 open reading frame 41	1.33
22097 2	221824_s_at	8-Mar	membrane-associated ring finger (C3HC4) 8	-1.54
9314	221841_s_at	KLF4	Kruppel-like factor 4 (gut)	4.92
11901 6	221850_x_at	CTGLF1	centaurin, gamma-like family, member 1	1.49
55793	221856_s_at	FAM63A	family with sequence similarity 63, member A	-1.34
	221861_a_t		NA	-1.33
5918	221872_a_t	RARRES1	retinoic acid receptor responder (tazarotene induced) 1	2.97
3134	221875_x_at	HLA-F	major histocompatibility complex, class I, F	2.23
1296	221900_a_t	COL8A2	collagen, type VIII, alpha 2	1.26
79848	221925_s_at	CSPP1	centrosome and spindle pole associated protein 1	1.34
2982	221942_s_at	GUCY1A3	guanylate cyclase 1, soluble, alpha 3	2.45
6169	221943_x_at	RPL38	ribosomal protein L38	1.63
84861	221948_s_at	KLHL22	kelch-like 22 (Drosophila)	-1.25
22207	221949_a	LOC2220	hypothetical protein LOC222070	-1.42

0	t	70		
57570	221952_x _at	TRMT5	TRM5 tRNA methyltransferase 5 homolog (<i>S. cerevisiae</i>)	1.89
	221973_a _t		NA	1.51
63968	221974_a _t	PWCR1	Prader-Willi syndrome chromosome region 1	1.98
3134	221978_a _t	HLA-F	major histocompatibility complex, class I, F	2.16
6134	221989_a _t	RPL10	ribosomal protein L10	1.94
11248	221991_a _t	NXPH3	neurexophilin 3	-1.34
51231	221998_s _at	VRK3	vaccinia related kinase 3	-1.63
10471	222019_a _t	PFDN6	prefoldin subunit 6	-1.46
11214	222023_a _t	AKAP13	A kinase (PRKA) anchor protein 13	1.28
72884 4	222040_a _t	LOC7288 44	hypothetical protein LOC728844	2.1
1191	222043_a _t	CLU	clusterin	-1.91
28432 5	222052_a _t	C19orf54	chromosome 19 open reading frame 54	-1.39
9466	222062_a _t	IL27RA	interleukin 27 receptor, alpha	1.3
35318 9	222071_s _at	SLCO4C 1	solute carrier organic anion transporter family, member 4C1	-3.2
14419 5	222088_s _at	SLC2A14	solute carrier family 2 (facilitated glucose transporter), member 14	2.02
54681	222125_s _at	PH-4	hypoxia-inducible factor prolyl 4- hydroxylase	1.5
7594	222136_x _at	ZNF43	zinc finger protein 43	1.35
54103	222150_s _at	tcag7.131 4	hypothetical protein LOC54103	2.28
26010	222154_s _at	LOC2601 0	viral DNA polymerase-transactivated protein 6	1.6
25945	222167_a _t	PVRL3	poliovirus receptor-related 3	-1.42
63876	222185_a _t	PKNOX2	PBX/knotted 1 homeobox 2	-1.36
29992	222218_s _at	PILRA	paired immunoglobulin-like type 2 receptor alpha	1.43
64421	222233_s _at	DCLRE1 C	DNA cross-link repair 1C (PSO2 homolog, <i>S. cerevisiae</i>)	1.6
55616	222236_s _at	DDEFL1	development and differentiation enhancing factor-like 1	-1.58
51477	222240_s _at	ISYNA1	myo-inositol 1-phosphate synthase A1	1.35
84928	222267_a _t	FLJ14803	hypothetical protein FLJ14803	-1.19

	222275_a_t		NA	-1.49
	222281_s_at		NA	1.44
	222288_a_t		NA	1.27
	222296_a_t		NA	-1.51
	222298_a_t		NA	-1.16
	222302_a_t		NA	-1.44
26628	222304_x_at	OR7E47P	olfactory receptor, family 7, subfamily E, member 47 pseudogene	-1.42
3708	222314_x_at	ITPR1	inositol 1,4,5-triphosphate receptor, type 1	1.31
	222363_a_t		NA	-1.47
8554	222371_a_t	PIAS1	protein inhibitor of activated STAT, 1	2.28
59344	222383_s_at	ALOXE3	arachidonate lipoxygenase 3	-1.22
9572	31637_s_at	NR1D1	nuclear receptor subfamily 1, group D, member 1	-1.95
5190	320_at	PEX6	peroxisomal biogenesis factor 6	-1.49
2145	32259_at	EZH1	enhancer of zeste homolog 1 (Drosophila)	1.26
8189	32402_s_at	SYMPK	symplekin	-1.3
5533	32541_at	PPP3CC	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform	1.71
4647	33197_at	MYO7A	myosin VIIA	-1.47
3669	33304_at	ISG20	interferon stimulated exonuclease gene 20kDa	2.58
9399	33736_at	STOML1	stomatin (EPB72)-like 1	-1.33
1762	33768_at	DMWD	dystrophia myotonica, WD repeat containing	-1.48
4626	34471_at	MYH8	myosin, heavy chain 8, skeletal muscle, perinatal	-1.16
816	34846_at	CAMK2B	calcium/calmodulin-dependent protein kinase (CaM kinase) II beta	-1.38
23381	34868_at	SMG5	Smg-5 homolog, nonsense mediated mRNA decay factor (C. elegans)	-1.51
8859	36019_at	STK19	serine/threonine kinase 19	-1.27
9905	36129_at	SGSM2	small G protein signaling modulator 2	-1.37
23201	36612_at	KIAA0280	KIAA0280	-1.56
23764	36711_at	MAFF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	5.51
4598	36907_at	MVK	mevalonate kinase (mevalonic aciduria)	-1.75
6439	37004_at	SFTPB	surfactant, pulmonary-associated protein B	-1.18

9902	37408_at	MRC2	mannose receptor, C type 2	1.45
7701	37586_at	ZNF142	zinc finger protein 142	-1.13
60343	38043_at	FAM3A	family with sequence similarity 3, member A	-1.46
9938	38149_at	ARHGAP25	Rho GTPase activating protein 25	1.42
10384	38241_at	BTN3A3	butyrophilin, subfamily 3, member A3	2.12
10636	38290_at	RGS14	regulator of G-protein signaling 14	-1.5
156	38447_at	ADRBK1	adrenergic, beta, receptor kinase 1	-1.42
6440	38691_s_at	SFTPC	surfactant, pulmonary-associated protein C	-1.62
1874	38707_r_at	E2F4	E2F transcription factor 4, p107/p130-binding	-2
55611	38710_at	OTUB1	OTU domain, ubiquitin aldehyde binding 1	-1.42
10847	38766_at	SRCAP	Snf2-related CBP activator protein	-1.25
9580	38918_at	SOX13	SRY (sex determining region Y)-box 13	-1.35
4862	39548_at	NPAS2	neuronal PAS domain protein 2	-1.25
1540	39582_at	CYLD	cylindromatosis (turban tumor syndrome)	1.57
2057	396_f_at	EPOR	erythropoietin receptor	-1.89
3263	39763_at	HPX	hemopexin	-1.54
29781	40640_at	NCAPH2	non-SMC condensin II complex, subunit H2	-1.29
5266	41469_at	PI3	peptidase inhibitor 3, skin-derived (SKALP)	-1.19
6794	41657_at	STK11	serine/threonine kinase 11	-1.67
32	43427_at	ACACB	acetyl-Coenzyme A carboxylase beta	-2.03
10025	43544_at	MED16	mediator complex subunit 16	-1.72
54929	43977_at	TMEM161A	transmembrane protein 161A	-1.29
90956	44120_at	ADCK2	aarF domain containing kinase 2	-1.24
55135	44563_at	WDR79	WD repeat domain 79	-1.44
54662	44696_at	TBC1D13	TBC1 domain family, member 13	-1.29
7776	47571_at	ZNF236	zinc finger protein 236	-2.38
10826	48030_i_at	C5orf4	chromosome 5 open reading frame 4	-1.97
30827	48580_at	CXXC1	CXXC finger 1 (PHD domain)	-1.28
9683	48612_at	N4BP1	Nedd4 binding protein 1	-1.42
83937	49306_at	RASSF4	Ras association (RalGDS/AF-6) domain family 4	1.71
222070	51774_s_at	LOC222070	hypothetical protein LOC222070	-2.06
59307	52940_at	SIGIRR	single immunoglobulin and toll-interleukin 1 receptor (TIR) domain	-1.51
83637	54970_at	ZMIZ2	zinc finger, MIZ-type containing 2	-1.55
91300	55705_at	C19orf22	chromosome 19 open reading frame 22	-1.46
55238	56821_at	FLJ10815	amino acid transporter	-1.27
222070	58900_at	LOC222070	hypothetical protein LOC222070	-1.88

8996	59625_at	NOL3	nucleolar protein 3 (apoptosis repressor with CARD domain)	1.38
27092	62987_r_at	CACNG4	calcium channel, voltage-dependent, gamma subunit 4	-1.6
51275	64432_at	C12orf47	chromosome 12 open reading frame 47	1.31
84818	64440_at	IL17RC	interleukin 17 receptor C	-1.74
54487	64474_g_at	DGCR8	DiGeorge syndrome critical region gene 8	-1.45
158747	64883_at	MOSPD2	motile sperm domain containing 2	-1.25
85002	65585_at	FAM86B1	family with sequence similarity 86, member B1	-1.54
57599	65591_at	WDR48	WD repeat domain 48	-1.38
25960	65718_at	GPR124	G protein-coupled receptor 124	1.4
54512	91682_at	EXOSC4	exosome component 4	-1.36
90379	91952_at	LOC90379	hypothetical protein BC002926	-1.34
6772	AFFX-HUMISG F3A/M97 935_3_at	STAT1	signal transducer and activator of transcription 1, 91kDa	2.34
6772	AFFX-HUMISG F3A/M97 935_MA_at	STAT1	signal transducer and activator of transcription 1, 91kDa	2.06
6772	AFFX-HUMISG F3A/M97 935_MB_at	STAT1	signal transducer and activator of transcription 1, 91kDa	2.39
	AFFX-M27830_3_at		NA	-1.41
	AFFX-M27830_M_at		NA	1.49

Appendix 3

Supplemental Table 3- Genes With Significant Estimate Value for the Interaction of HCV and Alcohol

Entrez ID	Affy ID	Symbol	Gene Name	Estimate
2101	1487_at	ESRRA	estrogen-related receptor alpha	0.86
8717	1729_at	TRADD	TNFRSF1A-associated via death domain	0.49
441263	179_at	PMS2L11	postmeiotic segregation increased 2-like 11	0.83
572	1861_at	BAD	BCL2-antagonist of cell death	0.59
4735	200015_s_at	SEPT2	septin 2	-0.92
23	200045_at	ABCF1	ATP-binding cassette, sub-family F (GCN20), member 1	0.78
6881	200055_at	TAF10	TAF10 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 30kDa	0.85
3550	200066_at	IK	IK cytokine, down-regulator of HLA II	-0.74
821	200068_s_at	CANX	calnexin	0.55
27013	200070_at	C2orf24	chromosome 2 open reading frame 24	-0.81
23326	200083_at	USP22	ubiquitin specific peptidase 22	0.88
10959	200087_s_at	TMED2	transmembrane emp24 domain trafficking protein 2	0.84
7184	200599_s_at	HSP90B1	heat shock protein 90kDa beta (Grp94), member 1	0.78
9761	200616_s_at	KIAA0152	KIAA0152	1.75
9761	200617_at	KIAA0152	KIAA0152	1.99
10397	200632_s_at	NDRG1	N-myc downstream regulated gene 1	-1.2
5792	200636_s_at	PTPRF	protein tyrosine phosphatase, receptor type, F	1.6
5792	200637_s_at	PTPRF	protein tyrosine phosphatase, receptor type, F	1.81

7534	200639_s_at	YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	-0.79
4924	200649_a_t	NUCB1	nucleobindin 1	1.35
5034	200654_a_t	P4HB	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide	0.93
5034	200656_s_at	P4HB	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide	1.35
3313	200692_s_at	HSPA9	heat shock 70kDa protein 9 (mortalin)	0.95
2934	200696_s_at	GSN	gelsolin (amyloidosis, Finnish type)	-1.93
11014	200698_a_t	KDEL2	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	1.3
11014	200700_s_at	KDEL2	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	1.24
1808	200762_a_t	DPYSL2	dihydropyrimidinase-like 2	-1.59
3915	200771_a_t	LAMC1	laminin, gamma 1 (formerly LAMB2)	-1.15
8682	200788_s_at	PEA15	phosphoprotein enriched in astrocytes 15	-0.98
8826	200791_s_at	IQGAP1	IQ motif containing GTPase activating protein 1	-1.35
8404	200795_a_t	SPARCL1	SPARC-like 1 (mast9, hevin)	-2.51
1153	200810_s_at	CIRBP	cold inducible RNA binding protein	-1.1
2950	200824_a_t	GSTP1	glutathione S-transferase pi	-1.21
10525	200825_s_at	HYOU1	hypoxia up-regulated 1	2.19
149934	200856_x_at	C20orf191	chromosome 20 open reading frame 191	1.08
2316	200859_x_at	FLNA	filamin A, alpha (actin binding protein 280)	-1.17
23019	200861_a_t	CNOT1	CCR4-NOT transcription complex, subunit 1	0.92
6745	200889_s_at	SSR1	signal sequence receptor, alpha (translocon-associated protein alpha)	1.58
6745	200890_s_at	SSR1	signal sequence receptor, alpha (translocon-associated protein alpha)	1.84
6745	200891_s_at	SSR1	signal sequence receptor, alpha (translocon-associated protein alpha)	1
2288	200894_s	FKBP4	FK506 binding protein 4, 59kDa	0.91

	_at			
23022	200897_s_at	PALLD	palladin, cytoskeletal associated protein	-1.38
23022	200907_s_at	PALLD	palladin, cytoskeletal associated protein	-1.21
6867	200911_s_at	TACC1	transforming, acidic coiled-coil containing protein 1	-1.12
5496	200913_at	PPM1G	protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform	0.59
10945	200922_at	KDEL1	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1	1.11
811	200935_at	CALR	calreticulin	2.4
3150	200944_s_at	HMG1	high-mobility group nucleosome binding domain 1	-0.91
2746	200946_x_at	GLUD1	glutamate dehydrogenase 1	1.3
10552	200950_at	ARPC1A	actin related protein 2/3 complex, subunit 1A, 41kDa	0.78
2521	200959_at	FUS	fusion (involved in t(12;16) in malignant liposarcoma)	-1.03
5479	200967_at	PPIB	peptidylprolyl isomerase B (cyclophilin B)	0.84
27230	200970_s_at	SERP1	stress-associated endoplasmic reticulum protein 1	0.99
27230	200971_s_at	SERP1	stress-associated endoplasmic reticulum protein 1	1.29
9784	200991_s_at	SNX17	sorting nexin 17	0.7
16	201000_at	AARS	alanyl-tRNA synthetase	0.82
10628	201008_s_at	TXNIP	thioredoxin interacting protein	-1.93
10628	201009_s_at	TXNIP	thioredoxin interacting protein	-1.86
10628	201010_s_at	TXNIP	thioredoxin interacting protein	-1.77
301	201012_at	ANXA1	annexin A1	-2.52
3945	201030_x_at	LDHB	lactate dehydrogenase B	-2.53
120	201034_at	ADD3	adducin 3 (gamma)	-1.46
4313	201069_at	MMP2	matrix metalloproteinase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)	-1.87
1611	201095_at	DAP	death-associated protein	0.92
378	201096_s_at	ARF4	ADP-ribosylation factor 4	1.24

3956	201105_a_t	LGALS1	lectin, galactoside-binding, soluble, 1 (galectin 1)	-1.31
7057	201110_s_at	THBS1	thrombospondin 1	-2.67
999	201131_s_at	CDH1	cadherin 1, type 1, E-cadherin (epithelial)	-1.07
3115	201137_s_at	HLA-DPB1	major histocompatibility complex, class II, DP beta 1	-2.38
10457	201141_a_t	GPNMB	glycoprotein (transmembrane) nmb	-2.42
7078	201150_s_at	TIMP3	TIMP metalloproteinase inhibitor 3 (Sorsby fundus dystrophy, pseudoinflammatory)	-1.68
3490	201162_a_t	IGFBP7	insulin-like growth factor binding protein 7	-1.87
3490	201163_s_at	IGFBP7	insulin-like growth factor binding protein 7	-1.32
372	201176_s_at	ARCNI	archain 1	0.84
5510	201213_a_t	PPP1R7	protein phosphatase 1, regulatory (inhibitor) subunit 7	0.47
1488	201220_x_at	CTBP2	C-terminal binding protein 2	-1.06
9789	201240_s_at	SPCS2	signal peptidase complex subunit 2 homolog (<i>S. cerevisiae</i>)	0.93
5704	201252_a_t	PSMC4	proteasome (prosome, macropain) 26S subunit, ATPase, 4	0.7
633	201261_x_at	BGN	biglycan	-1.66
11316	201264_a_t	COPE	coatamer protein complex, subunit epsilon	0.9
1601	201278_a_t	DAB2	disabled homolog 2, mitogen-responsive phosphoprotein (<i>Drosophila</i>)	-1.59
1601	201280_s_at	DAB2	disabled homolog 2, mitogen-responsive phosphoprotein (<i>Drosophila</i>)	-1.47
3491	201289_a_t	CYR61	cysteine-rich, angiogenic inducer, 61	-2.34
307	201301_s_at	ANXA4	annexin A4	-1.43
307	201302_a_t	ANXA4	annexin A4	-1.58
6451	201312_s_at	SH3BGR L	SH3 domain binding glutamic acid-rich protein like	-1.29
2012	201324_a_t	EMP1	epithelial membrane protein 1	-3.2
9341	201336_a_t	VAMP3	vesicle-associated membrane protein 3 (cellubrevin)	-0.9
2319	201350_a_t	FLOT2	flotillin 2	1.04
10131	201391_a_t	TRAP1	TNF receptor-associated protein 1	0.64

23471	201399_s_at	TRAM1	translocation associated membrane protein 1	1.31
5691	201400_a_t	PSMB3	proteasome (prosome, macropain) subunit, beta type, 3	0.74
5690	201404_x_at	PSMB2	proteasome (prosome, macropain) subunit, beta type, 2	0.73
6659	201418_s_at	SOX4	SRY (sex determining region Y)-box 4	-0.92
8314	201419_a_t	BAP1	BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase)	0.45
79084	201421_s_at	WDR77	WD repeat domain 77	0.66
7431	201426_s_at	VIM	vimentin	-1.92
9791	201433_s_at	PTDSS1	phosphatidylserine synthase 1	0.61
1293	201438_a_t	COL6A3	collagen, type VI, alpha 3	-1.74
4629	201496_x_at	MYH11	myosin, heavy chain 11, smooth muscle	-0.82
3912	201505_a_t	LAMB1	laminin, beta 1	-2.03
14	201511_a_t	AAMP	angio-associated, migratory cell protein	0.56
9868	201512_s_at	TOMM70A	translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	1.02
6723	201516_a_t	SRM	spermidine synthase	0.98
22883	201561_s_at	CLSTN1	calsyntenin 1	-1.02
2803	201567_s_at	GOLGA4	golgi autoantigen, golgin subfamily a, 4	0.93
10483	201582_a_t	SEC23B	Sec23 homolog B (S. cerevisiae)	1.79
10483	201583_s_at	SEC23B	Sec23 homolog B (S. cerevisiae)	1.22
302	201590_x_at	ANXA2	annexin A2	-1.25
800	201615_x_at	CALD1	caldesmon 1	-1.25
27044	201622_a_t	SND1	staphylococcal nuclease and tudor domain containing 1	0.82
400	201657_a_t	ARL1	ADP-ribosylation factor-like 1	1.33
2697	201667_a_t	GJA1	gap junction protein, alpha 1, 43kDa	-2.81
9231	201681_s_at	DLG5	discs, large homolog 5 (Drosophila)	-0.65
7163	201688_s_at	TPD52	tumor protein D52	1.52
7163	201689_s_at	TPD52	tumor protein D52	1.94

7283	201714_a _t	TUBG1	tubulin, gamma 1	1.34
2037	201719_s _at	EPB41L2	erythrocyte membrane protein band 4.1-like 2	-1.2
9703	201728_s _at	KIAA010 0	KIAA0100	1.1
9703	201729_s _at	KIAA010 0	KIAA0100	1.86
4060	201744_s _at	LUM	lumican	-4.04
120	201752_s _at	ADD3	adducin 3 (gamma)	-0.91
120	201753_s _at	ADD3	adducin 3 (gamma)	-1.23
55884	201760_s _at	WSB2	WD repeat and SOCS box- containing 2	1.31
10797	201761_a _t	MTHFD2	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase	-2.68
165	201792_a _t	AEBP1	AE binding protein 1	-1.52
5007	201799_s _at	OSBP	oxysterol binding protein	1.09
5007	201800_s _at	OSBP	oxysterol binding protein	0.96
9467	201810_s _at	SH3BP5	SH3-domain binding protein 5 (BTK-associated)	-1.17
9467	201811_x _at	SH3BP5	SH3-domain binding protein 5 (BTK-associated)	-1.19
9690	201817_a _t	UBE3C	ubiquitin protein ligase E3C	0.97
10440	201821_s _at	TIMM17 A	translocase of inner mitochondrial membrane 17 homolog A (yeast)	1.03
4072	201839_s _at	TACSTD 1	tumor-associated calcium signal transducer 1	-3.22
2202	201842_s _at	EFEMP1	EGF-containing fibulin-like extracellular matrix protein 1	-3.29
2202	201843_s _at	EFEMP1	EGF-containing fibulin-like extracellular matrix protein 1	-2.97
6455	201851_a _t	SH3GL1	SH3-domain GRB2-like 1	0.56
5552	201858_s _at	SRGN	serglycin	-2.25
5552	201859_a _t	SRGN	serglycin	-1.2
5327	201860_s _at	PLAT	plasminogen activator, tissue	-1.91
1634	201893_x _at	DCN	decorin	-1.7
1634	201894_s _at	DCN	decorin	1.27

369	201895_a_t	ARAF	v-raf murine sarcoma 3611 viral oncogene homolog	0.77
10217	201904_s_at	CTDSPL	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like	-1.09
80347	201913_s_at	COASY	Coenzyme A synthase	0.97
11231	201915_a_t	SEC63	SEC63 homolog (S. cerevisiae)	1.07
55186	201918_a_t	SLC25A36	solute carrier family 25, member 36	-1.49
55186	201919_a_t	SLC25A36	solute carrier family 25, member 36	-1.02
10549	201923_a_t	PRDX4	peroxiredoxin 4	1.03
4299	201924_a_t	AFF1	AF4/FMR2 family, member 1	-0.86
23064	201964_a_t	SETX	senataxin	1.03
4651	201976_s_at	MYO10	myosin X	-1.35
6480	201998_a_t	ST6GAL1	ST6 beta-galactosamide alpha-2,6-sialyltransferase 1	1
9220	202039_a_t	TIAF1	TGFB1-induced anti-apoptotic factor 1	0.99
9158	202041_s_at	FIBP	fibroblast growth factor (acidic) intracellular binding protein	0.89
2909	202046_s_at	GRLF1	glucocorticoid receptor DNA binding factor 1	0.82
6400	202062_s_at	SEL1L	sel-1 suppressor of lin-12-like (C. elegans)	1.6
6400	202063_s_at	SEL1L	sel-1 suppressor of lin-12-like (C. elegans)	0.74
6400	202064_s_at	SEL1L	sel-1 suppressor of lin-12-like (C. elegans)	1.52
3476	202105_a_t	IGBP1	immunoglobulin (CD79A) binding protein 1	-0.77
23647	202109_a_t	ARFIP2	ADP-ribosylation factor interacting protein 2 (arfaptin 2)	1.22
6522	202111_a_t	SLC4A2	solute carrier family 4, anion exchanger, member 2 (erythrocyte membrane protein band 3-like 1)	0.97
7450	202112_a_t	VWF	von Willebrand factor	-1.85
25937	202132_a_t	WWTR1	WW domain containing transcription regulator 1	-1.07
25937	202133_a_t	WWTR1	WW domain containing transcription regulator 1	-1.53
10120	202135_s_at	ACTR1B	ARP1 actin-related protein 1 homolog B, contractin beta (yeast)	0.53
4739	202149_a_t	NEDD9	neural precursor cell expressed, developmentally down-regulated 9	-2.13
10659	202157_s	CUGBP2	CUG triplet repeat, RNA binding	-2.11

	_at		protein 2	
2621	202177_a_t	GAS6	growth arrest-specific 6	-0.86
50999	202195_s_at	TMED5	transmembrane emp24 protein transport domain containing 5	1.31
6732	202199_s_at	SRPK1	SFRS protein kinase 1	0.64
10123	202207_a_t	ARL4C	ADP-ribosylation factor-like 4C	-1.97
10123	202208_s_at	ARL4C	ADP-ribosylation factor-like 4C	-1
4802	202215_s_at	NFYC	nuclear transcription factor Y, gamma	0.66
10443	202258_s_at	PFAAP5	phosphonoformate immuno-associated protein 5	-1.05
5159	202273_a_t	PDGFRB	platelet-derived growth factor receptor, beta polypeptide	-0.9
4070	202286_s_at	TACSTD2	tumor-associated calcium signal transducer 2	-3.25
4256	202291_s_at	MGP	matrix Gla protein	-3.47
1512	202295_s_at	CTSH	cathepsin H	-1.31
11079	202296_s_at	RER1	RER1 retention in endoplasmic reticulum 1 homolog (<i>S. cerevisiae</i>)	1.01
10277	202316_x_at	UBE4B	ubiquitination factor E4B (UFD2 homolog, yeast)	0.54
1454	202332_a_t	CSNK1E	casein kinase 1, epsilon	-1.01
5066	202336_s_at	PAM	peptidylglycine alpha-amidating monooxygenase	-1.49
23321	202341_s_at	TRIM2	tripartite motif-containing 2	-0.96
1861	202348_s_at	TOR1A	torsin family 1, member A (torsin A)	0.61
2962	202356_s_at	GTF2F1	general transcription factor IIF, polypeptide 1, 74kDa	0.52
399979	202358_s_at	SNX19	sorting nexin 19	0.87
9632	202361_a_t	SEC24C	SEC24 related gene family, member C (<i>S. cerevisiae</i>)	0.64
84747	202365_a_t	UNC119B	unc-119 homolog B (<i>C. elegans</i>)	1.05
9697	202369_s_at	TRAM2	translocation associated membrane protein 2	1.24
9871	202375_a_t	SEC24D	SEC24 related gene family, member D (<i>S. cerevisiae</i>)	2.13
12	202376_a_t	SERPINA3	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3	0.88
5997	202388_a_t	RGS2	regulator of G-protein signaling 2, 24kDa	-2.76
3064	202389_s	HD	huntingtin (Huntington disease)	0.66

	_at			
1278	202403_s_at	COL1A2	collagen, type I, alpha 2	-2.1
10897	202418_at	YIF1A	Yip1 interacting factor homolog A (S. cerevisiae)	1
5605	202424_at	MAP2K2	mitogen-activated protein kinase kinase 2	0.92
6256	202426_s_at	RXRA	retinoid X receptor, alpha	1.29
10237	202433_at	SLC35B1	solute carrier family 35, member B1	1.5
6256	202449_s_at	RXRA	retinoid X receptor, alpha	1.08
5209	202464_s_at	PFKFB3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	-1.59
4351	202472_at	MPI	mannose phosphate isomerase	0.58
9474	202511_s_at	ATG5	ATG5 autophagy related 5 homolog (S. cerevisiae)	0.89
5528	202513_s_at	PPP2R5D	protein phosphatase 2, regulatory subunit B', delta isoform	0.55
9255	202541_at	SCYE1	small inducible cytokine subfamily E, member 1 (endothelial monocyte-activating)	1.2
51232	202551_s_at	CRIM1	cysteine rich transmembrane BMP regulator 1 (chordin-like)	-1.83
51232	202552_s_at	CRIM1	cysteine rich transmembrane BMP regulator 1 (chordin-like)	-1.65
6782	202558_s_at	STCH	stress 70 protein chaperone, microsome-associated, 60kDa	1.69
55308	202578_s_at	DDX19A	DEAD (Asp-Glu-Ala-As) box polypeptide 19A	1.04
51573	202593_s_at	MIR16	membrane interacting protein of RGS16	1.26
3340	202607_at	NDST1	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	0.85
4221	202645_s_at	MEN1	multiple endocrine neoplasia I	0.94
9772	202650_s_at	KIAA0195	KIAA0195	0.71
7873	202655_at	ARMET	arginine-rich, mutated in early stage tumors	1.44
7456	202664_at	WIPF1	WAS/WASL interacting protein family, member 1	-1.4
8566	202671_s_at	PDXK	pyridoxal (pyridoxine, vitamin B6) kinase	0.95
29890	202689_at	RBM15B	RNA binding motif protein 15B	0.64
7372	202707_at	UMPS	uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase)	0.41
10282	202710_at	BET1	BET1 homolog (S. cerevisiae)	1.13

2673	202721_s_at	GFPT1	glutamine-fructose-6-phosphate transaminase 1	1.37
2673	202722_s_at	GFPT1	glutamine-fructose-6-phosphate transaminase 1	1.88
23428	202752_x_at	SLC7A8	solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 8	0.74
7867	202788_a_t	MAPKAPK3	mitogen-activated protein kinase-activated protein kinase 3	0.74
5566	202801_a_t	PRKACA	protein kinase, cAMP-dependent, catalytic, alpha	0.93
6924	202819_s_at	TCEB3	transcription elongation factor B (SIII), polypeptide 3 (110kDa, elongin A)	0.82
4026	202822_a_t	LPP	LIM domain containing preferred translocation partner in lipoma	-0.89
2877	202831_a_t	GPX2	glutathione peroxidase 2 (gastrointestinal)	1.5
4189	202842_s_at	DNAJB9	DnaJ (Hsp40) homolog, subfamily B, member 9	1.15
9267	202880_s_at	PSCD1	pleckstrin homology, Sec7 and coiled-coil domains 1 (cytohesin 1)	-0.69
10497	202893_a_t	UNC13B	unc-13 homolog B (C. elegans)	0.99
976	202910_s_at	CD97	CD97 molecule	-1.32
9826	202913_a_t	ARHGEF11	Rho guanine nucleotide exchange factor (GEF) 11	0.65
287	202920_a_t	ANK2	ankyrin 2, neuronal	-1.26
6662	202935_s_at	SOX9	SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal)	-2.2
6662	202936_s_at	SOX9	SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal)	-1.45
2995	202947_s_at	GYPC	glycophorin C (Gerbich blood group)	-0.82
2274	202949_s_at	FHL2	four and a half LIM domains 2	-1.78
5996	202988_s_at	RGS1	regulator of G-protein signaling 1	-3.3
730	202992_a_t	C7	complement component 7	-2.37
2192	202994_s_at	FBLN1	fibulin 1	-1.78
51421	203002_a_t	AMOTL2	angiominin like 2	-1.28
5799	203029_s_at	PTPRN2	protein tyrosine phosphatase, receptor type, N polypeptide 2	-0.86
3145	203040_s_at	HMBS	hydroxymethylbilane synthase	0.93
8914	203046_s_at	TIMELESS	timeless homolog (Drosophila)	0.86

51363	203066_a_t	GALNAC4S-6ST	B cell RAG associated protein	-1.04
7869	203071_a_t	SEMA3B	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3B	-0.84
10516	203088_a_t	FBLN5	fibulin 5	-2.43
4247	203102_s_at	MGAT2	mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	1.16
9040	203109_a_t	UBE2M	ubiquitin-conjugating enzyme E2M (UBC12 homolog, yeast)	0.87
9924	203117_s_at	USP52	ubiquitin specific peptidase 52	1
4891	203123_s_at	SLC11A2	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	1.15
5156	203131_a_t	PDGFRA	platelet-derived growth factor receptor, alpha polypeptide	-2.43
10952	203133_a_t	SEC61B	Sec61 beta subunit	0.89
10567	203136_a_t	RABAC1	Rab acceptor 1 (prenylated)	1.55
10298	203154_s_at	PAK4	p21(CDKN1A)-activated kinase 4	0.67
2744	203159_a_t	GLS	glutaminase	-1.35
9197	203164_a_t	SLC33A1	solute carrier family 33 (acetyl-CoA transporter), member 1	1.73
9197	203165_s_at	SLC33A1	solute carrier family 33 (acetyl-CoA transporter), member 1	1.88
10257	203196_a_t	ABCC4	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	-1.02
4552	203200_s_at	MTRR	5-methyltetrahydrofolate-homocysteine methyltransferase reductase	1.2
9650	203207_s_at	MTFR1	mitochondrial fission regulator 1	1.26
9650	203208_s_at	MTFR1	mitochondrial fission regulator 1	1.12
8869	203217_s_at	ST3GAL5	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	0.89
5830	203244_a_t	PEX5	peroxisomal biogenesis factor 5	0.75
3660	203275_a_t	IRF2	interferon regulatory factor 2	0.91
9695	203279_a_t	EDEM1	ER degradation enhancer, mannosidase alpha-like 1	1.1
9667	203280_a_t	SAFB2	scaffold attachment factor B2	-1.01
9653	203285_s_at	HS2ST1	heparan sulfate 2-O-sulfotransferase 1	0.95
3998	203294_s	LMAN1	lectin, mannose-binding, 1	1.15

	_at			
3720	203297_s_at	JARID2	jumonji, AT rich interactive domain 2	-0.75
8440	203315_a_t	NCK2	NCK adaptor protein 2	-1.45
23550	203317_a_t	PSD4	pleckstrin and Sec7 domain containing 4	0.61
3416	203327_a_t	IDE	insulin-degrading enzyme	0.98
3416	203328_x_at	IDE	insulin-degrading enzyme	1.42
3635	203331_s_at	INPP5D	inositol polyphosphate-5-phosphatase, 145kDa	-0.73
7358	203343_a_t	UGDH	UDP-glucose dehydrogenase	1.36
9776	203364_s_at	KIAA0652	KIAA0652	0.57
2800	203383_s_at	GOLGA1	golgi autoantigen, golgin subfamily a, 1	0.68
2800	203384_s_at	GOLGA1	golgi autoantigen, golgin subfamily a, 1	0.53
1487	203392_s_at	CTBP1	C-terminal binding protein 1	1.25
6304	203408_s_at	SATB1	SATB homeobox 1	-0.91
10106	203445_s_at	CTDSP2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2	0.72
6697	203458_a_t	SPR	sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase)	0.98
8662	203462_x_at	EIF3B	eukaryotic translation initiation factor 3, subunit B	0.97
23480	203484_a_t	SEC61G	Sec61 gamma subunit	0.94
5195	203503_s_at	PEX14	peroxisomal biogenesis factor 14	0.74
9391	203536_s_at	CIAO1	cytosolic iron-sulfur protein assembly 1 homolog (S. cerevisiae)	0.68
79053	203545_a_t	ALG8	asparagine-linked glycosylation 8 homolog (S. cerevisiae, alpha-1,3-glucosyltransferase)	0.8
8836	203560_a_t	GGH	gamma-glutamyl hydrolase (conjugase, foylpolypolygammaglutamyl hydrolase)	1.85
7709	203601_s_at	ZBTB17	zinc finger and BTB domain containing 17	-1.24
23017	203619_s_at	FAIM2	Fas apoptotic inhibitory molecule 2	0.29
51704	203632_s_at	GPRC5B	G protein-coupled receptor, family C, group 5, member B	-1.1
4281	203637_s_at	MID1	midline 1 (Opitz/BBB syndrome)	-1.43

2263	203638_s_at	FGFR2	fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer syndrome, Jackson-Weiss syndrome)	-2.5
2263	203639_s_at	FGFR2	fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer syndrome, Jackson-Weiss syndrome)	-1.67
22879	203644_s_at	MON1B	MON1 homolog B (yeast)	0.83
5433	203664_s_at	POLR2D	polymerase (RNA) II (DNA directed) polypeptide D	0.63
6387	203666_a_t	CXCL12	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)	-1.79
4925	203675_a_t	NUCB2	nucleobindin 2	1.83
6895	203677_s_at	TARBP2	TAR (HIV-1) RNA binding protein 2	0.54
596	203685_a_t	BCL2	B-cell CLL/lymphoma 2	-1.22
8324	203706_s_at	FZD7	frizzled homolog 7 (Drosophila)	-2.09
5261	203709_a_t	PHKG2	phosphorylase kinase, gamma 2 (testis)	0.69
578	203728_a_t	BAK1	BCL2-antagonist/killer 1	0.63
28955	203733_a_t	DEXI	dexamethasone-induced transcript	1.04
360	203747_a_t	AQP3	aquaporin 3 (Gill blood group)	1.11
5937	203748_x_at	RBMS1	RNA binding motif, single stranded interacting protein 1	-1.2
6925	203753_a_t	TCF4	transcription factor 4	-1.65
6503	203761_a_t	SLA	Src-like-adaptor	-1.28
644	203771_s_at	BLVRA	biliverdin reductase A	-0.82
644	203773_x_at	BLVRA	biliverdin reductase A	-1.05
7103	203824_a_t	TSPAN8	tetraspanin 8	-1.91
26610	203829_a_t	ELP4	elongation protein 4 homolog (S. cerevisiae)	0.67
2199	203886_s_at	FBLN2	fibulin 2	-0.92
1613	203891_s_at	DAPK3	death-associated protein kinase 3	-1.47
5909	203911_a_t	RAP1GA P	RAP1 GTPase activating protein	1.17

1525	203917_a_t	CXADR	coxsackie virus and adenovirus receptor	-1.18
10062	203920_a_t	NR1H3	nuclear receptor subfamily 1, group H, member 3	1.05
1479	203947_a_t	CSTF3	cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kDa	0.69
2167	203980_a_t	FABP4	fatty acid binding protein 4, adipocyte	-2.49
2149	203989_x_at	F2R	coagulation factor II (thrombin) receptor	-1.53
5774	203997_a_t	PTPN3	protein tyrosine phosphatase, non-receptor type 3	1.28
6619	204001_a_t	SNAPC3	small nuclear RNA activating complex, polypeptide 3, 50kDa	0.57
5074	204004_a_t	PAWR	PRKC, apoptosis, WT1, regulator	-0.95
26751	204019_s_at	SH3YL1	SH3 domain containing, Ysc84-like 1 (S. cerevisiae)	-2.57
23637	204028_s_at	RABGAP1	RAB GTPase activating protein 1	-0.73
1902	204037_a_t	EDG2	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2	-0.87
4199	204058_a_t	ME1	malic enzyme 1, NADP(+)-dependent, cytosolic	1.44
116987	204066_s_at	CENTG2	centaurin, gamma 2	0.65
10609	204078_a_t	SC65	synaptonemal complex protein SC65	-0.6
8459	204079_a_t	TPST2	tyrosylprotein sulfotransferase 2	1.14
7169	204083_s_at	TPM2	tropomyosin 2 (beta)	-1.69
6604	204099_a_t	SMARD3	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3	-0.5
2309	204131_s_at	FOXO3	forkhead box O3	-1.83
11259	204135_a_t	FILIP1L	filamin A interacting protein 1-like	-1.98
27252	204177_s_at	KLHL20	kelch-like 20 (Drosophila)	-0.72
10432	204178_s_at	RBM14	RNA binding motif protein 14	0.85
5481	204186_s_at	PPID	peptidylprolyl isomerase D (cyclophilin D)	1.14
3454	204191_a_t	IFNAR1	interferon (alpha, beta and omega) receptor 1	0.84
8732	204207_s_at	RNGTT	RNA guanylyltransferase and 5'-phosphatase	0.72
25906	204218_a_t	C11orf51	chromosome 11 open reading frame 51	0.59

9535	204220_a_t	GMFG	glia maturation factor, gamma	-1.27
9759	204225_a_t	HDAC4	histone deacetylase 4	0.65
4316	204259_a_t	MMP7	matrix metalloproteinase 7 (matrilysin, uterine)	-2.24
3960	204272_a_t	LGALS4	lectin, galactoside-binding, soluble, 4 (galectin 4)	-2.1
8470	204288_s_at	SORBS2	sorbin and SH3 domain containing 2	-0.83
1307	204345_a_t	COL16A1	collagen, type XVI, alpha 1	-1.32
2152	204363_a_t	F3	coagulation factor III (thromboplastin, tissue factor)	-2.61
10978	204370_a_t	CLP1	CLP1, cleavage and polyadenylation factor I subunit, homolog (<i>S. cerevisiae</i>)	0.81
27301	204408_a_t	APEX2	APEX nuclease (apurinic/aprimidinic endonuclease) 2	0.72
10959	204427_s_at	TMED2	transmembrane emp24 domain trafficking protein 2	1.33
2669	204472_a_t	GEM	GTP binding protein overexpressed in skeletal muscle	-3.11
7701	204474_a_t	ZNF142	zinc finger protein 142	0.7
5091	204476_s_at	PC	pyruvate carboxylase	1.66
1802	204514_a_t	DPH2	DPH2 homolog (<i>S. cerevisiae</i>)	0.52
4673	204528_s_at	NAP1L1	nucleosome assembly protein 1-like 1	-1.05
1346	204570_a_t	COX7A1	cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)	-1.22
54471	204594_s_at	SMCR7L	Smith-Magenis syndrome chromosome region, candidate 7-like	1.19
1462	204620_s_at	VCAN	versican	-2.08
7033	204623_a_t	TFF3	trefoil factor 3 (intestinal)	-0.6
540	204624_a_t	ATP7B	ATPase, Cu ⁺⁺ transporting, beta polypeptide	1.2
8986	204632_a_t	RPS6KA4	ribosomal protein S6 kinase, 90kDa, polypeptide 4	0.81
3169	204667_a_t	FOXA1	forkhead box A1	0.98
3127	204670_x_at	HLA-DRB5	major histocompatibility complex, class II, DR beta 5	-1.99
9771	204681_s_at	RAPGEF5	Rap guanine nucleotide exchange factor (GEF) 5	-1.92
4625	204737_s_at	MYH7	myosin, heavy chain 7, cardiac muscle, beta	-1.12

6236	204803_s_at	RRAD	Ras-related associated with diabetes	-1.28
9183	204812_a_t	ZW10	ZW10, kinetochore associated, homolog (Drosophila)	0.94
9704	204816_s_at	DHX34	DEAH (Asp-Glu-Ala-His) box polypeptide 34	-0.56
5883	204828_a_t	RAD9A	RAD9 homolog A (S. pombe)	0.44
8411	204841_s_at	EEA1	early endosome antigen 1	0.29
2644	204867_a_t	GCHFR	GTP cyclohydrolase I feedback regulator	1.08
1497	204925_a_t	CTNS	cystinosis, nephropathic	0.91
9815	204982_a_t	GIT2	G protein-coupled receptor kinase interactor 2	-0.55
2239	204983_s_at	GPC4	glypican 4	-0.52
11020	205037_a_t	RABL4	RAB, member of RAS oncogene family-like 4	0.92
5004	205040_a_t	ORM1	orosomucoid 1	0.78
5004	205041_s_at	ORM1	orosomucoid 1	0.73
9904	205115_s_at	RBM19	RNA binding motif protein 19	0.6
3908	205116_a_t	LAMA2	laminin, alpha 2 (merosin, congenital muscular dystrophy)	-1.89
5891	205130_a_t	RAGE	renal tumor antigen	-0.82
6320	205131_x_at	CLEC11A	C-type lectin domain family 11, member A	-0.63
2585	205219_s_at	GALK2	galactokinase 2	1.03
9122	205234_a_t	SLC16A4	solute carrier family 16, member 4 (monocarboxylic acid transporter 5)	-1.07
3625	205258_a_t	INHBB	inhibin, beta B	-1.53
10531	205273_s_at	PITRM1	pitrilysin metalloproteinase 1	1.11
51101	205308_a_t	C8orf70	chromosome 8 open reading frame 70	-0.66
9071	205328_a_t	CLDN10	claudin 10	-2.24
580	205345_a_t	BARD1	BRCA1 associated RING domain 1	-1.04
8821	205376_a_t	INPP4B	inositol polyphosphate-4-phosphatase, type II, 105kDa	-0.56
1880	205419_a_t	EBI2	Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor)	-2.11
9358	205422_s_at	ITGBL1	integrin, beta-like 1 (with EGF-like repeat domains)	-2.77

3092	205426_s _at	HIP1	huntingtin interacting protein 1	0.57
9848	205442_a _t	MFAP3L	microfibrillar-associated protein 3-like	1.9
5502	205478_a _t	PPP1R1A	protein phosphatase 1, regulatory (inhibitor) subunit 1A	1.76
10420	205486_a _t	TESK2	testis-specific kinase 2	0.56
2626	205517_a _t	GATA4	GATA binding protein 4	0.9
7410	205536_a _t	VAV2	vav 2 guanine nucleotide exchange factor	0.76
23708	205541_s _at	GSPT2	G1 to S phase transition 2	1.07
6876	205547_s _at	TAGLN	transgelin	-2.23
313	205639_a _t	AOAH	acyloxyacyl hydrolase (neutrophil)	-0.79
2243	205650_s _at	FGA	fibrinogen alpha chain	0.48
486	205674_x _at	FXVD2	FXVD domain containing ion transport regulator 2	-2.62
10301	205677_s _at	DLEU1	deleted in lymphocytic leukemia, 1	1.21
2674	205696_s _at	GFRA1	GDNF family receptor alpha 1	0.43
10745	205702_a _t	PHTF1	putative homeodomain transcription factor 1	0.53
8886	205763_s _at	DDX18	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	0.76
26240	205775_a _t	FAM50B	family with sequence similarity 50, member B	0.86
1852	205777_a _t	DUSP9	dual specificity phosphatase 9	-0.77
3575	205798_a _t	IL7R	interleukin 7 receptor	-3.29
22914	205821_a _t	KLRK1	killer cell lectin-like receptor subfamily K, member 1	-0.95
120	205882_x _at	ADD3	adducin 3 (gamma)	-0.99
10537	205890_s _at	UBD	ubiquitin D	-2.91
4776	205897_a _t	NFATC4	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4	0.74
5427	205909_a _t	POLE2	polymerase (DNA directed), epsilon 2 (p59 subunit)	0.74
5334	205934_a _t	PLCL1	phospholipase C-like 1	-0.3
22843	205938_a _t	PPM1E	protein phosphatase 1E (PP2C domain containing)	0.42
	205955_a _t		NA	0.29

22832	206005_s _at	KIAA100 9	KIAA1009	-0.61
10216	206007_a _t	PRG4	proteoglycan 4	2.08
22887	206015_s _at	FOXP3	forkhead box J3	-0.87
2042	206070_s _at	EPHA3	EPH receptor A3	-3.18
9651	206080_a _t	PLCH2	phospholipase C, eta 2	-0.78
7148	206093_x _at	TNXB	tenascin XB	-1.03
7168	206116_s _at	TPM1	tropomyosin 1 (alpha)	-1.63
411	206129_s _at	ARSB	arylsulfatase B	0.31
27304	206141_a _t	MOCS3	molybdenum cofactor synthesis 3	0.4
57834	206153_a _t	CYP4F11	cytochrome P450, family 4, subfamily F, polypeptide 11	1.44
65988	206180_x _at	ZNF747	zinc finger protein 747	0.75
1041	206192_a _t	CDSN	corneodesmosin	0.75
22821	206221_a _t	RASA3	RAS p21 protein activator 3	-0.51
22847	206225_a _t	ZNF507	zinc finger protein 507	0.73
1369	206256_a _t	CPN1	carboxypeptidase N, polypeptide 1	1.74
3428	206332_s _at	IFI16	interferon, gamma-inducible protein 16	-2
6372	206336_a _t	CXCL6	chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2)	-2.98
288	206385_s _at	ANK3	ankyrin 3, node of Ranvier (ankyrin G)	-2.77
6097	206419_a _t	RORC	RAR-related orphan receptor C	0.9
8710	206421_s _at	SERPINB 7	serpin peptidase inhibitor, clade B (ovalbumin), member 7	0.56
57447	206453_s _at	NDRG2	NDRG family member 2	-0.95
51603	206468_s _at	KIAA085 9	KIAA0859	0.88
10736	206510_a _t	SIX2	SIX homeobox 2	0.43
5680	206570_s _at	PSG11	pregnancy specific beta-1- glycoprotein 11	0.36
30008	206580_s _at	EFEMP2	EGF-containing fibulin-like extracellular matrix protein 2	-0.66
1813	206590_x _at	DRD2	dopamine receptor D2	0.49
8943	206592_s _at	AP3D1	adaptor-related protein complex 3, delta 1 subunit	0.99

3003	206666_a_t	GZMK	granzyme K (granzyme 3; tryptase II)	-1.56
10462	206682_a_t	CLEC10A	C-type lectin domain family 10, member A	-0.95
10898	206688_s_at	CPSF4	cleavage and polyadenylation specific factor 4, 30kDa	0.56
22865	206732_a_t	SLITRK3	SLIT and NTRK-like family, member 3	1.03
55503	206827_s_at	TRPV6	transient receptor potential cation channel, subfamily V, member 6	-0.76
6299	206893_a_t	SALL1	sal-like 1 (Drosophila)	1.65
10021	206946_a_t	HCN4	hyperpolarization activated cyclic nucleotide-gated potassium channel 4	0.37
51471	206963_s_at	NAT8B	N-acetyltransferase 8B (gene/pseudogene)	-2.47
10663	206974_a_t	CXCR6	chemokine (C-X-C motif) receptor 6	-0.87
10050	207051_a_t	SLC17A4	solute carrier family 17 (sodium phosphate), member 4	-1.25
10246	207097_s_at	SLC17A2	solute carrier family 17 (sodium phosphate), member 2	2.22
11238	207129_a_t	CA5B	carbonic anhydrase VB, mitochondrial	0.89
420	207220_a_t	ART4	ADP-ribosyltransferase 4 (Dombrock blood group)	-1.28
4286	207233_s_at	MITF	microphthalmia-associated transcription factor	-1.24
4842	207309_a_t	NOS1	nitric oxide synthase 1 (neuronal)	0.45
4050	207339_s_at	LTB	lymphotoxin beta (TNF superfamily, member 3)	-0.69
9389	207408_a_t	SLC22A14	solute carrier family 22 (organic cation transporter), member 14	0.82
3950	207409_a_t	LECT2	leukocyte cell-derived chemotaxin 2	-1.98
486	207434_s_at	FXYP2	FXYP domain containing ion transport regulator 2	-2.47
6425	207468_s_at	SFRP5	secreted frizzled-related protein 5	-1.22
6532	207519_a_t	SLC6A4	solute carrier family 6 (neurotransmitter transporter, serotonin), member 4	0.54
358	207542_s_at	AQP1	aquaporin 1 (Colton blood group)	-1.98
27284	207601_a_t	SULT1B1	sulfotransferase family, cytosolic, 1B, member 1	1.07
29909	207651_a_t	GPR171	G protein-coupled receptor 171	-1.97
10130	207668_x_at	PDIA6	protein disulfide isomerase family A, member 6	1.19
3626	207687_a_t	INHBC	inhibin, beta C	1.08

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6683	207724_s_at	SPAST	spastin	0.43
1443	207770_x_at	CSH2	chorionic somatomammotropin hormone 2	0.5
26003	207812_s_at	GORASP2	golgi reassembly stacking protein 2, 55kDa	1.43
7982	207871_s_at	ST7	suppression of tumorigenicity 7	1.23
4629	207961_x_at	MYH11	myosin, heavy chain 11, smooth muscle	-1.11
1805	207977_s_at	DPT	dermatopontin	-2.14
81030	208087_s_at	ZBP1	Z-DNA binding protein 1	-0.62
81875	208114_s_at	ISG20L2	interferon stimulated exonuclease gene 20kDa-like 2	0.75
4121	208116_s_at	MAN1A1	mannosidase, alpha, class 1A, member 1	1.9
4142	208210_at	MAS1	MAS1 oncogene	0.84
6585	208221_s_at	SLIT1	slit homolog 1 (Drosophila)	-0.63
2263	208228_s_at	FGFR2	fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer syndrome, Jackson-Weiss syndrome)	-2.23
711	208247_at	C3orf51	chromosome 3 open reading frame 51	-0.77
1755	208250_s_at	DMBT1	deleted in malignant brain tumors 1	0.67
553	208260_at	AVPR1B	arginine vasopressin receptor 1B	0.87
3126	208306_x_at	HLA-DRB4	major histocompatibility complex, class II, DR beta 4	-1.97
2494	208337_s_at	NR5A2	nuclear receptor subfamily 5, group A, member 2	0.63
2494	208343_s_at	NR5A2	nuclear receptor subfamily 5, group A, member 2	0.95
9875	208395_s_at	URB1	URB1 ribosome biogenesis 1 homolog (S. cerevisiae)	0.37
57019	208424_s_at	CIAPIN1	cytokine induced apoptosis inhibitor 1	0.83
5631	208447_s_at	PRPS1	phosphoribosyl pyrophosphate synthetase 1	0.9
23039	208459_s_at	XPO7	exportin 7	0.55
2557	208463_at	GABRA4	gamma-aminobutyric acid (GABA) A receptor, alpha 4	0.53
2912	208465_at	GRM2	glutamate receptor, metabotropic 2	0.48

581	208478_s_at	BAX	BCL2-associated X protein	-0.72
690	208529_a_t	BTF3L1	basic transcription factor 3, like 1	-0.7
26582	208582_s_at	DUX3	double homeobox, 3	-0.75
10075	208598_s_at	HUWE1	HECT, UBA and WWE domain containing 1	0.8
6641	208608_s_at	SNTB1	syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1)	1.16
7430	208623_s_at	VIL2	villin 2 (ezrin)	-1.35
1981	208625_s_at	EIF4G1	eukaryotic translation initiation factor 4 gamma, 1	0.77
24597_3	208638_a_t	ATP6V1C2	ATPase, H ⁺ transporting, lysosomal 42kDa, V1 subunit C2	1.17
10130	208639_x_at	PDIA6	protein disulfide isomerase family A, member 6	1.33
142	208644_a_t	PARP1	poly (ADP-ribose) polymerase family, member 1	0.94
7415	208649_s_at	VCP	valosin-containing protein	0.75
10983	208656_s_at	CCNI	cyclin I	-0.81
9601	208658_a_t	PDIA4	protein disulfide isomerase family A, member 4	1.2
1192	208659_a_t	CLIC1	chloride intracellular channel 1	-0.98
7267	208664_s_at	TTC3	tetratricopeptide repeat domain 3	0.61
824	208683_a_t	CAPN2	calpain 2, (m/II) large subunit	-1.13
10211	208748_s_at	FLOT1	flotillin 1	0.59
8775	208751_a_t	NAPA	N-ethylmaleimide-sensitive factor attachment protein, alpha	1.2
4673	208752_x_at	NAP1L1	nucleosome assembly protein 1-like 1	-1.17
4673	208754_s_at	NAP1L1	nucleosome assembly protein 1-like 1	-1.26
471	208758_a_t	ATIC	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	0.77
1831	208763_s_at	TSC22D3	TSC22 domain family, member 3	-2.22
28411_9	208789_a_t	PTRF	polymerase I and transcript release factor	-1.23
23015	208797_s_at	GOLGA8A	golgi autoantigen, golgin subfamily a, 8A	-1.03
6731	208800_a_t	SRP72	signal recognition particle 72kDa	1.44
4218	208819_a	RAB8A	RAB8A, member RAS oncogene	0.79

	t		family	
5694	208827_a_t	PSMB6	proteasome (prosome, macropain) subunit, beta type, 6	0.77
54107	208828_a_t	POLE3	polymerase (DNA directed), epsilon 3 (p17 subunit)	1.18
483	208836_a_t	ATP1B3	ATPase, Na ⁺ /K ⁺ transporting, beta 3 polypeptide	-2.1
821	208853_s_at	CANX	calnexin	1.34
23710	208868_s_at	GABAR APL1	GABA(A) receptor-associated protein like 1	-1.41
23710	208869_s_at	GABAR APL1	GABA(A) receptor-associated protein like 1	-1.11
5062	208875_s_at	PAK2	p21 (CDKN1A)-activated kinase 2	1.09
3122	208894_a_t	HLA-DRA	major histocompatibility complex, class II, DR alpha	-2.44
708	208910_s_at	C1QBP	complement component 1, q subcomponent binding protein	1.31
65220	208918_s_at	NADK	NAD kinase	1.35
65220	208919_s_at	NADK	NAD kinase	1.14
3958	208949_s_at	LGALS3	lectin, galactoside-binding, soluble, 3	-3.3
1316	208960_s_at	KLF6	Kruppel-like factor 6	-1.96
1316	208961_s_at	KLF6	Kruppel-like factor 6	-2.03
149628	208965_s_at	PYHIN1	pyrin and HIN domain family, member 1	-1.8
3428	208966_x_at	IFI16	interferon, gamma-inducible protein 16	-1.85
8402	209003_a_t	SLC25A11	solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11	1.22
3855	209016_s_at	KRT7	keratin 7	-1.9
9361	209017_s_at	LONP1	lon peptidase 1, mitochondrial	0.92
65018	209018_s_at	PINK1	PTEN induced putative kinase 1	0.99
9776	209021_x_at	KIAA0652	KIAA0652	0.92
4191	209036_s_at	MDH2	malate dehydrogenase 2, NAD (mitochondrial)	1.2
358	209047_a_t	AQP1	aquaporin 1 (Colton blood group)	-3.11
8202	209061_a_t	NCOA3	nuclear receptor coactivator 3	-0.74
182	209099_x_at	JAG1	jagged 1 (Alagille syndrome)	-1.58
7866	209100_a	IFRD2	interferon-related developmental	1.07

	t		regulator 2	
1490	209101_a_t	CTGF	connective tissue growth factor	-3.67
7353	209103_s_at	UFD1L	ubiquitin fusion degradation 1 like (yeast)	0.76
23558	209117_a_t	WBP2	WW domain binding protein 2	1.25
7846	209118_s_at	TUBA1A	tubulin, alpha 1a	-1.57
3535	209138_x_at	IGL@	immunoglobulin lambda locus	-3.04
9266	209158_s_at	PSCD2	pleckstrin homology, Sec7 and coiled-coil domains 2 (cytohesin-2)	-0.84
1534	209163_a_t	CYB561	cytochrome b-561	0.88
1534	209164_s_at	CYB561	cytochrome b-561	0.93
11067	209183_s_at	C10orf10	chromosome 10 open reading frame 10	-2.24
488	209186_a_t	ATP2A2	ATPase, Ca ⁺⁺ transporting, cardiac muscle, slow twitch 2	1.46
112	209195_s_at	ADCY6	adenylate cyclase 6	0.61
7852	209201_x_at	CXCR4	chemokine (C-X-C motif) receptor 4	-2.2
7936	209219_a_t	RDBP	RD RNA binding protein	-0.69
23095	209234_a_t	KIF1B	kinesin family member 1B	0.95
23008	209256_s_at	KIAA0265	KIAA0265 protein	0.9
50814	209279_s_at	NSDHL	NAD(P) dependent steroid dehydrogenase-like	1.08
1410	209283_a_t	CRYAB	crystallin, alpha B	-2.72
10602	209286_a_t	CDC42EP3	CDC42 effector protein (Rho GTPase binding) 3	-1.8
4781	209289_a_t	NFIB	nuclear factor I/B	-1.08
3400	209291_a_t	ID4	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	-2.97
25977	209300_s_at	NECAP1	NECAP endocytosis associated 1	0.79
599	209311_a_t	BCL2L2	BCL2-like 2	0.73
3123	209312_x_at	HLA-DRB1	major histocompatibility complex, class II, DR beta 1	-2.24
5715	209334_s_at	PSMD9	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	0.4
1634	209335_a_t	DCN	decorin	-2.08
55361	209345_s	PI4K2A	phosphatidylinositol 4-kinase type	0.96

	_at		2 alpha	
6452	209370_s_at	SH3BP2	SH3-domain binding protein 2	0.71
8818	209391_at	DPM2	dolichyl-phosphate mannosyltransferase polypeptide 2, regulatory subunit	0.78
5168	209392_at	ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	-2.48
10488	209432_s_at	CREB3	cAMP responsive element binding protein 3	0.92
288	209442_x_at	ANK3	ankyrin 3, node of Ranvier (ankyrin G)	-1.55
5910	209444_at	RAP1GDS1	RAP1, GTP-GDP dissociation stimulator 1	1.33
1798	209509_s_at	DPAGT1	dolichyl-phosphate (UDP-N-acetylglucosamine) N-acetylglucosaminophosphotransferase 1 (GlcNAc-1-P transferase)	1.53
1384	209522_s_at	CRAT	carnitine acetyltransferase	1.37
9373	209532_at	PLAA	phospholipase A2-activating protein	0.46
9373	209533_s_at	PLAA	phospholipase A2-activating protein	0.99
9562	209585_s_at	MINPP1	multiple inositol polyphosphate histidine phosphatase, 1	1.13
9595	209606_at	PSCDBP	pleckstrin homology, Sec7 and coiled-coil domains, binding protein	-2.1
6509	209610_s_at	SLC1A4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	1.69
6509	209611_s_at	SLC1A4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	0.42
972	209619_at	CD74	CD74 molecule, major histocompatibility complex, class II invariant chain	-2.07
27295	209621_s_at	PDLIM3	PDZ and LIM domain 3	-1.38
64087	209624_s_at	MCCC2	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	0.96
11068	209665_at	CYB561D2	cytochrome b-561 domain containing 2	1.01
10560	209681_at	SLC19A2	solute carrier family 19 (thiamine transporter), member 2	-1.85
6387	209687_at	CXCL12	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)	-1.6
4824	209706_at	NKX3-1	NK3 homeobox 1	0.55
934	209771_x_at	CD24	CD24 molecule	-2.17

8605	209785_s_at	PLA2G4C	phospholipase A2, group IVC (cytosolic, calcium-independent)	-0.96
969	209795_a_t	CD69	CD69 molecule	-2.65
406	209824_s_at	ARNTL	aryl hydrocarbon receptor nuclear translocator-like	1.38
10197	209852_x_at	PSME3	proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)	0.91
23401	209864_a_t	FRAT2	frequently rearranged in advanced T-cell lymphomas 2	0.6
6696	209875_s_at	SPP1	secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1)	-3.72
8034	209910_a_t	SLC25A16	solute carrier family 25 (mitochondrial carrier; Graves disease autoantigen), member 16	0.54
7104	209937_a_t	TM4SF4	transmembrane 4 L six family member 4	-1.05
84720	209998_a_t	PIGO	phosphatidylinositol glycan anchor biosynthesis, class O	0.66
8651	209999_x_at	SOCS1	suppressor of cytokine signaling 1	0.58
2627	210002_a_t	GATA6	GATA binding protein 6	-1.44
84759	210022_a_t	PCGF1	polycomb group ring finger 1	0.6
3418	210045_a_t	IDH2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	1.65
3418	210046_s_at	IDH2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	1.43
6363	210072_a_t	CCL19	chemokine (C-C motif) ligand 19	-2.76
51257	210075_a_t	2-Mar	membrane-associated ring finger (C3HC4) 2	0.63
24	210082_a_t	ABCA4	ATP-binding cassette, sub-family A (ABC1), member 4	0.71
27130	210114_a_t	INVS	inversin	0.74
5376	210139_s_at	PMP22	peripheral myelin protein 22	-1.38
10211	210142_x_at	FLOT1	flotillin 1	0.72
7763	210275_s_at	ZFAND5	zinc finger, AN1-type domain 5	-1.4
2321	210287_s_at	FLT1	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)	-0.51
9027	210289_a_t	NAT8	N-acetyltransferase 8	-2.69
10483	210293_s_at	SEC23B	Sec23 homolog B (S. cerevisiae)	1.42

64410	210307_s_at	KLHL25	kelch-like 25 (Drosophila)	0.72
9356	210343_s_at	SLC22A6	solute carrier family 22 (organic anion transporter), member 6	-1.07
51752	210385_s_at	ARTS-1	type 1 tumor necrosis factor receptor shedding aminopeptidase regulator	1.11
1672	210397_a_t	DEFB1	defensin, beta 1	-3.64
302	210427_x_at	ANXA2	annexin A2	-1.23
10899	210434_x_at	JTB	jumping translocation breakpoint	0.63
11054	210443_x_at	OGFR	opioid growth factor receptor	0.81
254896	210483_a_t	MGC31957	hypothetical protein MGC31957	-1.56
5987	210541_s_at	TRIM27	tripartite motif-containing 27	0.95
3985	210582_s_at	LIMK2	LIM domain kinase 2	0.78
6303	210592_s_at	SAT1	spermidine/spermine N1-acetyltransferase 1	-1
9145	210613_s_at	SYNGR1	synaptogyrin 1	-0.63
8558	210622_x_at	CDK10	cyclin-dependent kinase (CDC2-like) 10	1.03
7841	210627_s_at	GCS1	glucosidase I	0.8
6442	210632_s_at	SGCA	sarcoglycan, alpha (50kDa dystrophin-associated glycoprotein)	-0.96
3858	210633_x_at	KRT10	keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris)	0.81
9474	210639_s_at	ATG5	ATG5 autophagy related 5 homolog (S. cerevisiae)	0.94
8209	210667_s_at	C21orf33	chromosome 21 open reading frame 33	0.99
4902	210683_a_t	NRTN	neurturin	1.2
29015	210692_s_at	SLC43A3	solute carrier family 43, member 3	1.66
10653	210715_s_at	SPINT2	serine peptidase inhibitor, Kunitz type, 2	-2.08
6945	210752_s_at	MLX	MAX-like protein X	0.37
2047	210753_s_at	EPHB1	EPH receptor B1	0.65
1601	210757_x_at	DAB2	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	-1.19
3491	210764_s_at	CYR61	cysteine-rich, angiogenic inducer, 61	-2.64
28334	210822_a	LOC2833	RPL13-2 pseudogene	0.53

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1488	210835_s_at	CTBP2	C-terminal binding protein 2	-1.29
5168	210839_s_at	ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	-1.71
79071	210868_s_at	ELOVL6	ELOVL family member 6, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast)	1.63
26056	210879_s_at	RAB11FIP5	RAB11 family interacting protein 5 (class I)	-0.56
444	210896_s_at	ASPH	aspartate beta-hydroxylase	0.88
3597	210904_s_at	IL13RA1	interleukin 13 receptor, alpha 1	1.57
5204	210908_s_at	PFDN5	prefoldin subunit 5	-0.79
28639	210915_x_at	TRBC1	T cell receptor beta constant 1	-1.45
10402	210942_s_at	ST3GAL6	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	1.82
5873	210951_x_at	RAB27A	RAB27A, member RAS oncogene family	1.27
8908	210963_s_at	GYG2	glycogenin 2	0.96
8908	210964_s_at	GYG2	glycogenin 2	1.48
406	210971_s_at	ARNTL	aryl hydrocarbon receptor nuclear translocator-like	1.16
10922	210975_x_at	FASTK	Fas-activated serine/threonine kinase	0.65
3122	210982_s_at	HLA-DRA	major histocompatibility complex, class II, DR alpha	-2.61
7168	210986_s_at	TPM1	tropomyosin 1 (alpha)	-1.43
7531	210996_s_at	YWHAE	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	0.83
196515	211034_s_at	FLJ30092	AF-1 specific protein phosphatase	0.61
9601	211048_s_at	PDIA4	protein disulfide isomerase family A, member 4	1.57
4247	211061_s_at	MGAT2	mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	1.11
54499	211098_x_at	TMCO1	transmembrane and coiled-coil domains 1	0.61
1209	211136_s_at	CLPTM1	cleft lip and palate associated transmembrane protein 1	1.12
4664	211139_s_at	NAB1	NGFI-A binding protein 1 (EGR1 binding protein 1)	0.66

1737	211150_s_at	DLAT	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	1.16
7066	211155_s_at	THPO	thrombopoietin (myeloproliferative leukemia virus oncogene ligand, megakaryocyte growth and development factor)	1
1438	211286_x_at	CSF2RA	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)	-0.68
8480	211318_s_at	RAE1	RAE1 RNA export 1 homolog (S. pombe)	0.49
834	211368_s_at	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	-1.38
3502	211430_s_at	IGHG3	immunoglobulin heavy constant gamma 3 (G3m marker)	-3.24
23766	211458_s_at	GABARAPL3	GABA(A) receptors associated protein like 3	-1.14
148	211489_at	ADRA1A	adrenergic, alpha-1A-, receptor	1.84
377	211622_s_at	ARF3	ADP-ribosylation factor 3	0.82
	211642_at		NA	-0.48
	211645_x_at		NA	-2.7
3912	211651_s_at	LAMB1	laminin, beta 1	-1.38
3929	211652_s_at	LBP	lipopolysaccharide binding protein	1.6
3119	211656_x_at	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1	-1.44
6320	211709_s_at	CLEC11A	C-type lectin domain family 11, member A	-1
91369	211717_at	ANKRD40	ankyrin repeat domain 40	0.58
5730	211748_x_at	PTGDS	prostaglandin D2 synthase 21kDa (brain)	-2.24
25974	211774_s_at	MMACHC	methylmalonic aciduria (cobalamin deficiency) cblC type, with homocystinuria	1.24
10152	211793_s_at	ABI2	abl interactor 2	0.82
28639	211796_s_at	TRBC1	T cell receptor beta constant 1	-1.59
1634	211813_x_at	DCN	decorin	-2
7066	211831_s_at	THPO	thrombopoietin (myeloproliferative leukemia virus oncogene ligand, megakaryocyte growth and development factor)	0.68
9016	211855_s_at	SLC25A14	solute carrier family 25 (mitochondrial carrier, brain),	0.46

			member 14	
1634	211896_s_at	DCN	decorin	-1.96
5141	211901_s_at	PDE4A	phosphodiesterase 4A, cAMP-specific (phosphodiesterase E2 dunce homolog, Drosophila)	-0.89
7852	211919_s_at	CXCR4	chemokine (C-X-C motif) receptor 4	-2.34
3309	211936_a_t	HSPA5	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	1.22
1284	211964_a_t	COL4A2	collagen, type IV, alpha 2	-2.05
3516	211974_x_at	RBPJ	recombination signal binding protein for immunoglobulin kappa J region	-1.09
1282	211980_a_t	COL4A1	collagen, type IV, alpha 1	-2.14
79026	211986_a_t	AHNAK	AHNAK nucleoprotein	-1.39
3113	211990_a_t	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	-2.53
3113	211991_s_at	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	-2.59
23117	211996_s_at	LOC23117	KIAA0220-like protein	-1.62
26099	212003_a_t	C1orf144	chromosome 1 open reading frame 144	0.64
23190	212006_a_t	UBXD2	UBX domain containing 2	0.98
5411	212036_s_at	PNN	pinin, desmosome associated protein	-1.34
9114	212041_a_t	ATP6V0D1	ATPase, H ⁺ transporting, lysosomal 38kDa, V0 subunit d1	0.82
8565	212048_s_at	YARS	tyrosyl-tRNA synthetase	1.1
23061	212052_s_at	TBC1D9B	TBC1 domain family, member 9B (with GRAM domain)	0.9
113419	212083_a_t	TEX261	testis expressed 261	1.07
2907	212090_a_t	GRINA	glutamate receptor, ionotropic, N-methyl D-aspartate-associated protein 1 (glutamate binding)	1.12
23516	212110_a_t	SLC39A14	solute carrier family 39 (zinc transporter), member 14	1.02
23107	212145_a_t	MRPS27	mitochondrial ribosomal protein S27	0.93
5087	212151_a_t	PBX1	pre-B-cell leukemia homeobox 1	-1.04
11260	212160_a_t	XPOT	exportin, tRNA (nuclear export receptor for tRNAs)	1.72
92703	212165_a_t	TMEM183A	transmembrane protein 183A	0.69

204	212174_a_t	AK2	adenylate kinase 2	0.89
31	212186_a_t	ACACA	acetyl-Coenzyme A carboxylase alpha	1.29
5730	212187_x_at	PTGDS	prostaglandin D2 synthase 21kDa (brain)	-2.34
115207	212188_a_t	KCTD12	potassium channel tetramerisation domain containing 12	-1.86
115207	212192_a_t	KCTD12	potassium channel tetramerisation domain containing 12	-1.9
25963	212202_s_at	TMEM87A	transmembrane protein 87A	-1.21
25963	212204_a_t	TMEM87A	transmembrane protein 87A	-0.94
90411	212245_a_t	MCFD2	multiple coagulation factor deficiency 2	1.57
90411	212246_a_t	MCFD2	multiple coagulation factor deficiency 2	1.32
92140	212248_a_t	MTDH	metadherin	1.24
92140	212250_a_t	MTDH	metadherin	1.34
23175	212276_a_t	LPIN1	lipin 1	1.09
200081	212300_a_t	TXLNA	taxilin alpha	1.14
23231	212314_a_t	KIAA0746	KIAA0746 protein	-1.33
23351	212356_a_t	KIAA0323	KIAA0323	1.05
23201	212357_a_t	KIAA0280	KIAA0280	0.75
488	212361_s_at	ATP2A2	ATPase, Ca ⁺⁺ transporting, cardiac muscle, slow twitch 2	1.61
4628	212372_a_t	MYH10	myosin, heavy chain 10, non-muscle	-0.9
2618	212379_a_t	GART	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase	0.89
535	212383_a_t	ATP6V0A1	ATPase, H ⁺ transporting, lysosomal V0 subunit a1	0.75
6925	212386_a_t	TCF4	transcription factor 4	-1.54
6925	212387_a_t	TCF4	transcription factor 4	-1.63
89910	212404_s_at	UBE3B	ubiquitin protein ligase E3B	0.39
51603	212405_s_at	KIAA0859	KIAA0859	0.82
219654	212419_a_t	C10orf56	chromosome 10 open reading frame 56	1.28

219654	212423_a_t	C10orf56	chromosome 10 open reading frame 56	1.04
80273	212434_a_t	GRPEL1	GrpE-like 1, mitochondrial (E. coli)	0.89
9807	212439_a_t	IHPK1	inositol hexaphosphate kinase 1	0.8
9645	212472_a_t	MICAL2	microtubule associated monooxygenase, calponin and LIM domain containing 2	1.12
23030	212496_s_at	JMJD2B	jumonji domain containing 2B	0.86
439921	212509_s_at	MXRA7	matrix-remodelling associated 7	-1.48
27351	212527_a_t	D15Wsu75e	DNA segment, Chr 15, Wayne State University 75, expressed	1.5
	212528_a_t		NA	1.08
124801	212532_s_at	LSM12	LSM12 homolog (S. cerevisiae)	0.92
80308	212541_a_t	FLAD1	FAD1 flavin adenine dinucleotide synthetase homolog (S. cerevisiae)	0.75
55023	212542_s_at	PHIP	pleckstrin homology domain interacting protein	-1.1
202	212543_a_t	AIM1	absent in melanoma 1	-1.57
10252	212558_a_t	SPRY1	sprouty homolog 1, antagonist of FGF signaling (Drosophila)	-1.9
23246	212563_a_t	BOP1	block of proliferation 1	0.69
1737	212568_s_at	DLAT	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	1.31
23052	212573_a_t	ENDOD1	endonuclease domain containing 1	-1.17
23295	212576_a_t	MGRN1	mahogunin, ring finger 1	1.04
5788	212588_a_t	PTPRC	protein tyrosine phosphatase, receptor type, C	-1.57
3512	212592_a_t	IGJ	immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu polypeptides	-3.35
23220	212611_a_t	DTX4	deltex 4 homolog (Drosophila)	1.51
440026	212623_a_t	TMEM41B	transmembrane protein 41B	1.32
8417	212631_a_t	STX7	syntaxin 7	-0.6
3097	212642_s_at	HIVP2	human immunodeficiency virus type I enhancer binding protein 2	-1.09
25976	212665_a_t	TIPARP	TCDD-inducible poly(ADP-ribose) polymerase	-1.64
6678	212667_a_t	SPARC	secreted protein, acidic, cysteine-rich (osteonectin)	-1.63

3117	212671_s_at	HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1	-2.62
91289	212682_s_at	TMEM112B	transmembrane protein 112B	0.64
57460	212686_a_t	PPM1H	protein phosphatase 1H (PP2C domain containing)	0.57
192683	212699_a_t	SCAMP5	secretory carrier membrane protein 5	0.56
83660	212701_a_t	TLN2	talin 2	0.64
4239	212713_a_t	MFAP4	microfibrillar-associated protein 4	-1.55
390	212724_a_t	RND3	Rho family GTPase 3	-1.08
4833	212739_s_at	NME4	non-metastatic cells 4, protein expressed in	1.2
23274	212786_a_t	CLEC16A	C-type lectin domain family 16, member A	0.82
6509	212811_x_at	SLC1A4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	1.08
5305	212829_a_t	PIP4K2A	phosphatidylinositol-5-phosphate 4-kinase, type II, alpha	-0.9
23172	212835_a_t	KIAA0157	KIAA0157	0.68
7373	212865_s_at	COL14A1	collagen, type XIV, alpha 1 (undulin)	-1.76
8550	212871_a_t	MAPKAPK5	mitogen-activated protein kinase-activated protein kinase 5	0.66
23276	212882_a_t	KLHL18	kelch-like 18 (Drosophila)	0.43
26112	212886_a_t	CCDC69	coiled-coil domain containing 69	1.39
124565	212890_a_t	MGC15523	hypothetical protein MGC15523	0.82
7779	212907_a_t	SLC30A1	solute carrier family 30 (zinc transporter), member 1	1.29
253725	212929_s_at	FAM21C	family with sequence similarity 21, member C	-1.04
23315	212947_a_t	SLC9A8	solute carrier family 9 (sodium/hydrogen exchanger), member 8	0.69
5066	212958_x_at	PAM	peptidylglycine alpha-amidating monooxygenase	-1.09
4673	212967_x_at	NAP1L1	nucleosome assembly protein 1-like 1	-1.11
	212993_a_t		NA	1.89
9875	212996_s_at	URB1	URB1 ribosome biogenesis 1 homolog (<i>S. cerevisiae</i>)	0.54
23452	213004_a_t	ANGPTL2	angiopoietin-like 2	-0.58
4781	213032_a_t	NFIB	nuclear factor I/B	-1.28

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9862	213043_s_at	MED24	mediator complex subunit 24	0.73
5576	213052_at	PRKAR2A	protein kinase, cAMP-dependent, regulatory, type II, alpha	1.02
23354	213053_at	KIAA0841	KIAA0841	-0.7
1805	213071_at	DPT	dermatopontin	-2.2
90121	213079_at	TSR2	TSR2, 20S rRNA accumulation, homolog (S. cerevisiae)	-0.75
115201	213115_at	ATG4A	ATG4 autophagy related 4 homolog A (S. cerevisiae)	1.02
9570	213144_at	GOSR2	golgi SNAP receptor complex member 2	0.91
9570	213180_s_at	GOSR2	golgi SNAP receptor complex member 2	0.72
10302	213203_at	SNAPC5	small nuclear RNA activating complex, polypeptide 5, 19kDa	0.89
	213215_at		NA	0.77
113178	213244_at	SCAMP4	secretory carrier membrane protein 4	0.68
107	213245_at	ADCY1	adenylate cyclase 1 (brain)	1.05
79987	213247_at	SVEP1	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	-1.08
10346	213293_s_at	TRIM22	tripartite motif-containing 22	-2.16
23264	213323_s_at	ZC3H7B	zinc finger CCCH-type containing 7B	0.72
25945	213325_at	PVRL3	poliovirus receptor-related 3	1.35
4191	213333_at	MDH2	malate dehydrogenase 2, NAD (mitochondrial)	1.47
23461	213353_at	ABCA5	ATP-binding cassette, sub-family A (ABC1), member 5	1.24
10402	213355_at	ST3GAL6	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	1.78
	213393_at		NA	1.16
	213429_at		NA	-2.57
91316	213502_x_at	LOC91316	similar to bK246H3.1 (immunoglobulin lambda-like polypeptide 1, pre-B-cell specific)	-1.7
302	213503_x_at	ANXA2	annexin A2	-1.28
10980	213504_at	COPS6	COP9 constitutive photomorphogenic homolog subunit 6 (Arabidopsis)	0.94

3908	213519_s_at	LAMA2	laminin, alpha 2 (merosin, congenital muscular dystrophy)	-1.71
3945	213564_x_at	LDHB	lactate dehydrogenase B	-2.5
6039	213566_a_t	RNASE6	ribonuclease, RNase A family, k6	-1.5
65220	213607_x_at	NADK	NAD kinase	0.82
402055	213608_s_at	CTB-1048E9.5	similar to SRR1-like protein	0.74
3384	213620_s_at	ICAM2	intercellular adhesion molecule 2	-0.87
374655	213657_s_at	ZNF710	zinc finger protein 710	1.13
374655	213658_a_t	ZNF710	zinc finger protein 710	0.9
7542	213740_s_at	ZFPL1	zinc finger protein-like 1	-1.38
26156	213750_a_t	RSL1D1	ribosomal L1 domain containing 1	0.98
28996	213763_a_t	HIPK2	homeodomain interacting protein kinase 2	1.18
80765	213820_s_at	STARD5	StAR-related lipid transfer (START) domain containing 5	2.1
84705	213835_x_at	GTPBP3	GTP binding protein 3 (mitochondrial)	0.46
375346	213851_a_t	TMEM110	transmembrane protein 110	0.87
4673	213864_s_at	NAP1L1	nucleosome assembly protein 1-like 1	-1.08
6925	213891_s_at	TCF4	transcription factor 4	-1.53
633	213905_x_at	BGN	biglycan	-1.98
	213929_a_t		NA	0.81
23048	213940_s_at	FNBP1	formin binding protein 1	-0.95
4069	213975_s_at	LYZ	lysozyme (renal amyloidosis)	-2.41
6421	214016_s_at	SFPQ	splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated)	-1.27
6146	214042_s_at	RPL22	ribosomal protein L22	-1.13
56901	214095_a_t	NDUFA4L2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4-like 2	0.8
56901	214096_s_at	NDUFA4L2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4-like 2	0.98
10922	214114_x_at	FASTK	Fas-activated serine/threonine kinase	0.9

4588	214133_a_t	MUC6	mucin 6, oligomeric mucus/gel-forming	-1.03
25924	214156_a_t	MYRIP	myosin VIIA and Rab interacting protein	1.51
2168	214158_s_at	FABP1	fatty acid binding protein 1, liver	0.45
708	214214_s_at	C1QBP	complement component 1, q subcomponent binding protein	1.27
23062	214233_a_t	GGA2	golgi associated, gamma adaptin ear containing, ARF binding protein 2	0.56
27122	214247_s_at	DKK3	dickkopf homolog 3 (Xenopus laevis)	-2.95
9110	214268_s_at	MTMR4	myotubularin related protein 4	1.04
3166	214386_a_t	HMX1	H6 family homeobox 1	-0.65
9814	214402_s_at	SFI1	Sfi1 homolog, spindle assembly associated (yeast)	-0.82
10737	214408_s_at	RFPL3S	ret finger protein-like 3 antisense	-0.48
47438_1	214412_a_t	H2AFB2	H2A histone family, member B2	-0.41
6472	214437_s_at	SHMT2	serine hydroxymethyltransferase 2 (mitochondrial)	0.91
3929	214461_a_t	LBP	lipopolysaccharide binding protein	1.49
5005	214465_a_t	ORM2	orosomucoid 2	0.8
11212	214545_s_at	PROSC	proline synthetase co-transcribed homolog (bacterial)	0.97
32	214584_x_at	ACACB	acetyl-Coenzyme A carboxylase beta	0.61
2861	214586_a_t	GPR37	G protein-coupled receptor 37 (endothelin receptor type B-like)	0.77
35337_6	214658_a_t	TICAM2	toll-like receptor adaptor molecule 2	1.21
3514	214669_x_at	IGKC	immunoglobulin kappa constant	-2.33
28831	214677_x_at	IGLJ3	immunoglobulin lambda joining 3	-3.34
6641	214708_a_t	SNTB1	syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1)	1.4
56252	214713_a_t	YLPM1	YLP motif containing 1	0.59
84124	214714_a_t	ZNF394	zinc finger protein 394	-0.51
54432	214733_s_at	YIPF1	Yip1 domain family, member 1	1.32
	214769_a_t		NA	0.46
	214809_a		NA	-0.9

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7626	214813_a_t	ZNF75	zinc finger protein 75 (D8C6)	0.43
3514	214836_x_at	IGKC	immunoglobulin kappa constant	-2.53
222658	214849_a_t	KCTD20	potassium channel tetramerisation domain containing 20	0.91
8295	214908_s_at	TRRAP	transformation/transcription domain-associated protein	0.49
9358	214927_a_t	ITGBL1	integrin, beta-like 1 (with EGF-like repeat domains)	-2.42
55660	214941_s_at	PRPF40A	PRP40 pre-mRNA processing factor 40 homolog A (<i>S. cerevisiae</i>)	0.84
2971	215091_s_at	GTF3A	general transcription factor IIIA	0.8
3535	215121_x_at	IGL@	immunoglobulin lambda locus	-3.01
5937	215127_s_at	RBMS1	RNA binding motif, single stranded interacting protein 1	-1.33
9639	215139_a_t	ARHGEF10	Rho guanine nucleotide exchange factor (GEF) 10	-0.33
4917	215176_x_at	NTN2L	netrin 2-like (chicken)	-3.05
	215185_a_t		NA	0.58
3123	215193_x_at	HLA-DRB1	major histocompatibility complex, class II, DR beta 1	-2
729148	215207_x_at	LOC729148	similar to lethal (2) k00619 CG4775-PA	0.81
23348	215238_s_at	DOCK9	dedicator of cytokinesis 9	-0.69
114781	215261_a_t	BTBD9	BTB (POZ) domain containing 9	0.88
400642	215283_a_t	LOC400642	hypothetical gene supported by BC041875; BX648984	0.7
255057	215325_x_at	C19orf26	chromosome 19 open reading frame 26	-1.1
10914	215374_a_t	PAPOLA	poly(A) polymerase alpha	0.58
3535	215379_x_at	IGL@	immunoglobulin lambda locus	-3.13
2260	215404_x_at	FGFR1	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome)	-1.07
55016	215445_x_at	1-Mar	membrane-associated ring finger (C3HC4) 1	-0.57
6955	215540_a_t	TRA@	T cell receptor alpha locus	0.68
22888	215544_s_at	UBOX5	U-box domain containing 5	0.62
6597	215714_s_at	SMARCA4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily	0.83

			a, member 4	
64689	215749_s _at	GORASP 1	golgi reassembly stacking protein 1, 65kDa	0.86
249	215783_s _at	ALPL	alkaline phosphatase, liver/bone/kidney	1.69
5364	215807_s _at	PLXNB1	plexin B1	0.98
56928	215833_s _at	SPPL2B	signal peptide peptidase-like 2B	0.69
10564	215931_s _at	ARFGEF 2	ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibited)	0.4
91353	215946_x _at	CTA- 246H3.1	similar to omega protein	-2.15
10825	216083_s _at	NEU3	sialidase 3 (membrane sialidase)	0.56
182	216268_s _at	JAG1	jagged 1 (Alagille syndrome)	-2.09
3183	216302_a _t	HNRNPC	heterogeneous nuclear ribonucleoprotein C (C1/C2)	0.48
8841	216326_s _at	HDAC3	histone deacetylase 3	0.63
	216337_a _t		NA	0.38
23223	216360_x _at	RRP12	ribosomal RNA processing 12 homolog (<i>S. cerevisiae</i>)	0.53
	216376_x _at		NA	0.95
934	216379_x _at	CD24	CD24 molecule	-2.15
80344	216389_s _at	WDR23	WD repeat domain 23	1.08
	216401_x _at		NA	-2.39
3956	216405_a _t	LGALS1	lectin, galactoside-binding, soluble, 1 (galectin 1)	-1.17
19695 1	216411_s _at	C15orf33	chromosome 15 open reading frame 33	0.36
7114	216438_s _at	TMSB4X	thymosin, beta 4, X-linked	-0.74
	216463_a _t		NA	-0.33
89795	216466_a _t	NAV3	neuron navigator 3	-0.2
56005	216483_s _at	C19orf10	chromosome 19 open reading frame 10	1.05
39102 0	216565_x _at	LOC3910 20	interferon induced transmembrane protein pseudogene	0.92
	216612_x _at		NA	-1.02
10130	216640_s	PDIA6	protein disulfide isomerase family	1.35

	_at		A, member 6	
6760	216684_s_at	SS18	synovial sarcoma translocation, chromosome 18	-0.75
392	216689_x_at	ARHGAP1	Rho GTPase activating protein 1	0.88
7204	216700_a_t	TRIO	triple functional domain (PTPRF interacting)	0.5
5996	216834_a_t	RGS1	regulator of G-protein signaling 1	-4.23
6648	216841_s_at	SOD2	superoxide dismutase 2, mitochondrial	1.72
23264	216844_a_t	ZC3H7B	zinc finger CCCH-type containing 7B	-0.96
1028	216894_x_at	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	-0.88
23223	216909_a_t	RRP12	ribosomal RNA processing 12 homolog (S. cerevisiae)	0.4
995	216914_a_t	CDC25C	cell division cycle 25 homolog C (S. pombe)	0.55
3493	217022_s_at	IGHA1	immunoglobulin heavy constant alpha 1	-4.36
7852	217028_a_t	CXCR4	chemokine (C-X-C motif) receptor 4	-4.23
	217029_a_t		NA	0.51
9757	217069_a_t	MLL4	myeloid/lymphoid or mixed-lineage leukemia 4	-1.26
81855	217226_s_at	SFXN3	sideroflexin 3	-1.19
6208	217298_a_t	RPS14	ribosomal protein S14	0.25
160313	217338_a_t	KRT19P2	keratin 19 pseudogene 2	0.34
	217423_a_t		NA	0.42
	217458_a_t		NA	0.57
3108	217478_s_at	HLA-DMA	major histocompatibility complex, class II, DM alpha	-2.02
3416	217496_s_at	IDE	insulin-degrading enzyme	1.24
389537	217499_x_at	OR7E38P	olfactory receptor, family 7, subfamily E, member 38 pseudogene	1.2
	217549_a_t		NA	-0.85
441453	217551_a_t	LOC441453	similar to olfactory receptor, family 7, subfamily A, member 17	0.49
51550	217598_a_t	CINP	cyclin-dependent kinase 2-interacting protein	0.34
3240	217647_a_t	HP	haptoglobin	1.84
22007	217706_a	LRRC51	leucine rich repeat containing 51	-1.21

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3925	217714_x_at	STMN1	stathmin 1/oncoprotein 18	-1.04
29927	217716_s_at	SEC61A1	Sec61 alpha 1 subunit (S. cerevisiae)	1.26
55737	217727_x_at	VPS35	vacuolar protein sorting 35 homolog (S. cerevisiae)	-0.88
6277	217728_a_t	S100A6	S100 calcium binding protein A6	-1.96
9168	217733_s_at	TMSB10	thymosin, beta 10	-1.23
22820	217749_a_t	COPG	coatamer protein complex, subunit gamma	1.02
11031	217762_s_at	RAB31	RAB31, member RAS oncogene family	-1.69
11031	217763_s_at	RAB31	RAB31, member RAS oncogene family	-1.64
11031	217764_s_at	RAB31	RAB31, member RAS oncogene family	-1.38
51646	217783_s_at	YPEL5	yippee-like 5 (Drosophila)	-0.82
10419	217786_a_t	PRMT5	protein arginine methyltransferase 5	0.78
2590	217787_s_at	GALNT2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2)	1.63
2590	217788_s_at	GALNT2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2)	1.51
55666	217796_s_at	NPLOC4	nuclear protein localization 4 homolog (S. cerevisiae)	1.4
79109	217808_s_at	MAPKAP1	mitogen-activated protein kinase associated protein 1	1.18
51465	217825_s_at	UBE2J1	ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)	1.04
51652	217837_s_at	VPS24	vacuolar protein sorting 24 homolog (S. cerevisiae)	-1.1
51150	217855_x_at	SDF4	stromal cell derived factor 4	0.71
4282	217871_s_at	MIF	macrophage migration inhibitory factor (glycosylation-inhibiting factor)	1.3
64755	217891_a_t	C16orf58	chromosome 16 open reading frame 58	0.87
55037	217895_a_t	PTCD3	Pentatricopeptide repeat domain 3	0.76
53826	217897_a_t	FXVD6	FXVD domain containing ion transport regulator 6	-1.02
10905	217921_a_t	MAN1A2	mannosidase, alpha, class 1A, member 2	1.12
10905	217922_a_t	MAN1A2	mannosidase, alpha, class 1A, member 2	0.74

64771	217924_a_t	C6orf106	chromosome 6 open reading frame 106	0.88
79932	217929_s_at	KIAA0319L	KIAA0319-like	0.64
55245	217935_s_at	UQCC	ubiquinol-cytochrome c reductase complex chaperone, CBP3 homolog (yeast)	0.68
55624	217944_a_t	POMGN T1	protein O-linked mannose beta1,2-N-acetylglucosaminyltransferase	1.2
56993	217960_s_at	TOMM22	translocase of outer mitochondrial membrane 22 homolog (yeast)	0.57
27018	217963_s_at	NGFRAP 1	nerve growth factor receptor (TNFRSF16) associated protein 1	-1.2
116496	217966_s_at	FAM129 A	family with sequence similarity 129, member A	-1.22
51734	217977_a_t	SEPX1	selenoprotein X, 1	0.8
8635	217984_a_t	RNASET 2	ribonuclease T2	-1.11
8566	218019_s_at	PDXK	pyridoxal (pyridoxine, vitamin B6) kinase	1.25
51231	218022_a_t	VRK3	vaccinia related kinase 3	0.63
55706	218073_s_at	TMEM48	transmembrane protein 48	0.53
51304	218077_s_at	ZDHHC3	zinc finger, DHHC-type containing 3	0.58
64121	218088_s_at	RRAGC	Ras-related GTP binding C	-0.83
51073	218105_s_at	MRPL4	mitochondrial ribosomal protein L4	1.06
55177	218126_a_t	FAM82C	family with sequence similarity 82, member C	0.88
79415	218130_a_t	C17orf62	chromosome 17 open reading frame 62	1.29
58477	218140_x_at	SRPRB	signal recognition particle receptor, B subunit	1.19
57761	218145_a_t	TRIB3	tribbles homolog 3 (Drosophila)	1.4
56944	218162_a_t	OLFML3	olfactomedin-like 3	-1.43
56997	218168_s_at	CABC1	chaperone, ABC1 activity of bc1 complex homolog (S. pombe)	1.25
79139	218172_s_at	DERL1	Der1-like domain family, member 1	0.98
54187	218189_s_at	NANS	N-acetylneuraminic acid synthase (sialic acid synthase)	1.31
4338	218212_s_at	MOCS2	molybdenum cofactor synthesis 2	1.1
63901	218248_a_t	FAM111 A	family with sequence similarity 111, member A	-0.88
51128	218254_s_at	SAR1B	SAR1 gene homolog B (S. cerevisiae)	1.12

79876	218289_s_at	UBE1DC1	ubiquitin-activating enzyme E1-domain containing 1	1.26
55154	218296_x_at	MSTO1	misato homolog 1 (Drosophila)	0.99
79447	218300_a_t	C16orf53	chromosome 16 open reading frame 53	0.58
55253	218347_a_t	TYW1	tRNA-yW synthesizing protein 1 homolog (S. cerevisiae)	0.61
79174	218358_a_t	CRELD2	cysteine-rich with EGF-like domains 2	1.42
10069	218377_s_at	RWDD2B	RWD domain containing 2B	1.1
25796	218387_s_at	PGLS	6-phosphogluconolactonase	0.95
11267	218391_a_t	SNF8	SNF8, ESCRT-II complex subunit, homolog (S. cerevisiae)	0.96
10807	218427_a_t	SDCCAG3	serologically defined colon cancer antigen 3	0.95
55337	218429_s_at	FLJ11286	hypothetical protein FLJ11286	0.78
79646	218433_a_t	PANK3	pantothenate kinase 3	0.6
26015	218441_s_at	RPAP1	RNA polymerase II associated protein 1	0.6
55161	218465_a_t	TMEM33	transmembrane protein 33	1.09
56915	218481_a_t	EXOSC5	exosome component 5	0.56
8891	218488_a_t	EIF2B3	eukaryotic translation initiation factor 2B, subunit 3 gamma, 58kDa	0.75
51337	218500_a_t	C8orf55	chromosome 8 open reading frame 55	0.79
54928	218516_s_at	IMPAD1	inositol monophosphatase domain containing 1	0.84
79960	218517_a_t	PHF17	PHD finger protein 17	-1.47
79178	218540_a_t	THTPA	thiamine triphosphatase	0.7
63874	218581_a_t	ABHD4	abhydrolase domain containing 4	0.69
54662	218596_a_t	TBC1D13	TBC1 domain family, member 13	0.7
51696	218603_a_t	HECA	headcase homolog (Drosophila)	-1.04
51409	218620_s_at	HEMK1	HemK methyltransferase family member 1	0.51
10186	218656_s_at	LHFP	lipoma HMGIC fusion partner	-1.96
8291	218660_a_t	DYSF	dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive)	0.8
55014	218666_s_at	STX17	syntaxin 17	0.79
57402	218677_a_t	S100A14	S100 calcium binding protein A14	-1.22

23753	218681_s _at	SDF2L1	stromal cell-derived factor 2-like 1	1.97
2188	218689_a _t	FANCF	Fanconi anemia, complementation group F	0.65
54512	218695_a _t	EXOSC4	exosome component 4	0.58
28984	218723_s _at	C13orf15	chromosome 13 open reading frame 15	-3.07
64856	218731_s _at	VWA1	von Willebrand factor A domain containing 1	0.95
54929	218745_x _at	TMEM16 1A	transmembrane protein 161A	0.64
80024	218749_s _at	SLC24A6	solute carrier family 24 (sodium/potassium/calcium exchanger), member 6	0.78
55113	218753_a _t	XKR8	XK, Kell blood group complex subunit-related family, member 8	0.84
55151	218772_x _at	TMEM38 B	transmembrane protein 38B	1.33
51205	218795_a _t	ACP6	acid phosphatase 6, lysophosphatidic	0.87
60559	218817_a _t	SPCS3	signal peptidase complex subunit 3 homolog (<i>S. cerevisiae</i>)	1.25
56967	218820_a _t	C14orf13 2	chromosome 14 open reading frame 132	0.87
55191	218840_s _at	NADSYN 1	NAD synthetase 1	-1.11
64838	218843_a _t	FNDC4	fibronectin type III domain containing 4	1.11
27242	218856_a _t	TNFRSF2 1	tumor necrosis factor receptor superfamily, member 21	-2.07
55843	218870_a _t	ARHGAP 15	Rho GTPase activating protein 15	-1.18
54997	218872_a _t	TESC	tescalcin	-1.11
51069	218887_a _t	MRPL2	mitochondrial ribosomal protein L2	0.73
4771	218915_a _t	NF2	neurofibromin 2 (bilateral acoustic neuroma)	0.7
1486	218923_a _t	CTBS	chitobiase, di-N-acetyl-	1.39
54925	218937_a _t	ZNF434	zinc finger protein 434	0.65
55278	218949_s _at	QRSL1	glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1	0.74
25984	218963_s _at	KRT23	keratin 23 (histone deacetylase inducible)	-2.83
56521	218976_a _t	DNAJC1 2	DnaJ (Hsp40) homolog, subfamily C, member 12	1.99
57001	218981_a _t	ACN9	ACN9 homolog (<i>S. cerevisiae</i>)	1.32
64924	218989_x _at	SLC30A5	solute carrier family 30 (zinc transporter), member 5	1.42

79694	219003_s _at	MANEA	mannosidase, endo-alpha	1.58
55500	219017_a _t	ETNK1	ethanolamine kinase 1	1.47
51236	219071_x _at	C8orf30A	chromosome 8 open reading frame 30A	0.64
55778	219086_a _t	C14orf13 1	chromosome 14 open reading frame 131	0.35
54829	219087_a _t	ASPN	asporin	-2.47
55661	219108_x _at	DDX27	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27	-0.76
65003	219162_s _at	MRPL11	mitochondrial ribosomal protein L11	0.69
9388	219181_a _t	LIPG	lipase, endothelial	1.56
79072	219200_a _t	FASTKD 3	FAST kinase domains 3	1.12
64218	219259_a _t	SEMA4A	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A	0.92
79034	219261_a _t	C7orf26	chromosome 7 open reading frame 26	0.75
26577	219295_s _at	PCOLCE 2	procollagen C-endopeptidase enhancer 2	1.21
80310	219304_s _at	PDGFD	platelet derived growth factor D	-2.41
55315	219344_a _t	SLC29A3	solute carrier family 29 (nucleoside transporters), member 3	0.63
80162	219359_a _t	ATHL1	ATH1, acid trehalase-like 1 (yeast)	-1.03
57099	219366_a _t	AVEN	apoptosis, caspase activation inhibitor	0.7
5429	219380_x _at	POLH	polymerase (DNA directed), eta	-1.41
56833	219386_s _at	SLAMF8	SLAM family member 8	-1.16
55128	219405_a _t	TRIM68	tripartite motif-containing 68	0.72
11264	219428_s _at	PXMP4	peroxisomal membrane protein 4, 24kDa	0.68
55286	219450_a _t	C4orf19	chromosome 4 open reading frame 19	1.31
79639	219462_a _t	TMEM53	transmembrane protein 53	0.72
55176	219499_a _t	SEC61A2	Sec61 alpha 2 subunit (S. cerevisiae)	0.87
79697	219526_a _t	C14orf16 9	chromosome 14 open reading frame 169	0.93
65987	219545_a _t	KCTD14	potassium channel tetramerisation domain containing 14	1.28

3773	219564_a_t	KCNJ16	potassium inwardly-rectifying channel, subfamily J, member 16	-4.06
93664	219572_a_t	CADPS2	Ca ²⁺ -dependent activator protein for secretion 2	1.04
2266	219612_s_at	FGG	fibrinogen gamma chain	0.67
10158	219630_a_t	PDZK1IP1	PDZK1 interacting protein 1	-2.86
24146	219640_a_t	CLDN15	claudin 15	0.78
6926	219682_s_at	TBX3	T-box 3 (ulnar mammary syndrome)	1.6
79713	219690_a_t	TMEM149	transmembrane protein 149	1.28
55277	219718_a_t	FLJ10986	hypothetical protein FLJ10986	1.22
79983	219756_s_at	POF1B	premature ovarian failure, 1B	-0.79
54885	219771_a_t	TBC1D8B	TBC1 domain family, member 8B (with GRAM domain)	1.34
56978	219835_a_t	PRDM8	PR domain containing 8	-0.79
7561	219854_a_t	ZNF14	zinc finger protein 14	-0.66
78989	219873_a_t	COLEC11	collectin sub-family member 11	-1.6
11153	219910_a_t	HYPE	Huntingtin interacting protein E	1.4
29925	219920_s_at	GMPPB	GDP-mannose pyrophosphorylase B	1.66
64752	219943_s_at	FLJ11850	hypothetical protein FLJ11850	0.53
55034	219959_a_t	MOCOS	molybdenum cofactor sulfurase	1.93
51377	219960_s_at	UCHL5	ubiquitin carboxyl-terminal hydrolase L5	1.65
6866	219992_a_t	TAC3	tachykinin 3 (neuromedin K, neurokinin beta)	0.7
54518	219994_a_t	APBB1IP	amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein	0.8
56605	220012_a_t	ERO1LB	ERO1-like beta (<i>S. cerevisiae</i>)	1.09
93	220028_a_t	ACVR2B	activin A receptor, type IIB	0.83
80235	220041_a_t	PIGZ	phosphatidylinositol glycan anchor biosynthesis, class Z	0.58
79831	220070_a_t	JMJD5	jumonji domain containing 5	1.06
63933	220094_s_at	CCDC90A	coiled-coil domain containing 90A	1.06
54875	220095_a_t	C9orf39	chromosome 9 open reading frame 39	0.44
79722	220112_a_t	ANKRD5	ankyrin repeat domain 55	0.66

	t	5		
80323	220180_a_t	CCDC68	coiled-coil domain containing 68	-1.19
64924	220181_x_at	SLC30A5	solute carrier family 30 (zinc transporter), member 5	0.56
56260	220216_a_t	C8orf44	chromosome 8 open reading frame 44	-0.59
55791	220235_s_at	C1orf103	chromosome 1 open reading frame 103	1.66
27042	220251_a_t	C1orf107	chromosome 1 open reading frame 107	0.67
64064	220256_s_at	OXCT2	3-oxoacid CoA transferase 2	-0.6
55146	220261_s_at	ZDHHC4	zinc finger, DHHC-type containing 4	0.79
64800	220271_x_at	EFCAB6	EF-hand calcium binding domain 6	0.45
50624	220275_a_t	CUZD1	CUB and zona pellucida-like domains 1	0.32
29116	220319_s_at	MYLIP	myosin regulatory light chain interacting protein	-0.76
54457	220325_a_t	TAF7L	TAF7-like RNA polymerase II, TATA box binding protein (TBP)-associated factor, 50kDa	0.4
441024	220346_a_t	MTHFD2L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like	0.73
55199	220353_a_t	FAM86C	family with sequence similarity 86, member C	0.39
222487	220404_a_t	GPR97	G protein-coupled receptor 97	0.41
10164	220446_s_at	CHST4	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 4	-1.87
79015	220449_a_t	MGC5566	hypothetical protein MGC5566	0.46
25897	220483_s_at	RNF19A	ring finger protein 19A	-1.08
	220489_s_at		NA	-1.08
64223	220587_s_at	GBL	G protein beta subunit-like	0.67
55179	220643_s_at	FAIM	Fas apoptotic inhibitory molecule	-1.38
79978	220674_a_t	FLJ22814	hypothetical protein FLJ22814	-0.56
50854	220755_s_at	C6orf48	chromosome 6 open reading frame 48	-1.22
10243	220773_s_at	GPHN	gephyrin	1.11
80069	220904_a_t	C6orf208	chromosome 6 open reading frame 208	0.53
81876	220964_s_at	RAB1B	RAB1B, member RAS oncogene family	0.94

81855	220974_x _at	SFXN3	sideroflexin 3	-0.8
81031	221024_s _at	SLC2A10	solute carrier family 2 (facilitated glucose transporter), member 10	2.04
81575	221031_s _at	APOLD1	apolipoprotein L domain containing 1	-2.89
26503	221041_s _at	SLC17A5	solute carrier family 17 (anion/sugar transporter), member 5	0.81
63891	221063_x _at	RNF123	ring finger protein 123	0.92
55798	221079_s _at	METTL2 B	methyltransferase like 2B	0.9
10530	221127_s _at	RIG	regulated in glioma	-0.78
	221159_a _t		NA	2.61
81554	221247_s _at	WBSCR1 6	Williams-Beuren syndrome chromosome region 16	0.53
81557	221261_x _at	MAGED4 B	melanoma antigen family D, 4B	-0.54
81537	221268_s _at	SGPP1	sphingosine-1-phosphate phosphatase 1	1.54
2850	221306_a _t	GPR27	G protein-coupled receptor 27	0.62
8385	221341_s _at	OR1D4	olfactory receptor, family 1, subfamily D, member 4	0.29
26476	221346_a _t	OR10J1	olfactory receptor, family 10, subfamily J, member 1	0.36
665	221478_a _t	BNIP3L	BCL2/adenovirus E1B 19kDa interacting protein 3-like	-1.34
58528	221524_s _at	RRAGD	Ras-related GTP binding D	1.05
1978	221539_a _t	EIF4EBP 1	eukaryotic translation initiation factor 4E binding protein 1	1.14
83716	221541_a _t	CRISPLD 2	cysteine-rich secretory protein LCCL domain containing 2	-1.98
51540	221575_a _t	SCLY	selenocysteine lyase	1.83
9501	221614_s _at	RPH3AL	rabphilin 3A-like (without C2 domains)	0.91
51236	221629_x _at	C8orf30A	chromosome 8 open reading frame 30A	0.64
55769	221645_s _at	ZNF83	zinc finger protein 83	-1.6
3514	221651_x _at	IGKC	immunoglobulin kappa constant	-2.56
3514	221671_x _at	IGKC	immunoglobulin kappa constant	-2.54
55168	221693_s _at	MRPS18 A	mitochondrial ribosomal protein S18A	1.07
29086	221711_s _at	C19orf62	chromosome 19 open reading frame 62	0.63

11214	221718_s_at	AKAP13	A kinase (PRKA) anchor protein 13	-1.32
1462	221731_x_at	VCAN	versican	-2.75
3069	221767_x_at	HDLBP	high density lipoprotein binding protein (vigilin)	0.68
6120	221770_a_t	RPE	ribulose-5-phosphate-3-epimerase	0.61
376267	221810_a_t	RAB15	RAB15, member RAS oncogene family	1.14
84861	221838_a_t	KLHL22	kelch-like 22 (Drosophila)	0.38
81570	221845_s_at	CLPB	ClpB caseinolytic peptidase B homolog (E. coli)	0.65
408050	221853_s_at	NOMO3	NODAL modulator 3	1.52
9683	221867_a_t	N4BP1	Nedd4 binding protein 1	0.68
400961	221868_a_t	PAIP2B	poly(A) binding protein interacting protein 2B	1.11
	221877_a_t		NA	0.66
58986	221882_s_at	TMEM8	transmembrane protein 8 (five membrane-spanning domains)	0.9
9563	221892_a_t	H6PD	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	1.17
10443	221899_a_t	PFAAP5	phosphonoformate immun-associated protein 5	-1.39
114112	221906_a_t	TXNRD3	thioredoxin reductase 3	0.77
27079	221940_a_t	RPUSD2	RNA pseudouridylate synthase domain containing 2	0.51
283232	221951_a_t	TMEM80	transmembrane protein 80	-0.85
5165	221957_a_t	PDK3	pyruvate dehydrogenase kinase, isozyme 3	0.65
56834	221966_a_t	GPR137	G protein-coupled receptor 137	0.76
51150	221972_s_at	SDF4	stromal cell derived factor 4	1.19
196483	222013_x_at	FAM86A	family with sequence similarity 86, member A	0.69
11214	222024_s_at	AKAP13	A kinase (PRKA) anchor protein 13	-1.35
10399	222034_a_t	GNB2L1	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	-0.71
1285	222073_a_t	COL4A3	collagen, type IV, alpha 3 (Goodpasture antigen)	-1.59
125058	222116_s_at	TBC1D16	TBC1 domain family, member 16	1.04
3268	222126_a_t	HRBL	HIV-1 Rev binding protein-like	1.37

6925	222146_s_at	TCF4	transcription factor 4	-1.89
9236	222156_x_at	CCPG1	cell cycle progression 1	1.19
60526	222192_s_at	C2orf43	chromosome 2 open reading frame 43	0.9
56926	222206_s_at	NCLN	nicalin homolog (zebrafish)	0.75
29956	222212_s_at	LASS2	LAG1 homolog, ceramide synthase 2	0.83
55379	222231_s_at	LRRC59	leucine rich repeat containing 59	1.28
55000	222244_s_at	TUG1	taurine upregulated gene 1	-1.13
25896	222250_s_at	INTS7	integrator complex subunit 7	0.98
79939	222263_a_t	SLC35E1	solute carrier family 35, member E1	0.7
542767	222277_a_t	PCOTH	prostate collagen triple helix	0.67
283491	222327_x_at	OR7E156P	olfactory receptor, family 7, subfamily E, member 156 pseudogene	0.58
	222335_a_t		NA	0.28
646808	222338_x_at	LOC646808	hypothetical LOC646808	0.59
79791	222352_a_t	FBXO31	F-box protein 31	0.56
29984	31846_at	RHOD	ras homolog gene family, member D	1.3
3508	31861_at	IGHMBP2	immunoglobulin mu binding protein 2	0.66
23625	32209_at	FAM89B	family with sequence similarity 89, member B	0.57
10554	32836_at	AGPAT1	1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha)	0.74
8484	33579_i_at	GALR3	galanin receptor 3	0.68
10298	33814_at	PAK4	p21(CDKN1A)-activated kinase 4	0.57
1043	34210_at	CD52	CD52 molecule	-1.55
9894	34260_at	TELO2	TEL2, telomere maintenance 2, homolog (S. cerevisiae)	-0.75
8517	36004_at	IKBKG	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma	0.69
9647	37384_at	PPM1F	protein phosphatase 1F (PP2C domain containing)	0.55
374655	37590_g_at	ZNF710	zinc finger protein 710	0.98
23549	38703_at	DNPEP	aspartyl aminopeptidase	0.5
4862	39549_at	NPAS2	neuronal PAS domain protein 2	1.27

6305	39835_at	SBF1	SET binding factor 1	0.51
374655	39891_at	ZNF710	zinc finger protein 710	0.4
55794	40255_at	DDX28	DEAD (Asp-Glu-Ala-Asp) box polypeptide 28	0.53
8045	40359_at	RASSF7	Ras association (RalGDS/AF-6) domain family 7	0.68
53615	41160_at	MBD3	methyl-CpG binding domain protein 3	0.88
79676	44617_at	OGFOD2	2-oxoglutarate and iron-dependent oxygenase domain containing 2	1.15
79903	45526_g_at	FLJ14154	hypothetical protein FLJ14154	0.75
54985	45714_at	HCFC1R1	host cell factor C1 regulator 1 (XPO1 dependent)	-0.74
55615	47069_at	PRR5	proline rich 5 (renal)	0.73
79034	47083_at	C7orf26	chromosome 7 open reading frame 26	0.6
60672	48659_at	RP5-1077B9.4	invasion inhibitory protein 45	0.8
23410	49327_at	SIRT3	sirtuin (silent mating type information regulation 2 homolog) 3 (<i>S. cerevisiae</i>)	0.55
9409	49878_at	PEX16	peroxisomal biogenesis factor 16	0.51
58525	52005_at	WIZ	widely interspaced zinc finger motifs	0.7
84065	52078_at	C1orf160	chromosome 1 open reading frame 160	0.6
80789	53968_at	INTS5	integrator complex subunit 5	0.96
63892	54632_at	THADA	thyroid adenoma associated	1.66
54480	55093_at	CSGcA-T	chondroitin sulfate glucuronyltransferase	1
57473	55872_at	ZNF512B	zinc finger protein 512B	1.11
83696	56829_at	NIBP	NIK and IKK {beta} binding protein	0.61
26119	57082_at	LDLRAP1	low density lipoprotein receptor adaptor protein 1	0.6
4718	58916_at	NDUFC2	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kDa	1.52
114112	59631_at	TXNRD3	thioredoxin reductase 3	0.5
376267	59697_at	RAB15	RAB15, member RAS oncogene family	1.38
8681	60528_at	PLA2G4B	phospholipase A2, group IVB (cytosolic)	0.82
11094	61874_at	C9orf7	chromosome 9 open reading frame 7	0.73
57175	64486_at	CORO1B	coronin, actin binding protein, 1B	1.14
78992	65086_at	YIPF2	Yip1 domain family, member 2	0.78
51619	65521_at	UBE2D4	ubiquitin-conjugating enzyme E2D 4 (putative)	0.51

79939	79005_at	SLC35E1	solute carrier family 35, member E1	0.4
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Vita

Ryan Christopher Fassnacht was born on July 12, 1983, at the Fairfax Memorial Hospital in Fairfax County, Virginia and is an American citizen. He graduated from James W. Robinson Secondary School, Fairfax, Virginia in 2001. He received his Bachelor of Science in Biology from Hampden-Sydney College, Hampden-Sydney, Virginia in 2005. He completed his requirements in the Certificate Program in Physiology from Virginia Commonwealth University, Richmond, Virginia in 2007. He joined the Molecular Biology Research Team as a part time Laboratory Specialist in the Transplant Department in the Hume-Lee Transplant Center at the Medical College of Virginia Campus of Virginia Commonwealth University, Richmond, Virginia in 2007, where he presently continues to work for VCU Health Systems, Richmond, Virginia