Microarray Analysis of Hepatic Gene Expression During the Development of Diet-Induced Obesity

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ABSTRACT

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Obesity is known to result in insulin resistance, Type 2 diabetes and the eventual development of non-alcoholic steatohepatitis (NASH). The underlying molecular mechanisms involved in the progression of these diseases are currently unknown. To obtain a better understanding of these molecular pathways, DNA microarray analysis was used to examine gene expression profiles during the development of diet-induced obesity (DIO) in the mouse. Mice fed a high fat diet (HFD) quickly become obese primarily due to fat deposition, resulting in a significant increase in body weight and marked hyperinsulinemia in comparison to chow fed (ND) controls. Hepatic gene expression profiles were examined using trend and correlation analysis in HFD and ND groups at 0, 2, 4, 8 and 12 weeks after high fat feeding. Statistical analysis using ANOVA identified 1947 genes to have a significant diet effect ($P < 0.05$). Analysis of the data revealed significant changes in gene expression in genes involved in protective mechanisms in the early weeks of HFD such as those in glycolysis and beta-oxidation. At the later time points there was down regulation of gene expression in pathways of leptin signaling, liver regeneration and protective radical scavengers. In addition, expression of genes involved in gluconeogenesis and fat synthesis pathways were also more highly expressed at the later time points. This microarray analysis has identified several novel pathways that are involved in the development of insulin resistance and steatosis in the liver.

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Table of Contents

Page

List of figures..........ix

List of tables..........xi

Abbreviations..........xii

Chapter 1: Introduction

Introduction..........1

1.1 Messenger RNA (mRNA) and microarray technology..........3
1.2 Obesity and Type 2 diabetes..........5
1.3 Insulin resistance and hyperinsulinemia..........7
1.4 Non-alcoholic steatohepatitis (NASH)..........7
1.5 The role of liver in glucose homeostasis and high fat diet..........8
1.6 The diet-induced obese mouse model..........10
1.7 Contributions from colleagues..........11
1.8 Thesis organization..........11

Chapter 2: Materials and Methods

Experimental Procedures

2.1 Strain and time course..........12
2.2 Blood glucose, insulin and leptin measurements..........12
2.3 Dual energy X-ray Absorptiometry (DEXA) analysis at 8 weeks and Oil red O staining for fat..........13
2.4 Isolation of total RNA and quality control..........13
2.5 Pooling and synthesis of cDNA..........14
2.6. Incorporation of biotinylated ribonucleotides and quality control..........14
2.7 Fragmentation of cRNA and quality control..........14
2.8 Hybridization, washing, staining and scanning of chips..........15

Microarray Data Analysis

2.9 Initial quality control of microarray scans and upload of data into Resolver..........16
2.10 Identification of outlier chips and combining triplicate chips..........16
2.11 2D cluster analysis of intensity experiments..........17
2.12 Normalization of microarray expression data..........17
2.13 Expression analysis of diet affected genes and linear trend analysis..........18
2.14 Correlations: gene expression profiles to pharmacological data and biological processes..........19

Page

Chapter 3: Results

3.1 Diet-induced obesity time course: food and water consumption..........20
3.2 Development of obesity and insulin resistance: body weight, blood glucose, insulin and leptin..........21
3.3 Dual energy X-ray Absorptiometry (DEXA) analysis and Oil red O staining at 8 weeks of time course..........24
3.4 Summary of Diet-Induced Obesity (DIO)..........26
3.5 Microarray experimental design..........27
3.6 Generation of target cRNA..........28
3.7 Isolation and quality control of total RNA..........30
3.8 Quality control of cRNA..........32
3.9 Quality control of fragmented cRNA..........33
3.10 Initial quality control of microarray scans..........35
3.11 Identification of outlier microarrays (chips)..........36
3.12 2D cluster of intensity experiments..........39
3.13 Diet affected genes..........39
3.14 Linear trend and correlation analysis..........41
3.15 Regulation of glycolysis and gluconeogenesis..........42
3.16 Regulation of fat metabolism..........46
3.17 Regulations of CYPs, GSTs and HSPs..........50
3.18 Energy metabolism alteration..........52
3.19 Regulation of growth factors..........53
3.20 Microarray analysis summary..........54

Chapter 4: Discussion

4.1 Validation of the diet-induced obese mouse model..........55
4.2 Microarray design issues..........55
4.3 Statistical issues with analysis of microarray data..........57
4.4 1947 genes were identified to have a significant diet affect..........59
4.5 Linear Trend and correlation analysis..........61
4.6 Biological mechanisms in early weeks (0-4) of obesity and insulin resistance development..........62
4.7 Biological mechanisms in late weeks (8-12) of obesity and insulin resistance development..........64
4.8 Summary..........67
4.9 Future studies..........68
4.10 References..........70

Page

Appendix A Variance stabilizing transformation..80

Appendix B 1947 diet affected genes ($P < 0.05$)..81

Appendix C Trend analysis: Genes that are significantly up-regulated ($P < 0.01$)..147

Appendix D Trend analysis: Genes that are significantly down-regulated ($P < 0.01$)..148

List of Figures

Page

1 (A) Food consumption of high fat diet (HFD) and chow diet (ND)................20

1 (B) Water consumption of high fat diet (HFD) and chow diet (ND)...............20

1 (C) Caloric intake of high fat diet (HFD) and chow diet (ND).........................20

2 (A) Body weight of C57BL/6J on high fat diet (HFD) or chow diet (ND).........21

2 (B) Non fasting plasma glucose levels of mice on high fat diet (HFD) or chow diet (ND)..22

2 (C) Insulin levels of mice on high fat diet (HFD) or chow diet (ND)...............23

2 (D) Leptin levels of mice on high fat diet (HFD) or chow diet (ND)...............24

3 (A) DEXA scan reveals differences between the high fat diet (HFD) and chow diet (ND) treatment group..25

3 (B) Percentage (%) of body fat of HFD and ND mice also revealed differences (* P $\leq$0.001) 25

4 Histology of liver sections of high fat diet (HFD) and chow diet (ND) animals...26

5 (A) High fat feeding 12 week time course experiment...............................27

5 (B) Microarray design..28

6 cRNA sample preparation...29

7 Quality control assessment of total liver RNA by examination of 28S and 18S rRNA bands using RNA Nano LabChip.....................................31

8 (A) Quality control assessment of biotin labeled cRNA synthesis reactions.......33

8 (B) cRNA synthesis profiles..34

9 Fragmented cRNA quality control...34

10 Correlation plot of two chips from the week 12 HFD group........................37

List of Figures

Continued

Page

11 2D agglomerative cluster..40

12 Glycolysis and gluconeogenesis regulatory genes..................................43

13 Normalized intensity of PPARα gene expression of chow diet (ND) and high fat diet (HFD) for a period of 12 weeks..47

14 Normalized intensity of SREBP-1 gene expression of chow diet (ND) and high fat diet (HFD) for a period of 12 weeks..49

15 HFD-ND transformed intensity of Atp5c1...52

16 Down regulation of Egfr and Hdgf upon high fat diet treatment...................53

17 Microarray analysis software...60

18 Identification of molecular mechanisms in the development of obesity, inulin resistance and steatosis (NASH)..64

List of Tables

Page

1 A260/A280 ratio after RNeasy purification and concentration of total RNA.....31

2 Affymetrix expression report.....36

3 Correlation coefficient of all the chip combinations.....38

4 Gene correlation/anti-correlation with body weight ($P < 0.05$).....44

5 Gene correlation/anti-correlation with insulin ($P < 0.05$).....45

6 Gene correlation/anti-correlation with blood glucose ($P < 0.05$).....46

7 Differences in expression levels (HFD-ND) and p-values at all time points of glutathione S transferases.....51

8 Differences in expression levels (HFD-ND) and p-values at all time points of heat shock proteins.....51

Abbreviations

Akt/PKB	Thymoma viral proto-oncogene 1
ANOVA	analysis of variance
Apoa4	apolipoprotein a4
ATP	adenosine triphosphate
BHLH	basic helix-loop helix
BMI	body mass index
cDNA	complementary deoxyribonucleic acid
chip	microarray = GeneChip
Cpt1	carnitine palmitoyl transferase
Cyp2b9	cytochrome P450 2b9
Cyp3a11	cytochrome P450 3a11
Cyp3a16	cytochrome P450 3a16
Cyps	cytochrome P450 isoforms
cRNA	complementary RNA
Decr1	2,4-dienoyl CoA reductase 1 mitochondrial
DEXA	dual energy x-ray absorptiometry
DNA	deoxyribonucleic acid
DIO	diet-induced obesity
Ech1	enoyl coenzyme A hydratase 1
EDTA	ethylenediaminetetraacetic acid
Egf	epidermal growth factor
Egfr	epidermal growth factor receptor

Abbreviations

Continued

Elov2	elongation of very long chain fatty acids-like 2
Elov3	elongation of very long chain fatty acids-like 3
ESTs	expressed sequence tags
Fabp2	fatty acid binding protein 2
Fabp6	fatty acid binding protein 6
Fbp1	fructose bisphosphatase 1
G6pc	glucose 6 phosphatase
Gapd	glyceraldehyde-3-phosphate dehydrogenase
Gck	glucokinase
Gdc1	glycerol phosphate dehydrogenase 1 cytoplasmic
Gdm1	glycerol phosphate dehydrogenase 1 mitochondrial
GSTs	gluathione S transferases
Hdgf	hepatoma derived growth factor
HDL	high density lipoprotein
HFD	high fat diet
Hmgcs2	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2
HSPs	heat shock proteins
mRNA	messenger RNA
NAFLD	non-alcoholic fatty liver disease
NASH	non-alcoholic steatohepatitis
ND	chow diet
NIDDM	non-insulin-dependent diabetes mellitus

Abbreviations

Continued

Pck1	phosphoenolpyruvate carboxykinase 1
PCR	polymerase chain reaction
Pfkfb1	6-phosphofructo-2-kinase/fructose-2-6-bisphosphatase 1
PIAS3	protein inhibitor of activated STAT 3
PPARα	peroxisome proliferative activated receptor alpha
PPRE	peroxisome proliferator responsive element
RNA	ribonucleic acid
Scd1	Stearoyl-coenzyme A desaturase 1
Slc25a20	Solute carrier family 25 member 20/carnitine-acylcarnitine translocase
SPOT14	Thyroid hormone responsive protein
STAT3	Signal transducer activator transcription 3
SRE	stearoyl regulatory element
SREBP1	sterol regulatory element binding protein 1
WHO	World Health Organization

Chapter 1

Introduction

The molecular mechanisms involved in obesity and insulin resistance are still poorly understood. The ability of the new technology of microarray analysis to survey genome-wide changes in gene expression should provide valuable insight into understanding these diseases and their complications at the molecular level.

Obesity is an excellent disease system in which to apply microarray technology for the following reasons. First, obesity is a multigenic disease and the Affymetrix MG-U74Av2 microarray has approximately 13000 genes. This technology has the potential of identifying multiple patterns of gene expression. Second, the diet-induced obese (DIO) mouse model is well characterized at the pharmacological level. Third, the liver is one of the major organs that is affected by obesity and can be readily isolated from mice.

Both obesity and diabetes are reaching epidemic proportions worldwide in all age spectrums and is most evident in the North American population (7,60). Non-alcoholic steatohepatitis (NASH), a liver disease which is a consequence of obesity also is emerging as an important metabolic syndrome. The role of obesity is so critical in the development of NASH that it is now considered as "another disease of affluence" (45,70).

A strong link exists between consumption of a high fat diet (HFD) and the development of adverse health effects (74). High fat feeding is known to result in the development of obesity, insulin resistance and steatosis (NASH) (53). This study defines a relationship between diet induced disease progression and gene expression.

The specific aims for these projects were to:

1. Design a microarray experiment of diet-induced obesity (DIO) that would support a thorough statistical analysis of the data.
2. Identify statistically significant changes in hepatic gene expression at 0, 2, 4, 8 and 12 weeks of high fat feeding.
3. Use trend and correlation analyses to provide biological insights into the data.
4. Identify molecular mechanisms associated with the development of obesity, insulin resistance and steatosis (NASH).

1.1 Messenger RNA (mRNA) and Microarray Technology

The etiology of multigenic diseases such as obesity, insulin resistance and steatosis (NASH) are not easily solved using single gene approaches. Alternative strategies in the field of gene discovery may prove to be beneficial in identification of genetic pathways associated with the above mentioned diseases. The combination of microarray technology and the appropriate animal model can be a powerful tool in understanding the underlying mechanisms of human multigenic diseases such as obesity and Type 2 diabetes (25).

In the past decade, there has been an explosion of knowledge and tools in both molecular biology and computational technology. Sequencing of the human and mouse genomes has mapped out the majority of the genes. Photolithography, robotics and miniaturization have created the analytical systems. These recent advances are facilitating the study of gene expression and the discovery of the roles played by specific genes in the development of diseases. Microarrays display in a single experiment the expression levels of thousands of genes within a cell (5).

Dr. Mark Schena and co-workers developed Microarrays at Stanford University in the early 1990s. This field emerged with the involvement of several major disciplines in science: biology, chemistry, physics, engineering, mathematics and computer science (71). Microarray technology includes arraying of DNA on a glass surface, hybridization, detection method (laser) and analysis software that facilitates management of large data sets (36). More specifically, the amount of mRNA bound to the spots on the microarray is precisely measured, generating a profile of gene expression in cells and tissues (5).

Today microarrays are available from several commercial vendors and are replacing traditional biological assays based on such as gels, filters and purification columns (71). Affymetrix GeneChip microarrays are becoming increasingly used in academic and industrial institutions. These microarrays offer several internal controls; each chip contains approximately 13000 different genes. The Affymetrix MG-U74Av2 contains ~6000 genes that have been functionally characterized and ~6000 expressed sequenced tags (ESTs). Each gene is represented minimally by one set of 16-20 different 'probe pairs'. A probe pair consists of a 25-base-pair (bp) 'perfect-match' oligonucleotide probe and a 25-bp 'mismatch' probe, in which the 13th position does not match the target sequence. The intensity across all the paired probes ('the probe set') is integrated by proprietary GeneChip software. The software compares the mRNA levels in two RNA preparations by analyzing probe-set signals from two GeneChips: one hybridized with complementary RNA (cRNA) made from the control RNA preparation, the other hybridized with cRNA generated from the experiment. The Affymetrix platform designates the cRNA made from the cellular RNA as the "target" and the oligonucleotide on the chip as the "probe" (59).

The powerful tool of microarray technology offers a significant advantage in terms of the number of genes that can be analyzed simultaneously. Large-scale gene expression analysis generates a detailed molecular profile thus allowing for the identification of previously unknown genes and pathways associated with particular biological processes (41). Several recent publications have demonstrated how genomic tools, in particular microarrays are beginning to offer unprecedented insights into complex diseases (11,12,24,38,62). Although, understanding the relationship between genes and diseases remains a particularly challenging task with the use of advanced genomic technologies such as GeneChip arrays, researchers can view complex diseases from a genome-wide perspective (40,41).

This is the first report to describe hepatic gene expression profiles throughout the development of obesity, insulin resistance and steatosis (NASH) in a mouse model of DIO. It would be expected that high fat feeding would cause dramatic changes in expression pattern particularly of genes involved in metabolic pathways. The purpose of this time course experiment was to gain insights into the expression of liver genes that are altered upon the development of obesity, insulin resistance and steatosis (NASH). Also to determine which genes most highly correlate with the pharmacological data on body weight, glucose and insulin. Additionally, we wanted to examine if the observed changes between the two diet groups were consistent with existing mechanisms in the development of the diseases.

1.2 Obesity and Type 2 Diabetes

Obesity is currently a public health concern with about 315 million people world-wide who fall into the World Health Organization (WHO) definition of obesity (21). Over 90% of the cases of diabetes worldwide are in the form known as Type 2 diabetes and approximately 85% of Type 2 diabetics are obese (37). Obesity and Type 2 diabetes are rapidly spreading under the new dietary habits and sedentary lifestyle of our age (42,88). Both diseases also are leading to increasing cases of NASH, which is a significant cause of morbidity and mortality in patients with obesity related Type 2 diabetes. Consistently, all three diseases are generating immense health care costs (1,43,51).

Obesity leads to several complications such as insulin resistance, Type 2 diabetes, heart disease, hypertension, stroke, sleep apnea, gestational diabetes, degenerative joint disease, liver diseases (NASH) and certain cancers (20,30,33,34,67). The risk of developing most of these conditions increases with weight gain and deposition of fat in cell types other than adipocytes. The result of excess lipid accumulation in cell types such as the liver and muscle leads to inhibition of insulin action. It has been shown that reduction of the levels of fat accumulation in liver and other tissues results in improved insulin sensitivity (33). Deregulated expression of genes that are involved in fat synthesis, satiety, insulin signaling and thermogenesis may lead to the development of obesity and its consequences. A number of gene products have been identified to be key players in this phenotype, for example leptin, however, many still remain unknown (35,79).

Type 2 diabetes or non-insulin-dependent diabetes mellitus (NIDDM) follows the onset of obesity and insulin resistance (32). The pathogenesis of the disease involves hyperglycemia, insulin resistance and hyperinsulinemia (8,33). In the healthy state, insulin is secreted from pancreatic beta-cells in response to increasing glucose concentrations in the blood. Insulin mediates its action on multiple points of both glucose and lipid metabolic pathways. Insulin attenuates gluconeogenesis, promotes glycogen synthesis in the liver, facilitates glucose uptake by peripheral tissues, inhibits lipolysis in adipose tissue and inhibits hepatic glucose production (61). As insulin resistance develops, many of these key regulatory mechanisms are lost and complications such as retinopathy, nephropathy, neuropathy, hypertension, dyslipidemia, coronary heart disease, stroke and cancer results (17,54,61). Much research has gone into understanding the insulin-signaling pathway in the hope of identification of the mechanisms of insulin resistance. However, many pathways involved in this disease remain unknown and a better understanding of the underlying mechanisms involved in the development of insulin resistance and obesity would provide new insights into these diseases and possibly the identification of novel therapeutic targets (37).

1.3 Insulin Resistance and Hyperinsulinemia

In response to rising levels of blood glucose the pancreas produces increasing amounts of insulin. Hyperinsulinemia is the body's way of counteracting insulin resistance. Thus insulin resistance gradually develops during excess weight gain. Obesity, Type 2 diabetes and NASH, all positively correlate with insulin resistance, suggesting that insulin resistance is critically involved in the pathogenesis of all three diseases (37,43,50). In fact, studies have shown that obesity is directly associated with insulin resistance and weight loss improves insulin sensitivity (47,68,87). The molecular mechanisms involved in the development of insulin resistance and its consequences are unknown. It would be of interest to examine on a genome-wide level the genes that correlate with the development of insulin resistance.

1.4 Non-alcoholic steatohepatitis (NASH)

NASH was considered a relatively uncommon disease and has only become evident recently because of the prevalence of obesity. More than 70% of people with NASH are obese and up to 75% of people with NASH have Type 2 diabetes. It is not unexpected that this population also would have associated hyperinsulinemia and hyperleptinemia. Most patients with NASH are between the ages of 40 and 60. However, the reports of children at the age of 10 having NASH, are a major concern (6,43,70).

This liver disease begins in its earliest stages with the development of fatty liver also known as steatosis and progresses to cirrhosis and eventually liver failure (70). The progression from start to finish involves several pathological processes. Initially steatosis develops with association to insulin resistance, obesity and development of Type 2 diabetes. The mechanisms involved in this first step are insulin resistance, which causes the mobilization of fatty acids in the hepatocytes thus leading to steatosis. The second phase of this disease is mediated by oxidative stress. Cytochrome P450 2E1 (CYP2E1) generates free radicals that damage the hepatocytes resulting in the secondary recruitment of inflammatory cells and leading to the occurrence of necrosis and inflammation. There are several mechanisms being proposed for the dramatic alterations in liver function that occur with these diseases, however, the exact molecular mechanisms involved in this broad-spectrum disease are currently unknown (6,23,28,43,45)

1.5 The Role of Liver in Glucose Homeostasis and High Fat Diet

High fat feeding has dramatic effects on liver function. It has been reported previously that upon high fat feeding there is conversion into a fatty liver and an altered gene expression profile (39). More specifically, liver abnormalities are being identified in diabetic patients, the majority being attributable to a fatty liver and altered metabolic processes (70,73). Clearly, both the development of Type 2 diabetes and obesity are leading to altered liver morphology, resulting in susceptibility to various liver diseases (cirrhosis, NASH, NAFLD, hepatitis C).

The liver is a relevant organ to analyze for changes in gene expression in the development of obesity, insulin resistance and steatosis (NASH) as it plays a central role in metabolism and its functional state has a profound effect on the entire body (39). The liver is the largest solid organ in the body and is strategically situated to carry out remarkable functions by receiving blood from the portal vein and hepatic artery. These inputs import large amounts of nutrients, toxic substances, endobiotics and xenobiotics. Some of the major functions of the liver include converting food into stored energy, removing toxic substances from the blood, defending against bacteria, drug metabolism and production of bile. Additionally, the liver is responsible for blood glucose homeostasis and providing glucose to extrahepatic tissue (9). Up to 60% of glucose absorbed from the digestive tract is taken up by the liver and stored either as glycogen or converted into amino acids or fatty acids (37). Therefore, the liver also acts as a metabolic fuel converter in order to provide extrahepatic tissues with appropriate fuels (9).

Tissue specific knockout mice lacking the insulin receptor (IR) in muscle, fat and also liver showed that the loss of the insulin signaling pathway in the liver results in a phenotype of severe insulin resistance and progressive hepatic dysfunction as seen with obesity, Type 2 diabetes and steatosis (NASH). Knockout mice, lacking the muscle and fat IR, only display some of the phenotypes. In context of the pathologies being investigated, the liver is the primary organ responsible for blood glucose homeostasis (18,46,55-57,89).

The liver also has been examined with respect to steatosis, which is commonly observed upon high fat feeding. This fatty liver syndrome can be reversed in a lipodystrophic mouse model upon administration of leptin. Leptin signaling results in down regulation of genes involved in triglyceride synthesis thereby preventing fat deposits in the liver and improving the symptoms of Type 2 diabetes (72,79,80).

Based on the work of many researchers, the liver has been shown to be significantly involved in the development of obesity, insulin resistance and steatosis (NASH). Therefore, further investigation of hepatic gene expression profiles may provide information into an understanding of the diseases.

1.6 The Diet-Induced Obese Mouse Model

An excellent animal model to study the changes in hepatic gene expression during the development of obesity, insulin resistance and steatosis (NASH), is the DIO mouse. For example C57BL/6J male mice have been reported to be the most common mouse model for DIO studies (4). In the late 1980s high fat feeding experiments were carried out on the C57BL/6J mouse strain and several other rodent models (76,77,86). Obesity resulted in this model without being chemically induced and further resulted in Type 2 diabetes. Upon high fat feeding these mice are susceptible to the development of obesity and Type 2 diabetes in a manner analogous to the majority of Type 2 diabetic symptoms in humans (75,76,78). In addition, for the mouse genome project the C57BL/6J strain was selected for sequencing, hence >90% of the DNA sequence for this strain is known. Sequencing of the mouse genome will help in the identification for many of the expressed sequence tags (ESTs) used on these microarrays. This is because 99% of genes within the mouse genome have counterparts in the human genome. Furthermore, since the sequence of genes with common functions are relatively well conserved between humans and mice and mice can be used experimentally, this will allow scientists to test and learn more about the function of human genes, leading to better understanding of human disease and improved treatments and cures (15,83).

1.7 Contributions from Colleagues

Microarray experiments require contributions from various disciplines of science and the successful completion of this thesis was due to the help of a number of collaborators. Dr. Chi-Chung Chan, Ms. Lijing-Xu and Jimmy Fourtounis from the Department of Pharmacology at Merck Frosst assisted in development of the DIO mouse model and were responsible for carrying out the animal work and providing me with tissue samples. In addition, Dr. Richard Raubertas from the Merck Biometrics Department in Rahway was responsible for statistical analysis of the data on the transformed scale using the R package software. Yves Bois in the Merck Frosst Genomics Group provided expertise for the use of Affymetrix chips and James Mortimer from the Bioinformatics Department at Merck Frosst contributed his efforts for the microarray analysis.

1.8 Thesis Organization

This thesis is divided into four chapters. The first chapter introduces microarray technology, diseases being examined in this project (obesity, insulin resistance, Type 2 diabetes and steatosis (NASH), the role of liver in glucose homeostasis and the animal model. The materials and methods used for the pharmacological and microarray experiments are outlined in chapter 2. In addition, this chapter outlines the microarray analysis. Details of the results obtained from the pharmacological characterization of the DIO mouse and results from hepatic gene expression profiles during HFD treatment over a 12 week time course are provided in chapter 3. Issues with microarray designs, the biological mechanisms identified in the DIO mouse model, summary and suggestions for future studies are all detailed in chapter 4.

Chapter 2

Materials and Methods

EXPERIMENTAL PROCEDURES

2.1 Strain and Time Course

The diet-induced obese (DIO) mouse model was developed and characterized by the Merck Frosst Pharmacology group (Dr. Chi-Chung Chan and Li-jing Xu). Complete details of this model will be published elsewhere. In this particular experiment microarray profiling was used to examine the effects of high fat feeding on hepatic gene expression during the development of obesity. C57BL/6J male mice, 7-8 weeks old were obtained from the Jackson Laboratory (Bar Harbor, Maine). All animals were housed in-group cages (6 mice per cage) at the Merck Frosst Animal Center. The animals were kept under controlled lighting (12-h light-dark cycle), temperature (72° ± 2°F) and humidity (50 ± 10%). Two days after their arrival they were randomly assigned to condensed HFD (24 animals) or a ND (30 animals). The HFD diet was composed of 35.5% fat, 20% protein, 0.1% fiber, 3.7% ASH, 32.7% carbohydrate and has a caloric profile of 5.36 Kcal/gram (Bio-serv). The ND diet was composed of 4.4% fat, 24.5% protein, 3.7% fiber, 7.8% ASH, 46.6% carbohydrate and has a caloric profile of 3.1 Kcal/gram (Harlan). Body weight, food and water consumption were recorded throughout the 12 week time course study.

2.2 Blood Glucose, Insulin and Leptin Measurements

At all time points, blood was collected via heparin tubes. The plasma samples were kept at -80°C until analyzed. Glucose, insulin and leptin levels were measured with a glucose meter, RIA-Insulin kit (Linco, St. Charles, MO, Cat #RI-13K) and RIA-Leptin kit (Alpco, Mouse/Rat-Leptin-RIA) respectively. At each time point (0, 2, 4, 8 and 12 weeks), six mice per diet (12 per time point with the exception of week 0, where n = 6) were sacrificed with carbon dioxide. A portion of the liver was collected in RNase-free tubes and snap frozen in liquid nitrogen. Frozen tissues were stored at -80°C until processed for RNA extraction.

2.3 Dual Energy X-ray Absorptiometry (DEXA) Analysis at 8 weeks and Oil Red O Staining for Fat

At time point 8 weeks, dual energy x-ray absorptiometry (DEXA) was performed to determine the lean tissue, fat tissue, total tissue and percentage of fat content. The animals were anesthetized for 15 to 20 min with an intraperitoneal injection of 5% xylazene, 8% ketanine and 5% dextrose. Additionally, at 8 weeks, liver histology samples from a representative experiment were evaluated on frozen sections. Sections of 14 μm were cut, fixed in formalin and stained with Oil Red O.

2.4 Isolation of Total RNA and Quality Control

Approximately 500 mg of liver tissue was homogenized in TRIzol (Life Technologies, Gaithersburg, MD) using a homogenizer and total RNA was isolated from each sample using a guanidine isothiocyanate phenol-chloroform extraction according to the manufacturer's protocol. Total RNA was reprecipitated using RNAmate (Biochain, San Leandro, CA) and RNA was further purified with RNeasy columns (Qiagen). RNA concentrations and purity were determined spectrophotometrically and its quality further assessed by RNA Nano LabChip (Agilent Technologies) according to the manufacturer's protocol. RNA analysis was performed with Agilent 2100 bioanalyzer software.

2.5 Pooling and Synthesis of cDNA

Equal amounts of RNA from pairs of individual samples within each group were pooled for microarray analysis. Thus each treatment was represented by three pooled samples, using two mouse livers per pool. Using the pooled total RNA (12 to 15 μg), first-strand cDNA was synthesized with SuperScript II reverse transcriptase (Invitrogen) using a T7-$(dT)_{24}$ primer (5′- GGCCAGTGAATTGTAATACGACTCACTATAGGGA-GGCGG-$(dT)_{24}$ - 3′) for 1 h at 42°C followed by second-strand synthesis using *E. coli* DNA polymerase I and RNase H (Invitrogen) at 16°C for 2 h. The cDNA was purified by Phase Lock Gels (Eppendorf) with phenol-chloroform extraction according to Affymetrix (GeneChip Expression Analysis Technical Manual 701021 Rev. 2).

2.6 Incorporation of Biotinylated Ribonucleotides and Quality Control

One half of the purified cDNA was used as a template for *in vitro* transcription with T7 RNA polymerase incorporating biotin-labeled UTP and CTP into the resulting copy of cRNA using the Bioarray High Yield RNA transcript labeling kit (Enzo). RNA concentrations were determined spectrophotometrically and its quality further assessed by RNA Nano LabChip (Agilent Technologies) according to the manufacturer's protocol. RNA analysis was performed with Agilent 2100 bioanalyzer software.

2.7 Fragmentation of cRNA and Quality Control

For each sample, 20 μg of adjusted biotinylated cRNA was fragmented to a mean size of 150 bases by incubating at 94°C for 35 min in 40 mM Tris-acetate, pH 8.1, 100 mM potassium acetate and 30 mM magnesium acetate. The adjusted cRNA yield is equal to RNA_m (amount of cRNA measured after cRNA synthesis) subtracted from the total

RNA_I (starting amount of total RNA) multiplied by Y (fraction of cDNA reaction used in cRNA synthesis). This calculation takes into account an estimate of 100% carryover for the unlabeled total RNA. Samples of cRNA were reprocessed for those that did not produce 20 μg of adjusted biotinylated cRNA. The cRNA samples also must meet concentration criteria of 0.6 μg/μl, in order to set up the fragmentation reaction. The quality of fragmented cRNA was assessed by RNA Nano LabChip (Agilent Technologies) according to the manufacturer's protocol. Data analysis was performed with Agilent 2100 bioanalyzer software.

2.8 Hybridization, Washing, Staining and Scanning of Chips

Fragmented cRNA (15 μg) was combined with control oligonucleotide B2, control cRNA (BioB, BioC, BioD), herring sperm DNA and acetylated BSA in the hybridization buffer (100 mM MES, 1 M [Na^+], 20 mM EDTA, 0.01 % Tween 20). The hybridization cocktail was heated at 99°C for 5 min followed by incubation at 45°C for 5 min before the sample was injected into the MG-U74Av2 microarray. Hybridization was carried out at 45°C for 14-16 h with mixing in a GeneChip Hybridization Oven 640 (Affymetrix) at 60 rpm. After hybridization, the hybridization cocktail was removed and the arrays were washed with non-stringent wash buffer (6X SSPE, 0.01 % Tween 20) at 25°C on a fluidics station (Affymetrix) and subsequently with stringent wash buffer (100 mM MES, o.1 M [Na^+], 0.01 % Tween 20) at 50°C. The arrays were then stained with streptavidin-phycoerythrin (10 µg/ml) (Molecular Probes) at 25°C for ten minutes, followed by wash cycles with non-stringent wash buffer at 25°C, then microarrays were stained with biotinylated antibody (3 µg/ml) (Vector Laboratories) for ten minutes at 25°C to further amplify the signal. Which was followed with a second staining using streptavidin-phycoerythrin (10 μg/ml) (Molecular Probes) at 25°C for ten minutes. The final washes were carried out with the non-stringent buffer at 30°C and the microarrays were scanned using the Hewlett-Packard GeneChip system confocal scanner at 570 nm.

MICROARRAY DATA ANALYSIS

2.9 Initial Quality Control of Microarray Scans and Upload of Data into Resolver

Initial quality control of the microarrays was assessed by analyzing the *.dat files for scratches, dust particles, grid alignments and intensities using the Affymetrix microarray suite V.4.0. In addition, expression reports were generated for each of the microarrays and analyzed by verifying the baseline noise, number of probe sets present, housekeeping controls and the spike controls. Microarray data was exported into Resolver and annotated with complete details of the experimental procedures.

2.10 Identification of Outlier Chips and Combining Triplicate Chips

Microarrays were tested for their reproducibility by correlation coefficients using the Rosetta Resolver Software. Triplicate chips were tested using the combination of n_c_k = n!/k!(n-k)!. In these sets of correlations we used 2_c_3. This allowed for a complete correlation of each chip within the triplicates. Therefore, for a set of three replicates, three comparisons were carried out to test the various combinations (31).

All intensity profiles (individual microarray intensities) were combined into intensity experiments using the Resolver Intensity Hyb manager. Both the intensity profiles and intensity experiments were used for further analysis.

2.11 2D Cluster Analysis of Intensity Experiments

Agglomerative cluster analysis was performed according to the Rosetta RESOLVER™ Expression Data Analysis System User Guide (2). Nine intensity experiments representing a combination of the triplicate experiments were used to identify similarities and differences between the groups.

2.12 Normalization of Microarray Expression Data

Affymetrix CEL files for each of the 27 arrays were processed in Rosetta Resolver to yield background-corrected intensity values for the 12488 probesets on the arrays. Collaboration was set up with Dr. Richard Raubertas to use a robust statistical approach for the microarray analysis. The intensities were exported from Resolver and analysis was carried out using the statistical program R (44). Intensities for each array were multiplied by a scale factor to equalize the medians for all arrays. The within-group variability of intensities increased approximately quadratically with the overall intensity level, so a variance stabilizing transformation suggested by Weng (85) was applied. The transformation is approximately linear at low intensities but approaches a logarithmic transformation at high intensities. The transformed values for each array were normalized to remove any biases in the intensity response for that array.

Normalization is a computational process in which data from different microarrays are equalized prior to analysis. This process corrects for minor imbalances that arise during the labeling, hybridization, scanning and other processes between microarray chips (71). Probesets with the least evidence of differential expression between groups (those with the smallest ratio of between-group to within-group variability) were identified. The median transformed intensity for each probeset across all arrays was calculated. For each array a smooth, nonparametric regression curve was fitted to a graph of deviations from the medians, versus the medians. The fitted curve was then subtracted from the data for the array (Appendix A). All subsequent analyses used these normalized, transformed intensity values.

2.13 Expression Analysis of Diet Affected Genes and Linear Trend Analysis

For each gene a nested series of ANOVA models were fit to the data. The models focused on identifying and characterizing diet-related effects on gene expression. The most general model allowed separate means for the nine week/diet combinations in the experiment. Successively more constrained models allowed (a) arbitrary main effects for week and diet, but specified that any interaction between them must take the form of a linear trend in diet effects across weeks; (b) main effects for week and diet, but no interactions between them (i.e., any diet effect must be constant across weeks); and (c) only week effects (no diet effect at all). By comparing the fits of these models, we obtained p-values for tests of various hypotheses about diet effects. In addition, contrasts among means were used to estimate the magnitudes of these effects. The primary filter for genes of interest was that there should be evidence of some diet effect on expression level. This was implemented by requiring a small p-value for a test of diet effect, obtained by comparing the fits of model (c) and the general model above. For genes with a significant diet effect, the effect was estimated separately at each week and a test for trend in the effects across week was carried out (comparing models (a) and (b)).

2.14 Correlations: Gene Expression Profiles to Pharmacological Data and Biological Processes

For genes with a significant diet effect, the correlation of expression level with body weight, blood glucose level, and insulin level at sacrifice also was examined. Each RNA sample hybridized to an array was a pool of material from two animals, so the values of the physiologic variables for the pair of animals were averaged when calculating correlations (adjusted p-value). The gene symbols used in the Figures and Tables are from the NetAffx™ and Mg_U74Av2 annotations. The biological processes for the gene level transcripts are derived from the gene ontology consortium (Gene Ontology), although in some cases the term is derived from published reports as shown (10). All expression profile data and gene ontology terms were placed into a single database in Microsoft Access for generation of Figures and Tables.

Chapter 3

Results

This chapter describes the characterization of the DIO mice throughout the 12 weeks of high fat feeding. The data support the use of these mice for microarray profiling in the development of obesity and insulin resistance. The remainder of the chapter outlines the results obtained from total RNA isolation, cDNA synthesis, cRNA synthesis, cRNA fragmentation, hybridization and microarray analysis.

3.1 Diet-Induced Obesity Time Course: Food and Water Consumption

C57BL/6J male mice were fed for a period of 12 weeks a high fat diet (HFD, n = 24) containing ~36% fat or a chow diet (ND, n = 30) containing ~5% fat. The high fat diet group's food and water consumption were less than the ND group (Figure 1A and 1B) but both groups consumed the same amount of calories (Figure 1C).

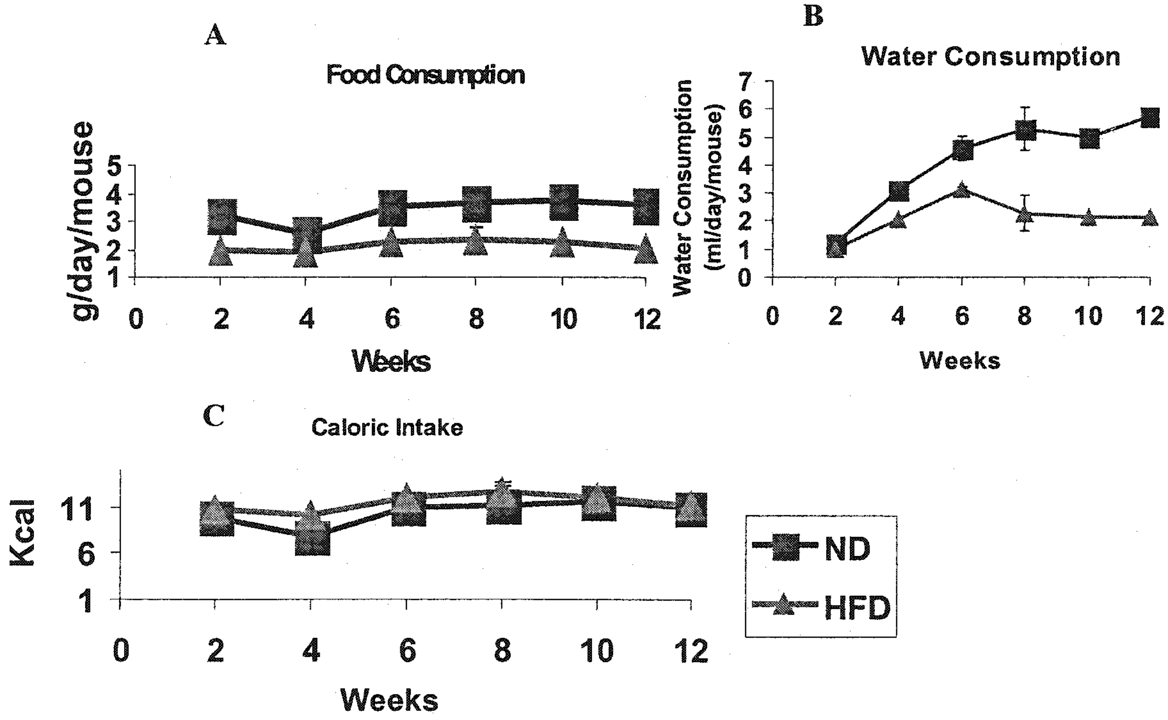


Figure 1A. Food consumption of high fat diet (HFD) and chow diet (ND). **B**. Water consumption of high fat diet (HFD) and chow diet (ND) **C**. Caloric intake of high fat diet (HFD) and chow diet (ND).

3.2 Development of Obesity and Insulin Resistance: Body Weight, Blood Glucose, Insulin and Leptin

The body weights of the HFD and ND group mice were measured at 0, 2, 4, 6, 8, 10 and 12 weeks (Figure 2A). A significant difference in body weight between the two groups was evident as early as two weeks ($P \leq 0.01$), weight gain trends are also in agreement with a previous report (84). At the conclusion of the 12 week time course, the HFD group (43 ± 2 g) was significantly heavier than the control group (31 ± 2 g) animals ($P \leq 0.0001$).

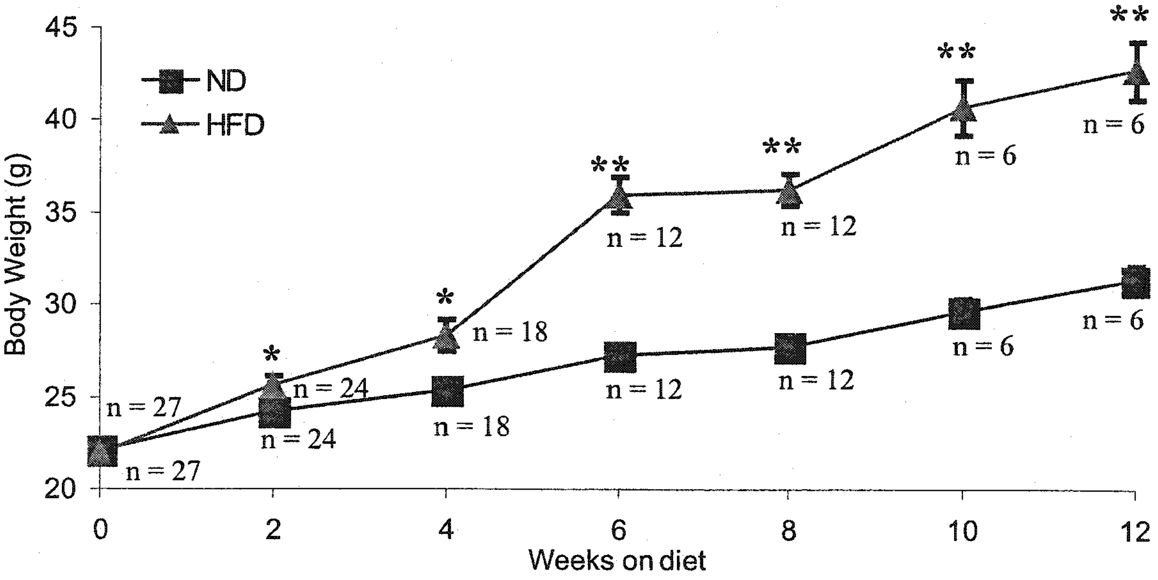


Figure 2A. Body weight of C57BL/6J on high fat diet (HFD) or chow diet (ND). Mice were 6 weeks of age at start of time course. Data are means ± SE. No difference detected between two groups at week zero ($p = 0.5$). Significant difference between groups at all other weeks (*$p \leq 0.01$; **$p \leq 0.0001$). In the graph, the n values denote the number of animals used to calculate the body weight at the corresponding time points.

To further characterize the effects of high fat feeding, blood glucose and insulin levels were measured in both HFD and ND groups. Similar to body weight, significant diet effects were seen with blood glucose at all time points except week 0 (Figure 2B). The HFD group mice became mildly hyperglycemic by week 2 and glucose levels remained elevated throughout the time course experiment (~10 mM versus ~8 mM). Insulin levels of the HFD and ND group mice were measured at 0, 2, 4, 8 and 12 weeks (Figure 2C). By 8 weeks, insulin levels were 3 times higher than that of ND controls and by week 12 the HFD group had plasma insulin levels ~10 times higher than the control group.

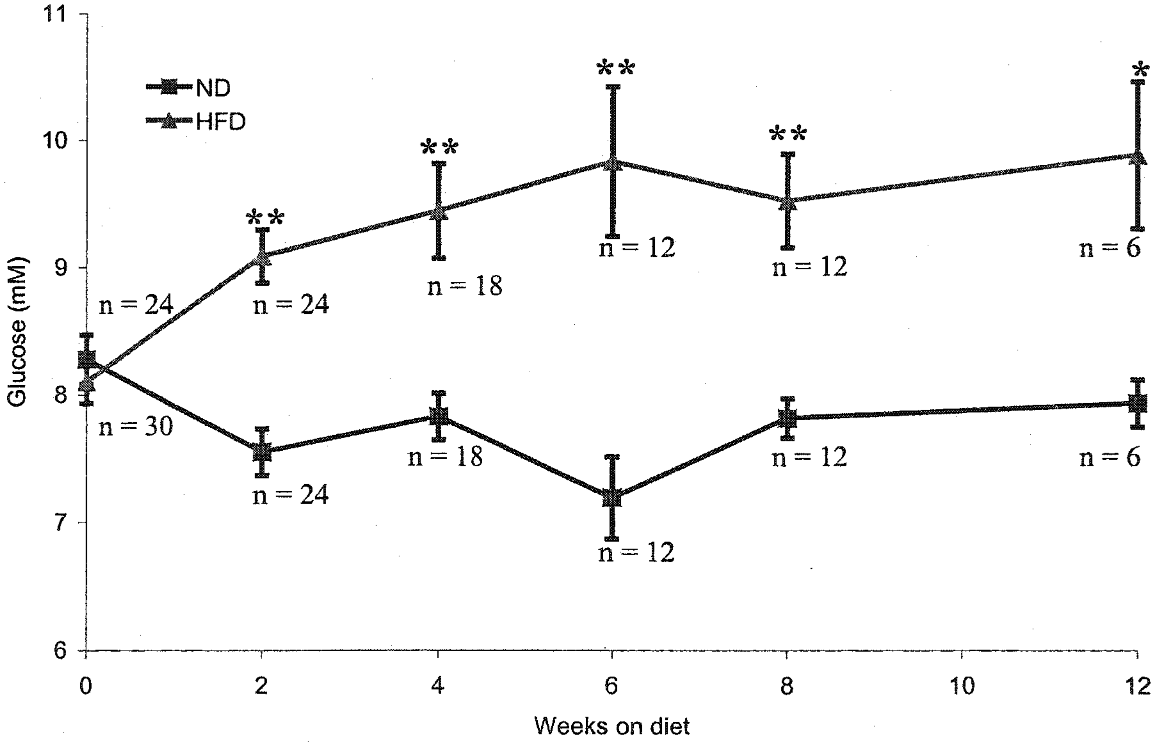


Figure 2B. Non fasting plasma glucose levels of mice on high fat diet (HFD) or chow diet (ND). Data are means ± SE. No difference detected between two groups at week zero ($p = 0.5$, $n = 30$ and $n = 24$ for ND and HFD respectively). Significant differences between groups at all other weeks (*$p \leq 0.01$; **$p \leq 0.001$). In the graph, the n values denote the number of animals used to calculate the glucose levels at the corresponding time points.

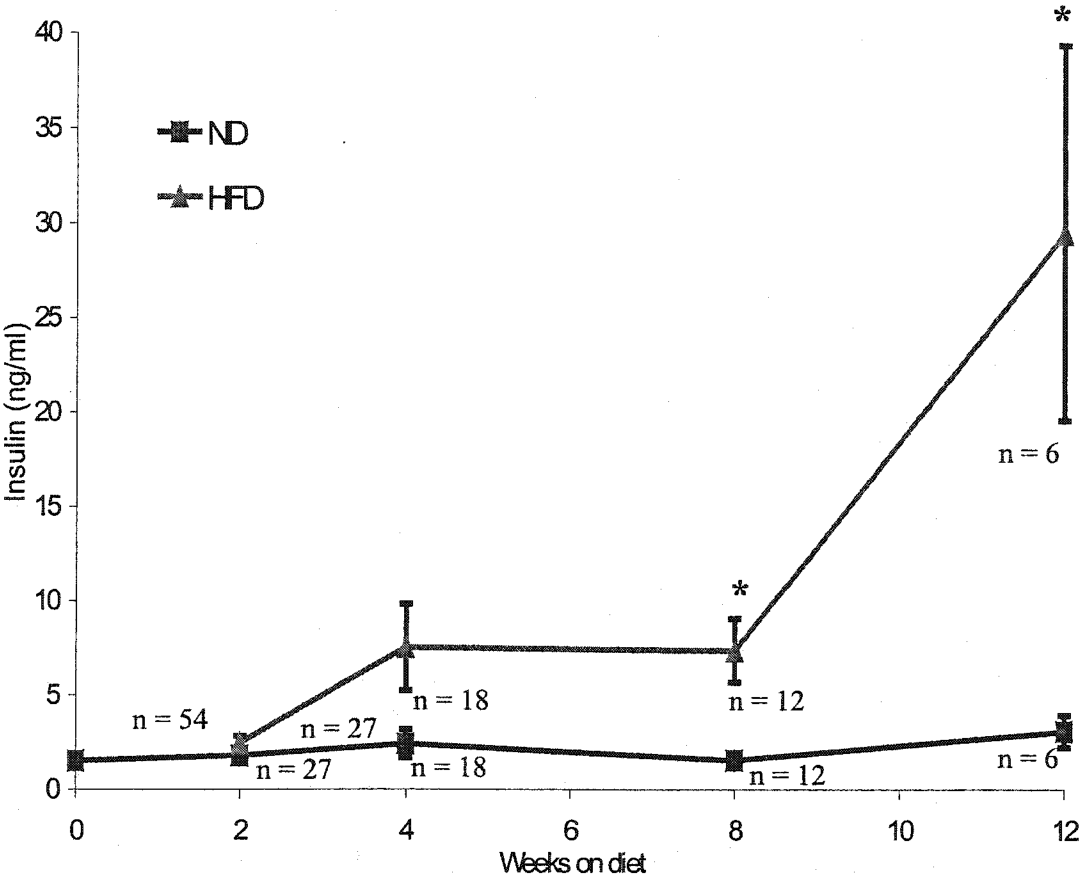


Figure 2C. Insulin levels of mice on high fat diet (HFD) or chow diet (ND). Data are means ± SE. No difference detected between two groups from week zero to week 4. Significant difference between groups at week 8 and week 12 (*p ≤ 0.03). In the graph, the n values denote the number of animals used to calculate the insulin levels at the corresponding time points.

Leptin levels were measured throughout the 12 weeks of high fat feeding. At all of the time points the HFD group had higher levels of leptin than the ND group. Significant differences in leptin levels were seen as early as two weeks ($p \leq 0.001$). By 2 weeks, leptin levels of HFD group were 3 times that of the control group and by week 12 they were ~5 times that of the control group as shown in Figure 2D.

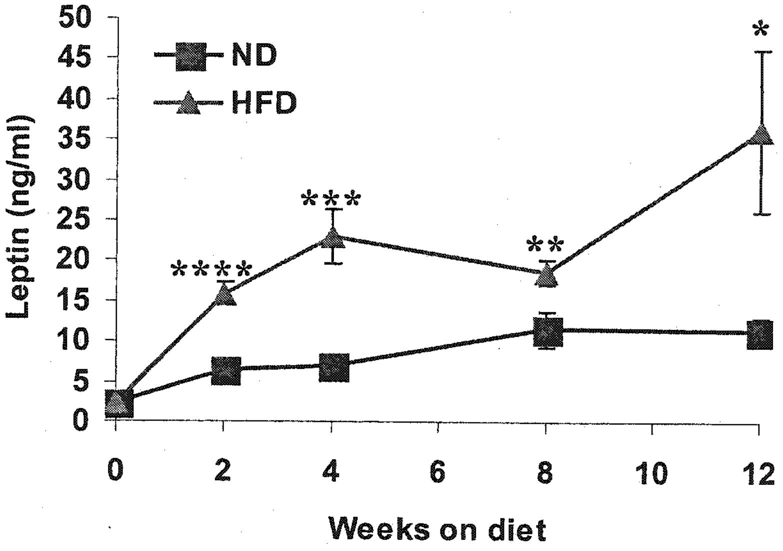


Figure 2D. Leptin levels of mice on high fat diet (HFD) or chow diet (ND). Data are means ± SE. No difference detected between two groups at week zero. Significant difference between groups at weeks 2, 4, 8 and 12 (*p ≤ 0.05; **p ≤ 0.03; ***p ≤ 0.006; **** p ≤ 0.001).

3.3 Dual Energy X-ray Absorptiometry (DEXA) Analysis and Oil Red O Staining at 8 Weeks of Time Course

Eight weeks after initiation of high fat feeding, dual energy x-ray absorptiometry (DEXA) analysis revealed a significant difference in the total tissue content. The HFD (33.2 ± 0.7 g) was heavier in comparison to the ND (25.7 ± 0.7 g) group ($P < 1.6E\text{-}0.5$). As expected the lean tissue and length (HFD vs ND: 9.5 vs 9.4 cm) of mice were similar in both groups while fat tissue was significantly higher in the HFD (9.2 ± 0.9 g) in comparison to the ND (3.2 ± 0.3 g) group ($P < 0.001$) (Figure 3A). The percentage of fat was also significantly higher in the HFD group in comparison to the ND group (Figure 3B). Body weight gain was primarily due to increased fat tissue (HFD vs ND: 27.4 % vs. 12.6 % fat of the body mass, *p ≤0.001).

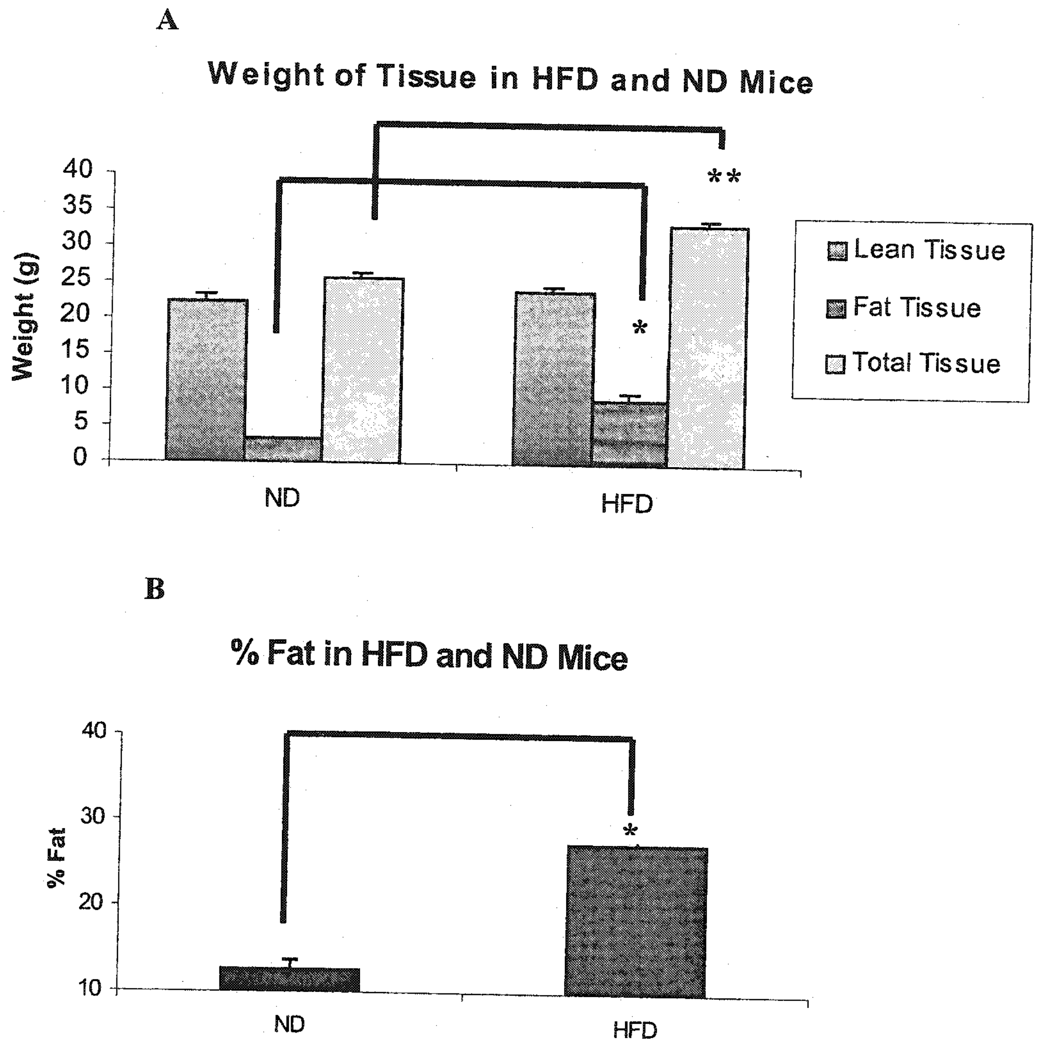


Figure 3A. DEXA scan reveals differences between the high fat diet (HFD) and chow diet (ND) treatment group. At 8 weeks differences were observed in total tissue (**$p \leq 1.6E\text{-}05$) and fat tissue (*$p \leq 0.001$). **3B.** Percentage (%) of body fat of HFD and ND mice also revealed differences (*$p \leq 0.001$).

Also at eight weeks a histological examination for fat accumulation was performed on liver sections. Staining of sections with the lipid specific Oil Red O stain as shown in Figure 4 revealed excessive lipid accumulation in HFD versus ND liver.

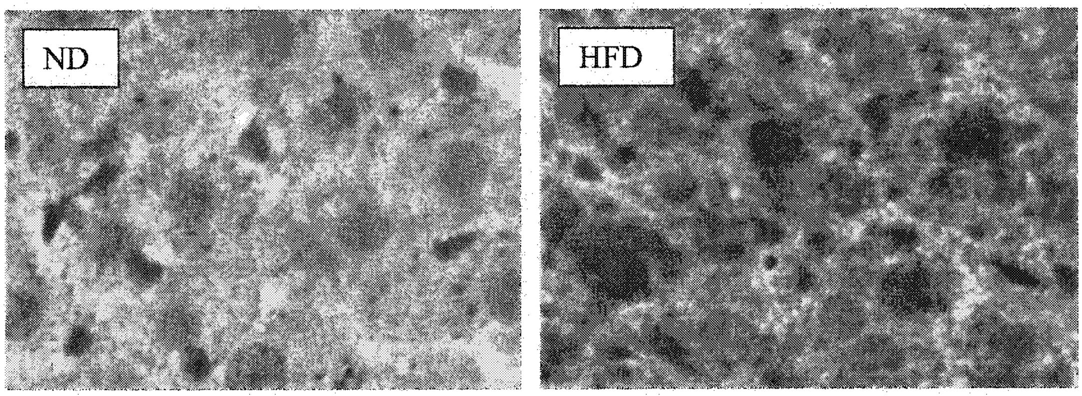


Figure 4. Histology of liver sections of high fat diet (HFD) and chow diet (ND) animals. Oil Red O stains fat deposits red and nuclei blue. Staining indicates large amounts of fat deposits upon high fat feeding at 8 weeks (40X magnification).

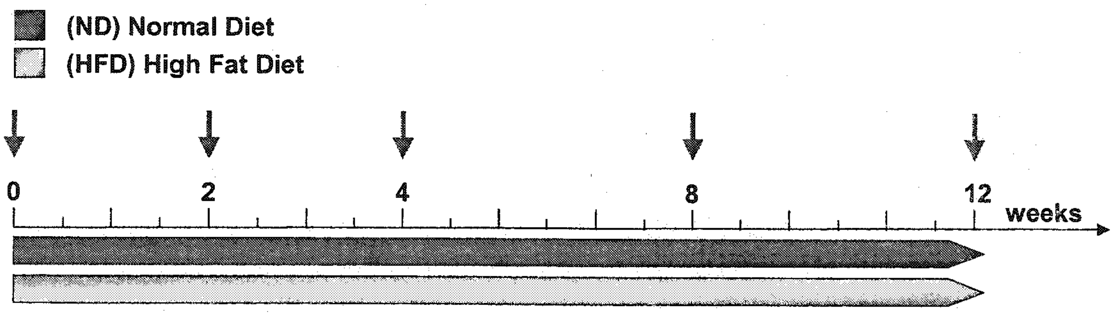
3.4 Summary of Diet-Induced Obesity (DIO)

Taken together all of the pharmacological results described above show the development of weight gain, hyperglycemia, hyperinsulinemia, hyperleptinemia and steatosis upon HFD treatment. All the results support the use of mice from the DIO experiment for further microarray profiling.

3.5 Microarray Experimental Design

The goal of this study was to determine hepatic gene expression changes resulting from the development of obesity. In particular, we were interested in identifying the molecular mechanisms involved in the development of obesity, insulin resistance and steatosis (NASH). To identify changes correlated with the development of obesity a time course experiment was set up for a period of 12 weeks as described above and depicted below in Figure 5A. Liver samples were collected at 0, 2, 4, 8 and 12 weeks of treatment. The sample preparation for each treatment group is outlined in Figure 5B. In this study 6 animals were used per treatment time point, however their expression profile was determined using 3 microarrays. Therefore, there was random pooling of 2 RNA samples per array at the cDNA synthesis step. This generated 27 microarray datasets for microarray analysis.

A



- 54 C57BL/6 mice, 9 groups of 6
- group 1: fed chow diet (ND) for 12 weeks
- group 2: fed high fat diet (HFD) for 12 weeks
- mice 7-8 weeks old were fed either HFD or ND for 12 weeks
- sacrificed at weeks: 0, 2, 4, 8 and 12

Figure 5A. High fat feeding 12 week time course experiment. Liver samples were isolated at 0, 2,4, 8 and 12 weeks after treatment with high fat diet (HFD) and chow diet (ND).

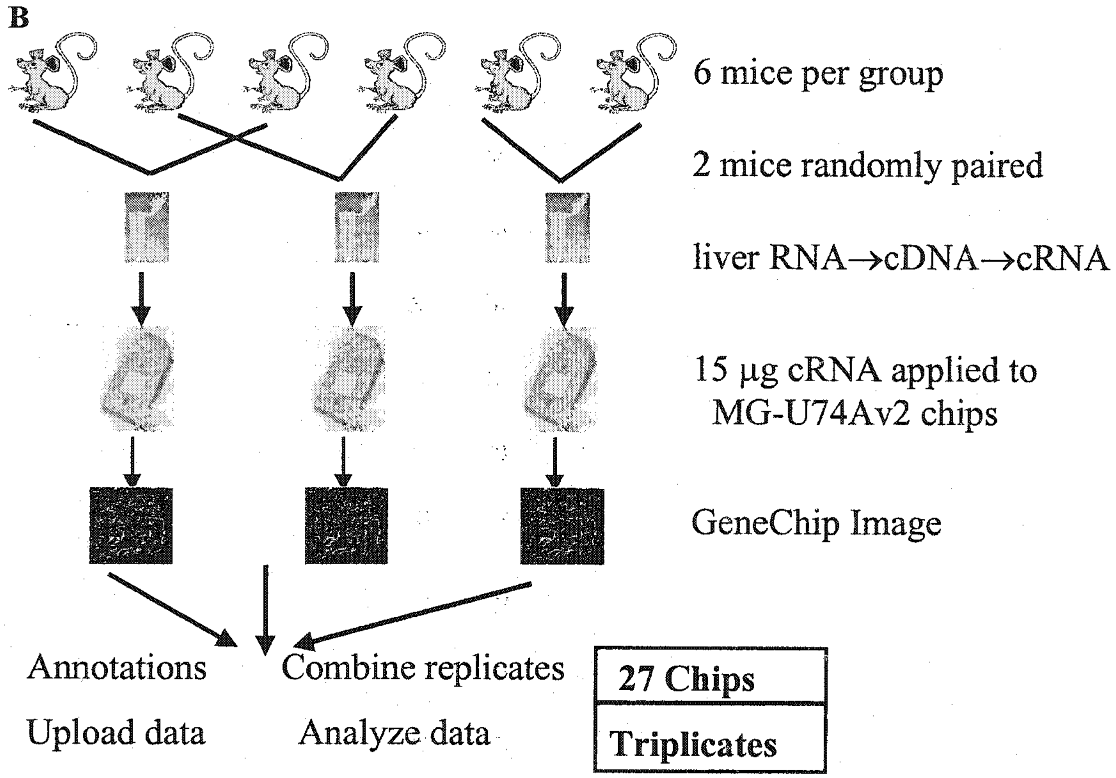


Figure 5B. Microarray design. This is a representation of sample preparation for each of the treatment groups. HFD and ND treatment groups were processed the same way. The time point for each treatment was analyzed using 3 microarrays.

3.6 Generation of Target cRNA

Quality control after total RNA isolation, cRNA synthesis and cRNA fragmentation was necessary to ensure that the highest quality of target cRNA was applied to the microarrays. The integrity of these samples must be confirmed at various steps of preparation to ensure the success of the microarray experiments (71). Shown below in Figure 6 are the number of steps that are required for generation of target cRNA samples. RNase free tubes were used and gloves were worn at all times. Liver tissue, is carefully removed and snap frozen in liquid nitrogen immediately after the mice have been sacrificed. The liver is stored at -80°C until time of processing the cRNA target samples. The sample may be stored at -80°C after total RNA processing or cDNA synthesis but must be applied to the microarrays immediately after cRNA synthesis since the cRNA can not be kept at -80°C for longer than five days.

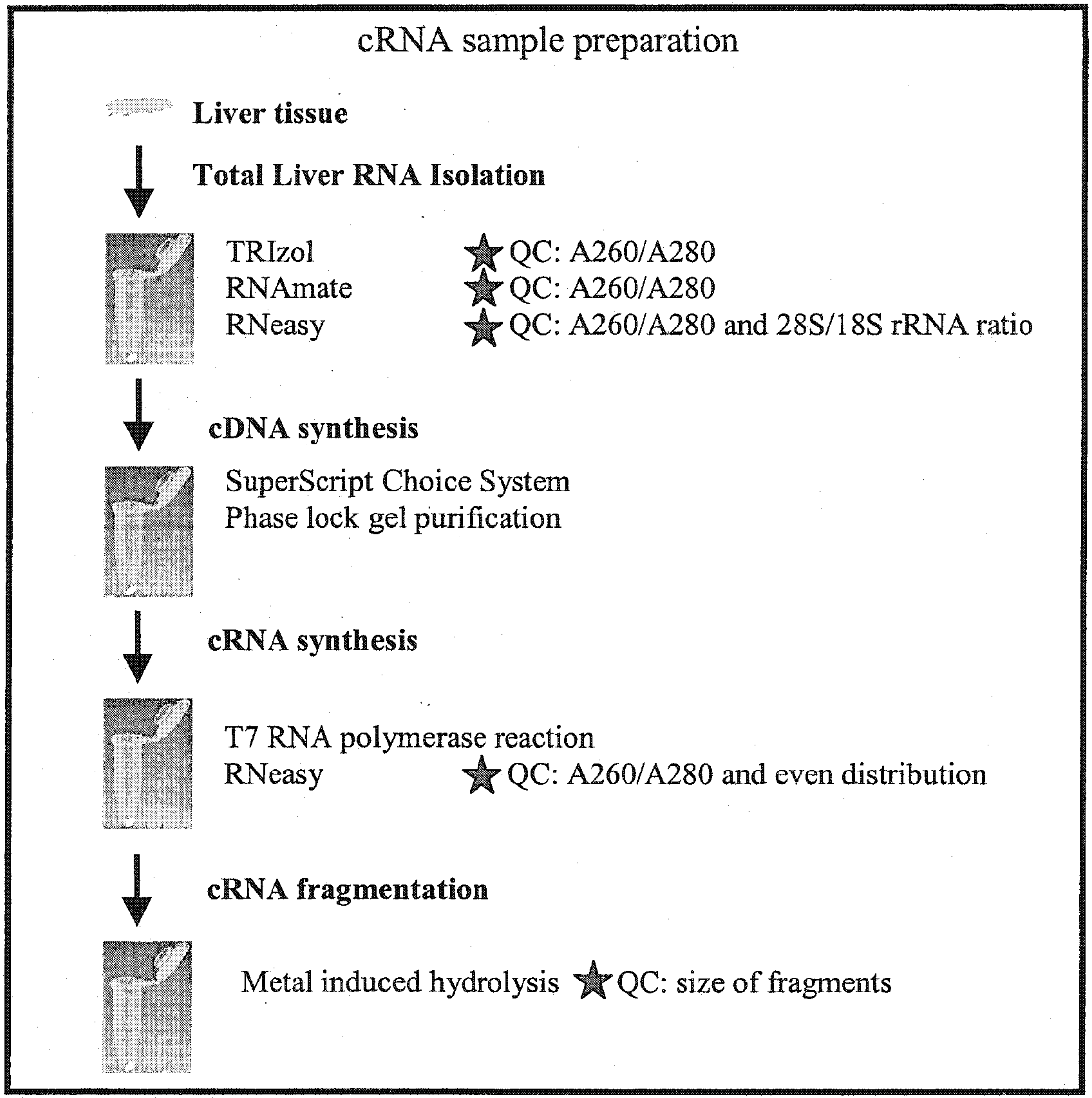


Figure 6. cRNA sample preparation. This figure highlights the steps for target cRNA sample preparation from liver tissue. All samples must pass the quality control (QC) steps prior to being hybridized on the microarray. The stars symbolize points of QC. Samples which do not pass QC have to be reprocessed from remaining frozen tissue.

3.7 Isolation and Quality Control of Total RNA

Total RNA was isolated from 54 liver samples using a three-step isolation protocol, which included TRIzol, RNAmate and RNeasy. After TRIzol and RNeasy isolation protocols, quality control procedures were carried out to assure the sample was free from contaminants and degradation products. The samples were assessed for their quality based on the absorbance ratio at A260 and A280. Ratios <1.5 indicated the presence of contamination. Table 1 summarizes representative absorbance values obtained from the week 2 liver samples after RNeasy treatment. The first six samples (N1-N6) were the HFD treatment mice and samples N7 to N12 were from the ND mice. All of the samples had A260/A280 ratios greater than 1.5 and were used for further experimentation. All 54 liver samples were processed until ratios greater than 1.5 were obtained for the RNA samples. A second step in analyzing the quality of the total RNA sample was to determine the 28S to 18S ribosomal RNA ratio by examining the integrity of the 28S (4800 base pairs) and 18S rRNA (1900 base pairs) using an Agilent bioanalyzer. Ratios <1 would indicate degradation which appears in the gel lane as an increase in low molecular weight products and the disappearance of the 28S band. Degraded samples were reprocessed from remaining frozen liver tissue. All 54 samples were processed until they were free from degradation and contaminants. Figure 7 is a representative gel image of samples from liver for week 2 from HFD (N1-N6) and ND (N7-N12). Lanes 11 and 12 in Figure 7 are examples of degradation.

Table 1. A260/A280 ratio after RNeasy purification and concentration of total RNA. The A260/A280 is an indication of sample purity. All these samples have values greater than 1.5 indicating acceptable samples. The concentration of the samples are calculated as follows:Abs $_{260nm}$ x 40 μg/mL x dilution(250) = [RNA] μg/mL.

	260	280	260/280	μg/mL
N1	0.424	0.271	1.6	4240
N2	0.585	0.364	1.6	5850
N3	0.343	0.221	1.6	3430
N4	0.279	0.179	1.6	2790
N5	0.48	0.305	1.6	4800
N6	0.398	0.247	1.6	3980
N7	0.467	0.297	1.6	4670
N8	0.478	0.299	1.6	4780
N9	0.537	0.341	1.6	5370
N10	0.417	0.266	1.6	4170
N11	0.394	0.251	1.6	3940
N12	0.466	0.296	1.6	4660

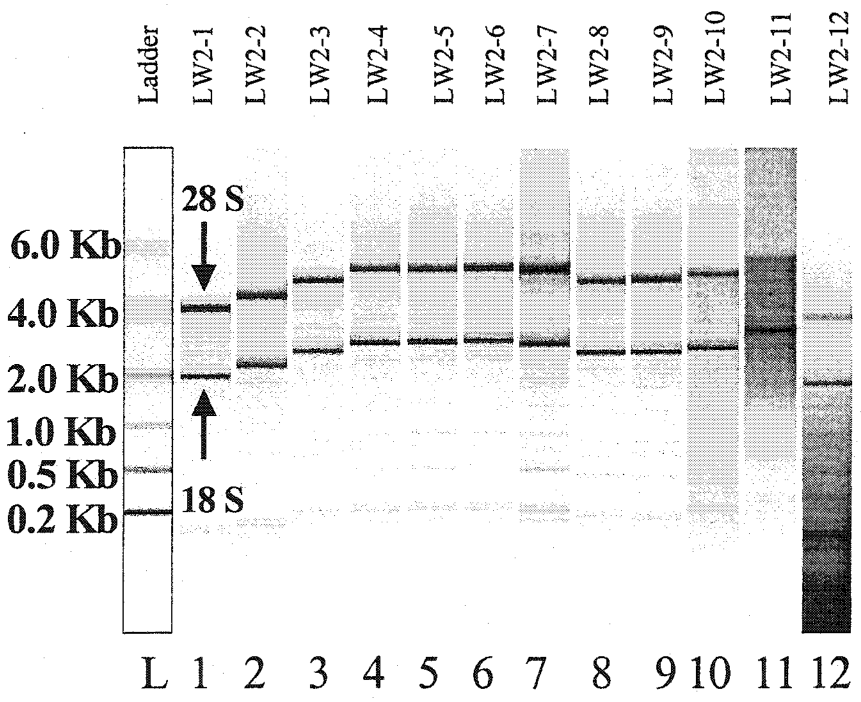


Figure 7. Quality control assessment of total liver RNA by examination of 28S and 18S rRNA band using RNA Nano LabChip. Representative samples from week 2: HFD lanes 1-6 and ND lanes 7-12.

3.8 Quality Control of cRNA

As mentioned above (3.5 Microarray Experimental Design) equal amounts of two RNA liver samples were pooled randomly at the time of cDNA synthesis for each of the treatment groups. The cDNA then was used to synthesize cRNA were biotin labeled ribonucleotides were incorporated. Quality control of this step also was assessed using the Agilent Bioanalyzer. The quality of cRNA synthesis was evaluated for each treatment group. Each time point was required to have consistent synthesis reactions. A good quality cRNA synthesis should show an even distribution of RNA products. Figure 8A is a representation of cRNA synthesis reactions from weeks 0, 2 and 4. Examination of the gel image revealed lanes 1 to 4 and 6 to 7 to have an even distribution of molecular weights. Lanes 8 to 10 had an uneven distribution of RNA products. Lanes 5, 11 and 12 show low intensity cRNA products. These gel image results also can be visualized by traces which give better intensity and determination for how even the synthesis was. A closer examination of the individual groups in Figure 8B reveals that only week 2 samples 1-4 and 6 have even distribution. Examination of the week 4 samples reveals even distribution for cRNAL4-1 (lane 7) with slightly more lower molecular weight products. While the remaining week 4 samples (lanes 8 to 10) have a higher distribution for the lower molecular weight RNA products. Week 0 liver samples indicate even distribution but low intensity. All 27 cRNA synthesis reactions were carried out until even synthesis of the reactions was obtained. Each sample also was assessed for adjusted cRNA concentrations of 0.6 $\mu g/\mu l$. This second step of quality control assures that the cRNA synthesis was essentially even across all the RNA species, thus removing biases from the cRNA synthesis reactions.

3.9 Quality Control of fragmented cRNA

Samples of cRNA were fragmented to a mean size of 35 to 200 base pairs. The quality of the fragmentation was assessed by the size of RNA products using the Agilent Bioanalyzer. Figure 9 is a gel image representation of samples from the week 2 liver HFD (lanes 1-3) and ND (lanes 4-6). All of these samples passed the quality control since all fragments were below 200 base pairs. This third quality control step assures that all samples are the appropriate size in order for optimal hybridization reactions with the microarray probes.

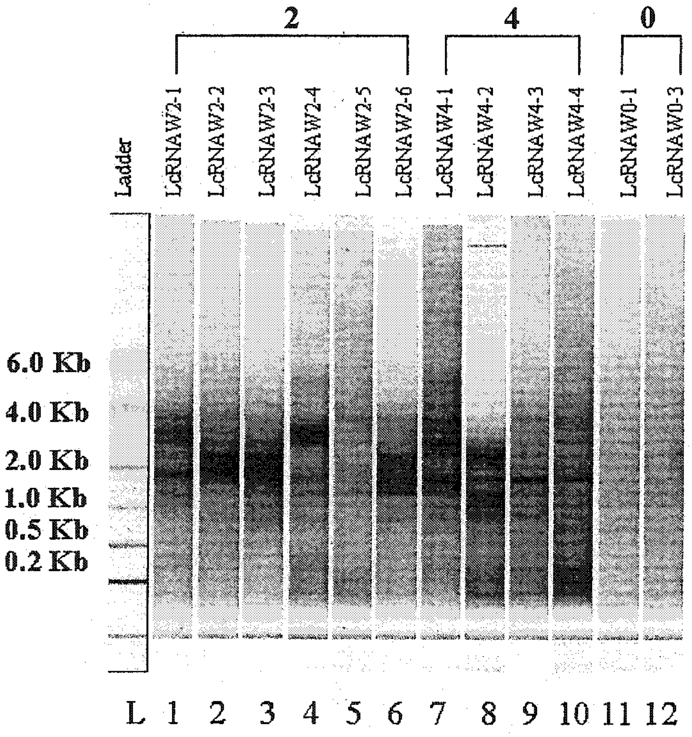


Figure 8A. Quality control assessment of biotin labeled cRNA synthesis reactions. Representative samples from weeks 0, 2 and 4. Samples are assessed using the Agilent Bioanalyzer. Lanes 1-4 and 6-7 show cRNA synthesis reactions with production of even molecular weight products. Lanes 8 to 10 show uneven cRNA synthesis reactions. Lanes 5, 11 and 12 show synthesis of only low molecular weight products.

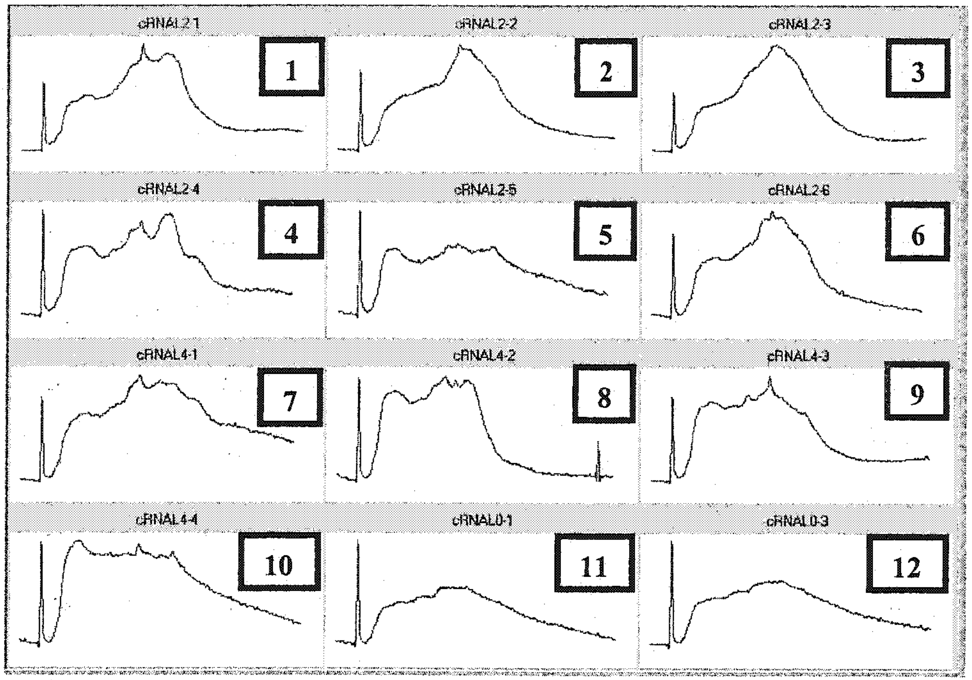


Figure 8B. cRNA synthesis profiles. Representative samples from weeks 0, 2 and 4. Samples are assessed using the Agilent Bioanalyzer. The numbers in the square boxes correspond to lane numbers from the gel image Figure 8A. Lanes 1-4 and 6-7 have even distribution. Lanes 8-10 have increased lower molecular weight RNA products. Lanes 11-12 have low intensity but even distribution.

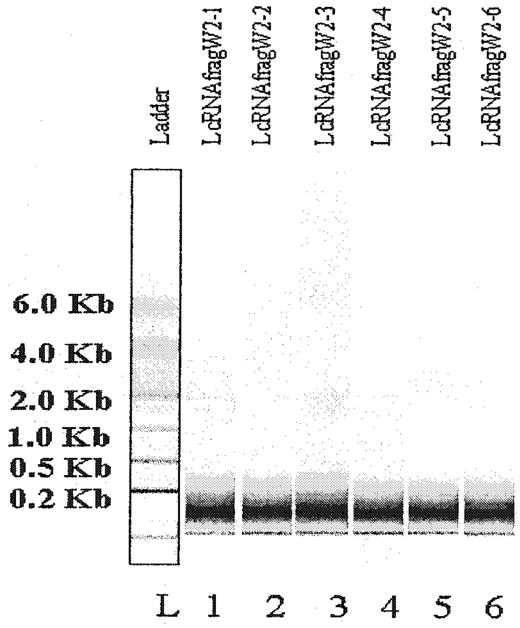


Figure 9. Fragmented cRNA quality control. Representative samples from week 2. Samples are assessed using the Agilent Bioanalyzer. Samples were fragmented to below 200 base pairs, indicating that these samples would have passed the quality control.

3.10 Initial Quality Control of Microarray Scans

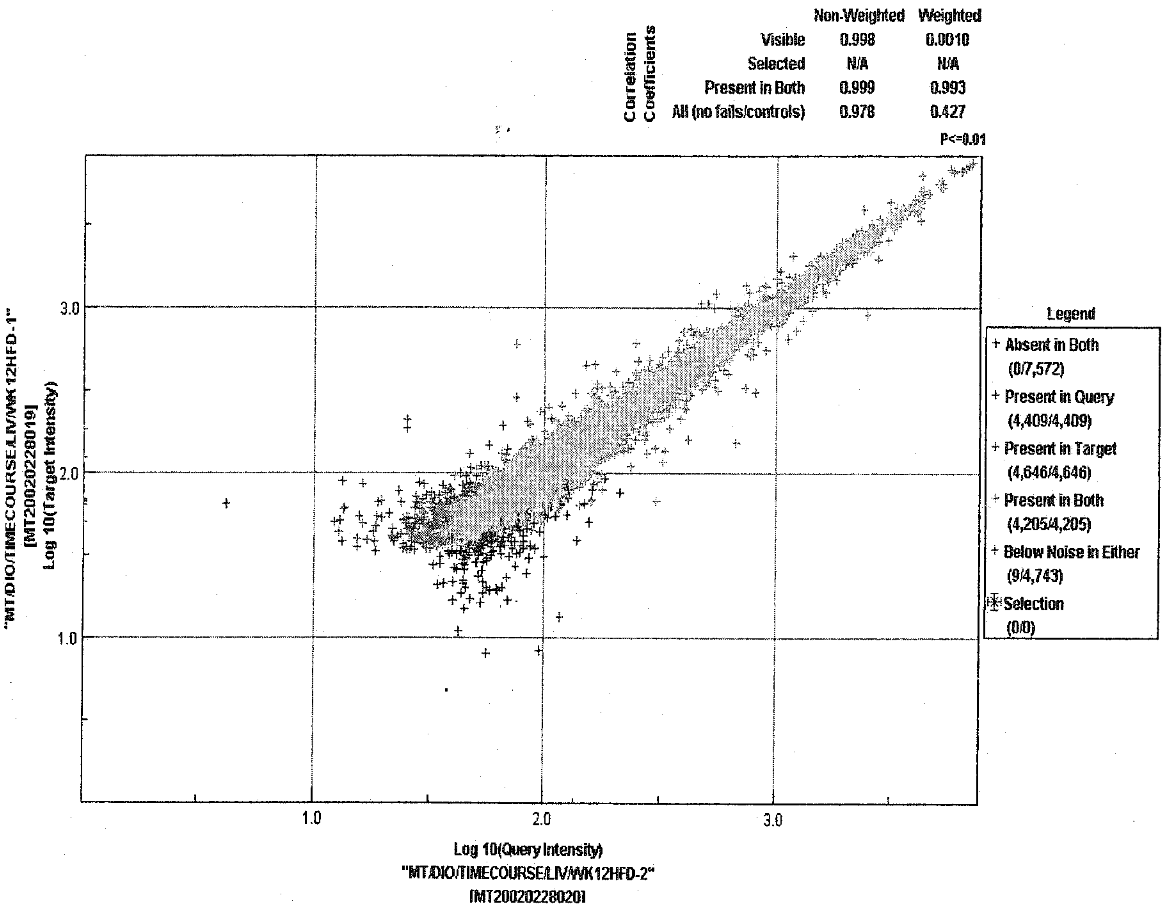
Once fragmented cRNAs were prepared, all 27 samples were hybridized to the microarrays. The microarrays were washed, stained and prepared for visualization as mentioned in Chapter 2 (Materials and Methods). The initial quality control carried out on the microarrays was to look for scratches and dust particles. All arrays passed this first step. In addition, all chips also had similar intensities and perfect grid alignments. To further assess the quality of the chips, Affymetrix expression reports were generated for all 27 chips. This was assessed using the background intensity value (50-100), scaled noise (Q 1.0-5.0), consistency of scaling factor between the chips, 3'/5' ratio of housekeeping controls (<3), probes present (~50%), and a present call for all of the spike controls (Table 2). The fact that the 3'/5' ratios were less than three fold was also a good indication that the RNA samples were not degraded. In addition, the increasing call of the spike controls indicates that the scanner detected gene expression from low transcript genes since the least abundant spike (BIOB) was detected with a value of 328.4.

Table 2. Affymetrix Expression Report. The report includes values for several controls which allows for assessment of cRNA synthesis reaction, hybridization and noise of the microarray.

Report Type	Expression Report
File Name	**U74A2-LIV-WK2-2HFD280202.chp**
Algorithm	**Expression**
Controls	**Antisense**
Probe array	MG_U74Av2
Scaled Noise (Q)	4.093
Scale Factor	1.215
Probe Present	48.6% (6067)
Background	58.44
Housekeeping Controls	3'/5' ratio
B-actinmur	1.2
GAPDH	1.1
18SRNA	1.5
Spike Controls	**Call**
BIOB	328.4
BIOC	802.5
BIODN	1231.5
CREX	7456.2

3.11 Identification of Outlier Microarrays (chips)

Individual chips for each triplicate was tested for reproducibility using correlation analysis prior to combining the results. Each microarray was plotted against each other within a group and the R factor was recorded. Figure 10 is a representation of a single correlation plot of microarrays from week 12 (HFD chip-1 versus HFD chip-2). The diagonal comes from plotting gene intensity for each individual gene from the 2 chips. The tighter the diagonal, the stronger the correlation is between the two microarrays. Gene expressions points that deviate from the diagonal are not correlated in the two chips. The high correlation coefficient obtained from the analysis (Table 3) indicates that no outlier chips were detected, hence the appropriate microarrays were then combined into intensity experiments and annotated in the Rosetta RESOLVER™ database.



Correlation Coefficients	Non-Weighted	Weighted
Visible	0.998	0.0010
Selected	N/A	N/A
Present in Both	0.999	0.993
All (no fails/controls)	0.978	0.427

Figure 10. Correlation plot of two chips from the week 12 HFD group. The Legend summarizes the results of the correlation analysis indicating genes that are absent in both, present in query, present in target, present in both, below noise in either and selection. Each + symbol on the correlation plot signifies a gene intensity.

Table 3. Correlation coefficient of all chip combinations. The high correlation coefficients indicate that the chips are highly reproducible.

Chip Comparisons	Correlation
Week 0-1 to 0-2	0.994
Week 0-1 to 0-3	0.999
Week 0-2 to 0-3	0.995
Week 2 ND 1 to 2	0.994
Week 2 ND 1 to 3	0.997
Week 2 ND 2 to 3	0.994
Week 2 HFD 1 to 2	0.994
Week 2 HFD 1 to 3	0.992
Week 2 HFD 2 to 3	0.995
Week 4 ND 1 to 2	0.994
Week 4 ND 1 to 3	0.994
Week 4 ND 2 to 3	0.996
Week 4 HFD 1 to 2	0.994
Week 4 HFD 1 to 3	0.994
Week 4 HFD 2 to 3	0.995
Week 8 ND 1 to 2	0.991
Week 8 ND 1 to 3	0.990
Week 8 ND 2 to 3	0.994
Week 8 HFD 1 to 2	0.992
Week 8 HFD 1 to 3	0.993
Week 8 HFD 2 to 3	0.991
Week 12 ND 1 to 2	0.990
Week 12 ND 1 to 3	0.982
Week 12 ND 2 to 3	0.989
Week 12 HFD 1 to 2	0.993
Week 12 HFD 1 to 3	0.995
Week 12 HFD 2 to 3	0.994

3.12 2D Cluster of Intensity Experiments

The initial clustering of the intensity experiments revealed that there was a distinct separation of the ND and HFD animals at 0, 4, 8 and 12 weeks, whereas the 2 week ND and HFD mice clustered together as shown in Figure 11. The clustering of the 2 week time point, independent of diet, was due to a very strong signature from a group of developmentally regulated genes as shown in Figure 11 boxes A and B. This result stresses the importance of comparing age matched treated and non-treated animals instead of comparison to time = 0.

3.13 Diet Affected Genes

To identify genes, whose expression was affected by diet for any of the time points, the intensity values from the microarrays were normalized and transformed as described in Chapter 2 Materials and Methods and analyzed separately using analysis of variance (ANOVA) and of covariance. Expression was analyzed using transformed intensity (not fold change), so as to identify all significantly affected genes. This method should be more sensitive in picking up the small but significant changes in gene expression that are known to have profound affects on phenotype. Using this method the differences in expression level between HFD and ND for each of the time points can be calculated with an associated p-value. Based on this analysis, of the 12422 non-control genes on the arrays, a total of 1947 genes (~16%) were found to have a significant diet effect ($p < 0.05$) see Appendix B. Appendix B lists the gene names, symbols, description, mean expression level for week 0 (on the transformed scale), diet affected p-value (pANY) and the differences in expression level between HFD and ND for weeks 2, 4, 8 and 12 with the corresponding p-values.

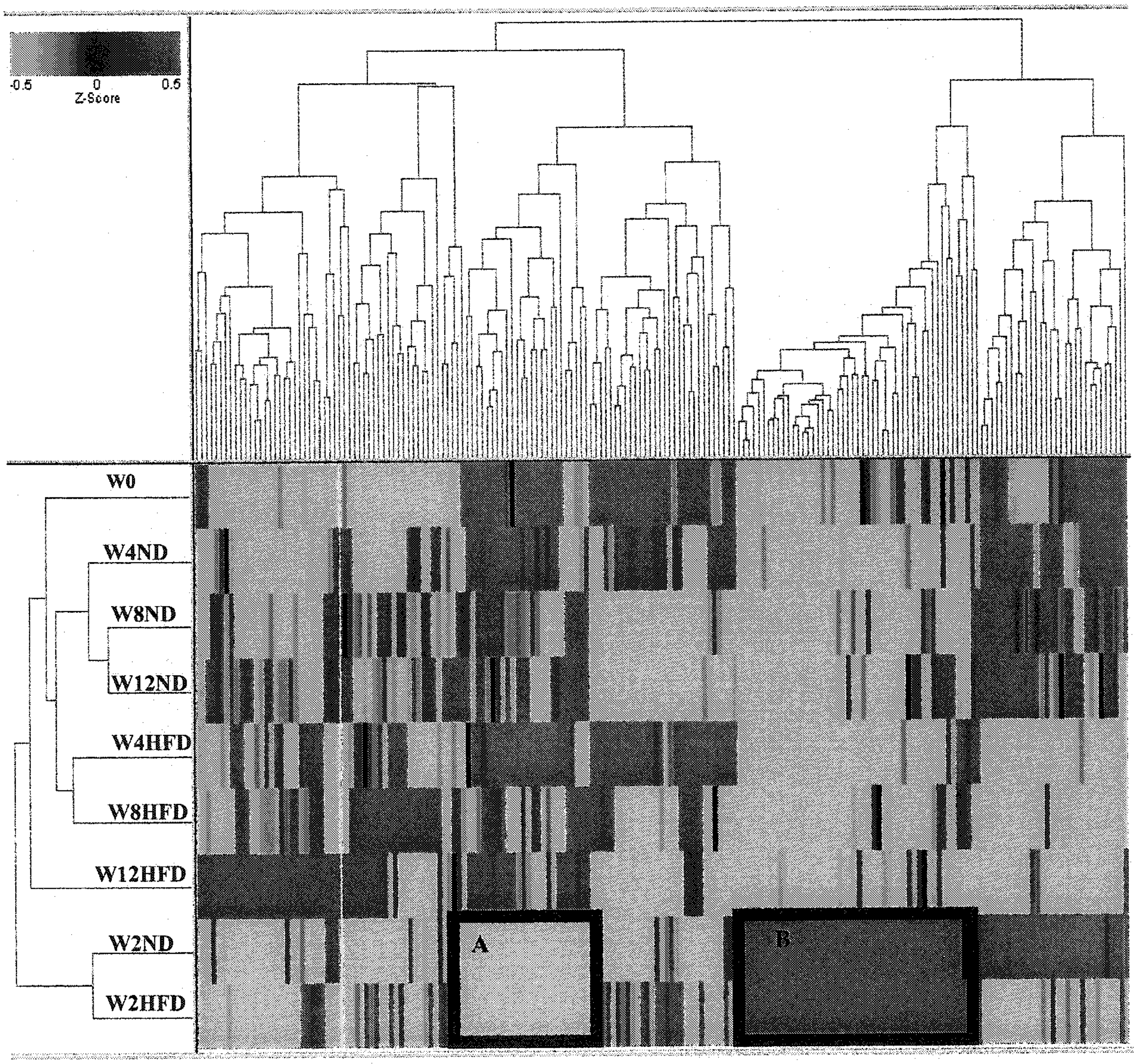


Figure 11. 2D agglomerative cluster. The lines at the top of the dendrogram represent the genes used to generate this cluster. The red intensity signifies genes that are up regulated and the green signifies genes that are down regulated. The left side of the cluster are the grouping results. Boxes A and B are the genes responsible for clustering week 2 separately.

3.14 Linear Trend and Correlation Analysis

After having identified 1947 genes to have a significant diet effect at $P < 0.05$ we utilized two approaches, linear trend and correlation analysis to parse the data in order to identify the more significant affected pathways and to reduce the size of the lists. One of our initial approaches was to use magnitude and direction of genes that followed a linear trend throughout the 12 weeks of high fat feeding. Trend analysis was based on differences in gene expression level between HFD and ND for weeks 2, 4, 8 and 12. Based on the analysis 211 genes were identified to have significant trends ($P < 0.01$). These genes were classified into 2 separate tables without the ESTs: upward trend 65 and downward trend 81 (Appendix C and D). However, analysis of the gene list revealed that linear trends were not always relevant in identifying the biological significance. For example, tubulin beta 3 (Tubb3) showed a positive linear trend (2.54) (Appendix C) although expression increased during HFD feeding, expression levels in HFD group were still below ND in three of the time points as shown in Appendix B. Therefore, caution was required interpreting the linear trend results since they did not always reflect the biology

In order to introduce the biology into the analysis we correlated the pharmacological data with the expression profiles. This analysis would identify all genes whose expression was significantly correlated or anti-correlated with a particular physiological trait. Tables 4, 5 and 6 list the genes whose expression is significantly correlated or anti-correlated to body weight, insulin and glucose levels during the development of obesity. For example, one of the genes that was correlated with weight gain and insulin profiles was fructose bisphospatase1 (Fbp1), a key regulatory protein in gluconeogenesis. Further in depth analysis of the gene list from Appendix B showed that all the genes for the key regulatory enzymes involved in glycolysis and gluconeogenesis were affected at some point during the time course. A number of critical biological pathways whose expression was significantly affected by high fat feeding were identified and are described below.

3.15 Regulation of Glycolysis and Gluconeogenesis

Upon examining the correlation results, Fbp1, as mentioned above was identified to have significant positive correlations with weight gain (0.834) and insulin profiles (0.761). Also one of the top genes that is anti-correlated with body weight is phosphoenolpyruvate carboxykinase 1 (Pckl) which is involved in gluconeogenesis. Upon identification of the above-mentioned genes in the correlation analysis, we further examined Appendix B and the genes for all six key enzymes involved in hepatic glucose metabolism were present, which would indicate that these genes are significantly affected by diet. In addition, 6-phosphofructo-2-kinase/fructose-2-6-bisphophatase 1 (Pfkfb1), the bifunctional enzyme responsible for controlling hepatic gluconeogenesis and glycolysis also was significantly affected by diet (64). Shown in Figure 12 is the plot of data from Appendix B for all six genes that are involved in glycolysis and gluconeogenesis. The plot represents the HFD-ND transformed intensity at all of the time points. Figure 12 suggests that in the early stages of the high fat feeding, glycolysis predominates (weeks 2 and 4) as indicated by up regulation of Glucose kinase (Gck), Phosphofructokinase (Pfkm) and Pyruvate kinase (Pklr). While, at the earlier time points gluconeogenesis genes such as Glucose 6 phosphatase (G6pc) and (Pck1) are being down regulated. With the development of insulin resistance (weeks 8 and 12) there is a switch to gluconeogenesis as shown with up regulation of G6pc and Fructose bisphosphate 1 (Fbp1).

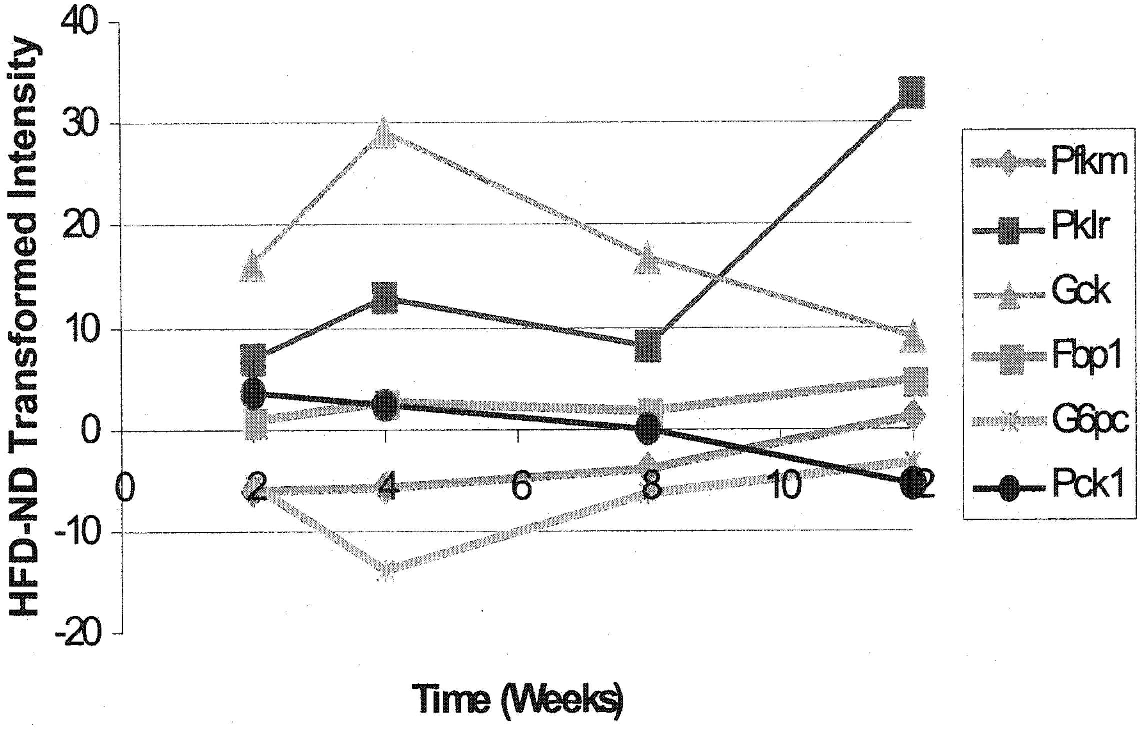


Figure 12. Glycolysis and gluconeogenesis regulatory genes. All six genes were identified to be affected by the high fat diet (HFD) treatment. The expression levels are displayed as high diet (HFD)-chow diet (ND) transformed intensity for Phosphofructokinase (Pfkm), Pyruvate kinase (Pklr), Glucose kinase (Gck), Fructose bisphosphatase 1 (Fbp1), Glucose 6 phosphatase (G6pc) and Phosphoenolpyruvate carboxykinase 1 (Pck1). p-values for each of the time points can be found in Appendix B.

Table 4. Gene correlation/anti-correlation with body weight ($P < 0.05$)

Name	CorrBW	Sequence Description	Biological Process
Gdc1	0.858	Glycerol phosphate dehydrogenase 1, cytoplasmic adult	Glycerol metabolism
Fbp1	0.834	Fructose bisphosphatase 1	Gluconeogenesis
Aatk	0.816	Apoptosis-associated tyrosine kinase	Protein kinase
Hadhsc	0.809	L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain	Fatty acid metabolism
Cyp2b9	0.799	Cytochrome P450, 2b9, phenobarbitol inducible, type a	Metabolism
Cd72	0.796	CD72 antigen	Immune response
Rad51l1	0.787	RAD51-like 1 (S. cerevisiae)	DNA repair/binding ATPase
Umpk	0.771	Uridine monophosphate kinase	Nucleotide biosynthesis
Tcea3	0.768	Transcription elongation factor A (SII), 3	Nucleotide binding
Lgals1	0.752	Lectin, galactose binding, soluble 1	Sugar binding
Inhbe	0.750	Inhibin beta E	Receptor binding/glycopeptide hormone
Mpp1	0.748	Membrane protein, palmitoylated (55 kDa)	Signal transducer
Akap1	0.748	A kinase (PRKA) anchor protein 1	Integral membrane protein
Prkab1	0.743	Protein kinase, AMP-activated, beta 1 non-catalytic subunit	Fatty acid biosynthesis
Capn2	0.740	Calpain 2	Protein catabolism
Glns	0.739	Glutamine synthetase	Nitrogen metabolism
Anxa2	0.729	Annexin A2	Actin binding
Skd3	0.728	Suppressor of K+ transport defect 3	Nucleotide binding
Sec14l2	0.726	SEC14-like 2 (S. cerevisiae)	Transcription
Sorbs1	0.719	Sorbin and SH3 domain containing 1	Cell adhesion/glucose uptake/insulin receptor signaling
Pck1	-0.717	Phosphoenolpyruvate carboxykinase 1, cytosolic	Gluconeogenesis
Aldo3	-0.723	Aldolase 3, C isoform	Glucose catabolism
Cyp2c40	-0.730	Cytochrome P450, 2c40	Metabolism
Egfr	-0.735	Epidermal growth factor receptor	Transmembrane receptor protein tyrosine kinase
Usf1	-0.735	Upstream transcription factor 1	Transcription
Rps5	-0.736	Ribosomal protein S5	Protein biosynthesis
Agxt	-0.737	Alanine-glyoxylate aminotransferase	Amino acid metabolism
Rpl12	-0.738	Ribosomal protein L12	Protein biosynthesis
Igk-V20	-0.743	Mouse VK gene for kappa light chain variable region and J4 sequence.	Immune response
Irf6	-0.751	Interferon regulatory factor 6	Transcription
Tctex3	-0.752	t-complex testis-expressed 3	Transcription
Igfbp2	-0.759	Insulin-like growth factor binding protein 2	Growth factor binding
Rps27a	-0.761	Ribosomal protein S27a	Protein biosynthesis
Tle1	-0.779	Transducin-like enhancer of split 1, homolog of Drosophila E(spl)	Cell growth and/or maintenance
Lamp2	-0.783	Lysosomal membrane glycoprotein 2	Lysosome
Ccl9	-0.799	Chemokine (C-C motif) ligand 9	Immune response
Rpl5	-0.800	Ribosomal protein L5	Cell growth and/or maintenance
Lifr	-0.801	Leukemia inhibitory factor receptor	Integral membrane protein
Lbcl1	-0.804	Lymphoid blast crisis-like 1	Signal transducer

Table 5. Gene correlation/anti-correlation with insulin ($P < 0.05$)

Name	CorrIns	Sequence Description	Biological Process
Anxa2	0.875	Annexin A2	Actin binding
Inhbe	0.833	Inhibin beta E	Receptor binding/glycopeptide hormone
Slc22a1	0.814	Solute carrier family 22 (organic cation transporter), member 1	Cell growth and/or maintenance
Apoc2	0.798	Apolipoprotein C-II	Lipid catabolism
Cyp2b9	0.798	Cytochrome P450, 2b9, phenobarbital inducible, type a	Metabolism
Hadhsc	0.798	L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain	Fatty acid metabolism
Aatk	0.767	Apoptosis-associated tyrosine kinase	Protein kinase
Slc16a2	0.767	Solute carrier family 16 (monocarboxylic acid transporters), member 2	Integral plasma membrane protein/transport
Lgals1	0.766	Lectin, galactose binding, soluble 1	Sugar binding
Skd3	0.763	Suppressor of K+ transport defect 3	Nucleotide binding
Fbp1	0.761	Fructose bisphosphatase 1	Gluconeogenesis
Tuba1	0.757	Tubulin, alpha 1	Microtubule-based process
Vnn1	0.755	Vanin 1	Hydrolase
Aldh3a2	0.754	Aldehyde dehydrogenase family 3, subfamily A2	Metabolism
Umpk	0.754	Uridine monophosphate kinase	Nucleotide biosynthesis
Gapd	0.753	Glyceraldehyde-3-phosphate dehydrogenase	Glucose catabolism
Hmgcs2	0.751	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2	Cholesterol biosynthesis
Anxa4	0.750	Annexin A4	Lipid binding
Mpp1	0.746	Membrane protein, palmitoylated (55 kDa)	Signal transduction
Rad51l1	0.742	RAD51-like 1 (S. cerevisiae)	DNA repair/binding, ATPase
Akap1	0.736	A kinase (PRKA) anchor protein 1	Integral membrane protein
Wars	0.735	Tryptophanyl-TrNA synthetase	Protein biosynthesis/tRNA ligase
Sorbs1	0.735	Sorbin and SH3 domain containing 1	Cell adhesion/glucose uptake/insulin receptor signaling
Mgll	0.729	Monoglyceride lipase	Hydrolase
Slc25a20	0.726	Solute carrier family 25 (mitochondrial carnitine/acylcarnitine translocase), member 20	Integral plasma membrane protein/transport
G0s2	0.723	G0/G1 switch gene 2	Cell growth and/or maintenance
Dp1l1	0.721	Deleted in polyposis 1-like 1	Cell growth and/or maintenance
Lect2	0.720	Leukocyte cell-derived chemotaxin 2	Chemotaxis
Gdm1	0.718	Glycerol phosphate dehydrogenase 1, mitochondrial	Glycerol metabolism
Rps5	-0.721	Ribosomal protein S5	Protein biosynthesis
Agxt	-0.731	Alanine-glyoxylate aminotransferase	Amino acid metabolism
Igfbp1	-0.738	Insulin-like growth factor binding protein 1	Regulation of cell growth
Lifr	-0.747	Leukemia inhibitory factor receptor	Integral membrane protein
Egfr	-0.758	Epidermal growth factor receptor	Transmembrane receptor protein tyrosine kinase
Tat	-0.765	Tyrosine aminotransferase	Transaminase
Eef1a2	-0.791	Eukaryotic translation elongation factor 1 alpha 2	Protein biosynthesis

Table 6. Gene correlation/anti-correlation with blood glucose ($P < 0.05$)

Name	CorrGlu	Sequence Description	Biological Process
Mgll	0.7835	Monoglyceride lipase	Hydrolase
Inhbc	0.7637	Inhibin beta-C	Receptor binding
Casp8	0.7455	Caspase 8	Induction of apoptosis
Ephx2	0.7222	Epoxide hydrolase 2, cytoplasmic	Cell communication
Cyp3a16	-0.7249	Cytochrome P450, 3a16	Metabolism
Arsdr1	-0.7296	Androgen-regulated short-chain dehydrogenase/reductase 1	Metabolism
Ccl9	-0.7525	Chemokine (C-C motif) ligand 9	Immune response
Cyp3a11	-0.7566	Cytochrome P450, steroid inducible 3a11	Metabolism
Gstm3	-0.8107	Glutathione S-transferase, mu 3	Glutathione conjugation reaction

3.16 Regulation of Fat Metabolism

One of the other major metabolic pathways identified by the use of correlation analysis was fat metabolism. Beta-oxidation genes were significantly affected by HFD. Several genes show changes in gene expression within the time course that are consistent with our model. We identified in the body weight (0.809) and insulin (0.798) correlation Tables 4 and 5 expression profiles of L-3-hydroxyacyl-Coenzyme A dehydrogenase (Hadhsc), a gene that plays an essential role in the mitochondrial beta-oxidation of short chain fatty acids. In addition monoglyceride lipase was also identified as the sole gene to positively correlate with blood glucose (0.7835) and insulin (0.729) trends. This enzyme is involved in hydrolyzing triglycerides.

Therefore, we went back to our diet affected gene list (Appendix B) to see if PPARα a known transcription factor to activate genes involved in beta-oxidation and peroxisome proliferation was included in Appendix B. PPARα was identified on the list and had similar gene expression patterns in both groups till 2 weeks of high fat feeding. Between 4 to 12 weeks, the expression of this gene continues to increase in the HFD group while the expression in the ND group decreases (Figure 13). The response of PPARα at 4 weeks of high fat feeding suggests that it may be involved in initiating the cascades that lead to full activation of the beta-oxidation of fatty acids. One cascade that follows this pathway is the activation and the increase in expression of carnitine acyltransferase 1 (crat1) also located in Appendix B.

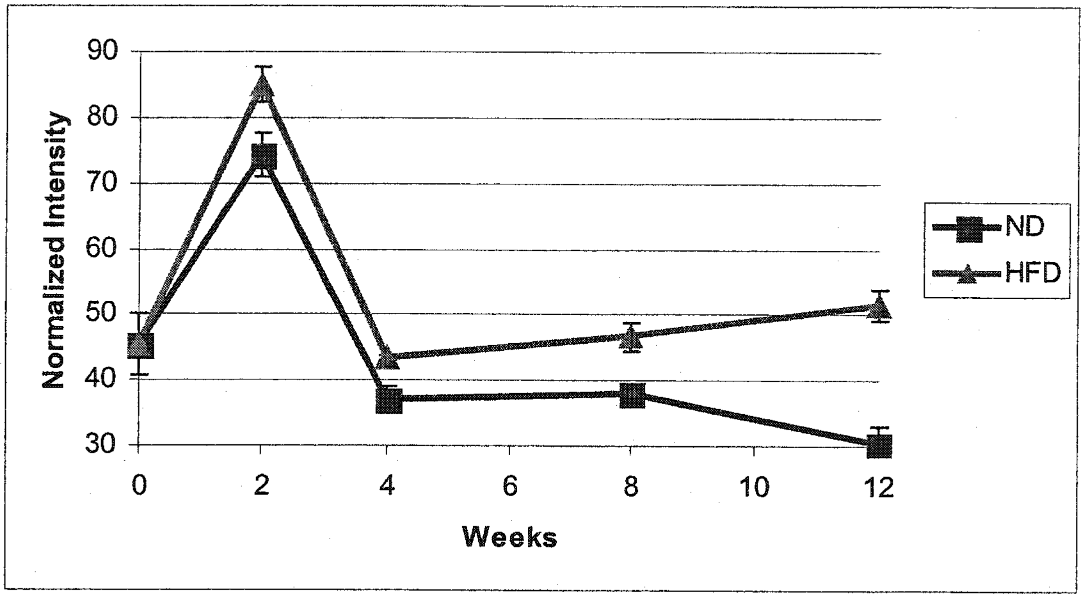


Figure 13 Normalized intensity of PPARα gene expression of chow diet (ND) and high fat diet (HFD) for a period of 12 weeks.

Carnitine acyltransferases have a crucial role in the transport of fatty acids for beta-oxidation and they are targets for therapeutic development against diabetes. In addition, carnitine palmitoyltransferase 1 and carnitine palmitoyltransferase 2 also are affected by high fat feeding. Solute carrier family 25 (mitochondrial carnitine/acylcarnitine translocase) member 20 (Slc25a20) is also positively correlated (0.726) with the insulin profiles. These four genes are involved in facilitating the transport of fatty acids across the mitochondrial membrane. In addition, 2,4-dienoyl CoA reductase 1 mitochondrial (Decr1) also continues to increase its gene expression profile over the 12 weeks of high fat feeding in comparison to the normal diet group. This enzyme is involved in the beta-oxidation of polyunsaturated fats. By using the correlation tables as a primary screen to identify the biological pathways that are being affected by diet we can further search our larger list to get a more complete picture of each pathway.

The other major metabolic pathway in fat metabolism affected by high fat feeding is fat synthesis. Two genes that are highly correlated with both body weight and insulin are the cytoplasmic and mitochondrial glycerol phosphate dehydrogenase 1 genes (Gdc1: 0.858 and Gdm1: 0.718). These two proteins are used for formation of the glycerol backbone for triglycerides (fat synthesis). Cytoplasmic glycerol phosphate dehydrogenase 1 reduces dihydroxyacetone phosphate to form glycerol 3-phosphate. Glycerol can then be incorporated into triglyceride molecules or can enter the glycolytic pathway. The 5'-AMP-activated protein kinase (AMPK/Prkab1) is correlated positively with body weight (0.743) and also is involved fatty acid synthesis.

Once again, we obtained a more detailed view of fat synthesis by examining in further depth Appendix B. There, sterol regulatory element binding protein 1 (SREBP-1) a transcription factor involved in the cholesterol and lipid metabolism was identified to have a higher expression in the HFD treatment group at all of the time points in comparison to the ND treatment group as shown in Figure 14. Several other genes such as (Scd1, SPOT14, Elov2, Elov3, Fabp2, Fabp6) involved in fat synthesis also had significant diet effects.

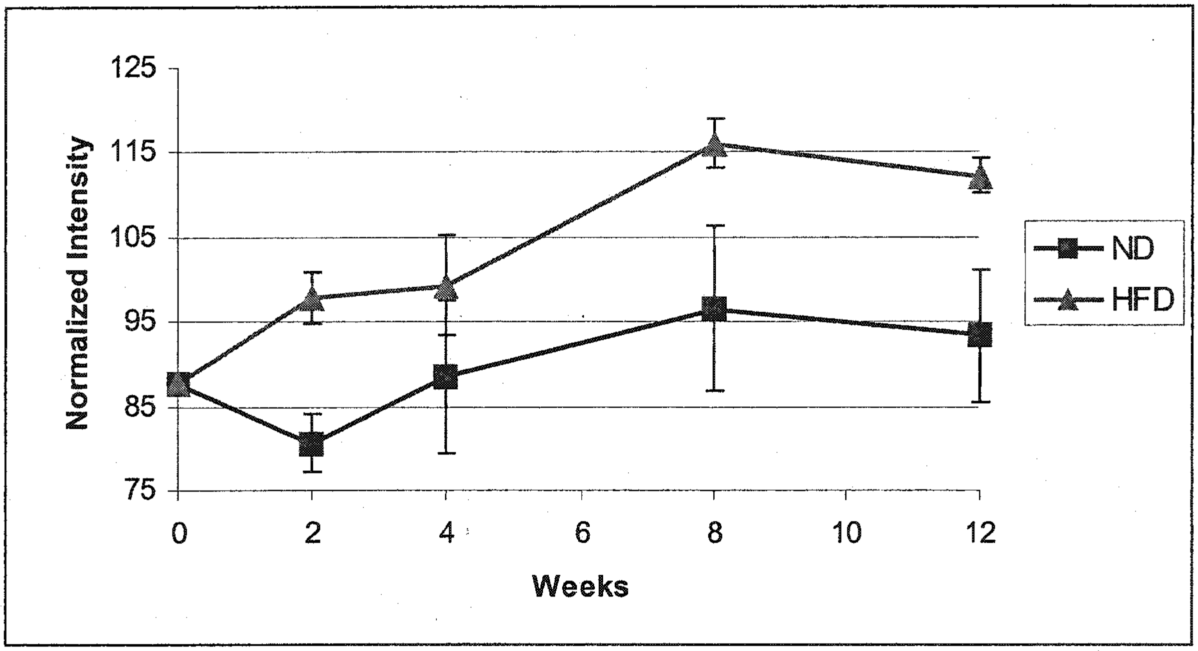


Figure 14 Normalized intensity of SREBP-1 gene expression of chow diet (ND) and high fat diet (HFD) for a period of 12 weeks.

Leptin signaling also is involved in regulation of fat synthesis. The plasma leptin levels were significantly higher in the HFD treatment group than in the ND treatment group at all time points in our model as shown in Figure 2D (consistent with the level of leptin resistance). At the molecular level protein inhibitor of activated STAT3 (PIAS3), is more highly expressed in the high fat diet treatment group than in the normal diet treatment group at weeks 8 (4.87) and 12 (11.65), corresponding with the development of hyperleptinemia and hyperinsulinemia. Leptin is required to keep the liver tissue free from excess lipid deposition and inhibitors of this pathway such as PIAS3 maybe contributing to the development of leptin resistance and steatosis.

3.17 Regulation of CYPs, GSTs and HSPs

Oxidative stress has been implicated in the pathogenesis of obesity and its complications. Stress proteins such as cytochrome P450 isoforms (CYPs), heat shock proteins (HSPs) and glutathione S transferases (GSTs) have been shown to protect organisms *in vitro* and *in vivo* against oxidative stress (65,66). Examination of the anti-correlated results in Tables 6 to 8 revealed Cyp3a11 (-0.7566), Cyp3a16 (-0.7249) and Gstm3 (-0.8107) to be anti-correlated with the blood glucose profiles. Also Cyp2c40 (-0.730) was anti-correlated with the body weight list. A closer examination of other members of genes in this family revealed that a large number of the GSTs were down regulated in the HFD treatment group as early as week 2 and this trend continued till the end of the time course as shown in Table 7. Examination of the CYPs in Appendix B revealed that 15 out of 20 of the diet affected CYPs also were down regulated in the HFD treatment group at week 2. This pattern continued till week 12. Examination of the HSPs in Appendix B also revealed that the number of HSP genes being affected by diet increased with the duration of HFD treatment. Therefore, there was a decrease in expression of these genes in the HFD treatment group in comparison to the ND treatment group over time as shown in Table 8. In the DIO model as insulin resistance, obesity and fatty liver are progressing, the protective mechanisms are being lost.

Table 7. Differences in expression levels (HFD-ND) and p-values at all time points of glutathione S transferases.

Symbol	Desc	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
Gsta2	glutathione S-transferase, alpha 2 (Yc2)	-41.29	0.00	-44.99	0.00	-60.60	0.00	-28.85	0.02
Gsta3	glutathione S-transferase, alpha 3	-4.53	0.03	-1.40	0.47	-6.04	0.01	-0.61	0.75
Gsta4	glutathione S-transferase, alpha 4	-16.58	0.01	-28.17	0.00	-27.77	0.00	-16.91	0.01
Gstm1	glutathione S-transferase, mu 1	-11.57	0.00	-12.41	0.00	-15.92	0.00	-4.76	0.03
Gstm2	glutathione S-transferase, mu 2	-15.88	0.00	-15.92	0.00	-16.71	0.00	1.08	0.79
Gstm3	glutathione S-transferase, mu 3	-17.41	0.00	-19.13	0.00	-23.65	0.00	-10.78	0.00
Gstm5	glutathione S-transferase, mu 5	38.68	0.00	11.91	0.16	-3.88	0.64	-3.44	0.68
Gstm6	glutathione S-transferase, mu 6	-14.55	0.01	-14.21	0.01	-24.96	0.00	-12.42	0.02
Gsto1	glutathione S-transferase omega 1	-5.16	0.00	-6.49	0.00	-9.96	0.00	-6.62	0.00
Gstp2	glutathione S-transferase, pi 2	-1.09	0.57	-2.39	0.22	-2.91	0.14	-6.74	0.00
Gstt2	glutathione S-transferase, theta 2	-15.68	0.01	-19.58	0.00	-22.98	0.00	-11.23	0.05

Table 8. Differences in expression levels (HFD-ND) and p-values at all time points of heat shock proteins.

Symbol	Desc	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
Hsp105	**heat shock protein, 105 kDa**	**7.45**	**0.12**	**18.57**	**0.00**	**1.97**	**0.67**	**-18.45**	**0.00**
Hsp60	**heat shock protein, 60 kDa**	**-1.61**	**0.18**	**2.62**	**0.03**	**-1.86**	**0.12**	**-6.55**	**0.00**
Hsp70-1	**heat shock protein, 70 kDa 1**	**13.92**	**0.17**	**25.20**	**0.02**	**-10.63**	**0.29**	**-37.20**	**0.00**
Hsp84-1	**heat shock protein, 84 kDa 1**	**-7.38**	**0.01**	**0.01**	**1.00**	**-3.25**	**0.19**	**-4.26**	**0.09**
Hspa4	**heat shock 70 kDa protein 4**	**5.93**	**0.02**	**4.47**	**0.07**	**-1.28**	**0.59**	**-5.04**	**0.05**
Hspa5	**heat shock 70kD protein 5 (glucose-regulated protein, 78kD)**	**1.90**	**0.53**	**12.32**	**0.00**	**2.98**	**0.33**	**-8.20**	**0.01**
Hspa8	**heat shock 70kD protein 8**	**6.26**	**0.01**	**9.59**	**0.00**	**5.64**	**0.02**	**-11.93**	**0.00**

3.18 Energy Metabolism Alteration

Upon high fat feeding there was increased lipid accumulation in the liver (Figure 4) and increased expression of genes involved in beta-oxidation (Figure 13) which leads to increased production of free radicals. These alterations in the liver have been noted previously to cause mitochondrial oxidative injury resulting in an impaired production of ATP and damage to organs in other models of steatosis. Therefore, examination of the FoF1-ATP synthase was of interest since it has been identified in male Wistar rats to be down regulated (35% lower) by immunoblot analysis from fatty livers. In the diet affected genes list (Appendix B) ATP synthase mitochondrial F1 complex (ATP5c1) was identified with an ANOVA p-value of 0.03. As expected from previous published reports there is down regulation of this gene at the RNA level in the HFD group in comparison to the ND group as shown in Figure 15 which follows with the decreased protein expression (81).

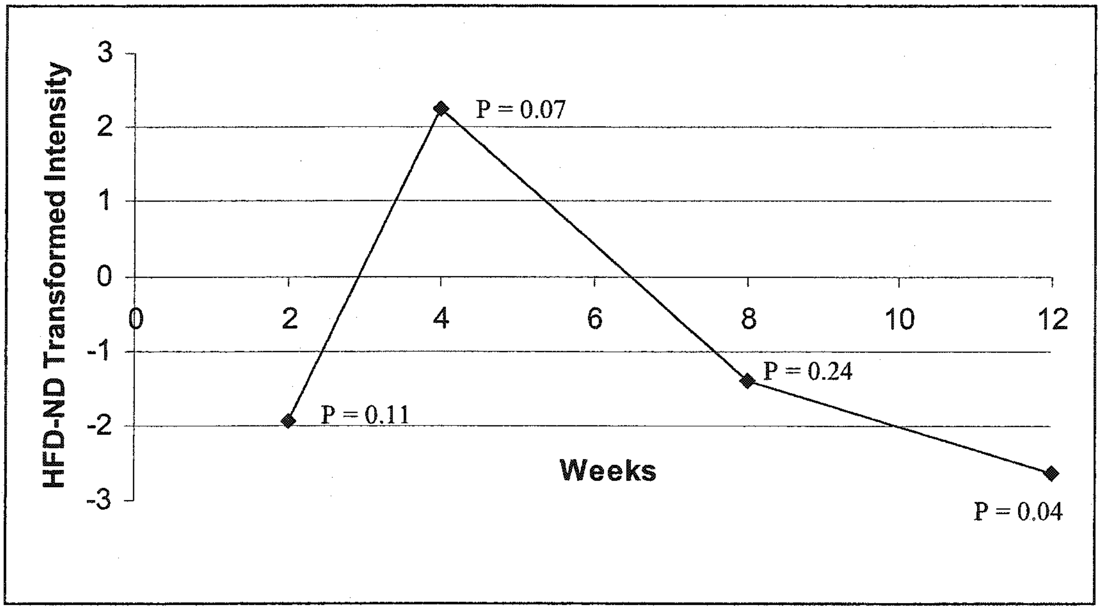


Figure 15 HFD-ND transformed intensity of Atp5c1. The high fat diet (HFD) group has a lower expression in ATP synthase mitochondrial F1 complex (ATP5c1) than the chow diet (ND) group for the majority of the time course experiment.

3.19 Regulation of Growth Factors

The presence of steatosis and the eventual development of NASH result in liver degeneration. One critical growth factor involved in liver regeneration is the epidermal growth factor (Egf). In our experiments epidermal growth factor receptor (Egfr) was identified to be anti-correlated to both body weight and insulin profiles. Hepatoma derived growth factor (Hdgf) also was found on the diet affected gene list and also is down regulated in a similar pattern as Egfr (Figure 16).

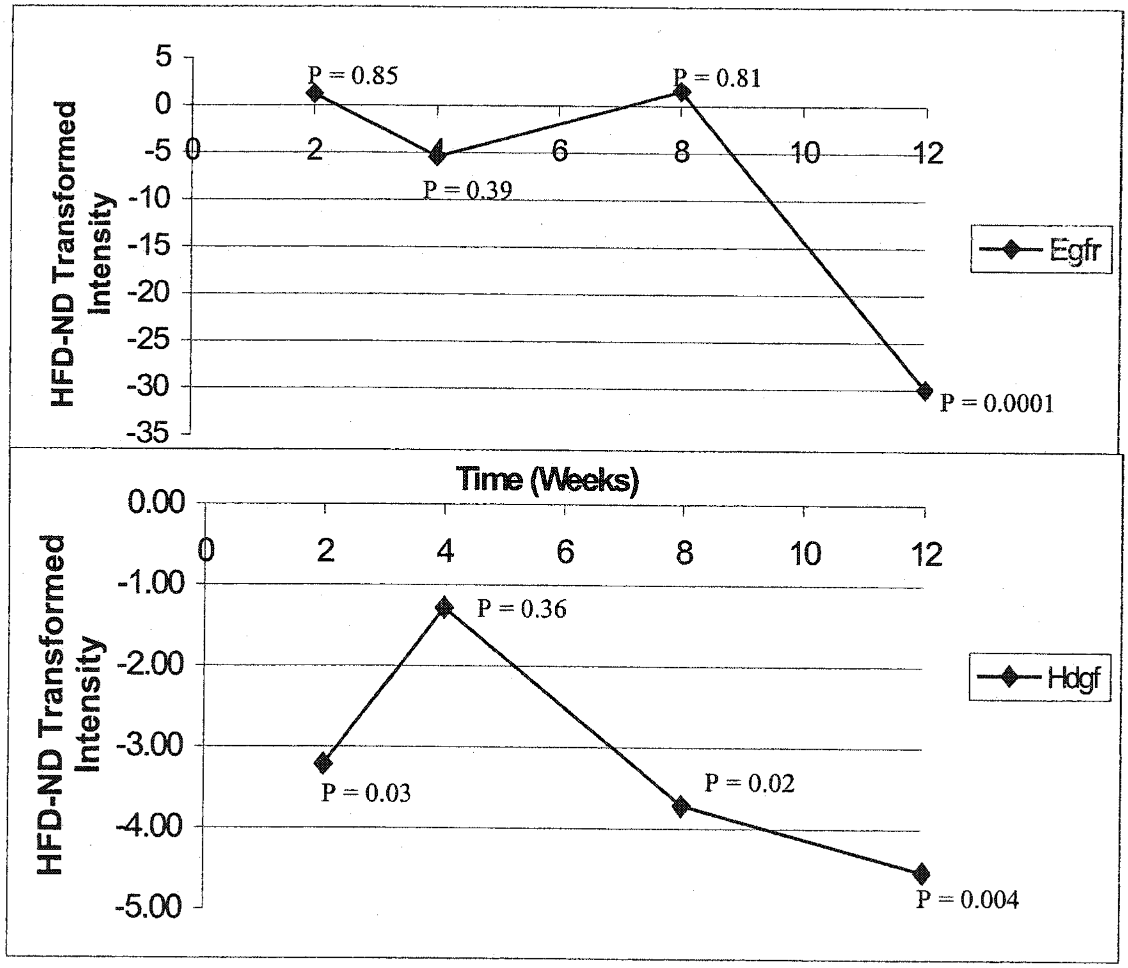


Figure 16 Down regulation of Egfr and Hdgf upon high fat diet treatment. This graph represents the HFD-ND transformed intensity throughout the time course.

The Egfr receptor dramatically decreases between week 8 and 12. This is at the same time points where we see a sharp increase in the insulin and leptin levels as shown in Figure 2C and D. Progressive down regulation of essential growth factors for liver regeneration indicates progression of steatosis and a transition into NASH at week 12 upon HFD treatment.

3.20 Microarray Analysis Summary

What has been reported in this thesis is one approach in analyzing the list of genes affected by diet. There are several other methods that also can be used to analyze the data. As well, additional pathways can be examined. This analysis will be an ongoing process.

Chapter 4

Discussion

4.1 Validation of the Diet-Induced Obese Mouse Model

Twelve weeks of feeding mice a HFD resulted in significant weight gain, hyperglycemia, hyperinsulinemia and hyperleptinemia all hallmarks of insulin resistance and obesity. Insulin resistance followed the onset of increased body weight and hyperglycemia in this 12 week time course experiment. In addition, measurements of the food intake revealed that the HFD group consumed less food by weight than the ND group but when the caloric profiles were calculated both groups consumed the same amount of calories over a period of 12 weeks. This indicates that the number amount of calories consumed does not account for the development of obesity, but more importantly it is the source of calories in the diet. Therefore, only the HFD group which consumed food with a fat content of 35.5% in comparison to 4.4% fat in the ND developed significant weight gain, hyperglycemia and hyperinsulinemia (Figures 2A-C). The pharmacological characterization is an essential first step and can be regarded as the first quality control step in the microarray process to ensure that the correct biology is being profiled.

4.2 Microarray Design Issues

The goal of this study was to profile hepatic gene expression changes during development of obesity. However, other sources affecting gene expression changes can be introduced during this time course which can complicate interpretation. To minimize the effects of these variables, we used the experimental strategy outlined in Figure 5A and B. First, 6 animals were used per treatment time point to provide sufficient sample numbers for measurements of physiological parameters in order to compensate for animal variability.

Second, each treatment time point was determined using 3 microarrays. Therefore, there was random pooling of 2 animals per array as described in Chapter 2 (Materials and Methods). To minimize variation in expression patterns between different mice, we studied 2 liver samples simultaneously, with equal amounts of cRNA mixed for each of the treatment groups and the resulting cRNA pools then were hybridized to a single microarray. The triplicate microarrays would be expected to control for both tissue and experimental variability including tissue heterogeneity, variables in RNA isolation, biotinylated cRNA production and variability in hybridization to GeneChip microarrays. Variations in gene expression profiles should be normalized by this method, while gene expression changes correlating with the development of obesity should be preserved (22). Replication is necessary for reducing the variation in microarray experiments. In particular biological replicates instead of technical replicates are essential for identifying the natural biological variability in the system (69). Biological replicates have the potential of highlighting the potentially important and reproducible changes between treatment comparisons. Also, increasing the number of replicates decreases the probability of identifying false positives and negatives (48). The microarray experimental design has to include a minimum of three replicates to perform statistical analysis. The triplicate approach as shown in this experiment generates a data set on which robust statistical analysis can be applied.

Third, the 5 point time course adds significance to the gene expression profiles since we are getting data from a single gene in two treatment groups over 5 time points which provides 27 values for a single gene. The design of this experiment allowed identification of low expressers at the early weeks and high expressers at the end of the 12 weeks and the reverse profile since microarray analysis was carried out to identify correlated and anti-correlated gene expression profiles to the pharmacological data. This experimental design and microarray analysis approach emphasizes the necessity of multiple time points in expression time course studies, thereby providing complete details of gene expression profiles over 12 weeks of high fat feeding.

Fourth, we analyzed age-matched controls in order to extract the fundamental patterns of gene expression profiles inherent in the data. Based on our results it is evident that the gene expression profiles be compared to the same time point rather than time 0, which has been the case for many microarray analyses (19,39). For example, at week 2, gene signatures occurring during sexual maturation were more significant than those induced by diet. At 2 weeks of the time course experiment these mice are at 8 to 10 weeks of age which is approximately the sexual maturation phase for male mice (52). Hence, this development stage has a more profound effect on gene expression than 2 weeks of HFD treatment. A comparison of the time-matched controls allows for identification of significant differential expression based on diet effects rather than developmental changes.

4.3 Statistical Issues with Analysis of Microarray Data

Contrary to conventional biological experiments that consist of relatively small data sets, microarray experiments generate enormous data sets. Data mining of ~13000 gene expression profiles over a 5 point time course is a challenging task especially when ~50% of the genes represented on the array are not well characterized. This overwhelming task was handled by integration of information from the various databases into Microsoft Access as mentioned in Chapter 2 (Materials and Methods). By importing the expression profiles and gene information into a single database it was more convenient to search for profiles. This approach allowed us to generate queries from a single database. For example, we generated using our own database (gene expression profiles and gene functions) Tables 4 to 8 and Appendices B, C and D.

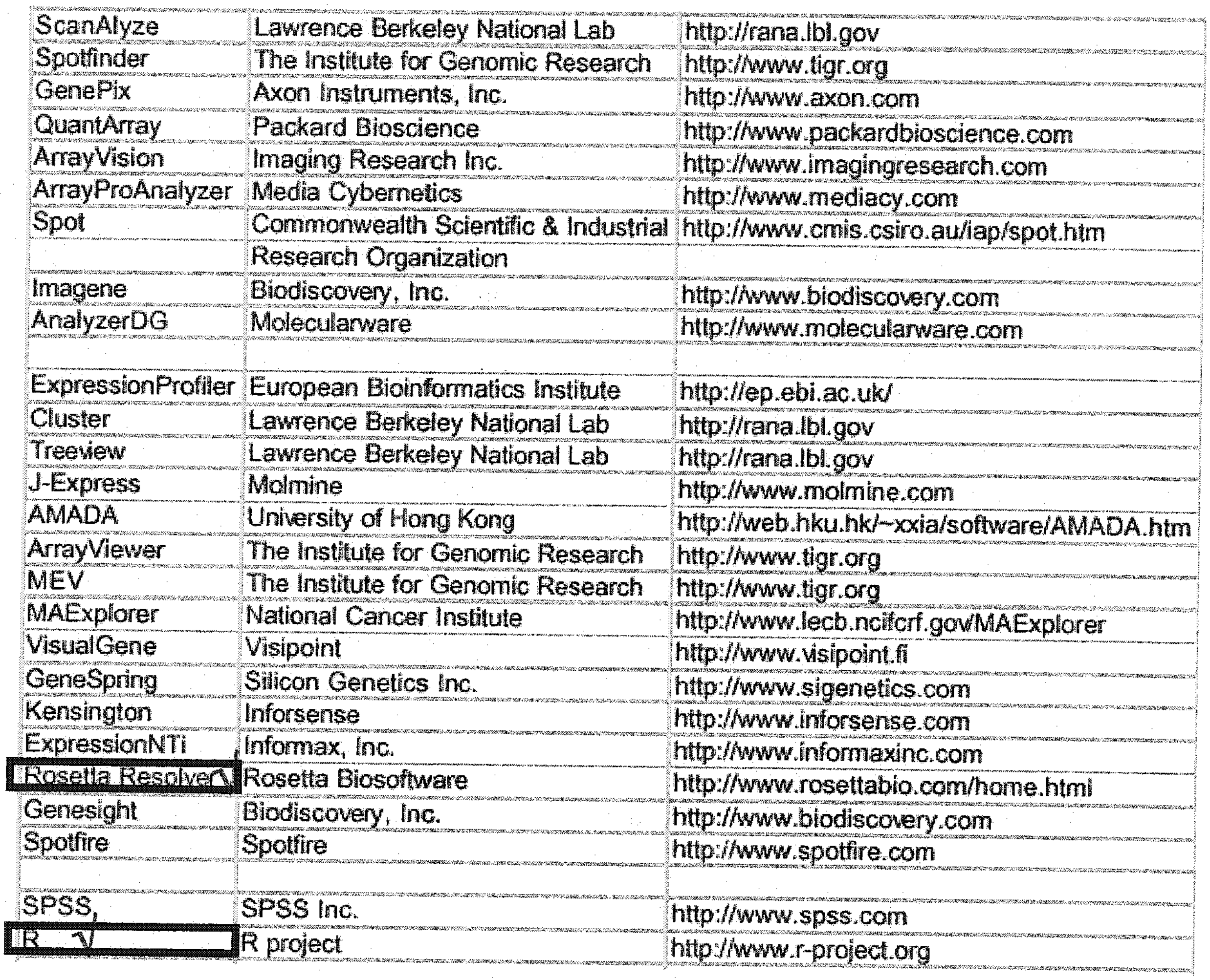
Microarray analysis is an emerging discipline and multiple approaches can be used and various software packages are available (3). We selected for our analysis the Rosetta Resolver and R packages as shown selected in Figure 17. Rosetta Resolver is one of the more advanced microarray analysis softwares. The R package was chosen since it is powerful statistical software that can handle large datasets for normalization. Variance stabilizing transformation was applied to our data set using the R software in order to remove the additive and multiplicative errors, which are introduced in microarray experiments. This generated a data set with a normal distribution and constant variance throughout all the genes. To further identify genes, which had the most significant changes between groups rather than within groups, ANOVA was used in the data analysis. ANOVA defines the significance of gene changes by examining the mean and variance of the two distributions and calculates the probability that they were sampled from the same distribution. This analysis differs from the more common analysis method that identifies significant changes in gene expression using fold change. Most publications state that a 2 fold or higher difference between the mean intensity of the groups is a significant change. However, this analysis method fails to account for sample variation and possibly leads to false positives. Miller et al. (58) have shown, using a study with 10000 genes, that the ratios of 450 genes can be higher than 2 by chance. Additionally, this ratio-based analysis ignores the fact that differences less than 2 fold may also elicit meaningful biological effects (58,82).

The field of microarray analysis is at present in its nascent stage. Recently, Minimum Information About a Microarray Experiment (MIAME) has been established to standardize the presentation of microarray experiments to include complete details of the experiment (16). Henceforth, journal publications will have to outline not only the details on the pharmacological experiments but also the details of the microarray analysis in the hopes of establishing a standardized method to perform microarray experiments. This experiment passes each of the requirements for MIAME and even surpasses their detailed protocols. Advances in this field will lead to a more concrete method for analyzing these large data sets.

4.4 1947 Genes were Identified to have a Significant Diet Affect

Based on our analysis, 1947 genes (of 12488) were significantly affected by high fat feeding at some point during the 12 week time course. Some of these significant gene changes upon high fat feeding have been reported previously in other tissues and models. For example, there was an increased expression of Apoa4, a gene which is well documented to have higher gene expression upon high fat feeding at all of the time points in the HFD group in comparison to the ND group. Over expression of Apoa4 is known to elevate plasma triglyceride, free fatty acid, total cholesterol and HDL cholesterol (39). We also observed up regulation of other genes such as those involved in macronutrient metabolism: fatty acid binding protein 2 (Fabp2), glycerol phosphate dehydrogenase 1

(Gdc1), enoyl coenzyme A hydratase 1 (Ech1) and stearoyl-Coenzyme A desaturase 1 (Scd1) that have been reported in DIO experiments (49).



ScanAlyze	Lawrence Berkeley National Lab	http://rana.lbl.gov
Spotfinder	The Institute for Genomic Research	http://www.tigr.org
GenePix	Axon Instruments, Inc.	http://www.axon.com
QuantArray	Packard Bioscience	http://www.packardbioscience.com
ArrayVision	Imaging Research Inc.	http://www.imagingresearch.com
ArrayProAnalyzer	Media Cybernetics	http://www.mediacy.com
Spot	Commonwealth Scientific & Industrial Research Organization	http://www.cmis.csiro.au/iap/spot.htm
Imagene	Biodiscovery, Inc.	http://www.biodiscovery.com
AnalyzerDG	Molecularware	http://www.molecularware.com
ExpressionProfiler	European Bioinformatics Institute	http://ep.ebi.ac.uk/
Cluster	Lawrence Berkeley National Lab	http://rana.lbl.gov
Treeview	Lawrence Berkeley National Lab	http://rana.lbl.gov
J-Express	Molmine	http://www.molmine.com
AMADA	University of Hong Kong	http://web.hku.hk/~xxia/software/AMADA.htm
ArrayViewer	The Institute for Genomic Research	http://www.tigr.org
MEV	The Institute for Genomic Research	http://www.tigr.org
MAExplorer	National Cancer Institute	http://www.lecb.ncifcrf.gov/MAExplorer
VisualGene	Visipoint	http://www.visipoint.fi
GeneSpring	Silicon Genetics Inc.	http://www.sigenetics.com
Kensington	Inforsense	http://www.inforsense.com
ExpressionNTi	Informax, Inc.	http://www.informaxinc.com
Rosetta Resolver √	Rosetta Biosoftware	http://www.rosettabio.com/home.html
Genesight	Biodiscovery, Inc.	http://www.biodiscovery.com
Spotfire	Spotfire	http://www.spotfire.com
SPSS,	SPSS Inc.	http://www.spss.com
R √	R project	http://www.r-project.org

Figure 17. Microarray analysis software. The first column is the software name. The second column is the organization and the third column is the website. Boxed in black is the software selected for the analysis.

4.5 Linear Trend and Correlation Analysis

With the identification of such a large number of genes (1947) affected by diet, it was necessary to further narrow down the list and two approaches were used (linear and correlation analysis). Linear trend analysis was initially used by Nadler et al. (63), to identify genes that increased or decreased with obesity. In our hands this method identified genes that had either positive or negative linear trends (Appendix C and D). This was one approach to reduce the large data set from 1947 to 211 genes. This method allows identification of some important trends. However, this method fails in interpreting a detailed overview of the meaningful biological data, since not all-biological changes are linear and the trend sometimes did not convey biological results. Therefore, correlation analysis was used in order to introduce biological components.

The correlation tables generated indicate that this method provides an insight into the biological pathways that may be involved in the development of obesity, insulin resistance and steatosis (NASH). In addition, obtaining multiplicity-adjusted p-values using the Holm's method identified the most significant biological changes. This method provides more significant p-values generated from repetitious testing of experiments. In addition, this method eliminates and reduces the number of false positives that may be seen without multiple testing (48).

These results suggest that the approach using the correlation multiplicity adjusted testing can identify genes that are more likely to be involved directly with the biological effect.

4.6 Biological Mechanisms in Early Weeks (0 to 4) of Obesity and Insulin Resistance Development

With the correlation analysis as a starting point, a number of biological pathways that were involved in the development of fatty liver pathology were identified (as shown in Figure 18). Highlighted in the solid arrow lines are the molecular mechanisms that have been identified by microarray analysis in the development of fatty liver. The dotted arrow lines are the pharmacological traits that occur due to high fat feeding.

For example, microarray analysis has identified the genes for regulatory enzymes involved in glycolysis to be up regulated in the HFD treatment group in comparison to the ND group during the initial weeks of high fat feeding. Up regulation of this pathway acts as a protective mechanism to reduce increasing blood glucose levels. Gluconeogenic genes are down regulated in the HFD group at the same time point since they are still insulin sensitive.

In the early weeks of high fat feeding, an increase in expression for some of the genes involved in beta-oxidation was also observed. Once again, this early response acts as a defense mechanism to protect from excess fat deposition in the liver, however increased beta-oxidation of fatty acids also generates increased levels of reactive oxygen species which can be detrimental. Clearly up regulation of PPARα further increases gene expression of genes involved in beta-oxidation. PPARα is the predominant PPAR subtype expressed in the liver and regulates genes involved in fatty acid transport, synthesis and oxidation, glucose and lipid metabolism, ketogenesis and desaturation (13). HFD treatment affected various genes containing a peroxisome proliferator responsive element (PPRE), with roles in fatty acid oxidation (carnitine palmitoyl transferase, Cpt1;

enoyl coenzyme A hydratase 1, Ech1), fatty acid desaturation (stearoyl-coenzyme A desaturase, Scd1), gluconeogenesis (cytosolic phosphoenolpyruvate 1, Pck1 or PEPCK; glucose 6 phosphatase, G6pc), cholesterol metabolism (apolipoprotein A4, Apoa4) and ketone body formation (3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2, Hmgcs2). Some of these genes appeared to have relevance to the mechanisms of the PPARα signaling pathway. For example, Hmgcs2 and cytochrome P450 2b9 (Cyp2b9) both have been reported to be under the control of PPARα and both are more highly expressed in the HFD group (13).

Although there is increased beta-oxidation we observed increased fat deposition in the liver. At the gene level there was an increase in genes that were involved in fat synthesis. At the early weeks (0-4 weeks) of high fat feeding sterol regulatory element binding protein 1 (SREBP1) is more highly expressed in the HFD group than the ND group. SREBPS are basic helix-loop helix (bHLH) transcription factors activated in response to variations in intracellular cholesterol levels that induce transcription of genes with sterol regulatory element (SRE) and E-box containing promoters. Genes containing SRE promoters have roles in fatty acid synthesis (13). In this experiment several SRE promoter-containing genes were also affected by HFD such as Scd1, SPOT14, Elov2, Elov3, Fabp2 and Fabp6.

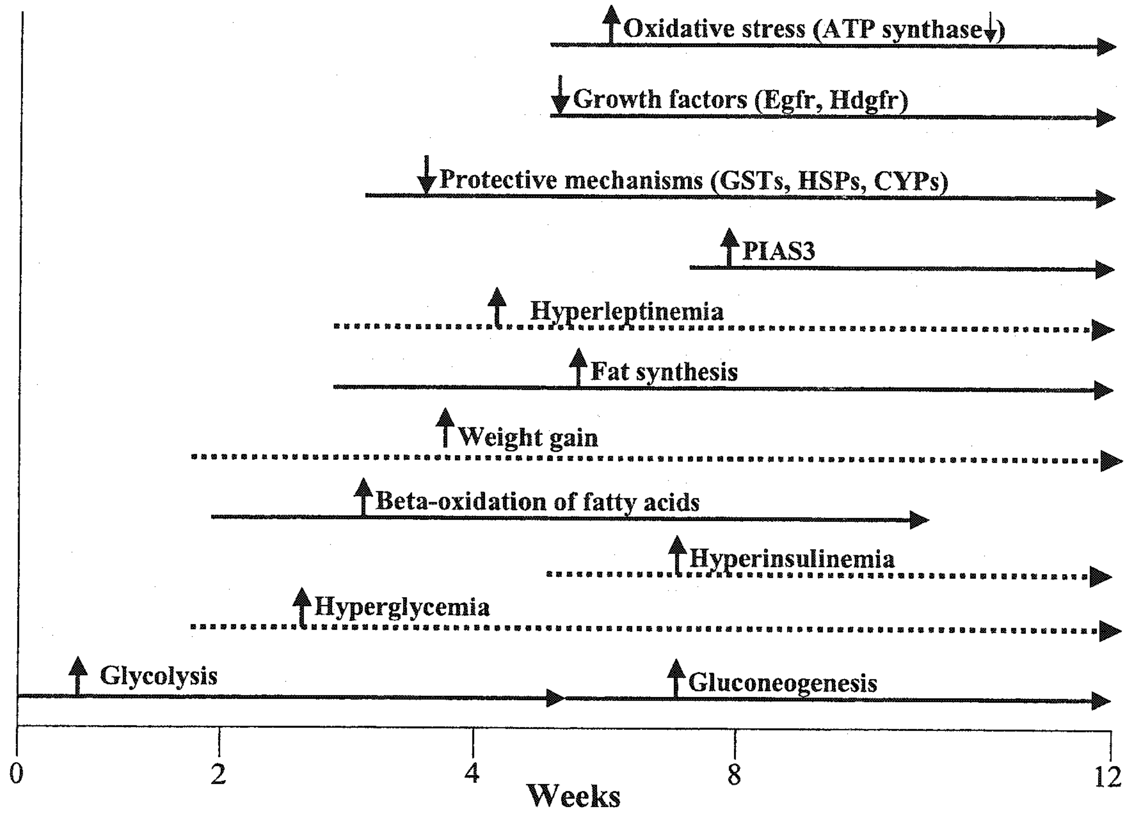


Figure 18. Identification of molecular mechanisms in the development of obesity, insulin resistance and steatosis (NASH). Solid line arrows are molecular pathways that were identified in the HFD group. The dotted line arrows are the pharmacological changes in the HFD group. The upward arrow (↑) signifies genes of that particular pathway or the pharmacological measurement being up-regulated. While the downward arrow (↓) signifies the inverse.

4.7 Biological Mechanisms in Late Weeks (8-12) of Obesity and Insulin Resistance Development

Between 8 to 12 weeks of high fat feeding microarray analysis reveals down regulation of gene expression profiles for enzymes involved in protective mechanisms (Figure 18). At the pharmacological level increased hyperinsulinemia occurs as the body attempts to compensate for insulin resistance. The increased insulin resistance to insulin signaling turns on genes in the gluconeogenesis pathway leading to further increases in hepatic glucose production. Turning off glycolysis and turning on gluconeogenesis contributes to the hyperglycemia syndrome seen upon high fat feeding (Figure 18).

In addition, there is development of leptin resistance. Plasma leptin levels were significantly elevated as early as 2 weeks upon high fat feeding and this trend continued till week 12. In the healthy state, leptin mediates its effects by binding to its receptor, leading to activation of Jak2. Jak2 then phosphorylates STAT3, which translocates into the nucleus to activate the transcription of genes involved in lipid homeostasis. In this way leptin spares tissues of lipid overload. In situations where there is development of hyperleptinemia and leptin resistance this pathway is turned off and leads to increased fat deposition. In this DIO model by week 12 there are indications of leptin resistance at the pharmacological and molecular level. At week 8 the HFD liver has greater fat depositions than the ND liver by staining with lipid specific Oil red O indicating steatosis. This excess lipid accumulation in the liver may be occurring through an increase of gene expression levels of the protein inhibitor of activated stat 3 (PIAS3). Increased levels of PIAS3 prevent activation of the leptin-signaling pathway thus leading to an increase in steatosis. It has been reported that lipid loading is involved in the development of insulin resistance (33). Perhaps induction of PIAS3, which inhibits leptin signaling and increases lipid deposition, may be one possible mechanism for the development of insulin resistance (26,79).

At 8 to 12 weeks of high fat feeding there is down regulation in gene expression for protective enzymes such as HSPs, GSTs and CYPs. HSPs allow cells to survive under stressful conditions such as environments rich in free radicals. By week 8 all the diet affected HSPs from Appendix B are more down regulated in the HFD group than the ND group also shown in Table 8. Hyperinsulinemia and hyperleptinemia seemed to reduce their expression to an even greater extent. Loss of gene expression in HSPs can result in protein misfolding, degradation of unstable proteins, accumulation of abnormally folded protein, aggregation and cell death (65). Mice placed on HFD have decreased gene expression for glutathione transferase (GSTs) enzymes in comparison to the ND group by early as two weeks. These enzymes play a key role in cellular detoxification. The enzymes protect the cells against toxicants by conjugating them to glutathione. The conjugated products are often less toxic and generally have greater water solubility, facilitating their removal from the cell. Therefore, loss of GST gene expression can lead to increased toxic compounds in the cellular environment (27). The CYPs have similar profiles to the GSTs. They too are down regulated at 2 weeks in the HFD group in comparison to the ND group and the trend continues till week 12. CYPs play a major role in the metabolism of endogenous compounds and in the detoxification of xenobiotic molecules. Factors such as age, gender, nutrition and hormone can affect CYPs and hence the biotransformation of compounds (90).

With an increased HFD is shown an increase in gene expression of enzymes involved in beta-oxidation. An increase in this pathway causes increased oxidative damage as seen with the loss of HSPs, CYPs and GSTs. The loss of gene expression of enzymes involved in protective mechanisms is more prevalent at the later time points (8-12 weeks). One other major target for oxidative damage is the ATP synthase mitochondrial F1 complex (ATP5c1), required for ATP production. Once this synthase is affected there are major consequences on the whole tissue. We observed down regulation of this ATP synthase at the gene expression level at 8 weeks, whether this is due to beta-oxidation is not known but a recent publication has shown down regulation of this synthase at the protein level in male Wistar rats with steatosis (81).

Also at 8 weeks, the DIO mice displayed increased weight gain, hyperinsulinemia, hyperleptinemia and steatosis when placed on a HFD. These are all well characterized physiological traits of obesity and Type 2 diabetes. What causes these molecular defects still remains unknown, however, a previous study on three distinct mice models of obesity and Type 2 diabetes described similar physiological traits and reported that all three models had significantly decreased levels of Egfr in comparison to their control group (14). In this study Egfr also was found to be anti-correlated to both body weight and insulin trends as in our model. Down regulation of the Egfr upon high fat feeding may be involved in the development of insulin resistance, since insulin and epidermal growth factor (Egf) share several metabolic actions. In addition, Egf is involved in proliferation and survival of hepatocytes during liver regeneration. Therefore, loss of the Egfr may have many deleterious effects(14,29).

4.8 Summary

Microarrays are powerful tools to investigate genome-wide expression of diseased and non-diseased tissues. This technology generates large data sets of valuable information when the experimental design is set up with the appropriate controls, replicates and animal model.

The DIO mouse model was used to investigate the development of obesity, insulin resistance and steatosis (NASH). Upon examination of the hepatic gene expression profiles throughout the 12 weeks of high fat feeding and through comparison with the appropriate time matched controls, several mechanisms were identified in the development of obesity, insulin resistance and steatosis (NASH). The initial findings indicated that a large number of genes ~1947 ($P < 0.05$) were affected upon high fat feeding at some point during the time course. This was a large list to interpret and therefore, the most significant biological changes were identified by directly correlating the pharmacological data with the gene expression profiles. This method was proven to be useful in identifying biological pathways that identified protective mechanisms in the early weeks of high fat feeding such as those involved in glucose removal (glycolysis) and excess fat removal (beta-oxidation of fatty acids). Additionally, other pathways such as those leading to liver degeneration (growth factors), free radical scavengers (GSTs), heat shock proteins (HSPs), leading to increased glucose production (gluconeogenesis), increased fat deposition (SREBP1) and leptin resistance (PIAS3) were identified to be contributing to the pathogenesis. Some of these pathways and genes have been examined for the first time in context of obesity, insulin resistance and steatosis (NASH).

4.9 Future Studies

This microarray study provides results based on triplicate replicates. In addition, correction for multiple testing was used in this analysis. Therefore, the results are highly reproducible and robust. Since this was an exploratory analysis, no other normalization or analysis methods were used for this project. Still, this study does provide a foundation for further research into identification of mechanisms involved in the development of obesity, insulin resistance and steatosis (NASH).

There are many potential experiments that would be useful in confirming the results of this study. As a first approach, the results can be confirmed either by traditional methods such as Northern blot analysis or more recent technologies such as quantitative real time PCR (82). This would provide an alternative approach for validating the gene expression profiles. In addition to validating the gene expression profiles, it would be of interest to follow up this series of experiments with analysis at the protein level.

Additionally, it is believed that genes, which are co-regulated, may contain common promoter regions. Therefore, correlation Tables 4 to 6 which list genes that have similar expression profiles can be used in identification of regulatory elements. Since the mouse genome has been sequenced and software programs have the ability to detect regulatory motifs it is possible to get a better view of how the gene expression levels are being coordinated in response to HFD treatment. This analysis may highlight more detailed molecular mechanisms on gene expression control.

Another potential direction is to examine these large data sets using other normalization or microarray analysis procedures. At the current moment there is no defined protocol for the analysis. Therefore, the analysis method depends on the questions and answers that are of interest. Re-analysis of the data by different techniques would be interesting to determine the reproducibility, significance and weaknesses of the various methods. It is recognized that the particular methods that we have used for microarray analysis are not the only approaches available. Many alternative approaches are continually being developed and our data once published will be archived in an open access database, which could allow other scientists to examine our large data set.

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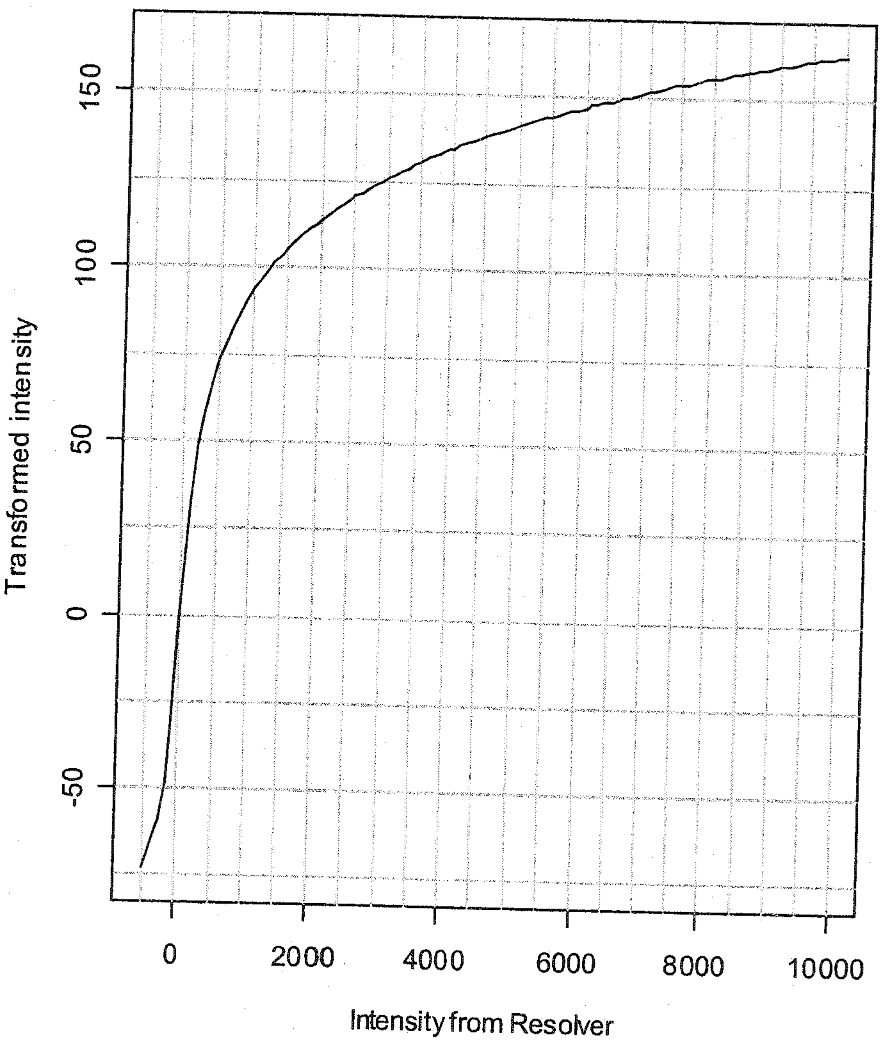
APPENDIX A

Variance stabilizing transformation



Normalization: transformation of data from Resolver scale of values ranging from 0 to 10 000 to transformed intensities of 0 to 160. The transformed values are on an additive scale.

APPENDIX B

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	WK08	pWK08	WK12	pWK12
160393_at		Mus musculus, clone IMAGE:4952607, mRNA	45.32	0.01	1.49	0.51	-5.24	0.03	-1.80	0.42	-8.15	0.00
104741_at		ESTs, Highly similar to T47144 hypothetical protein DKFZp761E1347.1 - human (fragment) [H.sapiens]	61.95	0.01	3.51	0.11	-2.12	0.32	2.43	0.26	7.94	0.00
102368_at		Mus musculus, Similar to hypothetical protein dJ122O8.2, clone MGC:41400 IMAGE:1446940, mRNA, complete cds	18.08	0.00	2.05	0.16	0.41	0.77	2.03	0.16	6.88	0.00
97115_at		ESTs, Moderately similar to S12207 hypothetical protein (B2 element) - mouse [M.musulus]	33.04	0.00	-4.41	0.07	-3.59	0.14	-7.48	0.00	-7.82	0.00
103733_at		ESTs	32.63	0.02	1.83	0.43	-0.93	0.68	-4.79	0.05	7.53	0.00
161050_at		ESTs	12.42	0.00	-5.02	0.47	-29.46	0.00	-0.81	0.91	11.18	0.11
96965_at			-18.16	0.01	-1.05	0.61	-8.12	0.00	1.03	0.62	-1.58	0.44
160316_at		Mus musculus, clone IMAGE:5039804, mRNA	37.39	0.01	1.33	0.50	3.15	0.12	-4.17	0.04	-6.15	0.01
97162_at		ESTs	1.82	0.01	-1.40	0.44	-6.92	0.00	-0.67	0.63	2.56	0.18
94048_at		Mus musculus, Similar to KIAA0677 gene product, clone MGC:28562 IMAGE:4207552, mRNA, complete cds	57.56	0.00	-4.58	0.14	-8.50	0.01	-10.91	0.00	-0.07	0.98
95575_r_at		Mus musculus, clone IMAGE:5037053, mRNA, partial cds	15.78	0.00	-0.80	0.82	-14.28	0.00	3.13	0.37	9.86	0.01
94261_at		UI-1-CF0-alw-a-07-0-UI.s1 Mus musculus cDNA, 3' end	56.38	0.02	-1.47	0.53	-8.75	0.00	-1.64	0.49	-2.43	0.31
102575_at			16.56	0.01	-4.67	0.27	6.07	0.15	14.89	0.00	-1.17	0.78
161107_r_at		ESTs, Weakly similar to W01A11.2.p [Caenorhabditis elegans] [C.elegans]	1.44	0.01	1.70	0.20	0.02	0.98	0.22	0.87	5.12	0.00
95385_at		ESTs	29.79	0.01	-5.44	0.00	3.21	0.06	-0.04	0.98	2.13	0.19
99849_at			126.21	0.01	2.20	0.36	0.82	0.73	-1.92	0.42	-10.08	0.00
103703_f_at		Mus musculus cDNA fis, clone TRACH2000665, moderately similar to Rattus norvegicus mRNA for putative integral membrane transport protein (UST1r)	98.42	0.01	-3.64	0.15	-5.31	0.04	-5.95	0.02	-6.33	0.02
101287_s_at			139.64	0.01	1.70	0.19	2.52	0.06	-0.62	0.62	4.09	0.00
100323_at			24.06	0.00	7.33	0.01	2.63	0.33	4.61	0.10	-8.67	0.00
96594_at		ESTs	66.06	0.00	-0.01	1.00	7.46	0.00	3.46	0.02	-2.14	0.15
99406_at			6.52	0.01	-4.80	0.05	8.09	0.00	-2.16	0.34	-2.51	0.27
102102_at		ESTs, Highly similar to POL2_MOUSE Retrovirus-related POL polyprotein [Contains: Reverse transcriptase ; Endonuclease] [M.musulus]	14.52	0.00	1.76	0.32	3.65	0.05	3.87	0.04	-7.29	0.00

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
97710_f_at		ESTs, Highly similar to S12207 hypothetical protein (B2 element) - mouse [M.musulus]	16.33	0.02	0.24	0.91	-5.35	0.02	6.55	0.01	-0.96	0.66
160252_at		Mus musculus, Similar to clathrin, heavy polypeptide (Hc), clone IMAGE:5369419, mRNA	80.88	0.00	-1.44	0.36	-6.61	0.00	-5.53	0.00	5.65	0.00
93488_at		Mus musculus, Similar to hypothetical protein FLJ10534, clone MGC:28320 IMAGE:4014819, mRNA, complete cds	21.55	0.00	5.25	0.08	6.12	0.05	3.91	0.19	-10.01	0.00
162317_r_at		EST, Weakly similar to RS12_MOUSE 40S RIBOSOMAL PROTEIN S12 [M.musulus]	27.56	0.00	-4.48	0.23	-4.95	0.18	1.78	0.62	-15.49	0.00
97088_at		ESTs, Weakly similar to C53B4.2.p [Caenorhabditis elegans] [C.elegans]	-7.37	0.01	4.06	0.13	6.56	0.02	7.01	0.01	-2.74	0.30
100754_at			0.52	0.01	-2.30	0.45	6.88	0.03	3.45	0.26	-9.34	0.01
103312_f_at		Mus musculus, clone MGC:41415 IMAGE:1529010, mRNA, complete cds	28.09	0.00	-3.00	0.13	-1.38	0.47	3.45	0.08	-7.73	0.00
99913_at			29.37	0.02	-10.36	0.03	4.27	0.33	-12.68	0.01	-3.01	0.49
162132_f_at		ESTs, Weakly similar to MAF2_MOUSE TRANSCRIPTION FACTOR MAF2 (PROTO-ONCOGENE C-MAF) [M.musulus]	-1.61	0.00	-2.58	0.01	-0.49	0.58	0.23	0.79	-3.30	0.00
101664_at			114.72	0.01	-1.15	0.42	-1.59	0.27	2.29	0.12	-5.61	0.00
94262_at		UI-1-CF0-alw-a-07-0-UI.s1 Mus musculus cDNA, 3' end	-10.13	0.00	7.56	0.13	-21.00	0.00	-6.90	0.16	2.81	0.56
97751_f_at		ESTs, Moderately similar to G3P_MOUSE Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) [M.musulus]	85.84	0.01	-2.72	0.55	10.63	0.03	6.37	0.17	13.61	0.01
98321_at			-7.05	0.02	-1.90	0.47	5.52	0.05	-8.30	0.01	2.82	0.29
97178_at			34.50	0.00	-11.25	0.02	-11.96	0.02	-13.93	0.01	-6.65	0.16
101614_at		ESTs	4.48	0.00	-1.54	0.19	4.27	0.00	-1.82	0.13	-2.49	0.04
99501_at		Mus musculus, Similar to translocation protein 1, clone IMAGE:5347105, mRNA, partial cds	34.77	0.01	13.26	0.05	-1.48	0.82	6.58	0.32	-22.73	0.00
96789_i_at		Mus musculus, Similar to hypothetical protein BC014916, clone MGC:36399 IMAGE:5135570, mRNA, complete cds	59.47	0.01	4.00	0.02	0.48	0.75	-0.72	0.64	5.37	0.00
97598_at			7.23	0.02	-7.12	0.02	-0.98	0.72	-7.16	0.02	-3.38	0.22
93409_at		ESTs	22.40	0.01	-6.68	0.24	-22.89	0.00	-2.21	0.69	-4.94	0.38
160983_at		ESTs	18.36	0.01	-11.87	0.00	9.80	0.01	1.26	0.72	-2.45	0.49
104643_at		Mus musculus, clone IMAGE:3963643, mRNA, partial cds	49.63	0.01	7.59	0.00	-0.71	0.71	-2.50	0.20	3.18	0.11
104419_at		Mus musculus, clone IMAGE:5101040, mRNA, partial cds	36.09	0.01	3.19	0.20	7.28	0.01	4.01	0.11	-4.41	0.08
96424_at			13.35	0.00	-5.22	0.05	-0.75	0.77	-7.38	0.01	-8.04	0.00
94106_at		ESTs	33.36	0.01	-3.51	0.06	-4.57	0.02	-3.69	0.05	2.21	0.21
101768_at			-3.36	0.02	3.29	0.02	-2.01	0.14	2.28	0.09	-2.65	0.06

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
102647_g_at		Mus musculus cDNA fis, clone TRACH2017498	36.75	0.00	2.04	0.23	-6.35	0.00	-2.58	0.14	4.26	0.02
95587_at		ESTs, Moderately similar to hypothetical protein FLJ13448 [Homo sapiens] [H.sapiens]	45.93	0.02	-1.05	0.61	-7.30	0.00	-2.69	0.20	2.28	0.28
103845_at		Mus musculus, RIKEN cDNA 4930445G01 gene, clone MGC:28108 IMAGE:3968084, mRNA, complete cds	70.16	0.02	5.03	0.02	-2.35	0.26	0.87	0.67	5.87	0.01
103303_at		ESTs	15.07	0.01	4.70	0.01	3.02	0.10	4.31	0.02	-1.89	0.29
101157_at			-1.84	0.01	1.66	0.49	-5.61	0.03	5.64	0.03	7.06	0.01
160990_r_at		Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:1700009J18:intercellular adhesion molecule, full insert sequence	22.17	0.01	6.40	0.02	0.75	0.76	4.49	0.08	-6.95	0.01
160682_at		UI-1-CF0-aml-d-08-0-UI.s1 Mus musculus cDNA, 3' end	52.33	0.00	11.83	0.00	5.17	0.11	-0.87	0.78	9.25	0.01
160697_at		Mus musculus, clone IMAGE:4982645, mRNA, partial cds	51.36	0.01	2.37	0.53	-13.03	0.00	-3.40	0.36	8.04	0.04
102645_at		ESTs	20.51	0.01	6.55	0.01	-2.86	0.25	2.05	0.40	-6.27	0.02
101204_at		EST	-25.47	0.01	5.14	0.09	1.96	0.51	6.07	0.05	10.52	0.00
95978_at		ESTs, Weakly similar to ATY1_MOUSE Probable cation-transporting ATPase 1 [M.musulus]	27.15	0.00	2.09	0.07	3.91	0.00	2.70	0.02	-1.85	0.10
93752_at		Mus musculus, clone IMAGE:3491909, mRNA, partial cds	49.19	0.01	1.48	0.29	3.91	0.01	1.23	0.37	-3.92	0.01
103211_at		ESTs, Weakly similar to beta-transducin [Caenorhabditis elegans] [C.elegans]	47.34	0.00	-6.17	0.05	-4.88	0.11	-4.00	0.19	-10.78	0.00
102171_r_at		Mus musculus, clone MGC:46897 IMAGE:5052215, mRNA, complete cds	73.17	0.01	-0.42	0.87	1.81	0.49	0.06	0.98	11.43	0.00
160313_at		Mus musculus, clone IMAGE:4460274, mRNA, partial cds	35.01	0.00	1.78	0.52	2.50	0.37	0.03	0.99	-14.20	0.00
100389_at		ESTs, Highly similar to COLQ_MOUSE Acetylcholinesterase collagenic tail peptide (AChE Q subunit) (Acetylcholinesterase-associated collagen) [M.musulus]	33.34	0.01	-3.77	0.39	6.43	0.15	-12.87	0.01	-8.89	0.05
103702_i_at		Mus musculus cDNA fis, clone TRACH2000665, moderately similar to Rattus norvegicus mRNA for putative integral membrane transport protein (UST1r)	90.43	0.00	-4.44	0.04	-2.06	0.32	-3.67	0.09	-10.94	0.00
94423_at		Mus musculus, Similar to hypothetical protein from clone 643, clone MGC:7903 IMAGE:3582955, mRNA, complete cds	36.20	0.00	5.94	0.05	-8.32	0.01	-3.49	0.23	9.28	0.00
104351_at		Mus musculus, clone IMAGE:5369808, mRNA	26.48	0.00	1.96	0.48	11.87	0.00	7.78	0.01	3.02	0.28

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
102233_at		Mus musculus, clone IMAGE:3500612, mRNA, partial cds	66.69	0.00	-5.93	0.18	-3.73	0.39	0.53	0.90	-25.53	0.00
93145_at		ESTs	12.23	0.01	1.65	0.38	-5.10	0.01	4.74	0.02	4.29	0.03
94415_at		ESTs	42.67	0.02	7.76	0.17	-0.75	0.89	1.78	0.75	-20.10	0.00
93143_at		Mus musculus, similar to Unknown (protein for MGC:17624), clone MGC:41566 IMAGE:1245153, mRNA, complete cds	38.40	0.01	-2.83	0.37	-12.01	0.00	2.87	0.37	5.11	0.12
96980_at			0.70	0.00	-8.43	0.00	-0.33	0.88	-6.95	0.00	-3.29	0.14
101307_at			105.43	0.00	-6.89	0.12	-1.09	0.80	-25.20	0.00	-13.60	0.00
161108_r_at		ESTs, Weakly similar to B39898 phospholipase A2 (EC 3.1.1.4), cytosolic - mouse [M.musulus]	10.15	0.01	-0.35	0.96	-21.09	0.00	7.50	0.26	17.90	0.01
160676_at		Mus musculus, clone IMAGE:2647796, mRNA	67.09	0.00	-2.22	0.34	-1.83	0.42	-8.34	0.00	-11.21	0.00
96178_at		ESTs, Weakly similar to T46608 zinc finger protein Png-1 - mouse [M.musulus]	30.36	0.02	6.37	0.02	6.99	0.01	-0.78	0.76	2.76	0.29
101118_at		ESTs	1.78	0.00	1.81	0.13	0.91	0.43	-4.14	0.00	3.94	0.00
161112_at		Mus musculus, Similar to hypothetical protein FLJ20509, clone IMAGE:3489119, mRNA, partial cds	31.29	0.00	-6.35	0.02	5.33	0.04	3.12	0.21	10.16	0.00
100295_at			29.03	0.00	-0.47	0.81	3.67	0.07	-3.24	0.11	7.58	0.00
104562_at		ESTs, Weakly similar to TC17_MOUSE Zinc finger protein 354A (Transcription factor 17) (Renal transcription factor Kid-1) (Kidney, ischemia, and developmentally regulated protein-1) [M.musulus]	22.37	0.02	0.46	0.84	2.40	0.30	-1.50	0.51	8.46	0.00
99699_at		Mus musculus murine retrovirus readthrough RNA sequence	-8.53	0.00	-1.72	0.39	0.95	0.63	3.93	0.06	7.94	0.00
102807_at		ESTs, Weakly similar to S42578 gene prune protein - fruit fly (Drosophila melanogaster) [D.melanogaster]	39.55	0.02	-4.25	0.06	1.82	0.40	-3.80	0.09	5.94	0.01
101633_at			25.40	0.01	0.88	0.81	0.63	0.86	-3.63	0.33	-14.95	0.00
103055_r_at			59.30	0.00	-14.50	0.00	-2.49	0.40	-12.11	0.00	-8.20	0.01
95182_at		EST	-6.72	0.02	3.45	0.08	2.52	0.20	-2.36	0.23	5.75	0.01
102165_at			34.50	0.01	-3.53	0.06	4.48	0.02	-3.26	0.08	-2.77	0.13
162310_r_at		ESTs, Weakly similar to JN0533 finger protein pMLZ-4 - mouse [M.musulus]	-17.21	0.02	11.82	0.00	-2.82	0.43	-3.04	0.40	6.22	0.09
161498_at		EST, Moderately similar to ribosomal protein L23 [Mus musculus] [M.musulus]	52.37	0.01	-4.86	0.07	-1.07	0.68	-2.23	0.39	-9.63	0.00
162038_f_at		Mus musculus, Similar to hypothetical protein BC014916, clone MGC:36399 IMAGE:5135570, mRNA, complete cds	28.75	0.00	8.82	0.00	0.73	0.78	-6.22	0.03	6.54	0.02

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
100681_f_at			-2.36	0.03	-0.68	0.72	-6.62	0.00	-2.57	0.19	-0.12	0.95
95028_r_at		ESTs	40.55	0.05	-0.87	0.69	-1.23	0.57	-0.91	0.68	-7.21	0.00
161083_at		ESTs, Weakly similar to T17365 serine/threonine protein kinase TAO1 - rat [R.norvegicus]	11.91	0.03	2.26	0.24	-0.29	0.88	-3.86	0.05	5.43	0.01
160783_at		Mus musculus, Similar to KIAA0831 protein, clone IMAGE:4950756, mRNA, partial cds	40.05	0.03	1.80	0.35	3.56	0.07	5.59	0.01	-1.52	0.42
101152_at			36.87	0.02	0.43	0.91	14.23	0.00	-2.88	0.45	-1.39	0.71
92398_at		Mus musculus, Similar to hypothetical protein FLJ12750, clone MGC:25614 IMAGE:4163734, mRNA, complete cds	16.73	0.02	7.89	0.01	-2.05	0.42	-2.83	0.27	4.36	0.10
102965_at		Mus musculus, clone IMAGE:4168084, mRNA	44.71	0.04	3.11	0.18	3.98	0.09	5.91	0.02	1.70	0.45
161710_r_at		Mus musculus, clone IMAGE:3708675, mRNA, partial cds	6.61	0.04	-2.50	0.04	0.40	0.73	-2.16	0.07	2.42	0.05
102196_at			20.85	0.02	5.31	0.08	-3.23	0.28	-1.08	0.71	9.31	0.00
93183_at		Mus musculus, Similar to CDC91 cell division cycle 91-like 1 (S. cerevisiae), clone IMAGE:5374066, mRNA, partial cds	30.68	0.05	3.21	0.25	-1.53	0.58	3.20	0.25	8.08	0.01
94477_at		Mus musculus, clone MGC:6827 IMAGE:2649084, mRNA, complete cds	17.72	0.02	0.66	0.80	2.68	0.31	2.19	0.40	-9.28	0.00
97004_at			57.52	0.05	-6.82	0.04	0.86	0.79	-6.11	0.07	5.86	0.08
161764_r_at		ESTs	-0.21	0.05	-2.59	0.02	-1.04	0.30	-1.50	0.15	-1.23	0.23
100889_at		ESTs, Weakly similar to T17286 hypothetical protein DKFZp434H0350.1 - human (fragment) [H.sapiens]	27.50	0.05	2.85	0.40	-6.98	0.05	0.02	0.99	8.66	0.02
102646_at		Mus musculus cDNA fis, clone TRACH2017498	20.81	0.05	2.90	0.08	-4.41	0.01	0.71	0.66	0.97	0.55
103767_f_at		ESTs	-14.45	0.04	7.97	0.05	8.01	0.05	7.49	0.07	2.75	0.48
160379_at		Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310065B16:erythrocyte protein band 4.1, full insert sequence	38.71	0.03	2.62	0.33	-0.70	0.79	2.68	0.31	-8.57	0.00
97960_at		ESTs, Weakly similar to ubiquitin specific protease 8; putative deubiquitinating enzyme [Mus musculus] [M.musulus]	10.08	0.03	2.56	0.25	3.78	0.10	-1.95	0.38	6.11	0.01
95184_f_at			15.83	0.05	-4.25	0.02	-2.14	0.22	0.04	0.98	-3.42	0.06
104034_at		Mus musculus, clone IMAGE:4973354, mRNA	37.70	0.03	8.07	0.01	0.87	0.74	5.56	0.05	0.09	0.97
97572_at			32.50	0.05	-7.19	0.03	4.47	0.16	-6.45	0.05	0.60	0.85
97009_f_at			-0.22	0.03	7.94	0.01	4.81	0.11	1.27	0.66	-4.21	0.15
100415_at			6.04	0.05	-3.19	0.06	-3.57	0.04	0.67	0.68	2.59	0.12

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
104434_at		Mus musculus, clone IMAGE:3588380, mRNA, partial cds	52.01	0.03	-2.25	0.20	-3.84	0.04	-4.25	0.02	0.36	0.83
97647_at			115.41	0.03	-3.85	0.17	-8.00	0.01	0.28	0.92	-4.39	0.12
101298_g_at			-1.72	0.05	1.43	0.43	-1.88	0.30	1.31	0.47	-5.45	0.01
101877_at		Mus musculus, RIKEN cDNA 4930445G01 gene, clone MGC:28108 IMAGE:3968084, mRNA, complete cds	85.65	0.05	1.87	0.07	0.82	0.41	1.60	0.11	-2.09	0.04
160966_at		ESTs	38.33	0.05	-1.70	0.35	-1.01	0.58	-2.53	0.17	-5.26	0.01
104032_at		Mus musculus, clone MGC:37981 IMAGE:5137303, mRNA, complete cds	17.36	0.05	8.56	0.16	-12.24	0.05	12.69	0.04	-3.80	0.52
96191_at		Mus musculus, clone IMAGE:5037434, mRNA, partial cds	63.89	0.05	2.80	0.01	-0.06	0.96	-1.46	0.17	-1.56	0.14
95882_at		EST	-6.15	0.02	-3.78	0.02	-0.77	0.62	2.30	0.15	3.77	0.02
161769_r_at		EST	39.39	0.04	-14.74	0.01	6.96	0.17	-4.27	0.40	3.86	0.44
102144_f_at		EST	10.11	0.02	2.54	0.11	0.43	0.78	0.73	0.64	-5.22	0.00
101716_at			2.23	0.02	-3.37	0.01	0.70	0.54	1.27	0.28	-2.36	0.05
160539_at		M.musculus ASF mRNA	14.81	0.04	3.42	0.15	4.07	0.09	0.51	0.82	-5.85	0.02
99574_at		ESTs, Weakly similar to RN12_MOUSE RING finger protein 12 (LIM domain interacting RING finger protein) (RING finger LIM domain-binding protein) (R-LIM) [M.musulus]	41.66	0.04	1.02	0.68	-4.30	0.09	-5.40	0.04	-4.92	0.06
97010_at			-5.39	0.02	-3.56	0.56	13.88	0.03	-2.70	0.66	-17.74	0.01
97739_at			-3.75	0.02	2.84	0.11	2.04	0.24	1.62	0.34	-5.12	0.01
100965_at		ESTs	40.36	0.04	-8.71	0.01	-4.79	0.13	-3.60	0.25	0.13	0.97
161581_r_at		Mus musculus, Similar to MBD2 (methyl-CpG-binding protein)-interacting zinc finger protein, clone MGC:27746 IMAGE:2651006, mRNA, complete cds	9.79	0.04	-5.81	0.01	1.53	0.48	-2.38	0.27	-3.58	0.11
101735_f_at			68.42	0.04	4.39	0.42	-3.15	0.56	13.57	0.02	-11.60	0.04
95856_at		ESTs	0.71	0.02	-0.65	0.66	-2.71	0.08	-1.89	0.21	-4.54	0.01
97835_at		Mus musculus, Similar to RIKEN cDNA 0610007L05 gene, clone MGC:18838 IMAGE:4212222, mRNA, complete cds	124.38	0.04	2.44	0.27	3.00	0.18	-0.82	0.71	6.50	0.01
95069_at		Mus musculus, clone IMAGE:5355658, mRNA	35.19	0.04	4.72	0.09	-6.91	0.02	0.35	0.90	3.75	0.17
101409_at		Mus musculus, Similar to ligatin, clone IMAGE:4982955, mRNA, partial cds	29.03	0.04	3.88	0.04	-0.80	0.65	0.56	0.75	4.74	0.01
104450_at			-2.29	0.04	12.75	0.01	4.02	0.35	-3.90	0.36	-5.31	0.22
162466_at		Mus musculus, clone MGC:41303 IMAGE:3371464, mRNA, complete cds	21.97	0.04	-1.69	0.71	-6.23	0.17	2.76	0.54	-14.28	0.00
103756_at		ESTs, Moderately similar to hypothetical protein FLJ20979 [Homo sapiens] [H.sapiens]	25.23	0.02	3.34	0.16	-3.06	0.19	6.78	0.01	2.67	0.25

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
103988_at		Mus musculus, clone IMAGE:4219507, mRNA, partial cds	34.07	0.02	3.99	0.25	-6.12	0.08	-10.24	0.01	-1.55	0.65
100350_at		ESTs, Moderately similar to RIKEN cDNA 5730493B19 [Mus musculus] [M.musulus]	-3.54	0.02	-3.63	0.06	-4.30	0.03	-2.76	0.14	-3.18	0.10
160105_r_at		ESTs, Weakly similar to mitochondrial translational release factor 1 [Homo sapiens] [H.sapiens]	19.40	0.05	0.46	0.87	-4.96	0.11	3.55	0.24	8.05	0.01
92208_at		Mus musculus, Similar to hypothetical protein FLJ22569, clone MGC:41153 IMAGE:1434214, mRNA, complete cds	0.41	0.02	-0.51	0.86	-11.16	0.00	-0.59	0.84	-0.46	0.88
101330_f_at			2.94	0.05	-2.39	0.30	4.70	0.05	-0.73	0.75	-5.59	0.02
95904_at		ESTs, Weakly similar to T31613 hypothetical protein Y50E8A.i - Caenorhabditis elegans [C.elegans]	16.28	0.04	-4.60	0.09	7.56	0.01	2.35	0.37	0.21	0.94
95901_f_at		ESTs	26.76	0.02	0.05	0.98	2.01	0.43	2.20	0.38	-8.93	0.00
103308_at		Mus musculus, clone MGC:30866 IMAGE:4010593, mRNA, complete cds	40.56	0.02	-2.18	0.47	2.40	0.42	-0.01	1.00	-10.93	0.00
97422_at		Mus musculus, clone IMAGE:3982770, mRNA, partial cds	46.31	0.02	5.45	0.01	-3.13	0.09	-2.36	0.20	0.50	0.78
102211_r_at		UI-M-FI0-byr-j-10-0-UI.r1 Mus musculus cDNA, 5' end	5.26	0.04	-2.13	0.10	-1.48	0.24	-1.05	0.41	-3.38	0.01
100327_at			7.29	0.04	0.72	0.83	11.75	0.00	-1.29	0.70	-0.17	0.96
101336_at			-11.96	0.04	-6.82	0.11	-3.02	0.47	0.19	0.96	12.61	0.01
99804_at			10.48	0.04	-6.40	0.02	-1.39	0.57	3.93	0.12	3.77	0.13
104120_at		Mus musculus, similar to Unknown (protein for IMAGE:2907119), clone MGC:41405 IMAGE:1493971, mRNA, complete cds	46.96	0.03	-3.84	0.02	2.83	0.07	-1.92	0.21	-2.06	0.18
102553_at			4.75	0.05	1.40	0.75	-10.04	0.03	6.55	0.14	8.26	0.07
92654_at		ESTs, Weakly similar to RPA1_MOUSE DNA-directed RNA polymerase I largest subunit (RNA polymerase I 194 kDa subunit) (RPA194) [M.musulus]	4.39	0.03	4.72	0.08	-4.74	0.07	-0.75	0.77	6.27	0.02
99987_at		ESTs, Weakly similar to ZFP2_MOUSE Zinc finger protein 2 (Zfp-2) (mKR2 protein) [M.musulus]	7.19	0.03	-1.82	0.45	-5.90	0.02	-5.66	0.03	-2.47	0.30
103752_r_at		ESTs	10.77	0.02	1.79	0.50	8.66	0.00	-1.68	0.53	-4.89	0.08
98346_at		ESTs, Weakly similar to JG0193 G protein-coupled receptor FEX - mouse [M.musulus]	40.53	0.02	1.02	0.79	12.97	0.00	5.40	0.17	5.20	0.19
101326_at			3.08	0.05	1.91	0.39	-1.95	0.38	-5.38	0.02	-4.38	0.06
96485_at		ESTs	-5.46	0.03	7.01	0.06	3.95	0.28	8.48	0.03	6.43	0.09

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
101942_at		Mus musculus, clone IMAGE:3986304, mRNA, partial cds	21.86	0.02	2.37	0.43	3.49	0.25	10.23	0.00	3.37	0.27
93235_at		Mus musculus, clone IMAGE:3964696, mRNA, partial cds	21.16	0.03	6.17	0.01	2.60	0.27	3.14	0.18	4.08	0.09
104651_at		ESTs, Highly similar to SNXE_HUMAN Sorting nexin 14 [H.sapiens]	15.89	0.02	7.08	0.01	-3.90	0.11	4.04	0.10	0.80	0.73
94159_at			17.57	0.03	-8.95	0.01	-2.07	0.54	-7.93	0.03	-0.04	0.99
95914_at		ESTs, Weakly similar to E29149 proline-rich protein - mouse [M.musulus]	10.95	0.03	1.81	0.24	-1.29	0.39	0.54	0.72	-5.02	0.00
92182_at		ESTs, Weakly similar to Rap2 interacting protein; Rap2 interacting protein 8 [Mus musculus] [M.musulus]	14.90	0.05	4.10	0.02	-2.61	0.13	-1.02	0.54	2.74	0.11
96971_f_at			9.71	0.05	1.34	0.63	1.55	0.58	5.81	0.05	7.04	0.02
94823_at		Mus musculus, ribosomal protein L23a, clone IMAGE:4988735, mRNA, partial cds	104.05	0.03	-4.52	0.10	-6.73	0.02	-0.38	0.88	-4.98	0.07
96977_at			-2.90	0.05	-5.24	0.03	-0.02	0.99	-5.11	0.03	0.74	0.73
99364_at		Mus musculus, similar to hypothetical brain protein my038, clone MGC:32263 IMAGE:5011450, mRNA, complete cds	2.30	0.03	2.72	0.06	4.07	0.01	0.45	0.75	0.99	0.48
161085_r_at		ESTs, Moderately similar to Gb3 synthase [Rattus norvegicus] [R.norvegicus]	38.10	0.03	0.63	0.84	-7.59	0.02	-0.85	0.78	8.13	0.01
95128_at		Mus musculus, clone IMAGE:3966453, mRNA, partial cds	36.70	0.02	4.53	0.01	-1.65	0.31	0.34	0.83	3.96	0.02
102253_at		Mus musculus clone L2 uniform group of 2-cell-stage gene family mRNA, complete cds	-14.47	0.03	-0.86	0.82	0.15	0.97	9.91	0.02	9.51	0.02
102050_at		UI-1-CF0-axi-g-02-0-UI.s1 Mus musculus cDNA, 3' end	-5.12	0.03	-6.65	0.01	-3.25	0.14	-2.28	0.30	-1.59	0.46
92293_at		ESTs, Weakly similar to T42718 probable neural cell adhesion molecule L1 precursor - mouse [M.musulus]	-6.82	0.05	2.39	0.03	-1.75	0.11	-0.56	0.60	1.90	0.08
101822_at			-15.88	0.03	-0.28	0.93	-10.49	0.00	-3.59	0.25	-1.09	0.72
95000_g_at		Mus Musculus mRNA for hypothetical protein	8.58	0.03	-2.11	0.25	4.96	0.01	-0.63	0.72	3.58	0.06
97543_at	02-Sep	septin 2	49.46	0.02	3.12	0.02	2.37	0.06	0.27	0.82	-2.82	0.03
104617_at	0610005C13Rik	RIKEN cDNA 0610005C13 gene	78.54	0.01	4.96	0.08	0.28	0.92	8.82	0.00	5.17	0.07
97318_at	0610006H08Rik	RIKEN cDNA 0610006H08 gene	25.54	0.03	1.93	0.19	-2.34	0.11	3.65	0.02	-1.95	0.18
95725_at	0610006H10Rik	RIKEN cDNA 0610006H10 gene	60.09	0.00	8.33	0.00	3.34	0.12	3.72	0.08	6.57	0.00
93743_at	0610007A03Rik	RIKEN cDNA 0610007A03 gene	35.00	0.03	6.51	0.03	-1.59	0.58	5.98	0.05	5.29	0.08
160271_at	0610007C21Rik	RIKEN cDNA 0610007C21 gene	67.25	0.01	-0.71	0.75	-7.31	0.00	1.36	0.55	7.07	0.01

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
96653_at	0610007O07Rik	RIKEN cDNA 0610007O07 gene	99.33	0.05	0.26	0.79	-0.30	0.76	2.87	0.01	1.72	0.09
160349_at	0610010E05Rik	RIKEN cDNA 0610010E05 gene	34.14	0.02	-0.44	0.80	-3.66	0.04	1.49	0.39	5.58	0.00
97268_i_at	0610010I12Rik	RIKEN cDNA 0610010I12 gene	83.85	0.03	-1.63	0.30	-2.03	0.20	4.83	0.01	0.96	0.53
162280_f_at	0610011B04Rik	RIKEN cDNA 0610011B04 gene	-7.03	0.01	-3.35	0.01	-1.44	0.22	2.92	0.02	-0.34	0.77
98959_at	0610016J10Rik	RIKEN cDNA 0610016J10 gene	26.71	0.04	-1.10	0.49	-1.46	0.36	-4.13	0.02	3.20	0.06
96670_at	0610025I19Rik	RIKEN cDNA 0610025I19 gene	89.79	0.00	3.19	0.20	5.72	0.03	3.96	0.11	8.41	0.00
96069_at	0610025K21Rik	RIKEN cDNA 0610025K21 gene	94.16	0.01	1.33	0.59	-5.42	0.04	-3.77	0.14	8.06	0.00
95660_at	0610025L15Rik	RIKEN cDNA 0610025L15 gene	89.12	0.00	-17.38	0.00	-16.11	0.00	-21.99	0.00	-9.24	0.01
94047_at	0610031J06Rik	RIKEN cDNA 0610031J06 gene	71.91	0.03	0.23	0.92	-3.37	0.16	2.66	0.26	7.36	0.00
93531_at	0610033L03Rik	RIKEN cDNA 0610033L03 gene	78.15	0.00	-2.14	0.52	-2.62	0.43	2.30	0.49	15.15	0.00
161243_f_at	0910001L24Rik	RIKEN cDNA 0910001L24 gene	-12.93	0.03	-0.41	0.93	-5.23	0.27	6.82	0.16	14.36	0.01
93786_i_at	1010001C05Rik	RIKEN cDNA 1010001C05 gene	56.58	0.01	2.56	0.27	0.28	0.90	4.42	0.07	-8.96	0.00
94455_at	1010001J12Rik	RIKEN cDNA 1010001J12 gene	21.84	0.00	-1.31	0.50	7.38	0.00	4.69	0.02	4.97	0.02
96321_at	1010001N11Rik	RIKEN cDNA 1010001N11 gene	91.92	0.00	-0.88	0.54	-1.03	0.48	-2.16	0.15	6.50	0.00
96308_r_at	1100001I22Rik	RIKEN cDNA 1100001I22 gene	-30.10	0.03	-18.43	0.02	19.63	0.02	-0.80	0.92	-4.17	0.58
98061_at	1110001K21Rik	RIKEN cDNA 1110001K21 gene	36.96	0.00	4.72	0.00	0.69	0.60	-0.09	0.95	7.85	0.00
96685_at	1110002E23Rik	RIKEN cDNA 1110002E23 gene	30.44	0.05	1.79	0.46	0.43	0.86	6.93	0.01	4.15	0.10
160240_at	1110003E01Rik	RIKEN cDNA 1110003E01 gene	75.71	0.00	2.16	0.10	3.65	0.01	3.99	0.00	-0.36	0.77
96716_at	1110003E01Rik	RIKEN cDNA 1110003E01 gene	77.53	0.00	4.25	0.03	7.48	0.00	5.57	0.01	-1.05	0.57
95091_at	1110003H02Rik	RIKEN cDNA 1110003H02 gene	58.55	0.00	4.72	0.02	2.17	0.28	7.26	0.00	6.95	0.00
93805_at	1110003H09Rik	RIKEN cDNA 1110003H09 gene	38.62	0.01	2.46	0.42	-9.51	0.01	-2.80	0.36	9.17	0.01
98037_at	1110003H18Rik	RIKEN cDNA 1110003H18 gene	49.73	0.02	-0.95	0.48	3.96	0.01	2.62	0.06	1.27	0.34
104042_at	1110003M08Rik	RIKEN cDNA 1110003M08 gene	41.12	0.00	3.21	0.23	-9.65	0.00	5.62	0.04	4.67	0.09
97204_s_at	1110003P16Rik	RIKEN cDNA 1110003P16 gene	18.03	0.05	-3.10	0.29	-9.16	0.00	-0.12	0.97	0.95	0.74

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
92806_at	1110004D19Rik	RIKEN cDNA 1110004D19 gene	40.16	0.03	0.28	0.89	6.51	0.01	0.67	0.75	4.18	0.06
95657_f_at	1110004G16Rik	RIKEN cDNA 1110004G16 gene	39.99	0.01	2.58	0.30	2.26	0.36	-5.54	0.03	-7.68	0.01
161489_r_at	1110006I15Rik	RIKEN cDNA 1110006I15 gene	-0.28	0.05	4.85	0.02	-0.10	0.96	-0.52	0.78	3.93	0.04
104245_at	1110007I12Rik	RIKEN cDNA 1110007I12 gene	46.39	0.04	-7.32	0.00	0.69	0.74	0.22	0.92	-0.13	0.95
160703_at	1110008P04Rik	RIKEN cDNA 1110008P04 gene	-3.40	0.05	10.11	0.18	-15.97	0.04	4.05	0.58	15.31	0.05
94290_at	1110012J22Rik	RIKEN cDNA 1110012J22 gene	40.55	0.00	1.90	0.32	-4.00	0.05	-1.33	0.49	9.83	0.00
97305_at	1110017C15Rik	RIKEN cDNA 1110017C15 gene	34.56	0.02	3.92	0.74	42.70	0.00	0.01	1.00	-18.83	0.13
103739_at	1110017N23Rik	RIKEN cDNA 1110017N23 gene	29.31	0.02	-0.22	0.90	-5.76	0.00	-2.17	0.22	-1.92	0.27
161830_f_at	1110018O12Rik	RIKEN cDNA 1110018O12 gene	28.70	0.01	-16.40	0.01	-18.98	0.00	-3.20	0.59	1.62	0.78
96151_at	1110018O12Rik	RIKEN cDNA 1110018O12 gene	42.25	0.04	-3.41	0.27	-7.99	0.02	-1.55	0.61	-5.60	0.08
95592_at	1110019N10Rik	RIKEN cDNA 1110019N10 gene	40.69	0.01	-0.24	0.91	-5.97	0.01	-4.60	0.04	-4.66	0.04
97919_at	1110021E09Rik	RIKEN cDNA 1110021E09 gene	20.92	0.00	2.04	0.07	2.97	0.01	-0.71	0.51	-4.04	0.00
103848_at	1110025F07Rik	RIKEN cDNA 1110025F07 gene	14.62	0.02	5.35	0.03	5.49	0.03	-0.89	0.71	-5.42	0.03
160376_at	1110029F20Rik	RIKEN cDNA 1110029F20 gene	87.11	0.01	10.97	0.01	7.72	0.04	8.51	0.03	4.38	0.23
95690_at	1110030L07Rik	RIKEN cDNA 1110030L07 gene	66.61	0.04	-1.05	0.64	-3.87	0.10	-3.61	0.12	5.57	0.02
160309_at	1110030N06Rik	RIKEN cDNA 1110030N06 gene	49.01	0.03	-4.08	0.29	-12.47	0.00	-4.74	0.22	-1.12	0.77
160834_at	1110032C13Rik	RIKEN cDNA 1110032C13 gene	8.63	0.04	0.75	0.88	2.30	0.64	1.70	0.73	-16.90	0.00
98149_s_at	1110033J19Rik	RIKEN cDNA 1110033J19 gene	33.05	0.01	-8.24	0.01	-4.55	0.15	-1.45	0.64	8.63	0.01
97527_at	1110038L14Rik	RIKEN cDNA 1110038L14 gene	34.34	0.00	-7.30	0.00	-7.15	0.00	-5.87	0.02	5.80	0.02
93054_at	1110054N06Rik	RIKEN cDNA 1110054N06 gene	37.98	0.00	9.37	0.00	2.22	0.43	2.29	0.41	9.21	0.00
93055_at	1110054N06Rik	RIKEN cDNA 1110054N06 gene	32.48	0.00	7.96	0.00	5.12	0.02	2.14	0.32	1.90	0.37
93056_g_at	1110054N06Rik	RIKEN cDNA 1110054N06 gene	28.84	0.00	9.87	0.00	-1.66	0.46	0.43	0.85	6.45	0.01
160197_at	1110058B13Rik	RIKEN cDNA 1110058B13 gene	29.75	0.01	4.23	0.12	-3.83	0.15	1.84	0.48	9.10	0.00
93496_at	1110059L23Rik	RIKEN cDNA 1110059L23 gene	99.83	0.04	0.19	0.98	12.47	0.05	-2.98	0.62	16.33	0.01

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
101053_at	1190003A07Rik	RIKEN cDNA 1190003A07 gene	61.19	0.02	0.38	0.90	-5.53	0.08	-4.03	0.19	-9.47	0.01
160322_at	1190006A08Rik	RIKEN cDNA 1190006A08 gene	67.18	0.00	0.21	0.88	7.53	0.00	2.00	0.17	0.63	0.66
104076_at	1190017O12Rik	RIKEN cDNA 1190017O12 gene	18.27	0.02	1.64	0.54	-9.51	0.00	3.33	0.22	-1.39	0.60
96708_at	1200002G13Rik	RIKEN cDNA 1200002G13 gene	45.41	0.02	-1.65	0.58	10.80	0.00	1.81	0.55	2.12	0.48
94548_at	1200003O06Rik	RIKEN cDNA 1200003O06 gene	76.70	0.02	0.43	0.84	-2.38	0.25	3.08	0.15	6.73	0.00
160151_i_at	1200009B18Rik	RIKEN cDNA 1200009B18 gene	13.26	0.00	0.21	0.88	-0.27	0.84	0.06	0.96	-6.70	0.00
160195_at	1200013P24Rik	RIKEN cDNA 1200013P24 gene	74.18	0.03	2.75	0.07	2.45	0.10	2.61	0.08	2.49	0.10
93270_at	1200014I03Rik	RIKEN cDNA 1200014I03 gene	38.35	0.00	1.49	0.09	-0.80	0.35	2.30	0.01	2.74	0.00
96672_at	1200015P04Rik	RIKEN cDNA 1200015P04 gene	73.80	0.03	5.65	0.10	1.53	0.65	1.31	0.69	-10.56	0.00
97485_at	1200015P13Rik	RIKEN cDNA 1200015P13 gene	87.88	0.03	2.66	0.18	3.74	0.07	3.81	0.06	3.94	0.05
160182_at	1210001E11Rik	RIKEN cDNA 1210001E11 gene	49.54	0.04	-1.46	0.61	-4.86	0.10	-1.84	0.52	-8.07	0.01
96890_at	1300002A08Rik	RIKEN cDNA 1300002A08 gene	97.96	0.00	4.38	0.00	3.65	0.01	6.39	0.00	5.69	0.00
93975_at	1300002F13Rik	RIKEN cDNA 1300002F13 gene	128.53	0.00	1.05	0.45	0.90	0.52	0.79	0.57	-6.40	0.00
93974_at	1300002F13Rik	RIKEN cDNA 1300002F13 gene	108.10	0.00	3.48	0.12	1.59	0.46	-0.10	0.96	-11.96	0.00
98154_at	1300004C11Rik	RIKEN cDNA 1300004C11 gene	17.55	0.02	3.27	0.23	-7.39	0.01	-6.67	0.02	-0.06	0.98
95702_at	1300006C19Rik	RIKEN cDNA 1300006C19 gene	54.07	0.01	-2.71	0.49	3.77	0.34	10.11	0.02	11.96	0.01
94540_at	1300006E06Rik	RIKEN cDNA 1300006E06 gene	135.29	0.01	1.01	0.52	2.59	0.11	-0.68	0.66	6.32	0.00
160799_at	1300007C21Rik	RIKEN cDNA 1300007C21 gene	79.92	0.00	16.59	0.02	11.59	0.10	17.11	0.02	-20.68	0.01
103562_f_at	1300007C21Rik	RIKEN cDNA 1300007C21 gene	70.88	0.00	12.25	0.02	12.91	0.02	8.23	0.11	-16.47	0.00
93327_at	1300011C24Rik	RIKEN cDNA 1300011C24 gene	13.98	0.00	6.46	0.00	-4.22	0.02	2.17	0.19	4.15	0.02
162014_i_at	1300011C24Rik	RIKEN cDNA 1300011C24 gene	92.43	0.02	-0.60	0.90	-2.47	0.61	-12.04	0.02	-13.22	0.01
104311_at	1300013G12Rik	RIKEN cDNA 1300013G12 gene	49.83	0.03	-2.78	0.28	4.13	0.12	-3.93	0.14	-7.11	0.01
104277_at	1300013N08Rik	RIKEN cDNA 1300013N08 gene	30.12	0.00	4.70	0.10	12.97	0.00	1.07	0.70	3.28	0.24
98049_at	1300018I05Rik	RIKEN cDNA 1300018I05 gene	31.37	0.01	3.36	0.09	-3.79	0.06	-1.40	0.46	6.24	0.00

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
104164_at	1300019N10Rik	RIKEN cDNA 1300019N10 gene	44.28	0.00	5.75	0.00	1.70	0.32	2.25	0.20	6.94	0.00
94807_at	1300019P08Rik	RIKEN cDNA 1300019P08 gene	87.43	0.00	-3.68	0.04	-1.47	0.38	-5.12	0.01	-4.25	0.02
93358_at	1500010B24Rik	RIKEN cDNA 1500010B24 gene	38.54	0.02	-3.77	0.04	-3.49	0.06	-1.44	0.41	-4.30	0.02
98953_at	1500010M16Rik	RIKEN cDNA 1500010M16 gene	50.94	0.00	0.98	0.36	2.01	0.07	3.60	0.00	-3.56	0.00
98610_at	1500012D08Rik	RIKEN cDNA 1500012D08 gene	39.60	0.03	0.23	0.93	-1.74	0.49	3.44	0.18	8.57	0.00
103524_at	1500015A01Rik	RIKEN cDNA 1500015A01 gene	10.69	0.00	8.07	0.01	1.03	0.71	7.33	0.01	6.29	0.03
98138_at	1500016H10Rik	RIKEN cDNA 1500016H10 gene	13.62	0.01	-2.09	0.34	-4.26	0.06	6.73	0.01	-3.99	0.07
96793_at	1500016M21Rik	RIKEN cDNA 1500016M21 gene	17.73	0.05	1.18	0.67	-1.48	0.59	-2.66	0.34	8.90	0.00
102312_r_at	1500034J01Rik	RIKEN cDNA 1500034J01 gene	22.21	0.05	7.05	0.03	-0.11	0.97	-6.49	0.05	4.30	0.17
96068_at	1500034J20Rik	RIKEN cDNA 1500034J20 gene	48.58	0.05	0.52	0.81	-4.94	0.03	-5.14	0.03	-2.14	0.34
96643_at	1600023A02Rik	RIKEN cDNA 1600023A02 gene	6.74	0.00	9.29	0.04	11.95	0.01	8.60	0.05	24.32	0.00
97320_at	1600025H15Rik	RIKEN cDNA 1600025H15 gene	73.40	0.00	-6.66	0.08	-20.90	0.00	-12.90	0.00	-10.40	0.01
161837_r_at	1700013L23Rik	RIKEN cDNA 1700013L23 gene	-16.83	0.01	2.71	0.28	-8.82	0.00	4.69	0.07	-4.02	0.12
104122_at	1700016D08Rik	RIKEN cDNA 1700016D08 gene	27.18	0.02	3.95	0.31	0.03	0.99	4.13	0.29	13.60	0.00
161065_at	1700018F16Rik	RIKEN cDNA 1700018F16 gene	0.11	0.03	-3.52	0.03	-1.95	0.22	3.54	0.03	2.17	0.18
160124_r_at	1700025B18Rik	RIKEN cDNA 1700025B18 gene	36.16	0.00	4.23	0.02	0.71	0.66	5.49	0.00	-3.61	0.03
98344_f_at	1700030C10Rik	RIKEN cDNA 1700030C10 gene	77.03	0.04	-3.99	0.03	4.26	0.02	1.17	0.50	0.11	0.95
93046_at	1700030K07Rik	RIKEN cDNA 1700030K07 gene	40.34	0.01	4.32	0.01	3.71	0.02	1.02	0.50	3.06	0.05
95619_at	1700040I03Rik	RIKEN cDNA 1700040I03 gene	11.74	0.04	-0.66	0.71	-5.26	0.01	2.30	0.20	-1.90	0.29
95033_at	1700105C21Rik	RIKEN cDNA 1700105C21 gene	41.47	0.00	-0.42	0.81	-1.52	0.40	-1.30	0.47	-9.02	0.00
97857_at	1810006O10Rik	RIKEN cDNA 1810006O10 gene	14.31	0.02	3.67	0.03	-4.51	0.01	1.23	0.45	1.86	0.26
104041_at	1810009A16Rik	RIKEN cDNA 1810009A16 gene	71.10	0.02	-2.43	0.28	-6.70	0.01	-4.57	0.05	-1.68	0.45
97885_at	1810009M01Rik	RIKEN cDNA 1810009M01 gene	94.60	0.01	-3.84	0.17	-9.03	0.00	3.66	0.19	-3.52	0.21

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
95132_r_at	1810011O01Rik	RIKEN cDNA 1810011O01 gene	99.59	0.02	-2.20	0.61	-4.28	0.32	0.74	0.86	15.41	0.00
99139_at	1810012I05Rik	RIKEN cDNA 1810012I05 gene	20.52	0.00	9.19	0.01	-5.83	0.07	8.60	0.01	2.56	0.40
95137_at	1810014L12Rik	RIKEN cDNA 1810014L12 gene	76.23	0.01	-8.31	0.02	-8.98	0.01	-3.89	0.24	-5.32	0.11
95518_at	1810015C04Rik	RIKEN cDNA 1810015C04 gene	95.41	0.00	-2.17	0.39	-7.80	0.01	-5.99	0.03	-8.46	0.00
99604_at	1810015H18Rik	RIKEN cDNA 1810015H18 gene	65.84	0.04	2.60	0.08	1.92	0.19	3.18	0.04	-2.12	0.15
97277_at	1810015M01Rik	RIKEN cDNA 1810015M01 gene	30.27	0.00	3.06	0.06	3.27	0.05	1.53	0.33	5.79	0.00
103381_at	1810024J13Rik	RIKEN cDNA 1810024J13 gene	75.16	0.03	1.51	0.40	5.56	0.01	0.24	0.89	3.19	0.09
161888_r_at	1810029F08Rik	RIKEN cDNA 1810029F08 gene	43.00	0.04	-5.96	0.04	-1.01	0.71	-3.08	0.26	6.36	0.03
160250_at	1810029G24Rik	RIKEN cDNA 1810029G24 gene	49.11	0.00	-8.52	0.00	5.19	0.05	-2.99	0.24	-4.53	0.08
102042_at	1810037C20Rik	RIKEN cDNA 1810037C20 gene	18.70	0.04	5.17	0.02	2.27	0.27	-3.42	0.10	2.49	0.23
99988_at	1810041M12Rik	RIKEN cDNA 1810041M12 gene	30.36	0.03	6.52	0.03	2.46	0.38	0.73	0.79	7.41	0.01
103619_at	1810044O22Rik	RIKEN cDNA 1810044O22 gene	88.36	0.00	-6.78	0.01	-6.73	0.01	-6.83	0.01	-6.76	0.01
104293_at	1810045K06Rik	RIKEN cDNA 1810045K06 gene	58.65	0.01	22.89	0.00	5.34	0.36	3.09	0.60	-1.83	0.75
100877_at	1810058I24Rik	RIKEN cDNA 1810058I24 gene	67.58	0.00	12.42	0.00	4.20	0.17	16.00	0.00	15.16	0.00
95011_at	1810063B07Rik	RIKEN cDNA 1810063B07 gene	29.86	0.01	-4.35	0.05	-0.65	0.76	-5.21	0.02	5.83	0.01
97262_at	1810073N04Rik	RIKEN cDNA 1810073N04 gene	58.46	0.02	5.02	0.01	-1.36	0.47	-0.60	0.75	-5.44	0.01
102331_at	2010004M01Rik	RIKEN cDNA 2010004M01 gene	18.02	0.01	-3.28	0.39	-7.39	0.06	-11.10	0.01	9.80	0.02
94898_at	2010004P11Rik	RIKEN cDNA 2010004P11 gene	23.52	0.02	5.28	0.07	5.30	0.07	1.36	0.63	-7.36	0.02
102427_at	2010005M05Rik	RIKEN cDNA 2010005M05 gene	33.84	0.02	5.00	0.06	-2.16	0.39	1.03	0.68	-7.71	0.01
94417_at	2010008E23Rik	RIKEN cDNA 2010008E23 gene	19.61	0.04	-1.37	0.55	1.31	0.57	1.88	0.42	7.62	0.00
95613_at	2010200I23Rik	RIKEN cDNA 2010200I23 gene	82.50	0.01	-0.71	0.81	-1.56	0.60	-2.43	0.42	-12.28	0.00
94882_at	2010200I23Rik	RIKEN cDNA 2010200I23 gene	73.12	0.03	1.96	0.46	-0.67	0.80	-1.66	0.53	-9.38	0.00
160666_at	2010200J04Rik	RIKEN cDNA 2010200J04 gene	29.35	0.05	4.58	0.03	1.66	0.39	4.33	0.03	-0.44	0.82
93853_at	2010306G19Rik	RIKEN cDNA 2010306G19 gene	9.48	0.02	8.61	0.04	3.78	0.35	3.00	0.45	-12.08	0.01

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
160513_at	2210016F16Rik	RIKEN cDNA 2210016F16 gene	35.54	0.01	0.91	0.44	-4.43	0.00	-1.45	0.23	0.26	0.83
99093_at	2210402A09Rik	RIKEN cDNA 2210402A09 gene	112.60	0.03	-4.08	0.05	-5.44	0.01	1.37	0.49	-2.81	0.17
96761_at	2210409B01Rik	RIKEN cDNA 2210409B01 gene	40.17	0.02	-7.00	0.01	6.65	0.02	-0.07	0.98	-3.52	0.19
162285_r_at	2210409B01Rik	RIKEN cDNA 2210409B01 gene	0.39	0.03	-3.65	0.01	-1.23	0.34	-2.40	0.07	0.62	0.63
100321_f_at	2210418O10Rik	RIKEN cDNA 2210418O10 gene	7.62	0.00	0.86	0.50	1.53	0.24	-1.99	0.13	-6.55	0.00
93310_at	2300001E01Rik	RIKEN cDNA 2300001E01 gene	89.22	0.00	-1.59	0.28	-0.18	0.90	-2.31	0.12	-7.74	0.00
104343_f_at	2310004B05Rik	RIKEN cDNA 2310004B05 gene	52.79	0.00	3.21	0.45	-15.72	0.00	-2.95	0.49	-10.51	0.02
104342_i_at	2310004B05Rik	RIKEN cDNA 2310004B05 gene	4.16	0.03	4.12	0.33	-10.24	0.02	0.44	0.92	-11.01	0.02
96211_at	2310004I03Rik	RIKEN cDNA 2310004I03 gene	29.31	0.04	12.13	0.01	-6.89	0.11	-1.84	0.66	3.85	0.36
95102_at	2310008D10Rik	RIKEN cDNA 2310008D10 gene	45.48	0.00	3.60	0.09	0.14	0.95	7.00	0.00	7.92	0.00
102783_at	2310009E04Rik	RIKEN cDNA 2310009E04 gene	71.93	0.03	0.48	0.82	6.32	0.01	2.60	0.23	3.37	0.12
160801_at	2310009N05Rik	RIKEN cDNA 2310009N05 gene	71.79	0.04	2.10	0.38	0.21	0.93	-5.43	0.03	5.97	0.02
97419_at	2310010I22Rik	RIKEN cDNA 2310010I22 gene	23.66	0.01	1.90	0.35	-8.78	0.00	0.70	0.73	1.47	0.47
103251_at	2310010M10Rik	RIKEN cDNA 2310010M10 gene	42.61	0.00	4.80	0.01	-4.68	0.01	4.40	0.01	1.67	0.32
96122_at	2310016A09Rik	RIKEN cDNA 2310016A09 gene	96.99	0.00	-3.76	0.13	-2.22	0.36	-8.79	0.00	6.44	0.01
99142_at	2310021M12Rik	RIKEN cDNA 2310021M12 gene	48.31	0.00	-1.85	0.31	1.10	0.55	-1.17	0.52	8.76	0.00
95622_at	2310022K15Rik	RIKEN cDNA 2310022K15 gene	36.06	0.02	0.15	0.93	-4.96	0.01	1.57	0.37	-4.08	0.03
98942_r_at	2310032D16Rik	RIKEN cDNA 2310032D16 gene	21.52	0.00	-0.70	0.68	0.30	0.86	-3.34	0.06	-8.24	0.00
160475_at	2310034L04Rik	RIKEN cDNA 2310034L04 gene	48.24	0.02	4.57	0.02	0.24	0.90	-4.84	0.02	2.69	0.16
96819_at	2310035K24Rik	RIKEN cDNA 2310035K24 gene	51.33	0.03	-7.07	0.02	3.65	0.19	-5.05	0.08	-3.33	0.23
94978_at	2310037I24Rik	RIKEN cDNA 2310037I24 gene	40.50	0.02	-0.88	0.57	2.49	0.12	-2.54	0.11	4.67	0.01
95109_at	2310044F10Rik	RIKEN cDNA 2310044F10 gene	13.58	0.01	-0.66	0.69	0.55	0.74	1.80	0.29	-6.71	0.00
104298_at	2310044G17Rik	RIKEN cDNA 2310044G17 gene	30.81	0.00	4.32	0.03	6.48	0.00	4.64	0.02	-0.44	0.81
97347_at	2310046A13Rik	RIKEN cDNA 2310046A13 gene	31.27	0.00	4.50	0.06	-3.49	0.13	-9.43	0.00	2.61	0.25

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
161342_r_at	2310046H11Rik	RIKEN cDNA 2310046H11 gene	25.39	0.04	3.27	0.22	-1.74	0.51	0.55	0.83	-8.52	0.00
160461_f_at	2310057H16Rik	RIKEN cDNA 2310057H16 gene	60.01	0.00	-11.09	0.00	-4.96	0.04	-6.27	0.01	1.22	0.59
92718_at	2310061N23Rik	RIKEN cDNA 2310061N23 gene	20.87	0.02	2.42	0.49	-2.59	0.46	7.87	0.03	10.39	0.01
96271_at	2310075C12Rik	RIKEN cDNA 2310075C12 gene	47.27	0.04	3.43	0.11	6.00	0.01	1.25	0.55	-2.09	0.32
96352_at	2400001E08Rik	RIKEN cDNA 2400001E08 gene	52.55	0.01	-0.69	0.76	-7.13	0.00	-2.75	0.23	5.33	0.03
100074_at	2400003B06Rik	RIKEN cDNA 2400003B06 gene	61.46	0.00	-4.16	0.31	2.95	0.47	3.21	0.43	-17.61	0.00
98070_at	2400003N08Rik	RIKEN cDNA 2400003N08 gene	48.91	0.01	-0.07	0.96	0.34	0.80	0.00	1.00	5.59	0.00
160239_at	2400006A19Rik	RIKEN cDNA 2400006A19 gene	72.78	0.02	1.99	0.16	2.83	0.05	1.43	0.30	-3.98	0.01
95501_at	2410001C21Rik	RIKEN cDNA 2410001C21 gene	26.88	0.04	5.93	0.05	3.10	0.29	1.62	0.58	7.46	0.02
94556_at	2410004M09Rik	RIKEN cDNA 2410004M09 gene	29.05	0.00	5.83	0.05	10.34	0.00	7.27	0.02	-3.48	0.22
162003_at	2410005K20Rik	RIKEN cDNA 2410005K20 gene	20.14	0.05	6.35	0.08	4.83	0.17	7.35	0.04	-4.08	0.24
97276_at	2410007D12Rik	RIKEN cDNA 2410007D12 gene	27.58	0.02	4.99	0.20	-2.39	0.53	2.05	0.59	14.14	0.00
98975_at	2410008G02Rik	RIKEN cDNA 2410008G02 gene	19.33	0.00	-8.35	0.00	-2.01	0.22	-0.37	0.82	1.96	0.23
95433_at	2410015A15Rik	RIKEN cDNA 2410015A15 gene	30.72	0.01	3.59	0.07	-5.33	0.01	-5.25	0.01	0.02	0.99
96779_f_at	2410022L05Rik	RIKEN cDNA 2410022L05 gene	14.30	0.02	-3.22	0.11	-6.02	0.01	2.04	0.30	-1.58	0.42
103553_at	2410041F14Rik	RIKEN cDNA 2410041F14 gene	56.59	0.04	5.62	0.12	-0.60	0.87	-1.61	0.65	-10.64	0.01
96628_at	2410081F06Rik	RIKEN cDNA 2410081F06 gene	40.28	0.02	1.08	0.65	4.03	0.10	3.17	0.19	-7.47	0.00
97328_at	2410090P21Rik	RIKEN cDNA 2410090P21 gene	-7.94	0.04	-3.14	0.20	-5.25	0.04	2.55	0.29	-5.15	0.04
96329_at	2410104I19Rik	RIKEN cDNA 2410104I19 gene	43.87	0.05	1.54	0.56	-7.82	0.01	-2.15	0.42	3.26	0.22
104349_at	2410133M08Rik	RIKEN cDNA 2410133M08 gene	21.21	0.01	0.76	0.71	5.45	0.02	5.76	0.01	-5.01	0.02
96677_at	2410195B05Rik	RIKEN cDNA 2410195B05 gene	39.76	0.01	0.82	0.63	-4.00	0.03	-4.93	0.01	3.16	0.08
162292_r_at	2510039O18Rik	RIKEN cDNA 2510039O18 gene	76.62	0.00	-6.46	0.01	8.16	0.00	-0.28	0.89	7.24	0.00
160908_r_at	2510042P03Rik	RIKEN cDNA 2510042P03 gene	21.26	0.04	2.70	0.22	1.50	0.48	1.64	0.45	6.44	0.01
97866_at	2510049I19Rik	RIKEN cDNA 2510049I19 gene	31.73	0.00	2.22	0.26	-1.56	0.42	-1.02	0.60	8.71	0.00

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
104693_at	2600001M11Rik	RIKEN cDNA 2600001M11 gene	4.16	0.02	4.29	0.16	-6.38	0.04	4.31	0.16	7.72	0.02
93591_at	2600002E23Rik	RIKEN cDNA 2600002E23 gene	33.87	0.03	11.56	0.03	-3.31	0.49	-8.06	0.11	10.27	0.04
93980_at	2600016B03Rik	RIKEN cDNA 2600016B03 gene	5.72	0.00	0.88	0.52	-1.92	0.17	-1.54	0.27	-6.85	0.00
103529_at	2600017J23Rik	RIKEN cDNA 2600017J23 gene	45.06	0.00	4.84	0.15	9.44	0.01	6.57	0.06	19.51	0.00
160298_at	2610001E17Rik	RIKEN cDNA 2610001E17 gene	6.85	0.00	0.66	0.44	1.91	0.04	0.35	0.68	3.41	0.00
102056_f_at	2610002J02Rik	RIKEN cDNA 2610002J02 gene	33.89	0.03	-1.30	0.54	-5.74	0.01	1.45	0.49	-4.49	0.04
99151_at	2610002K22Rik	RIKEN cDNA 2610002K22 gene	46.49	0.04	4.40	0.08	5.17	0.04	3.88	0.11	2.69	0.26
162367_f_at	2610007A16Rik	RIKEN cDNA 2610007A16 gene	0.61	0.02	-2.63	0.01	0.82	0.40	0.16	0.87	2.34	0.02
97252_at	2610012O22Rik	RIKEN cDNA 2610012O22 gene	-43.97	0.03	-15.71	0.01	-6.64	0.24	-0.93	0.87	-10.91	0.06
98931_at	2610016K11Rik	RIKEN cDNA 2610016K11 gene	58.26	0.03	3.63	0.12	-5.52	0.02	2.17	0.35	-4.20	0.08
100902_at	2610019F03Rik	RIKEN cDNA 2610019F03 gene	23.08	0.01	3.48	0.18	3.56	0.17	0.90	0.73	10.18	0.00
96609_at	2610019N13Rik	RIKEN cDNA 2610019N13 gene	46.10	0.02	1.98	0.41	2.07	0.39	1.35	0.57	-8.34	0.00
161017_at	2610020P18Rik	RIKEN cDNA 2610020P18 gene	-0.53	0.03	6.00	0.00	-1.40	0.43	-1.55	0.38	-1.23	0.48
96266_at	2610023M21Rik	RIKEN cDNA 2610023M21 gene	53.05	0.00	7.08	0.01	-1.53	0.56	3.62	0.18	-9.69	0.00
104146_at	2610025P08Rik	RIKEN cDNA 2610025P08 gene	-12.68	0.00	2.21	0.40	0.23	0.93	3.09	0.24	14.11	0.00
97247_at	2610034N03Rik	RIKEN cDNA 2610034N03 gene	70.94	0.00	2.13	0.08	3.34	0.01	0.67	0.57	6.15	0.00
93059_at	2610204K14Rik	RIKEN cDNA 2610204K14 gene	48.52	0.02	1.20	0.10	1.31	0.07	0.78	0.27	1.86	0.01
96095_i_at	2610207I16Rik	RIKEN cDNA 2610207I16 gene	27.05	0.01	6.60	0.01	2.56	0.30	-3.59	0.15	6.18	0.02
97164_at	2610207P08Rik	RIKEN cDNA 2610207P08 gene	20.84	0.00	0.88	0.65	0.58	0.76	2.07	0.29	8.62	0.00
102384_at	2610209L14Rik	RIKEN cDNA 2610209L14 gene	37.59	0.00	-0.03	0.99	5.00	0.01	1.80	0.30	-6.13	0.00
103726_at	2610311I19Rik	RIKEN cDNA 2610311I19 gene	56.84	0.01	1.14	0.57	7.32	0.00	2.88	0.16	-2.36	0.25
94510_at	2610312E17Rik	RIKEN cDNA 2610312E17 gene	31.29	0.02	-0.30	0.86	2.78	0.12	-2.68	0.13	-5.41	0.01
98973_at	2610318G08Rik	RIKEN cDNA 2610318G08 gene	22.86	0.02	0.43	0.84	1.60	0.46	-0.35	0.87	-8.01	0.00
99182_at	2610511E03Rik	RIKEN cDNA 2610511E03 gene	30.20	0.01	2.81	0.03	1.12	0.36	3.60	0.01	1.40	0.26

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
96806_at	2610511G02Rik	RIKEN cDNA 2610511G02 gene	79.55	0.00	4.62	0.18	-2.99	0.38	8.71	0.02	-13.24	0.00
100306_at	2700007P21Rik	RIKEN cDNA 2700007P21 gene	4.34	0.02	3.28	0.02	-3.61	0.01	-2.28	0.11	0.82	0.55
92268_at	2700007P21Rik	RIKEN cDNA 2700007P21 gene	16.15	0.05	3.24	0.06	-4.08	0.02	-1.16	0.48	1.48	0.37
93767_i_at	2700059D21Rik	RIKEN cDNA 2700059D21 gene	65.89	0.00	-7.50	0.00	-5.91	0.00	-8.88	0.00	-11.59	0.00
97205_at	2700079K05Rik	RIKEN cDNA 2700079K05 gene	54.93	0.00	1.76	0.31	3.02	0.09	1.44	0.40	-7.93	0.00
104561_at	2700084A09Rik	RIKEN cDNA 2700084A09 gene	-10.79	0.02	2.24	0.60	4.34	0.31	8.55	0.06	-13.16	0.01
94410_f_at	2700094L05Rik	RIKEN cDNA 2700094L05 gene	45.88	0.03	-0.66	0.76	-6.89	0.00	-0.98	0.66	4.20	0.07
104118_at	2810037C14Rik	RIKEN cDNA 2810037C14 gene	11.08	0.03	-1.45	0.55	-2.74	0.27	3.79	0.13	7.12	0.01
104423_at	2810047L02Rik	RIKEN cDNA 2810047L02 gene	-3.41	0.05	4.64	0.08	-5.04	0.06	3.86	0.14	3.71	0.16
97434_at	2810405F18Rik	RIKEN cDNA 2810405F18 gene	11.63	0.00	4.41	0.00	-3.61	0.01	-0.51	0.70	-3.10	0.03
103631_at	2810407K09Rik	RIKEN cDNA 2810407K09 gene	11.48	0.04	1.61	0.51	-1.95	0.43	1.10	0.65	8.12	0.00
97936_at	2810407L07Rik	RIKEN cDNA 2810407L07 gene	-1.29	0.04	7.56	0.01	0.86	0.75	4.06	0.14	4.12	0.14
104109_at	2810425J22Rik	RIKEN cDNA 2810425J22 gene	56.55	0.00	-0.03	0.99	-14.06	0.00	-9.99	0.01	-9.40	0.02
160278_at	2810428I15Rik	RIKEN cDNA 2810428I15 gene	29.65	0.02	2.15	0.69	-10.70	0.06	-0.72	0.90	18.07	0.00
102194_at	2810432D09Rik	RIKEN cDNA 2810432D09 gene	37.60	0.04	0.51	0.84	-4.10	0.12	3.21	0.22	7.42	0.01
97446_at	2810477H02Rik	RIKEN cDNA 2810477H02 gene	33.21	0.01	7.30	0.00	-0.90	0.61	-1.90	0.28	1.74	0.33
99514_at	2900002K07Rik	RIKEN cDNA 2900002K07 gene	25.82	0.01	-3.14	0.51	13.49	0.01	2.99	0.53	15.24	0.00
99179_at	3010002G01Rik	RIKEN cDNA 3010002G01 gene	-3.75	0.01	2.82	0.58	-18.94	0.00	-6.71	0.19	4.06	0.43
100041_at	3010027G13Rik	RIKEN cDNA 3010027G13 gene	105.01	0.00	-1.47	0.18	-3.51	0.00	-3.20	0.01	0.85	0.43
99653_at	3100001N19Rik	RIKEN cDNA 3100001N19 gene	77.11	0.00	-4.63	0.01	-3.31	0.04	2.63	0.10	-5.43	0.00
96640_at	3110001A13Rik	RIKEN cDNA 3110001A13 gene	62.62	0.00	9.80	0.00	3.33	0.09	10.64	0.00	13.64	0.00
104212_at	3110001K13Rik	RIKEN cDNA 3110001K13 gene	82.06	0.00	2.88	0.04	4.82	0.00	3.75	0.01	0.16	0.90
96288_at	3110038B19Rik	RIKEN cDNA 3110038B19 gene	30.78	0.02	4.24	0.06	2.30	0.29	-0.13	0.95	6.49	0.01

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
94260_at	3110040D16Rik	RIKEN cDNA 3110040D16 gene	65.12	0.01	1.09	0.42	-1.00	0.46	-5.52	0.00	-0.31	0.82
95383_at	3110041O18Rik	RIKEN cDNA 3110041O18 gene	76.36	0.01	-5.60	0.19	-8.91	0.04	-10.95	0.01	-8.63	0.05
92437_at	3110041O18Rik	RIKEN cDNA 3110041O18 gene	70.86	0.00	-10.96	0.06	-12.34	0.04	-26.23	0.00	-8.45	0.14
160791_at	3300001P08Rik	RIKEN cDNA 3300001P08 gene	11.03	0.01	1.62	0.26	-0.69	0.63	-0.08	0.96	-5.65	0.00
103686_at	3300002C04Rik	RIKEN cDNA 3300002C04 gene	4.96	0.05	-2.71	0.34	1.14	0.68	4.27	0.14	7.98	0.01
96104_at	3732413I11Rik	RIKEN cDNA 3732413I11 gene	21.73	0.03	7.09	0.00	2.05	0.34	1.32	0.54	2.46	0.26
104463_at	3830408P06Rik	RIKEN cDNA 3830408P06 gene	28.71	0.03	-3.53	0.03	3.25	0.04	1.27	0.41	2.67	0.09
103471_at	4432405K22Rik	RIKEN cDNA 4432405K22 gene	50.29	0.00	2.76	0.16	6.05	0.00	-1.01	0.60	-7.89	0.00
104283_at	4432405K22Rik	RIKEN cDNA 4432405K22 gene	47.48	0.05	5.34	0.11	-6.96	0.04	-4.73	0.15	-4.75	0.15
99523_at	4432417N03Rik	RIKEN cDNA 4432417N03 gene	36.12	0.01	-3.00	0.30	10.08	0.00	-0.64	0.82	-5.50	0.06
161447_f_at	4631434O19Rik	RIKEN cDNA 4631434O19 gene	6.48	0.00	2.18	0.11	0.65	0.62	5.53	0.00	-1.99	0.14
160951_at	4632419J12Rik	RIKEN cDNA 4632419J12 gene	68.12	0.01	17.28	0.02	21.21	0.01	7.06	0.31	5.38	0.44
95752_at	4733401P19Rik	RIKEN cDNA 4733401P19 gene	61.23	0.02	2.01	0.53	-9.82	0.01	-4.96	0.13	-4.57	0.16
161333_f_at	4833408P15Rik	RIKEN cDNA 4833408P15 gene	10.40	0.01	-3.11	0.11	-4.67	0.02	-2.50	0.20	4.67	0.02
98908_at	4833416I09Rik	RIKEN cDNA 4833416I09 gene	35.29	0.05	4.54	0.11	-7.54	0.01	1.60	0.56	2.40	0.39
161756_at	4833420N02Rik	RIKEN cDNA 4833420N02 gene	6.57	0.04	-0.95	0.68	-6.35	0.01	3.19	0.18	3.63	0.13
102776_at	4833420O05Rik	RIKEN cDNA 4833420O05 gene	22.11	0.03	5.08	0.03	0.02	0.99	1.47	0.51	6.06	0.01
99163_at	4921506J03Rik	RIKEN cDNA 4921506J03 gene	15.07	0.04	15.10	0.00	-1.56	0.73	1.66	0.71	-4.04	0.38
98326_f_at	4921513E08Rik	RIKEN cDNA 4921513E08 gene	-1.65	0.04	-2.18	0.09	2.50	0.05	2.73	0.04	0.03	0.98
95655_at	4930434H03Rik	RIKEN cDNA 4930434H03 gene	13.38	0.00	0.25	0.92	1.78	0.47	1.94	0.43	-11.26	0.00
97240_g_at	4930455J02Rik	RIKEN cDNA 4930455J02 gene	86.02	0.02	0.07	0.97	-5.51	0.02	-5.93	0.01	0.59	0.78
104544_at	4930517K11Rik	RIKEN cDNA 4930517K11 gene	-0.65	0.03	-3.06	0.10	3.29	0.08	-2.47	0.18	-4.15	0.03
96145_at	4930534E15Rik	RIKEN cDNA 4930534E15 gene	27.09	0.00	-3.68	0.39	-18.41	0.00	-6.03	0.16	0.04	0.99
104639_i_at	4930553M18Rik	RIKEN cDNA 4930553M18 gene	17.24	0.02	0.75	0.60	-1.20	0.40	2.08	0.15	-4.91	0.00

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
160576_at	4930563P03Rik	RIKEN cDNA 4930563P03 gene	18.14	0.01	-10.47	0.01	2.37	0.48	-5.35	0.12	9.01	0.01
94504_at	4930570C03Rik	RIKEN cDNA 4930570C03 gene	20.25	0.02	-2.65	0.38	-10.22	0.00	-4.50	0.15	-1.26	0.68
161437_f_at	4930578F06Rik	RIKEN cDNA 4930578F06 gene	20.58	0.01	2.54	0.11	1.69	0.28	0.86	0.58	5.37	0.00
96717_at	4930588A18Rik	RIKEN cDNA 4930588A18 gene	30.48	0.03	4.89	0.05	-6.64	0.01	-1.78	0.45	1.65	0.48
160279_at	4930588M11Rik	RIKEN cDNA 4930588M11 gene	34.75	0.00	-1.32	0.34	3.39	0.02	0.48	0.72	-7.83	0.00
96089_at	4931406C07Rik	RIKEN cDNA 4931406C07 gene	49.12	0.02	-3.06	0.23	-2.90	0.25	-7.99	0.00	2.69	0.28
162239_at	4933407C03Rik	RIKEN cDNA 4933407C03 gene	-4.05	0.01	2.57	0.11	0.99	0.53	-1.42	0.37	6.18	0.00
162145_r_at	4933424M23Rik	RIKEN cDNA 4933424M23 gene	5.64	0.04	-2.82	0.30	-6.39	0.03	-4.28	0.12	4.55	0.10
160959_at	4933432H23Rik	RIKEN cDNA 4933432H23 gene	42.54	0.02	3.77	0.05	4.56	0.02	3.11	0.10	2.24	0.22
97705_at	5031401C21Rik	RIKEN cDNA 5031401C21 gene	-8.66	0.02	-9.25	0.00	-1.53	0.54	1.57	0.53	-2.60	0.31
101001_at	5031439A09Rik	RIKEN cDNA 5031439A09 gene	6.33	0.00	-2.77	0.07	-1.51	0.30	1.57	0.28	6.27	0.00
98495_at	5033414D02Rik	RIKEN cDNA 5033414D02 gene	16.05	0.03	1.87	0.42	-6.08	0.01	2.60	0.26	4.84	0.05
94345_at	5133400A03Rik	RIKEN cDNA 5133400A03 gene	36.92	0.00	2.46	0.18	-2.54	0.17	-0.71	0.69	8.24	0.00
99675_at	5330422J23Rik	RIKEN cDNA 5330422J23 gene	62.80	0.02	2.33	0.18	0.41	0.81	1.57	0.36	6.14	0.00
103863_at	5630401J11Rik	RIKEN cDNA 5630401J11 gene	70.30	0.00	4.66	0.00	-6.88	0.00	-0.59	0.65	6.33	0.00
100587_f_at	5730403B10Rik	RIKEN cDNA 5730403B10 gene	62.08	0.01	2.88	0.29	6.77	0.02	7.55	0.01	-2.41	0.37
94555_at	5730408C10Rik	RIKEN cDNA 5730408C10 gene	56.25	0.04	2.51	0.34	-3.28	0.22	-3.88	0.15	7.20	0.01
95496_at	5730409F23Rik	RIKEN cDNA 5730409F23 gene	37.56	0.03	4.51	0.26	-7.17	0.08	-10.72	0.01	2.88	0.46
94845_at	5730454B08Rik	RIKEN cDNA 5730454B08 gene	46.59	0.00	2.66	0.08	-1.65	0.27	-1.79	0.24	-6.06	0.00
103978_at	5730454B08Rik	RIKEN cDNA 5730454B08 gene	31.47	0.01	9.90	0.00	0.53	0.82	-0.38	0.87	-3.81	0.12
102813_f_at	5730525G14Rik	RIKEN cDNA 5730525G14 gene	48.05	0.00	1.99	0.46	6.71	0.02	0.67	0.80	-10.11	0.00
95980_at	5730552M22Rik	RIKEN cDNA 5730552M22 gene	36.89	0.00	-8.08	0.00	3.53	0.09	-4.29	0.05	-3.47	0.10
100004_at	5930412E23Rik	RIKEN cDNA 5930412E23 gene	29.74	0.01	-0.36	0.81	-1.62	0.28	3.17	0.04	5.06	0.00

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
161062_r_at	6330416M07Rik	RIKEN cDNA 6330416M07 gene	-3.19	0.02	7.07	0.02	-5.47	0.07	2.64	0.37	6.06	0.05
161396_f_at	6530403D07Rik	RIKEN cDNA 6530403D07 gene	2.74	0.01	6.27	0.05	-7.40	0.03	7.20	0.03	4.03	0.20
95916_at	6530405F15Rik	RIKEN cDNA 6530405F15 gene	-6.77	0.02	1.28	0.51	-3.34	0.10	5.77	0.01	-3.50	0.08
96655_g_at	8430408H12Rik	RIKEN cDNA 8430408H12 gene	30.57	0.03	-11.95	0.11	-15.85	0.04	-15.71	0.04	6.53	0.37
97398_at	9130022B02Rik	RIKEN cDNA 9130022B02 gene	-12.18	0.02	-5.55	0.20	-0.07	0.99	11.38	0.01	10.35	0.02
103754_at	9430029A22Rik	RIKEN cDNA 9430029A22 gene	43.89	0.01	5.36	0.02	6.94	0.00	-0.73	0.72	-0.41	0.84
96924_at	9430077D24Rik	RIKEN cDNA 9430077D24 gene	28.78	0.03	-0.98	0.80	3.80	0.33	-5.11	0.19	-12.09	0.00
94995_at	A030007L17Rik	RIKEN cDNA A030007L17 gene	17.06	0.00	-1.24	0.45	-0.14	0.93	0.69	0.67	7.58	0.00
97749_at	AA407862	expressed sequence AA407862	3.47	0.01	-0.34	0.77	-1.57	0.18	2.70	0.03	-4.16	0.00
103693_at	AA407980	expressed sequence AA407980	23.26	0.02	-2.58	0.24	5.73	0.01	0.51	0.81	-5.07	0.03
94352_at	AA408199	expressed sequence AA408199	17.22	0.00	2.40	0.17	-6.95	0.00	-1.80	0.30	-3.17	0.08
95666_at	AA408242	expressed sequence AA408242	42.49	0.01	4.17	0.02	1.15	0.51	-4.96	0.01	-2.23	0.21
160661_at	AA408683	expressed sequence AA408683	23.24	0.01	4.93	0.14	2.36	0.47	4.61	0.17	12.44	0.00
95458_s_at	AA408880	expressed sequence AA408880	40.78	0.01	4.08	0.00	0.43	0.71	0.97	0.40	2.54	0.04
94343_at	AA408985	expressed sequence AA408985	68.16	0.02	2.58	0.40	10.74	0.00	2.69	0.38	-2.99	0.33
97458_at	AA409223	expressed sequence AA409223	65.44	0.03	-9.13	0.00	1.56	0.55	-1.39	0.59	-1.18	0.65
104294_at	AA409502	expressed sequence AA409502	36.57	0.00	-0.79	0.68	7.73	0.00	5.95	0.01	-0.24	0.90
94662_at	AA409766	expressed sequence AA409766	2.67	0.02	2.50	0.34	3.78	0.15	2.22	0.39	-8.29	0.00
161606_f_at	AA409995	expressed sequence AA409995	21.00	0.02	-4.98	0.11	-2.80	0.36	7.84	0.02	7.06	0.03
103669_at	AA415275	expressed sequence AA415275	36.43	0.01	-8.55	0.02	7.42	0.03	-5.17	0.13	-6.85	0.05
97918_at	AA536743	expressed sequence AA536743	14.39	0.02	0.42	0.92	-4.85	0.26	-5.88	0.17	-14.68	0.00
102767_at	AA536815	EST AA536815	49.28	0.01	-2.93	0.07	3.06	0.06	3.88	0.02	3.74	0.02
97193_at	AA575098	expressed sequence AA575098	28.77	0.00	-10.62	0.00	0.92	0.71	-6.89	0.01	-1.62	0.51
101673_r_at	AA675035	expressed sequence AA675035	0.25	0.03	-0.69	0.35	0.86	0.24	-1.85	0.02	1.40	0.06
94486_at	AA959742	expressed sequence AA959742	71.59	0.00	0.81	0.69	9.99	0.00	4.39	0.04	5.05	0.02
94359_at	AA960558	expressed sequence AA960558	26.18	0.02	2.01	0.36	3.28	0.14	4.97	0.03	5.94	0.01
100994_at	Aatk	apoptosis-associated tyrosine kinase	0.17	0.00	6.57	0.17	8.32	0.09	9.26	0.06	20.08	0.00
97198_at	Abca1	ATP-binding cassette, sub-family A (ABC1), member 1	26.60	0.03	13.61	0.01	5.64	0.26	6.15	0.22	-8.83	0.08
94733_at	Abcb4	ATP-binding cassette, sub-family B (MDR/TAP), member 4	97.12	0.00	9.42	0.00	11.44	0.00	10.78	0.00	9.92	0.00

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
92763_at	Abcb7	ATP-binding cassette, sub-family B (MDR/TAP), member 7	5.89	0.02	0.73	0.59	4.14	0.01	2.76	0.05	-0.83	0.54
103689_at	Abcc3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	98.47	0.00	-15.73	0.02	-16.00	0.02	-22.03	0.00	11.87	0.07
93407_at	Abcc6	ATP-binding cassette, sub-family C (CFTR/MRP), member 6	39.58	0.05	3.67	0.17	6.28	0.02	0.93	0.72	4.98	0.07
160612_at	Abcg1	ATP-binding cassette, sub-family G (WHITE), member 1	27.95	0.00	1.29	0.45	4.50	0.01	2.86	0.10	6.05	0.00
93626_at	Abcg2	ATP-binding cassette, sub-family G (WHITE), member 2	59.36	0.01	3.00	0.43	12.14	0.00	9.06	0.02	-1.30	0.73
95425_at	Acadl	acetyl-Coenzyme A dehydrogenase, long-chain	57.83	0.03	7.27	0.03	6.86	0.04	1.09	0.73	5.97	0.07
92581_at	Acadm	acetyl-Coenzyme A dehydrogenase, medium chain	109.36	0.02	4.25	0.07	2.39	0.30	-0.02	0.99	7.56	0.00
161469_r_at	Acads	acetyl-Coenzyme A dehydrogenase, short chain	25.90	0.00	-8.02	0.00	7.04	0.01	-0.24	0.92	4.57	0.07
103401_at	Acads	acetyl-Coenzyme A dehydrogenase, short chain	70.53	0.03	2.52	0.44	-2.44	0.46	-2.02	0.54	11.24	0.00
94850_at	Acate3-pending	acyl-Coenzyme A thioesterase 3, mitochondrial	9.82	0.00	-0.25	0.82	0.90	0.41	2.76	0.02	5.12	0.00
99910_at	Accn1	amiloride-sensitive cation channel 1, neuronal (degenerin)	25.32	0.01	-4.24	0.07	2.69	0.25	-4.07	0.09	6.53	0.01
161659_f_at	Acp1	acid phosphatase 1, soluble	6.61	0.02	2.62	0.17	-5.21	0.01	1.26	0.50	-3.69	0.06
98859_at	Acp5	acid phosphatase 5, tartrate resistant	66.50	0.02	-2.17	0.19	-5.40	0.00	-2.07	0.21	0.60	0.71
93207_at	Acr	preproacrosin	-8.47	0.00	13.99	0.04	17.67	0.01	-12.04	0.07	-19.64	0.01
101029_f_at	Actc1	actin, alpha, cardiac	11.76	0.04	-5.52	0.01	0.81	0.68	0.97	0.63	3.83	0.07
96573_at	Actg	actin, gamma, cytoplasmic	80.34	0.04	10.49	0.04	9.89	0.06	9.93	0.06	0.19	0.97
92280_at	Actn1	actinin, alpha 1	7.78	0.03	3.80	0.05	-2.56	0.17	2.21	0.23	-4.11	0.03
93460_at	Acvr1	activin A receptor, type 1	1.66	0.01	6.12	0.00	0.05	0.98	-1.41	0.42	-3.41	0.06
101177_at	Acvr1b	activin A receptor, type 1B	18.29	0.00	-10.59	0.00	1.77	0.44	1.89	0.41	1.45	0.53
102832_at	Adam1	a disintegrin and metalloproteinase domain 1a (fertilin alpha)	9.41	0.04	-3.98	0.02	-2.74	0.09	-2.50	0.13	0.10	0.95
162388_r_at	Adam5	a disintegrin and metalloprotease domain 5	30.32	0.04	-2.43	0.79	-24.31	0.01	-18.63	0.05	-7.46	0.41
161436_s_at	Adarb1	adenosine deaminase, RNA-specific, B1	24.66	0.00	6.61	0.00	0.23	0.90	7.38	0.00	-0.80	0.67
98589_at	Adfp	adipose differentiation related protein	115.48	0.00	2.43	0.30	1.91	0.42	-2.27	0.33	10.16	0.00
97733_at	Adora2b	adenosine A2b receptor	1.51	0.01	-7.17	0.00	2.73	0.23	3.31	0.15	-5.09	0.03
93540_at	Adprh	ADP-ribosylarginine hydrolase	29.33	0.05	-5.31	0.02	-2.56	0.24	-3.63	0.10	-1.77	0.41
97875_at	Adrm1	adhesion regulating molecule 1	62.19	0.00	5.37	0.03	-0.74	0.74	-10.55	0.00	-6.80	0.01
99038_at	Adss2	adenylosuccinate synthetase 2, non muscle	51.27	0.04	2.83	0.21	6.68	0.01	-1.23	0.58	-2.00	0.37
93122_at	Aeg1	acidic epididymal glycoprotein 1	-4.47	0.04	-0.49	0.70	2.53	0.06	-3.63	0.01	0.42	0.74
161629_i_at	Afp	alpha fetoprotein	4.29	0.02	-3.64	0.02	-0.32	0.82	4.07	0.01	0.93	0.51

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
160807_at	Agpat3	1-acylglycerol-3-phosphate O-acyltransferase 3	53.15	0.02	1.13	0.54	1.31	0.47	-1.97	0.28	6.47	0.00
101887_at	Agt	angiotensinogen	113.10	0.00	1.77	0.33	-2.74	0.14	2.74	0.14	11.07	0.00
161212_r_at	Agtr2	angiotensin II receptor, type 2	-0.17	0.00	0.46	0.74	1.40	0.31	5.88	0.00	2.09	0.14
93625_at	Agxt	alanine-glyoxylate aminotransferase	98.79	0.00	-2.55	0.25	-7.08	0.00	-4.47	0.05	-7.96	0.00
96024_at	Ahcy	S-adenosylhomocysteine hydrolase	136.51	0.01	2.09	0.09	-0.05	0.97	-3.70	0.01	-2.07	0.09
96638_at	AI043088	expressed sequence AI043088	-7.47	0.02	7.86	0.04	-10.87	0.01	-1.62	0.65	4.04	0.27
94440_at	AI132487	expressed sequence AI132487	111.64	0.00	3.97	0.22	0.02	0.99	2.79	0.38	17.52	0.00
95283_at	AI173996	expressed sequence AI173996	63.74	0.02	5.61	0.02	1.05	0.64	1.79	0.42	5.84	0.02
95386_at	AI181996	expressed sequence AI181996	27.79	0.05	6.63	0.10	-8.63	0.04	3.07	0.44	7.12	0.08
93983_at	AI195141	expressed sequence AI195141	41.81	0.04	3.23	0.05	-1.28	0.41	-2.35	0.14	3.33	0.04
96074_at	AI255964	expressed sequence AI255964	111.33	0.01	2.96	0.16	1.24	0.55	5.97	0.01	6.19	0.01
104213_at	AI266885	expressed sequence AI266885	120.05	0.00	9.81	0.15	3.81	0.57	9.17	0.18	-29.62	0.00
94473_at	AI314311	expressed sequence AI314311	94.26	0.02	2.35	0.09	2.02	0.14	1.88	0.17	3.79	0.01
161749_r_at	AI316828	expressed sequence AI316828	16.79	0.03	-5.85	0.00	-2.05	0.27	-2.08	0.26	0.38	0.83
94433_at	AI316867	expressed sequence AI316867	55.31	0.00	1.51	0.67	-2.63	0.45	4.29	0.23	-17.70	0.00
102360_at	AI323986	expressed sequence AI323986	-4.12	0.01	-5.39	0.03	-3.67	0.12	-7.45	0.00	0.88	0.70
97226_at	AI414047	expressed sequence AI414047	64.19	0.02	6.05	0.11	1.40	0.70	0.46	0.90	12.68	0.00
94428_at	AI415009	expressed sequence AI415009	30.48	0.00	4.95	0.05	-6.76	0.01	0.56	0.81	7.53	0.00
160995_at	AI425994	EST AI425994	54.07	0.04	-4.24	0.03	0.07	0.97	-4.56	0.02	1.23	0.51
160630_at	AI427066	expressed sequence AI427066	22.70	0.01	-5.29	0.00	3.15	0.03	-0.58	0.68	-0.94	0.50
96239_at	AI428238	expressed sequence AI428238	39.50	0.03	1.97	0.20	-4.03	0.01	-0.22	0.88	3.22	0.04
103531_f_at	AI447560	expressed sequence AI447560	67.76	0.01	0.97	0.78	11.99	0.00	6.79	0.07	4.46	0.22
101235_f_at	AI450241	expressed sequence AI450241	4.62	0.00	-5.61	0.00	-0.98	0.55	5.17	0.00	1.96	0.23
93693_at	AI451877	expressed sequence AI451877	27.88	0.03	-1.78	0.58	-10.15	0.01	-0.17	0.96	-5.33	0.11
160672_at	AI462438	expressed sequence AI462438	18.38	0.04	4.69	0.15	2.16	0.49	1.29	0.68	-9.62	0.01
96284_at	AI463719	expressed sequence AI463719	63.90	0.00	4.15	0.13	-10.70	0.00	-6.94	0.02	-1.21	0.65
92202_g_at	AI467657	expressed sequence AI467657	65.72	0.00	-2.21	0.65	20.10	0.00	20.73	0.00	-10.89	0.04
92589_at	AI480570	expressed sequence AI480570	51.20	0.02	-5.73	0.01	4.25	0.05	-2.47	0.23	0.97	0.63
94784_at	AI593484	expressed sequence AI593484	11.90	0.05	-1.54	0.45	-0.13	0.95	-6.06	0.01	2.89	0.17
97119_at	AI596198	expressed sequence AI596198	-0.58	0.01	0.78	0.37	0.81	0.34	-1.42	0.11	-2.94	0.00
104361_at	AI646709	expressed sequence AI646709	20.86	0.02	2.41	0.39	-3.06	0.28	-5.39	0.06	8.95	0.00
103227_at	AI788959	expressed sequence AI788959	96.33	0.00	-2.87	0.18	-0.42	0.84	-2.91	0.17	-9.81	0.00
160831_at	AI838661	expressed sequence AI838661	14.95	0.05	-2.43	0.30	-1.44	0.54	-2.01	0.39	7.10	0.01
161031_at	AI842128	expressed sequence AI842128	1.53	0.05	1.22	0.27	-1.48	0.18	-1.39	0.21	2.78	0.02

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
92531_at	AI844545	expressed sequence AI844545	18.99	0.00	9.20	0.00	3.82	0.13	5.40	0.04	5.60	0.03
103216_f_at	AI848108	expressed sequence AI848108	31.58	0.00	-2.76	0.21	-9.24	0.00	-9.06	0.00	-2.01	0.36
94336_at	AI850305	expressed sequence AI850305	27.01	0.04	-4.42	0.08	-3.21	0.20	-1.50	0.54	6.23	0.02
160994_at	AI851343	expressed sequence AI851343	19.47	0.05	3.77	0.25	-6.26	0.06	-6.28	0.06	-5.08	0.13
97752_at	AI854265	expressed sequence AI854265	4.81	0.04	-2.28	0.29	-0.04	0.98	-2.99	0.17	-6.52	0.01
161119_at	AI854630	expressed sequence AI854630	5.21	0.05	-3.34	0.06	4.14	0.02	1.76	0.29	-0.94	0.57
99948_at	AI854876	expressed sequence AI854876	-6.59	0.04	-10.71	0.08	-4.36	0.47	-16.98	0.01	-0.83	0.89
104494_at	AI874685	expressed sequence AI874685	17.20	0.01	-0.18	0.91	3.91	0.02	2.73	0.09	4.30	0.01
103443_at	Aim1	absent in melanoma 1	40.52	0.01	1.00	0.66	-2.11	0.35	6.51	0.01	6.91	0.01
95148_at	Ak2	adenylate kinase 2	80.03	0.00	3.85	0.16	11.01	0.00	3.11	0.26	7.09	0.02
99959_at	Ak4	adenylate kinase 4	56.13	0.03	3.28	0.22	2.88	0.28	7.15	0.01	4.51	0.10
97367_at	Akap1	A kinase (PRKA) anchor protein 1	40.28	0.00	4.66	0.09	-1.28	0.62	2.74	0.30	12.56	0.00
92796_at	Akp2	alkaline phosphatase 2, liver	21.47	0.04	-0.62	0.75	-0.53	0.79	-0.60	0.76	6.75	0.00
98918_at	AL022641	expressed sequence AL022641	70.27	0.03	0.29	0.94	-1.06	0.78	-0.23	0.95	13.78	0.00
101044_at	Alad	aminolevulinate, delta-, dehydratase	81.48	0.00	0.60	0.78	-4.65	0.04	1.40	0.52	11.08	0.00
92768_s_at	Alas2	aminolevulinic acid synthase 2, erythroid	73.00	0.02	-0.17	0.92	-1.71	0.34	-2.57	0.16	5.85	0.00
94778_at	Aldh1a7	aldehyde dehydrogenase family 1, subfamily A7	91.31	0.00	-10.04	0.00	-8.12	0.01	-5.52	0.04	-1.92	0.46
162331_f_at	Aldh3a1	aldehyde dehydrogenase family 3, subfamily A1	-31.04	0.05	-0.91	0.65	-3.05	0.14	3.63	0.08	4.80	0.03
99559_at	Aldh3a2	aldehyde dehydrogenase family 3, subfamily A2	86.95	0.04	7.83	0.22	7.89	0.22	-1.90	0.76	19.12	0.01
160546_at	Aldo3	aldolase 3, C isoform	26.81	0.00	-7.88	0.01	-12.18	0.00	-4.51	0.13	-9.78	0.00
94045_at	Ambp	alpha 1 microglobulin/bikunin	138.24	0.00	-1.43	0.29	-4.81	0.00	3.72	0.01	0.70	0.60
101489_at	Amd1	S-adenosylmethionine decarboxylase 1	45.55	0.04	2.56	0.44	0.16	0.96	7.45	0.03	-8.03	0.02
98094_f_at	Amfr	autocrine motility factor receptor	56.87	0.00	-1.67	0.34	-8.36	0.00	-1.19	0.50	0.22	0.90
94392_f_at	Ang	angiogenin	108.54	0.04	3.17	0.55	-5.72	0.28	12.05	0.03	-12.38	0.03
100441_s_at	Ank1	ankyrin 1, erythroid	-2.20	0.05	0.40	0.77	-0.53	0.70	1.88	0.18	-4.18	0.01
98476_at	Ank3	ankyrin 3, epithelial	23.29	0.00	-2.38	0.42	-12.12	0.00	-4.35	0.15	-11.09	0.00
98477_s_at	Ank3	ankyrin 3, epithelial	6.47	0.04	1.97	0.49	-2.76	0.33	-5.23	0.08	-7.60	0.01
93372_at	Anp32a	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	16.72	0.00	3.28	0.45	-19.88	0.00	-10.90	0.02	1.53	0.72
99993_at	Anpep	alanyl (membrane) aminopeptidase	56.74	0.03	4.13	0.09	1.08	0.65	3.59	0.14	6.36	0.01
102815_at	Anxa11	annexin A11	53.48	0.02	2.77	0.19	-2.35	0.26	4.08	0.06	5.99	0.01
100569_at	Anxa2	annexin A2	21.52	0.00	-0.86	0.87	5.38	0.33	2.30	0.67	36.78	0.00
100584_at	Anxa4	annexin A4	47.26	0.00	1.37	0.45	1.22	0.50	1.44	0.43	10.60	0.00
104011_at	Aox1	aldehyde oxidase 1	56.26	0.01	-10.55	0.04	-13.51	0.01	-11.86	0.02	4.02	0.40
161439_f_at	Ap1m1	adaptor-related protein complex AP-1, mu subunit 1	45.80	0.03	-3.97	0.18	7.09	0.02	-6.38	0.04	1.88	0.52
102835_at	Ap2a2	adaptor protein complex AP-2, alpha 2 subunit	45.56	0.01	-0.71	0.76	-4.75	0.05	-2.37	0.31	7.86	0.00
94388_at	Ap3s2	adaptor-related protein complex AP-3, sigma 2 subunit	16.39	0.03	6.08	0.00	0.56	0.75	0.19	0.91	1.04	0.55
100392_at	Apel-pending	apelin	43.57	0.00	-14.61	0.03	-13.77	0.04	-27.20	0.00	-23.91	0.00

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
93559_at	Apex1	apurinic/apyrimidinic endonuclease 1	44.75	0.01	-1.64	0.22	-1.58	0.24	-2.02	0.14	-4.57	0.00
94225_at	Apg5l	autophagy 5-like (S. cerevisiae)	54.14	0.01	-1.13	0.57	6.97	0.00	-2.76	0.18	3.67	0.08
93445_at	Api6	apoptosis inhibitor 6	35.69	0.01	7.04	0.16	1.98	0.69	18.90	0.00	0.95	0.85
101529_g_at	Apoa1	apolipoprotein A-I	33.93	0.03	4.47	0.09	-0.01	1.00	-3.69	0.16	-7.19	0.01
94032_at	Apoa1bp	apolipoprotein A-I binding protein	71.32	0.01	-0.74	0.75	-1.29	0.59	-3.14	0.20	9.18	0.00
161359_s_at	Apoa1bp	apolipoprotein A-I binding protein	86.67	0.03	-2.76	0.25	-2.28	0.34	-2.40	0.31	7.60	0.00
100078_at	Apoa4	apolipoprotein A-IV	62.89	0.00	24.18	0.00	42.31	0.00	19.52	0.01	58.39	0.00
97236_r_at	Apobec2	apolipoprotein B editing complex 2	-7.76	0.01	-6.00	0.03	4.52	0.09	-0.26	0.92	-7.34	0.01
97887_at	Apoc2	apolipoprotein C-II	106.53	0.00	3.78	0.13	8.39	0.00	4.46	0.08	16.42	0.00
93840_at	Apom	apolipoprotein M	97.76	0.01	-8.45	0.03	-8.00	0.04	-0.24	0.95	-10.28	0.01
93283_at	Aprt	adenine phosphoribosyl transferase	26.40	0.00	-4.04	0.09	-11.76	0.00	-3.04	0.20	-5.39	0.03
161559_i_at	Aqp1	aquaporin 1	20.54	0.00	-3.98	0.04	4.97	0.01	-5.25	0.01	-2.86	0.14
93330_at	Aqp1	aquaporin 1	41.67	0.02	5.92	0.06	-5.89	0.06	-5.40	0.08	5.28	0.08
101213_at	Arbp	acidic ribosomal phosphoprotein PO	128.89	0.01	-2.37	0.07	-3.47	0.01	-0.80	0.52	-3.53	0.01
162353_at	Arbp	acidic ribosomal phosphoprotein PO	7.64	0.05	-2.94	0.13	0.74	0.69	4.66	0.02	3.07	0.11
97811_at	Arfgap1	ADP-ribosylation factor GTPase activating protein 1	-4.69	0.02	5.83	0.38	24.31	0.00	0.66	0.92	6.23	0.35
101113_at	Arha2	ras homolog gene family, member A2	78.42	0.02	-2.77	0.33	-2.20	0.44	-1.99	0.48	10.53	0.00
101112_g_at	Arha2	ras homolog gene family, member A2	53.10	0.03	1.52	0.70	-2.52	0.53	-7.49	0.07	11.82	0.01
95547_at	Arhd	ras homolog gene family, member D	42.40	0.00	-3.78	0.18	-9.54	0.00	-4.83	0.09	6.37	0.03
96747_at	Arhu	ras homolog gene family, member U	57.80	0.01	-2.64	0.38	-6.34	0.05	-5.37	0.09	8.68	0.01
160371_at	Arl6ip	ADP-ribosylation-like factor 6 interacting protein	89.19	0.00	0.08	0.95	0.85	0.48	0.72	0.55	5.76	0.00
104745_at	Arl6ip2	ADP-ribosylation-like factor 6 interacting protein 2	74.40	0.00	5.35	0.00	5.50	0.00	7.55	0.00	-0.06	0.97
95749_at	Armet	arginine-rich, mutated in early stage tumors	89.94	0.00	-3.97	0.35	17.43	0.00	6.43	0.14	-5.32	0.21
102382_at	Arntl	aryl hydrocarbon receptor nuclear translocator-like	12.36	0.01	-13.63	0.00	-5.46	0.20	-12.25	0.01	0.45	0.91
96357_at	Arpc1b	actin related protein 2/3 complex, subunit 1B (41 kDa)	30.99	0.04	3.91	0.11	3.86	0.12	-0.21	0.93	-6.13	0.02
97260_at	Arpp19-pending	cyclic AMP phosphoprotein, 19 kDa	-10.01	0.03	3.69	0.43	-2.47	0.59	-9.29	0.06	13.04	0.01
161286_f_at	Arsa	arylsulfatase A	11.93	0.04	1.59	0.72	-14.82	0.00	-3.46	0.44	-3.36	0.45
99592_f_at	Arsdr1	androgen-regulated short-chain dehydrogenase/reductase 1	62.19	0.00	-10.15	0.01	-15.44	0.00	-10.79	0.01	-13.18	0.00
99591_i_at	Arsdr1	androgen-regulated short-chain dehydrogenase/reductase 1	22.94	0.01	-12.82	0.07	-12.82	0.07	-15.76	0.03	-17.88	0.01
99403_at	Art2a	ADP-ribosyltransferase 2a	-3.47	0.01	-0.70	0.49	0.69	0.50	2.99	0.01	-2.97	0.01
100599_at	Atf4	activating transcription factor 4	66.97	0.00	-3.58	0.16	-5.85	0.03	-2.41	0.33	-10.56	0.00
103006_at	Atf5	activating transcription factor 5	77.37	0.01	9.96	0.01	-0.95	0.77	-2.93	0.37	9.42	0.01

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
101984_at	Atox1	ATX1 (antioxidant protein 1) homolog 1 (yeast)	97.07	0.03	-2.76	0.48	-4.04	0.30	1.06	0.78	13.21	0.00
92798_at	Atp5c1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	94.34	0.03	-1.95	0.11	2.23	0.07	-1.41	0.24	-2.63	0.04
96281_at	Atp6v1g1	ATPase, H+ transporting, lysosomal 13kD, V1 subunit G isoform 1	61.96	0.00	-2.12	0.23	-1.91	0.28	0.52	0.77	-8.77	0.00
160577_at	Atp9a	ATPase, class II, type 9A	56.89	0.01	1.13	0.61	3.30	0.15	-1.16	0.61	9.08	0.00
93174_at	AU016588	expressed sequence AU016588	20.96	0.04	-5.64	0.04	-5.23	0.05	-4.20	0.11	1.50	0.55
102381_at	AU018108	expressed sequence AU018108	50.99	0.00	-5.88	0.07	-5.57	0.08	-3.22	0.30	-21.08	0.00
95564_at	AU018638	expressed sequence AU018638	18.63	0.00	5.08	0.02	7.79	0.00	1.48	0.46	-10.29	0.00
104046_at	AU021774	expressed sequence AU021774	48.34	0.00	1.04	0.54	3.95	0.03	1.70	0.32	-6.94	0.00
101939_at	AU022812	expressed sequence AU022812	80.36	0.02	-2.54	0.29	-2.95	0.22	-8.43	0.00	-1.22	0.61
103667_at	AU022875	expressed sequence AU022875	65.88	0.02	3.18	0.14	0.68	0.74	-4.31	0.05	-6.26	0.01
161016_at	AV011803	expressed sequence AV011803	25.93	0.00	4.86	0.01	7.82	0.00	7.66	0.00	9.31	0.00
92532_at	Avpr1a	arginine vasopressin receptor 1A	35.34	0.04	-4.69	0.20	-9.70	0.01	-2.16	0.54	-6.16	0.09
103574_at	AW060987	expressed sequence AW060987	18.20	0.01	-0.36	0.89	-6.44	0.02	-4.66	0.09	-7.35	0.01
103697_at	AW061234	expressed sequence AW061234	55.47	0.04	-1.23	0.84	6.22	0.32	-4.96	0.43	-19.88	0.00
103257_at	AW109744	expressed sequence AW109744	94.52	0.01	5.10	0.02	1.78	0.37	-0.65	0.74	6.93	0.00
102920_at	AW215585	expressed sequence AW215585	18.52	0.01	0.68	0.59	-2.31	0.08	-0.31	0.81	-4.67	0.00
103969_at	AW226533	expressed sequence AW226533	39.37	0.03	0.81	0.78	-0.96	0.74	-0.56	0.84	-10.22	0.00
160261_i_at	AW228608	expressed sequence AW228608	40.56	0.00	2.43	0.21	0.71	0.71	-2.54	0.19	-8.61	0.00
160978_at	AW261577	expressed sequence AW261577	10.37	0.01	-18.41	0.01	-11.52	0.06	-11.81	0.06	3.78	0.53
103456_at	AW322500	expressed sequence AW322500	66.22	0.03	1.03	0.63	-2.60	0.23	1.57	0.47	7.19	0.00
102961_at	AW413091	expressed sequence AW413091	105.52	0.00	-0.03	0.98	0.18	0.90	8.62	0.00	-0.95	0.52
103890_at	AW538196	expressed sequence AW538196	12.51	0.04	12.61	0.00	-4.78	0.23	1.30	0.74	-3.06	0.44
97425_at	AW547365	expressed sequence AW547365	30.34	0.00	-1.91	0.47	-11.78	0.00	-8.96	0.00	0.58	0.83
104128_at	AW556797	expressed sequence AW556797	38.85	0.02	3.98	0.09	6.84	0.01	-2.55	0.27	3.10	0.18
94432_at	AW742324	expressed sequence AW742324	51.96	0.04	-4.72	0.18	-7.98	0.03	-2.33	0.50	7.51	0.04
160148_at	Bach2	BTB and CNC homology 2	11.34	0.04	2.45	0.38	-2.55	0.36	-3.51	0.21	8.30	0.01
96167_at	Bag3	Bcl2-associated athanogene 3	36.40	0.01	9.12	0.05	10.99	0.02	-6.84	0.14	-9.74	0.04
161980_f_at	Bag3	Bcl2-associated athanogene 3	18.78	0.00	8.29	0.01	11.78	0.00	2.27	0.44	-10.36	0.00
103098_at	Baiap2	brain-specific angiogenesis inhibitor 1-associated protein 2	49.55	0.00	-2.33	0.36	-0.35	0.89	-8.84	0.00	8.72	0.00
98512_at	Banp	Btg3 associated nuclear protein	37.83	0.04	-4.42	0.13	5.03	0.09	-0.90	0.75	-7.18	0.02
96155_at	BC002318	cDNA sequence BC002318	61.74	0.03	4.71	0.01	0.46	0.79	3.54	0.05	1.54	0.36
95517_i_at	BC004004	cDNA sequence BC004004	82.60	0.00	-3.62	0.02	-5.53	0.00	-5.43	0.00	3.06	0.05

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
100949_at	BC004044	cDNA sequence BC004044	-21.87	0.03	23.25	0.01	-11.35	0.16	6.97	0.38	11.84	0.15
94830_at	BC005537	cDNA sequence BC005537	50.03	0.04	7.92	0.00	2.79	0.27	-1.32	0.60	-0.93	0.71
104630_at	BC021611	cDNA sequence BC021611	13.56	0.01	9.15	0.02	-4.10	0.26	2.04	0.57	10.58	0.01
104632_at	BC021611	cDNA sequence BC021611	19.19	0.04	16.85	0.01	1.34	0.82	5.34	0.38	11.54	0.07
104110_at	BC031407	cDNA sequence BC031407	48.39	0.00	2.20	0.20	1.10	0.51	-4.99	0.01	-7.70	0.00
160677_at	BC031407	cDNA sequence BC031407	7.22	0.03	13.10	0.00	1.75	0.65	1.18	0.76	-4.41	0.26
161996_f_at	Bcan	brevican	-1.80	0.02	-3.30	0.41	2.33	0.56	-6.26	0.13	-13.66	0.00
92700_at	Bcan	brevican	-32.24	0.01	2.17	0.10	-1.79	0.16	2.51	0.06	3.85	0.01
93252_at	Bcap31	B-cell receptor-associated protein 31	74.90	0.01	-0.52	0.79	-3.99	0.05	-4.09	0.05	6.29	0.00
96035_at	Bckdha	branched chain ketoacid dehydrogenase E1, alpha polypeptide	70.97	0.02	4.35	0.07	-3.00	0.20	-1.82	0.43	6.95	0.01
102302_at	Bckdhb	branched chain ketoacid dehydrogenase E1, beta polypeptide	62.97	0.00	1.14	0.59	3.20	0.14	2.93	0.18	9.64	0.00
96044_at	Bcl2l10	Bcl2-like 10	8.65	0.04	-3.08	0.09	-4.91	0.01	0.08	0.96	1.92	0.28
160380_at	Becn1	beclin 1 (coiled-coil, myosin-like BCL2-interacting protein)	54.97	0.03	5.26	0.00	0.41	0.78	0.50	0.74	-1.22	0.42
104701_at	Bhlhb2	basic helix-loop-helix domain containing, class B2	63.45	0.01	3.42	0.48	17.03	0.00	11.44	0.03	5.76	0.24
101189_at	Bid3	BH3 interacting (with BCL2 family) domain, apoptosis agonist	-4.19	0.02	2.64	0.12	3.72	0.04	-2.80	0.10	-3.33	0.06
93288_at	Biklk	Bcl2-interacting killer-like	80.84	0.02	3.16	0.09	0.15	0.93	6.39	0.00	0.09	0.96
92220_s_at	Bin1	myc box dependent interacting protein 1	21.98	0.00	0.97	0.63	-7.89	0.00	-3.31	0.11	3.25	0.12
102734_at	Birc3	baculoviral IAP repeat-containing 3	16.13	0.00	9.98	0.01	10.67	0.00	8.45	0.02	6.70	0.05
161883_f_at	Birc3	baculoviral IAP repeat-containing 3	24.77	0.02	-3.72	0.15	3.75	0.15	-8.00	0.00	1.12	0.65
98055_at	Blcap	bladder cancer associated protein homolog (human)	24.45	0.00	-3.65	0.21	-7.09	0.02	-10.32	0.00	2.35	0.41
162221_i_at	Blmh	bleomycin hydrolase	13.91	0.02	1.57	0.33	5.61	0.00	2.08	0.20	-1.04	0.51
93455_s_at	Bmp4	bone morphogenetic protein 4	40.20	0.02	-9.85	0.00	2.78	0.35	-1.60	0.59	-3.93	0.19
161028_at	Bmp6	bone morphogenetic protein 6	-7.35	0.03	8.69	0.05	11.19	0.01	4.59	0.28	-3.56	0.40
101903_at	Bop	CD8beta opposite strand	-15.05	0.04	1.55	0.37	-3.70	0.04	2.32	0.19	3.78	0.04
98066_r_at	Brd2	bromodomain-containing 2	29.75	0.00	4.21	0.22	-7.76	0.03	-3.73	0.27	-23.70	0.00
98947_at	Brd3	bromodomain-containing 3	-4.48	0.04	0.38	0.82	-2.34	0.18	-5.51	0.00	0.06	0.97
96037_at	Bri3	brain protein I3	78.60	0.00	5.01	0.03	2.12	0.34	-0.85	0.70	8.61	0.00
93104_at	Btg1	B-cell translocation gene 1, anti-proliferative	39.78	0.03	-1.57	0.48	-6.70	0.01	-3.91	0.09	2.49	0.27
101583_at	Btg2	B-cell translocation gene 2, anti-proliferative	30.72	0.03	8.19	0.54	10.92	0.41	0.60	0.96	-46.81	0.00
160227_s_at	Bysl	bystin-like	13.25	0.00	12.14	0.00	9.89	0.01	4.02	0.28	-6.18	0.11
96644_at	Bysl	bystin-like	0.22	0.04	-3.22	0.00	-0.26	0.79	0.77	0.42	0.14	0.89
103331_at	C030006K11Rik	RIKEN cDNA C030006K11 gene	41.78	0.00	12.43	0.00	-1.10	0.70	0.01	1.00	4.33	0.14
93454_at	C1qr1	complement component 1, q subcomponent, receptor 1	9.69	0.04	-8.42	0.00	-0.74	0.77	1.77	0.48	-1.17	0.64

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
103673_at	C2	complement component 2 (within H-2S)	78.33	0.01	-1.26	0.68	-6.74	0.04	-2.84	0.36	-10.34	0.00
93497_at	C3	complement component 3	133.28	0.00	-2.29	0.01	-2.93	0.00	1.01	0.24	-3.86	0.00
103908_at	C330016H24Rik	RIKEN cDNA C330016H24 gene	19.55	0.01	6.78	0.00	-2.68	0.12	-1.34	0.43	-0.15	0.93
103033_at	C4	complement component 4 (within H-2S)	129.92	0.01	3.86	0.11	0.43	0.85	8.67	0.00	2.28	0.33
102799_at	C4bp	complement component 4 binding protein	109.10	0.01	3.06	0.20	1.99	0.39	9.09	0.00	2.54	0.28
97666_r_at	C76213	expressed sequence C76213	1.50	0.01	4.84	0.03	1.53	0.46	-7.91	0.00	-0.98	0.64
97179_at	C76683	expressed sequence C76683	28.96	0.00	-0.61	0.79	2.86	0.21	4.25	0.07	9.65	0.00
103681_at	C76904	expressed sequence C76904	44.29	0.01	4.42	0.00	2.01	0.14	2.39	0.08	0.80	0.54
161973_r_at	C76907	expressed sequence C76907	-5.90	0.00	19.50	0.00	8.09	0.12	12.11	0.03	8.89	0.09
95857_at	C76972	expressed sequence C76972	-3.88	0.02	3.26	0.07	4.04	0.03	0.75	0.66	-4.06	0.03
95965_at	C77545	expressed sequence C77545	0.20	0.02	-1.18	0.42	-4.83	0.00	2.66	0.08	1.18	0.42
160885_at	C78391	expressed sequence C78391	69.15	0.02	2.28	0.08	1.07	0.40	2.25	0.08	-3.37	0.01
95975_at	C78811	expressed sequence C78811	2.59	0.01	-2.23	0.14	-1.16	0.43	5.95	0.00	1.07	0.47
103132_at	C78948	expressed sequence C78948	0.85	0.04	-2.84	0.04	1.36	0.31	0.34	0.80	3.34	0.02
161111_f_at	C78960	expressed sequence C78960	1.00	0.04	5.03	0.03	-0.43	0.84	0.63	0.77	5.54	0.02
101057_at	C79672	expressed sequence C79672	46.67	0.05	2.96	0.22	-3.19	0.19	1.65	0.49	6.59	0.01
96736_at	C79715	expressed sequence C79715	43.83	0.05	-3.97	0.13	-5.60	0.04	-2.88	0.26	4.27	0.10
97084_at	C80993	expressed sequence C80993	-2.33	0.01	-7.87	0.01	-4.49	0.10	-3.44	0.20	-5.77	0.04
160907_at	C81234	expressed sequence C81234	46.85	0.01	-8.03	0.00	-1.59	0.44	-3.29	0.12	-2.44	0.24
94786_at	C81272	expressed sequence C81272	1.60	0.03	-0.41	0.78	-4.76	0.00	-0.16	0.91	2.31	0.12
95531_at	C81439	expressed sequence C81439	14.93	0.01	0.05	0.96	-3.57	0.01	-3.54	0.01	-0.03	0.98
95445_at	C81457	expressed sequence C81457	52.61	0.01	0.16	0.91	2.74	0.07	4.42	0.01	2.61	0.08
92445_at	Cacna1a	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	-19.14	0.01	7.55	0.09	-7.12	0.11	-5.93	0.18	-13.71	0.00
98483_at	Cacnb3	calcium channel, voltage-dependent, beta 3 subunit	7.78	0.02	-6.86	0.00	-4.30	0.06	-1.08	0.62	0.88	0.68
96522_at	Calm1	calmodulin 1	92.65	0.03	1.89	0.38	1.86	0.39	0.32	0.88	7.40	0.00
100932_at	Capn1	calpain 1	-35.34	0.04	11.57	0.01	-5.99	0.18	-3.17	0.47	7.16	0.11
101040_at	Capn2	calpain 2	44.10	0.01	4.88	0.00	-0.10	0.94	1.65	0.25	3.26	0.03
98127_at	Cappa2	capping protein alpha 2	43.52	0.01	2.01	0.33	-0.91	0.66	-3.02	0.15	8.00	0.00
160375_at	Car3	carbonic anhydrase 3	133.95	0.02	-5.12	0.01	-1.90	0.32	-3.81	0.06	-2.93	0.13
161263_f_at	Casp2	caspase 2	8.36	0.03	0.59	0.82	3.08	0.25	8.77	0.00	-2.75	0.30
98437_at	Casp3	caspase 3, apoptosis related cysteine protease	46.88	0.02	-5.99	0.04	-7.01	0.02	2.71	0.34	-4.20	0.14
94458_at	Casp6	caspase 6	25.74	0.00	3.17	0.33	-15.17	0.00	1.77	0.59	-0.78	0.81
102328_at	Casp8	caspase 8	27.20	0.00	7.50	0.00	5.15	0.00	3.07	0.04	1.32	0.36
95062_at	Cast	calpastatin	25.47	0.01	8.73	0.01	1.41	0.62	4.03	0.17	-7.22	0.02
92228_at	Catna2	catenin alpha 2	36.14	0.04	-3.12	0.29	4.60	0.12	-0.81	0.78	-8.53	0.01
98152_at	Catns	catenin src	69.47	0.00	-7.83	0.02	-0.69	0.82	-11.89	0.00	-5.67	0.08
99050_at	Cav3	caveolin 3	8.74	0.02	-7.25	0.14	9.46	0.06	8.70	0.08	10.00	0.05

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
102397_at	Cbfa2t3h	core-binding factor, runt domain, alpha subunit 2; translocated to, 3 homolog (human)	10.20	0.03	0.42	0.85	1.70	0.43	-5.48	0.02	-5.39	0.02
93546_s_at	Cbfb	core binding factor beta	50.36	0.01	0.52	0.83	4.91	0.05	3.83	0.12	-7.37	0.01
96110_at	Cbr1	carbonyl reductase 1	35.47	0.02	-4.39	0.25	-14.03	0.00	-2.25	0.55	-0.87	0.82
161042_at	Cbr3	carbonyl reductase 3	-16.40	0.05	13.72	0.00	1.34	0.74	-1.89	0.64	0.87	0.83
102833_at	Cbx2	chromobox homolog 2 (Drosophila Pc class)	6.03	0.02	1.76	0.59	0.79	0.81	0.27	0.93	12.54	0.00
102834_at	Cbx2	chromobox homolog 2 (Drosophila Pc class)	-2.28	0.03	3.16	0.04	3.23	0.04	-1.86	0.22	1.95	0.20
94166_g_at	Ccl1	chemokine (C-C motif) ligand 1	6.42	0.02	1.86	0.17	0.38	0.77	-3.92	0.01	-2.60	0.06
102424_at	Ccl3	chemokine (C-C motif) ligand 3	13.45	0.04	-7.88	0.00	-2.99	0.24	-1.13	0.65	-2.01	0.42
162198_f_at	Ccl6	chemokine (C-C motif) ligand 6	4.51	0.04	-0.16	0.91	2.12	0.14	2.64	0.07	3.57	0.02
104388_at	Ccl9	chemokine (C-C motif) ligand 9	82.51	0.00	-15.84	0.00	-24.28	0.00	-24.55	0.00	-24.68	0.00
160127_at	Ccng	cyclin G	13.43	0.00	1.11	0.44	6.38	0.00	2.92	0.05	5.84	0.00
98478_at	Ccng2	cyclin G2	39.30	0.04	-8.05	0.10	-13.06	0.01	-6.28	0.19	0.55	0.91
93908_f_at	Ccr4	carbon catabolite repression 4 homolog (S. cerevisiae)	23.42	0.00	2.47	0.26	5.85	0.01	-1.02	0.64	-8.16	0.00
99535_at	Ccr4	carbon catabolite repression 4 homolog (S. cerevisiae)	49.98	0.02	17.61	0.02	6.75	0.35	11.31	0.12	-16.65	0.03
162384_f_at	Ccr4	carbon catabolite repression 4 homolog (S. cerevisiae)	13.06	0.01	11.86	0.03	2.26	0.66	15.64	0.01	-9.55	0.07
93907_f_at	Ccr4	carbon catabolite repression 4 homolog (S. cerevisiae)	68.61	0.03	0.02	1.00	4.70	0.10	-2.22	0.43	-8.91	0.00
162052_i_at	Ccs	copper chaperone for superoxide dismutase	-0.59	0.03	-3.21	0.03	-1.79	0.19	0.00	1.00	-3.13	0.03
100600_at	Cd24a	CD24a antigen	15.97	0.02	-4.73	0.20	8.34	0.03	4.97	0.18	8.53	0.03
102971_at	Cd3e	CD3 antigen, epsilon polypeptide	-13.88	0.04	5.33	0.04	3.49	0.17	5.06	0.05	3.17	0.21
103480_at	Cd4	CD4 antigen	16.89	0.01	-2.42	0.69	23.68	0.00	1.67	0.78	-5.78	0.35
101878_at	Cd72	CD72 antigen	-0.84	0.01	0.65	0.51	-1.52	0.14	2.93	0.01	2.68	0.01
101495_at	Cd81	CD 81 antigen	82.81	0.03	3.39	0.15	0.02	0.99	0.88	0.70	7.79	0.00
95661_at	Cd9	CD9 antigen	30.79	0.00	-6.48	0.02	-10.03	0.00	-4.50	0.08	-1.36	0.59
102664_at	Cdk5r	cyclin-dependent kinase 5, regulatory subunit (p35)	18.76	0.04	8.78	0.02	-0.01	1.00	-7.87	0.03	-0.95	0.78
104159_at	Ceacam9	CEA-related cell adhesion molecule 9	7.18	0.01	-3.97	0.06	7.34	0.00	2.01	0.32	-2.68	0.19
94466_f_at	Cebpa-rs1	CCAAT/enhancer binding protein alpha (C/EBP), related sequence 1	30.19	0.00	3.42	0.10	0.34	0.86	-1.12	0.57	-9.75	0.00
92364_at	Celsr2	cadherin EGF LAG seven-pass G-type receptor 2	19.96	0.04	-7.22	0.02	-0.48	0.86	-3.02	0.29	-5.77	0.05
101539_f_at	Ces3	carboxylesterase 3	94.70	0.02	-10.61	0.08	-12.23	0.04	-15.87	0.01	-0.69	0.90
101538_i_at	Ces3	carboxylesterase 3	98.41	0.02	-11.95	0.09	-14.44	0.05	-18.16	0.02	-2.40	0.73
99927_at	Cfi	complement component factor i	119.85	0.02	-0.62	0.74	-0.32	0.86	6.47	0.00	-3.17	0.11
92659_at	Cgef2-pending	cAMP-regulated guanine nucleotide exchange factor II	36.06	0.00	4.64	0.26	3.02	0.46	2.13	0.60	-18.19	0.00
101459_at	Chd1	chromodomain helicase DNA binding protein 1	32.42	0.01	2.13	0.26	-0.27	0.89	-0.60	0.75	-7.22	0.00
92694_at	Chi3l3	chitinase 3-like 3	5.90	0.04	-4.66	0.01	-0.16	0.92	0.09	0.95	2.42	0.12
100516_at	Chk	choline kinase	19.70	0.02	-7.12	0.23	-11.16	0.07	-16.89	0.01	-9.13	0.13

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
160330_at	Chordc1	cysteine and histidine-rich domain (CHORD)-containing, zinc-binding protein 1	59.56	0.00	-0.92	0.69	10.06	0.00	1.02	0.66	-5.32	0.03
95050_at	Chordc1	cysteine and histidine-rich domain (CHORD)-containing, zinc-binding protein 1	47.99	0.00	-0.64	0.74	8.30	0.00	-0.33	0.86	-5.75	0.01
96607_at	Chp-pending	calcium binding protein P22	98.00	0.05	3.97	0.03	3.52	0.04	-0.25	0.88	-1.92	0.25
100126_at	Chrac1	chromatin accessibility complex 1	41.63	0.01	0.30	0.93	-12.42	0.00	-0.90	0.79	6.56	0.07
96996_at	Chrna6	cholinergic receptor, nicotinic, alpha polypeptide 6	-0.30	0.04	-1.40	0.68	3.73	0.28	-6.88	0.05	-9.13	0.01
102329_at	Cideb	cell death-inducing DNA fragmentation factor, alpha subunit-like effector B	114.56	0.01	3.55	0.06	2.33	0.20	0.72	0.68	6.78	0.00
93284_at	Cirbp	cold inducible RNA binding protein	36.03	0.01	-2.96	0.32	-8.80	0.01	-6.73	0.03	4.16	0.16
97468_at	Cks1	CDC28 protein kinase 1	20.90	0.02	-1.46	0.52	8.05	0.00	2.61	0.25	-0.22	0.92
101758_at	Cktsf1b1	cysteine knot superfamily 1, BMP antagonist 1	-2.39	0.03	-1.97	0.63	9.60	0.03	2.55	0.53	10.43	0.02
162287_r_at	Clca3	chloride channel calcium activated 3	0.60	0.02	3.75	0.03	-1.93	0.23	2.67	0.11	-3.60	0.03
160415_at	Cldn1	claudin 1	60.98	0.00	-9.28	0.03	-11.88	0.01	-10.74	0.01	6.22	0.14
94493_at	Cldn3	claudin 3	70.59	0.00	3.22	0.17	-5.77	0.02	-3.22	0.17	10.22	0.00
93274_at	Clk	CDC-like kinase	57.04	0.00	0.07	0.96	-5.21	0.00	-4.46	0.01	-9.49	0.00
92257_at	Clock	circadian locomoter output cycles kaput	38.53	0.04	-6.11	0.09	-4.59	0.19	-9.57	0.01	0.45	0.90
93048_at	Clpp	caseinolytic protease, ATP-dependent, proteolytic subunit homolog (E. coli)	69.22	0.01	-2.28	0.24	-6.07	0.00	-3.76	0.06	-2.39	0.22
161294_f_at	Clu	clusterin	108.15	0.02	0.87	0.64	2.81	0.14	6.02	0.00	-2.41	0.21
94173_at	Cmkar3	chemokine (C-X-C) receptor 3	21.50	0.01	-0.47	0.89	-0.23	0.94	-8.03	0.02	10.68	0.00
101086_f_at	Cnbp	cellular nucleic acid binding protein	72.31	0.03	-2.60	0.39	-7.81	0.02	-7.19	0.03	-0.20	0.95
101088_f_at	Cnbp	cellular nucleic acid binding protein	69.69	0.03	-2.99	0.28	-5.03	0.08	-7.70	0.01	1.89	0.49
160830_at	Cnil	cornichon-like (Drosophila)	-6.54	0.03	0.48	0.89	-10.54	0.01	-1.67	0.62	5.95	0.09
161636_r_at	Cnk	cytokine inducible kinase	108.54	0.05	-1.54	0.62	5.43	0.09	-1.43	0.65	-8.79	0.01
92313_at	Col12a1	procollagen, type XII, alpha 1	2.22	0.02	-0.48	0.80	-2.56	0.18	0.25	0.89	6.57	0.00
99638_at	Col15a1	procollagen, type XV	102.28	0.03	4.12	0.03	-3.57	0.05	1.99	0.27	2.79	0.13
101882_s_at	Col18a1	procollagen, type XVIII, alpha 1	100.82	0.01	7.58	0.01	-5.86	0.02	-2.76	0.26	3.57	0.15
104483_at	Col9a1	procollagen, type IX, alpha 1	30.50	0.03	-1.39	0.75	-3.16	0.47	-12.82	0.01	-8.22	0.07
94992_at	Copb1	coatomer protein complex, subunit beta 1	64.89	0.05	2.87	0.15	5.19	0.02	2.95	0.14	-1.01	0.61
93341_r_at	Copb2	coatomer protein complex, subunit beta 2 (beta prime)	84.32	0.01	4.89	0.01	1.76	0.30	3.34	0.06	4.28	0.02
93340_f_at	Copb2	coatomer protein complex, subunit beta 2 (beta prime)	63.64	0.00	5.92	0.00	2.91	0.09	3.70	0.03	3.15	0.06
93582_at	Coq7	demethyl-Q 7	39.28	0.03	0.08	0.98	-3.40	0.26	4.97	0.11	9.19	0.01
162319_i_at	Cox6c	cytochrome c oxidase, subunit VIc	52.45	0.01	-11.83	0.00	-7.47	0.05	2.11	0.55	1.85	0.60
98505_i_at	Cpo	coproporphyrinogen oxidase	84.58	0.01	1.73	0.31	5.98	0.00	0.79	0.64	2.52	0.14

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
104161_at	Cpsf2	cleavage and polyadenylation specific factor 2, 100kD subunit	3.88	0.05	5.62	0.01	1.75	0.38	3.39	0.10	0.42	0.83
96234_at	Cpsf3	cleavage and polyadenylation specificity factor 3	26.62	0.05	-0.80	0.75	-6.33	0.02	4.26	0.10	-3.61	0.16
93320_at	Cpt1a	carnitine palmitoyltransferase 1, liver	107.43	0.00	12.64	0.00	9.66	0.00	11.39	0.00	8.12	0.00
95646_at	Cpt2	carnitine palmitoyltransferase 2	98.79	0.01	2.64	0.08	4.20	0.01	-1.28	0.38	2.86	0.06
102951_at	Cradd	CASP2 and RIPK1 domain containing adaptor with death domain	6.29	0.02	7.11	0.00	-1.39	0.49	-1.87	0.36	2.57	0.21
103646_at	Crat	carnitine acetyltransferase	5.49	0.03	10.74	0.14	-3.05	0.67	-5.71	0.43	23.55	0.00
160502_at	Creg	cellular repressor of E1A-stimulated genes	79.93	0.00	-6.68	0.02	-7.62	0.01	-11.39	0.00	-2.28	0.38
93760_at	Cript-pending	postsynaptic protein Cript	65.84	0.01	-2.12	0.10	-1.13	0.37	-3.68	0.01	-2.89	0.03
101879_s_at	Crry	complement receptor related protein	36.61	0.02	3.10	0.31	2.77	0.36	4.87	0.12	9.88	0.00
161648_at	Crry	complement receptor related protein	37.15	0.05	0.47	0.88	0.66	0.83	9.10	0.01	4.60	0.14
99900_at	Crx	cone-rod homeobox containing gene	31.23	0.02	-10.69	0.00	2.77	0.41	0.03	0.99	6.33	0.07
94421_r_at	Cry1	cryptochrome 1 (photolyase-like)	0.38	0.04	3.96	0.01	0.86	0.51	-0.72	0.58	1.89	0.15
94420_f_at	Cry1	cryptochrome 1 (photolyase-like)	20.84	0.05	-1.48	0.75	0.31	0.95	-7.41	0.13	14.13	0.01
162448_f_at	Cryac	crystallin, alpha C	7.01	0.00	5.84	0.15	5.75	0.16	4.43	0.27	-16.16	0.00
160139_at	Cryac	crystallin, alpha C	90.58	0.02	0.34	0.94	5.97	0.16	0.00	1.00	-14.81	0.00
93457_at	Crygb	crystallin, gamma B	1.19	0.02	2.13	0.09	0.18	0.88	3.89	0.00	0.65	0.59
98131_at	Cryz	crystallin, zeta	64.67	0.01	2.84	0.31	0.80	0.77	-1.48	0.59	10.98	0.00
99666_at	Cs	citrate synthase	59.20	0.03	-2.48	0.18	-2.69	0.15	-1.11	0.54	5.44	0.01
99184_at	Csad	cysteine sulfinic acid decarboxylase	72.52	0.00	-15.64	0.01	-25.63	0.00	-27.21	0.00	-24.77	0.00
97940_at	Csh1	chorionic somatomammotropin hormone 1	3.97	0.04	-3.22	0.05	1.44	0.36	-0.74	0.64	3.97	0.02
94483_at	Csnk2a2	casein kinase II, alpha 2, polypeptide	12.24	0.02	0.34	0.77	-0.01	0.99	2.23	0.07	3.83	0.00
98798_at	Cspg3	chondroitin sulfate proteoglycan 3	0.82	0.03	3.77	0.23	-2.35	0.45	5.08	0.11	8.98	0.01
102853_at	Cspg6	chondroitin sulfate proteoglycan 6	6.99	0.03	5.30	0.05	-3.42	0.19	-0.92	0.72	-6.89	0.01
100581_at	Cstb	cystatin B	76.22	0.01	-3.68	0.10	-2.70	0.22	1.98	0.37	8.46	0.00
103581_at	Cte1	cytosolic acyl-CoA thioesterase 1	36.20	0.05	-3.21	0.46	-7.58	0.09	-10.30	0.03	6.59	0.14
95608_at	Ctsb	cathepsin B	14.53	0.01	4.21	0.09	0.57	0.81	9.39	0.00	-1.65	0.49
101020_at	Ctsc	cathepsin C	26.87	0.00	11.83	0.00	-3.53	0.27	9.39	0.01	2.79	0.39
101019_at	Ctsc	cathepsin C	47.00	0.04	6.65	0.14	0.49	0.91	13.42	0.01	0.61	0.89
92924_at	Ctsg	cathepsin G	4.33	0.00	-3.99	0.10	3.74	0.12	0.84	0.72	9.45	0.00
94834_at	Ctsh	cathepsin H	97.46	0.01	1.21	0.26	-0.90	0.40	3.28	0.01	2.23	0.04
101963_at	Ctsl	cathepsin L	105.80	0.01	-2.96	0.09	-3.44	0.05	4.54	0.01	-2.86	0.10
92214_at	Ctsw	cathepsin W	-12.27	0.05	0.86	0.75	-0.58	0.83	-7.41	0.01	-5.57	0.05
92633_at	Ctsz	cathepsin Z	64.22	0.03	-3.71	0.15	-7.50	0.01	-3.94	0.13	-0.35	0.89
104073_at	Cugbp1	CUG triplet repeat, RNA binding protein 1	5.81	0.01	-0.45	0.82	4.64	0.03	2.57	0.20	-6.46	0.00
94002_at	Cul1	cullin 1	46.44	0.03	-2.51	0.09	-3.48	0.02	-2.02	0.16	-1.71	0.23
92797_at	Cul3	cullin 3	40.83	0.04	2.13	0.27	-2.58	0.19	-1.41	0.46	-5.48	0.01
102025_at	Cxcl13	chemokine (C-X-C motif) ligand 13	-0.08	0.01	-0.64	0.65	-3.01	0.04	-1.55	0.27	-4.92	0.00
101160_at	Cxcl2	chemokine (C-X-C motif) ligand 2	-1.12	0.01	0.62	0.64	-0.96	0.47	4.89	0.00	-1.65	0.22
100059_at	Cyba	cytochrome b-245, alpha polypeptide	21.37	0.01	6.49	0.04	-1.94	0.53	8.36	0.01	7.41	0.02

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
162469_r_at	Cyc1	cytochrome c-1	74.09	0.02	-9.41	0.01	3.51	0.25	-2.49	0.41	-4.62	0.14
103467_g_at	Cyhr1	cysteine and histidine rich 1	23.51	0.01	3.51	0.14	-7.37	0.00	-0.39	0.87	6.52	0.01
98320_at	Cyp26a1	cytochrome P450, 26, retinoic acid A1	22.59	0.00	-30.33	0.01	-9.17	0.39	-20.83	0.06	-42.91	0.00
102847_s_at	Cyp2a4	cytochrome P450, 2a4	132.26	0.01	-1.17	0.74	-0.60	0.87	-3.38	0.35	-15.24	0.00
102701_at	Cyp2b10	cytochrome P450, 2b10, phenobarbitol inducible, type b	47.05	0.02	-17.28	0.04	-5.94	0.46	-24.76	0.01	-1.04	0.90
102820_at	Cyp2b13	cytochrome P450, 2b13, phenobarbitol inducible, type c	-2.43	0.00	3.33	0.34	3.37	0.34	5.93	0.10	15.86	0.00
101862_at	Cyp2b9	cytochrome P450, 2b9, phenobarbitol inducible, type a	-1.05	0.00	2.93	0.83	20.76	0.14	21.59	0.13	60.52	0.00
99083_at	Cyp2c37	cytochrome P450, 2c37	129.82	0.00	-4.37	0.06	-1.24	0.57	-7.09	0.00	-5.42	0.02
102084_f_at	Cyp2c38	cytochrome P450, 2c38	94.39	0.04	-5.38	0.23	-11.45	0.02	-9.28	0.05	-1.90	0.67
96334_f_at	Cyp2c40	cytochrome P450, 2c40	128.31	0.00	-11.01	0.00	-10.41	0.00	-12.15	0.00	-11.68	0.00
94539_f_at	Cyp2d9	cytochrome P450, 2d9	138.89	0.01	1.25	0.29	0.95	0.41	-3.41	0.01	2.87	0.02
162174_at	Cyp2d9	cytochrome P450, 2d9	103.22	0.00	0.28	0.77	0.99	0.31	-4.45	0.00	0.25	0.79
100069_at	Cyp2f2	cytochrome P450, 2f2	125.51	0.01	-0.66	0.78	-0.09	0.97	-5.72	0.03	-8.42	0.00
93770_at	Cyp3a11	cytochrome P450, steroid inducible 3a11	138.51	0.00	-24.54	0.00	-28.95	0.00	-37.26	0.00	-31.75	0.00
99463_at	Cyp3a13	cytochrome P450, steroid inducible 3a13	85.01	0.01	-3.48	0.10	-6.40	0.01	2.43	0.25	-5.15	0.02
101639_r_at	Cyp3a16	cytochrome P450, 3a16	84.46	0.00	-43.75	0.00	-55.10	0.00	-63.61	0.00	-55.56	0.00
101638_s_at	Cyp3a16	cytochrome P450, 3a16	145.09	0.00	-30.99	0.00	-41.97	0.00	-54.11	0.00	-37.38	0.00
104024_at	Cyp3a25	cytochrome P450, 3a25	102.19	0.00	-14.85	0.00	-14.71	0.00	-19.05	0.00	-11.98	0.00
103353_f_at	Cyp4b1	cytochrome P450, subfamily IV B, polypeptide 1	40.61	0.00	-0.65	0.73	-4.69	0.02	-7.92	0.00	1.77	0.36
94916_at	Cyp51	cytochrome P450, 51	51.88	0.00	-14.33	0.08	-17.12	0.04	-10.08	0.21	-31.83	0.00
99404_at	Cyp7a1	cytochrome P450, 7a1	4.98	0.00	1.40	0.73	2.69	0.51	14.13	0.00	-14.11	0.00
103284_at	Cyp8b1	cytochrome P450, 8b1, sterol 12 alpha-hydrolase	92.58	0.00	-9.99	0.03	-6.26	0.15	-11.60	0.01	10.81	0.02
96757_at	D10Jhu81e	DNA segment, Chr 10, Johns Hopkins University 81 expressed	69.36	0.02	2.78	0.23	-5.41	0.03	-3.88	0.10	5.23	0.03
95894_at	D12Ertd364e	DNA segment, Chr 12, ERATO Doi 364, expressed	-0.67	0.01	-1.86	0.40	-8.47	0.00	-2.65	0.23	1.23	0.57
93775_at	D12Ertd647e	DNA segment, Chr 12, ERATO Doi 647, expressed	80.12	0.02	4.82	0.08	2.85	0.28	8.09	0.01	2.30	0.38
94452_g_at	D13Wsu123e	DNA segment, Chr 13, Wayne State University 123, expressed	60.95	0.01	3.94	0.06	-0.26	0.89	-2.34	0.24	-7.12	0.00
94451_at	D13Wsu123e	DNA segment, Chr 13, Wayne State University 123, expressed	40.82	0.04	1.95	0.22	1.87	0.24	3.06	0.06	-3.82	0.02
93843_at	D14Ertd484e	DNA segment, Chr 14, ERATO Doi 484, expressed	90.18	0.01	2.96	0.08	5.31	0.00	-0.76	0.64	3.77	0.03
96678_at	D14Ucla2	DNA segment, Chr 14, University of California at Los Angeles 2	78.35	0.00	6.81	0.01	1.72	0.44	2.85	0.21	7.90	0.00
160347_at	D15Ertd785e	DNA segment, Chr 15, ERATO Doi 785, expressed	30.61	0.05	2.23	0.25	-5.21	0.01	-1.39	0.47	2.84	0.15

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
104055_at	D16Bwg1543e	DNA segment, Chr 16, Brigham & Women's Genetics 1543 expressed	0.69	0.02	-0.24	0.89	1.26	0.47	-0.25	0.88	-6.67	0.00
104079_at	D16Ertd272e	DNA segment, Chr 16, ERATO Doi 272, expressed	14.55	0.01	0.54	0.79	-2.03	0.32	-7.02	0.00	5.18	0.02
96884_at	D16Ertd465e	DNA segment, Chr 16, ERATO Doi 465, expressed	58.11	0.01	3.97	0.01	2.49	0.08	0.81	0.56	3.81	0.01
160135_at	D16Ertd502e	DNA segment, Chr 16, ERATO Doi 502, expressed	59.62	0.01	2.68	0.20	-3.27	0.12	2.08	0.31	7.29	0.00
95025_at	D16H22S680E	DNA segment, Chr 16, human D22S680E, expressed	59.71	0.00	3.57	0.05	6.96	0.00	7.04	0.00	5.38	0.01
95431_at	D16Wsu109e	DNA segment, Chr 16, Wayne State University 109, expressed	32.71	0.02	0.42	0.87	-1.74	0.49	8.88	0.00	-3.98	0.12
92610_at	D17H6S45	DNA segment, Chr 17, human D6S45	42.75	0.00	-6.40	0.04	-9.26	0.00	-6.73	0.03	-3.85	0.20
94413_at	D18386	expressed sequence D18386	32.74	0.00	0.62	0.73	-5.50	0.01	-3.58	0.06	-9.62	0.00
99823_r_at	D18Ertd232e	DNA segment, Chr 18, ERATO Doi 232, expressed	22.35	0.00	-9.14	0.00	-1.71	0.34	-1.16	0.51	4.28	0.02
95064_at	D18Ertd240e	DNA segment, Chr 18, ERATO Doi 240, expressed	142.33	0.02	0.18	0.87	2.37	0.05	-0.28	0.81	3.78	0.00
161990_f_at	D18Wsu154e	DNA segment, Chr 18, Wayne State University 154, expressed	47.97	0.05	-5.41	0.02	-0.43	0.84	2.19	0.30	-3.97	0.07
96113_at	D18Wsu98e	DNA segment, Chr 18, Wayne State University 98, expressed	59.65	0.02	2.27	0.06	-1.28	0.28	1.01	0.39	3.49	0.01
93841_at	D3Ertd194e	DNA segment, Chr 3, ERATO Doi 194, expressed	41.92	0.03	3.26	0.28	-4.60	0.13	-8.61	0.01	-2.66	0.37
97141_s_at	D3Ertd229e	DNA segment, Chr 3, ERATO Doi 229, expressed	6.52	0.01	-6.83	0.01	2.24	0.35	-0.25	0.92	-7.41	0.00
94395_at	D3Ertd330e	DNA segment, Chr 3, ERATO Doi 330, expressed	18.37	0.01	2.43	0.32	-2.15	0.37	-1.69	0.48	-9.41	0.00
101688_at	D4Ertd58e	DNA segment, Chr 4, ERATO Doi 58, expressed	9.91	0.00	-5.84	0.00	4.15	0.02	1.82	0.29	-2.59	0.13
160381_at	D4Wsu125e	DNA segment, Chr 4, Wayne State University 125, expressed	36.25	0.05	-4.03	0.08	0.43	0.85	-1.43	0.52	-6.29	0.01
160773_at	D4Wsu132e	DNA segment, Chr 4, Wayne State University 132, expressed	12.13	0.00	0.77	0.66	3.55	0.05	5.05	0.01	-4.93	0.01
162178_r_at	D4Wsu132e	DNA segment, Chr 4, Wayne State University 132, expressed	36.84	0.03	-7.06	0.02	6.26	0.03	1.81	0.51	3.28	0.24
161425_r_at	D4Wsu132e	DNA segment, Chr 4, Wayne State University 132, expressed	-4.77	0.03	-15.11	0.03	-15.12	0.03	-1.31	0.84	11.05	0.11
92542_at	D4Wsu53e	DNA segment, Chr 4, Wayne State University 53, expressed	94.30	0.00	-0.91	0.66	-2.11	0.31	1.38	0.50	-13.05	0.00
101225_at	D5Ertd102e	DNA segment, Chr 5, ERATO Doi 102, expressed	26.97	0.00	-5.68	0.00	3.89	0.03	1.17	0.48	-3.85	0.03
97397_at	D5Ertd33e	DNA segment, Chr 5, ERATO Doi 33, expressed	29.48	0.02	-2.40	0.07	-0.71	0.58	-3.60	0.01	-2.13	0.11

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
104418_at	D6Ertd365e	DNA segment, Chr 6, ERATO Doi 365, expressed	20.77	0.00	7.86	0.00	1.60	0.36	-1.18	0.50	-1.13	0.52
96874_g_at	D6Ertd772e	DNA segment, Chr 6, ERATO Doi 772, expressed	90.67	0.00	2.98	0.12	1.47	0.43	0.15	0.93	-8.22	0.00
96875_r_at	D6Ertd772e	DNA segment, Chr 6, ERATO Doi 772, expressed	9.39	0.04	-3.23	0.09	2.84	0.14	2.81	0.14	-3.99	0.04
96646_at	D6Wsu157e	DNA segment, Chr 6, Wayne State University 157, expressed	17.71	0.00	6.09	0.00	5.20	0.01	3.11	0.09	-4.41	0.02
161242_f_at	D6Wsu157e	DNA segment, Chr 6, Wayne State University 157, expressed	-5.56	0.02	0.59	0.78	6.64	0.01	-2.28	0.29	4.13	0.07
103860_at	D7Wsu128e	DNA segment, Chr 7, Wayne State University 128, expressed	-1.56	0.04	-0.48	0.73	2.05	0.16	4.27	0.01	-1.43	0.32
93195_at	D8Ertd91e	DNA segment, Chr 8, ERATO Doi 91, expressed	33.82	0.00	5.40	0.07	-4.64	0.11	5.48	0.06	-11.92	0.00
96520_at	D9Ertd720e	DNA segment, Chr 9, ERATO Doi 720, expressed	6.60	0.00	-4.23	0.01	4.24	0.01	-2.13	0.18	-3.92	0.02
95430_f_at	D9Wsu18e	DNA segment, Chr 9, Wayne State University 18, expressed	39.98	0.01	-1.27	0.52	-2.89	0.15	5.24	0.01	5.01	0.02
103789_at	D9Wsu18e	DNA segment, Chr 9, Wayne State University 18, expressed	16.59	0.03	1.88	0.70	-12.24	0.02	0.88	0.86	12.49	0.02
92198_s_at	Daf2	decay accelerating factor 2	1.28	0.05	3.95	0.05	-3.35	0.10	0.07	0.97	4.12	0.04
94524_at	Dap3	death associated protein 3	39.75	0.03	1.01	0.62	-4.74	0.03	-0.60	0.77	5.53	0.01
160841_at	Dbp	D site albumin promoter binding protein	46.23	0.00	26.68	0.00	25.02	0.00	29.59	0.00	9.06	0.25
98966_at	Dbt	dihydrolipoamide branched chain transacylase E2	37.16	0.04	-4.05	0.24	-2.69	0.43	-6.13	0.08	-8.68	0.02
103842_at	Dby	DEAD (aspartate-glutamate-alanine-aspartate) box polypeptide, Y chromosome	35.49	0.00	6.73	0.00	-0.32	0.87	1.57	0.43	-8.14	0.00
101367_at	Dctn1	dynactin 1	21.43	0.01	3.96	0.09	-5.70	0.02	-5.24	0.03	4.35	0.06
95682_at	Ddb1	damage specific DNA binding protein 1 (127 kDa)	88.06	0.00	3.52	0.02	-0.16	0.91	4.26	0.01	4.00	0.01
160074_at	Ddc	dopa decarboxylase	65.20	0.00	-3.53	0.39	-7.99	0.06	-12.93	0.00	-17.82	0.00
101429_at	Ddit3	DNA-damage inducible transcript 3	8.80	0.01	14.26	0.01	9.71	0.06	8.49	0.10	-6.39	0.21
99025_at	Ddx19	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 19	33.07	0.05	1.30	0.36	-1.64	0.25	-1.35	0.34	-4.12	0.01
94361_at	Ddx21	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 21 (RNA helicase II/Gu)	31.62	0.00	-2.49	0.24	2.02	0.34	0.92	0.66	-10.27	0.00
103598_at	Ddx9	DEAD (aspartate-glutamate-alanine-aspartate) box polypeptide 9	25.42	0.02	1.83	0.36	1.64	0.41	2.59	0.20	-6.84	0.00
160711_at	Decr1	2,4-dienoyl CoA reductase 1, mitochondrial	62.22	0.00	-0.47	0.87	3.52	0.24	2.61	0.38	15.94	0.00
97782_at	Defb2	defensin beta 2	5.62	0.05	-1.85	0.63	-4.30	0.27	-9.65	0.02	7.52	0.06
95688_at	Degs	degenerative spermatocyte homolog (Drosophila)	64.52	0.00	-0.94	0.57	-5.44	0.00	-3.84	0.03	-3.42	0.05

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
103250_at	Dfna5h	deafness, autosomal dominant 5 homolog (human)	0.92	0.02	2.77	0.13	-0.53	0.76	-1.57	0.37	6.21	0.00
98989_at	Dhcr7	7-dehydrocholesterol reductase	22.76	0.02	-1.84	0.62	-12.15	0.00	-1.96	0.60	-7.97	0.05
161397_r_at	Dhodh	dihydroorotate dehydrogenase	-1.56	0.00	-22.43	0.00	-16.41	0.01	-17.47	0.01	5.23	0.38
95552_at	Dio1	deiodinase, iodothyronine, type I	76.05	0.00	13.54	0.01	16.00	0.00	17.34	0.00	14.39	0.01
99881_at	Dkk1	dickkopf homolog 1 (Xenopus laevis)	-1.04	0.03	1.32	0.41	-4.18	0.02	-2.83	0.09	2.24	0.17
161117_at	Dkk2	dickkopf homolog 1 (Xenopus laevis)	1.96	0.01	-2.46	0.17	1.61	0.36	-1.30	0.46	6.83	0.00
97502_at	Dld	dihydrolipoamide dehydrogenase	85.02	0.04	-0.19	0.92	3.95	0.05	0.17	0.93	-5.45	0.01
160892_at	Dlgh3	discs, large homolog 3 (Drosophila)	11.28	0.05	0.28	0.94	-11.84	0.00	2.03	0.58	-2.66	0.47
92930_at	Dlx5	distal-less homeobox 5	3.68	0.02	-6.53	0.00	0.40	0.83	2.68	0.17	-1.85	0.34
96498_at	Dmc1h	disrupted meiotic cDNA 1 homolog	4.34	0.01	-3.69	0.01	-1.00	0.45	-0.65	0.62	-4.38	0.00
97261_at	Dnaja1	DnaJ (Hsp40) homolog, subfamily A, member 1	84.26	0.00	8.15	0.02	18.37	0.00	1.04	0.76	-17.14	0.00
96254_at	Dnajb1	DnaJ (Hsp40) homolog, subfamily B, member 1	25.35	0.00	18.22	0.10	4.84	0.65	-3.00	0.78	-45.57	0.00
96680_at	Dnajb9	DnaJ (Hsp40) homolog, subfamily B, member 9	52.07	0.00	1.58	0.71	18.44	0.00	2.86	0.50	-10.96	0.02
96679_at	Dnajb9	DnaJ (Hsp40) homolog, subfamily B, member 9	24.27	0.00	7.46	0.07	20.62	0.00	-1.13	0.78	-1.65	0.68
103344_at	Dnajc1	DnaJ (Hsp40) homolog, subfamily C, member 1	37.45	0.04	3.66	0.05	0.15	0.93	3.86	0.04	-3.04	0.09
101890_f_at	Dnajc2	DnaJ (Hsp40) homolog, subfamily C, member 2	34.41	0.01	0.32	0.83	2.10	0.18	-4.91	0.00	-3.18	0.05
160153_at	Dnajc7	DnaJ (Hsp40) homolog, subfamily C, member 7	45.29	0.03	-1.82	0.34	-3.21	0.10	-1.02	0.59	-5.71	0.01
94107_at	Dnase1l3	deoxyribonuclease 1-like 3	10.37	0.01	-3.41	0.13	-3.34	0.14	-5.24	0.03	5.57	0.02
100479_at	Dnmt3a	DNA methyltransferase 3A	8.23	0.00	3.90	0.01	-4.47	0.01	0.22	0.88	-2.73	0.07
161409_f_at	Dntt	deoxynucleotidyltransferase, terminal	22.90	0.03	-3.19	0.10	5.07	0.01	-2.74	0.16	1.31	0.49
103886_at	Dp1	deleted in polyposis 1	18.06	0.04	-1.57	0.35	-4.84	0.01	0.47	0.78	2.69	0.12
96134_at	Dp1l1	deleted in polyposis 1-like 1	119.21	0.00	1.37	0.48	3.23	0.11	-3.13	0.12	8.35	0.00
97776_at	Drd2	dopamine receptor 2	13.45	0.04	-6.86	0.01	1.47	0.52	-0.64	0.78	-3.95	0.10
103506_f_at	Dsc2	desmocollin 2	26.56	0.02	3.11	0.24	-6.68	0.02	-2.51	0.34	6.05	0.03
102374_at	Dscr1l2	Down syndrome critical region gene 1-like 2	-14.86	0.04	-6.16	0.04	-4.11	0.17	-2.19	0.45	6.56	0.03
94492_at	Dstn	destrin	99.89	0.04	-2.23	0.17	-3.99	0.02	-0.23	0.89	-3.07	0.07
98431_at	Dusp12	dual specificity phosphatase 12	26.71	0.00	3.10	0.12	-1.80	0.35	5.35	0.01	12.18	0.00
97740_at	Dusp16	dual specificity phosphatase 16	33.28	0.01	8.24	0.00	-0.39	0.84	2.50	0.22	-1.75	0.39
100495_at	Dvl2	dishevelled 2, dsh homolog (Drosophila)	-20.55	0.01	-19.42	0.00	-4.20	0.39	1.54	0.75	-0.05	0.99
96813_f_at	DXImx46e	DNA segment, Chr X, Immunex 46, expressed	44.68	0.00	-0.04	0.98	-1.96	0.14	-1.33	0.31	-5.92	0.00
92383_at	Dyrk1a	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1a	6.44	0.00	1.34	0.15	-3.36	0.00	-0.49	0.59	-4.03	0.00
160292_at	Ecgf1	endothelial cell growth factor 1 (platelet-derived)	90.71	0.01	1.27	0.57	-3.64	0.11	-6.03	0.01	7.15	0.00
93754_at	Ech1	enoyl coenzyme A hydratase 1, peroxisomal	102.72	0.02	1.84	0.55	-1.92	0.54	0.88	0.78	11.74	0.00
104065_at	Edem-pending	ER degradation enhancing alpha mannosidase-like	32.46	0.02	-1.56	0.24	-0.81	0.54	3.40	0.02	-3.20	0.02

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
100435_at	Edg2	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2	-20.72	0.01	7.64	0.01	-6.82	0.01	-1.80	0.48	3.43	0.19
100992_at	Edr1	early development regulator 1 (homolog of polyhomeotic 1)	4.24	0.02	-0.15	0.95	4.28	0.09	-3.76	0.13	7.28	0.01
103342_at	Eed	embryonic ectoderm development	26.85	0.04	0.27	0.83	-4.06	0.00	-0.15	0.90	-1.72	0.19
94429_at	Eef1a2	eukaryotic translation elongation factor 1 alpha 2	55.47	0.00	-2.46	0.21	1.22	0.53	1.59	0.41	-10.10	0.00
103007_at	Efna1	ephrin A1	20.20	0.05	0.31	0.96	8.42	0.16	-8.65	0.15	-15.75	0.01
102869_at	Efna2	ephrin A2	5.00	0.04	-2.95	0.41	-4.15	0.26	-9.02	0.02	6.79	0.07
100289_at	Efna3	ephrin A3	46.84	0.03	-1.97	0.54	5.64	0.09	-3.35	0.30	-9.66	0.01
160857_at	Efnb2	ephrin B2	-2.36	0.04	1.94	0.41	5.35	0.03	0.52	0.83	5.79	0.02
101842_g_at	Egfr	epidermal growth factor receptor	93.33	0.00	1.19	0.85	-5.45	0.39	1.55	0.81	-29.96	0.00
101840_at	Egfr	epidermal growth factor receptor	56.43	0.00	0.80	0.89	2.49	0.68	1.89	0.76	-36.81	0.00
101841_at	Egfr	epidermal growth factor receptor	79.88	0.00	1.80	0.76	-2.99	0.62	1.07	0.86	-30.86	0.00
99629_at	Ei24	etoposide induced 2.4 mRNA	79.90	0.01	-0.12	0.95	2.44	0.26	2.40	0.27	8.03	0.00
93058_at	Eif1a	eukaryotic translation initiation factor 1A	41.92	0.04	-0.82	0.81	10.23	0.01	-2.03	0.56	-5.47	0.12
103994_at	eIF2C2	Piwi/Argonaute family protain meIF2C2	12.53	0.00	10.04	0.00	-6.40	0.03	-4.31	0.12	6.87	0.02
94250_at	Eif3	eukaryotic translation initiation factor 3	49.97	0.00	-1.78	0.40	1.50	0.47	-0.19	0.93	-9.94	0.00
99101_at	Eif3s7	eukaryotic translation initiation factor 3, subunit 7 (zeta, 66/67 kDa)	67.49	0.02	0.70	0.66	-1.77	0.27	-2.92	0.08	-5.26	0.00
93089_at	Eif4a2	eukaryotic translation initiation factor 4A2	96.48	0.00	-2.03	0.17	0.22	0.88	-3.79	0.02	-5.25	0.00
99097_at	Eif4e	eukaryotic translation initiation factor 4E	7.16	0.03	-2.99	0.04	3.44	0.02	1.21	0.38	-2.00	0.16
94001_at	Elavl1	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)	57.50	0.02	1.98	0.16	1.01	0.46	-1.50	0.28	-4.63	0.00
103283_at	Elf5	E74-like factor 5	5.41	0.05	-0.25	0.90	-3.61	0.09	2.32	0.27	-5.52	0.01
102996_at	Ell	eleven-nineteen lysine-rich leukemia gene	55.23	0.05	0.24	0.90	3.39	0.07	0.06	0.97	-5.21	0.01
103891_i_at	Ell2	ELL-related RNA polymerase II, elongation factor	70.07	0.00	3.95	0.10	3.09	0.19	5.27	0.03	-9.84	0.00
97704_at	Ell2	ELL-related RNA polymerase II, elongation factor	9.32	0.01	5.46	0.01	4.30	0.04	-2.37	0.25	-3.89	0.06
92836_at	Eln	elastin	13.31	0.01	-10.75	0.06	-21.04	0.00	-5.70	0.29	-2.52	0.64
92207_at	Eln	elastin	12.65	0.01	-1.63	0.41	7.75	0.00	-0.83	0.67	-2.03	0.31
94393_r_at	Elovl2	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2	78.03	0.01	6.59	0.10	14.18	0.00	1.24	0.75	1.44	0.71
103469_at	Elovl3	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 3	21.21	0.04	-5.33	0.24	-11.13	0.02	-9.21	0.05	-1.27	0.78
161665_at	Emk3	ELKL motif serine-threonine protein kinase 3	4.44	0.01	-2.21	0.03	0.81	0.40	0.85	0.38	-2.91	0.01
97426_at	Emp1	epithelial membrane protein 1	6.29	0.00	3.73	0.06	3.75	0.06	8.48	0.00	4.34	0.03
100134_at	Eng	endoglin	68.70	0.00	1.86	0.25	-3.44	0.04	-2.91	0.08	8.84	0.00
160568_at	Eno1	enolase 1, alpha non-neuron	85.82	0.00	1.05	0.68	-0.78	0.76	-1.10	0.66	14.09	0.00
96344_at	Eno3	enolase 3, beta muscle	40.42	0.02	-14.20	0.00	4.59	0.27	-0.15	0.97	4.37	0.30

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
104174_at	Enpp1	ectonucleotide pyrophosphatase/phosphodiesterase 1	9.36	0.01	7.86	0.02	1.91	0.55	1.75	0.58	11.01	0.00
97317_at	Enpp2	ectonucleotide pyrophosphatase/phosphodiesterase 2	80.42	0.00	5.00	0.04	5.01	0.04	8.15	0.00	1.71	0.46
92561_at	Entpd5	ectonucleoside triphosphate diphosphohydrolase 5	50.33	0.01	0.45	0.83	-0.43	0.84	-9.09	0.00	-0.45	0.83
100051_at	Epb7.2	erythrocyte protein band 7.2	64.67	0.02	2.57	0.31	-1.61	0.52	-8.82	0.00	3.02	0.23
103263_at	Epc1	enhancer of polycomb homolog 1, (Drosophila)	35.56	0.04	1.04	0.67	-7.46	0.01	1.90	0.45	-3.98	0.12
95756_at	Epcs3	ectoplacental cone, invasive trophoblast giant cells, extraembryonic ectoderm and chorion sequence 3	15.52	0.02	0.44	0.73	1.85	0.17	2.36	0.08	-4.00	0.01
95298_at	Epha3	Eph receptor A3	-0.25	0.00	7.10	0.01	-4.02	0.13	0.00	1.00	-8.81	0.00
101587_at	Ephx1	epoxide hydrolase 1, microsomal	94.16	0.00	-10.70	0.00	-10.05	0.00	-13.75	0.00	0.08	0.98
93051_at	Ephx2	epoxide hydrolase 2, cytoplasmic	102.12	0.00	6.83	0.01	8.38	0.00	0.69	0.75	10.01	0.00
103483_at	Ercc5	excision repair cross-complementing rodent repair deficiency,complementation group 5	9.27	0.03	7.31	0.07	-5.09	0.20	-10.53	0.01	-1.53	0.69
98802_at	Ereg	epiregulin	-2.62	0.01	2.27	0.14	0.07	0.96	4.29	0.01	3.51	0.03
97871_at	Ero1l	ERO1-like (S. cerevisiae)	41.14	0.01	-3.24	0.17	6.04	0.02	-0.62	0.79	-6.80	0.01
96906_at	Etohi6	ethanol induced 6	-3.18	0.01	-0.95	0.43	0.09	0.94	-4.79	0.00	0.33	0.78
160119_at	Etv6	ets variant gene 6 (TEL oncogene)	78.74	0.02	0.54	0.94	28.64	0.00	3.01	0.69	-7.55	0.32
99391_at	Evi1	ecotropic viral integration site 1	10.51	0.01	-4.93	0.02	2.36	0.25	-3.96	0.06	-4.76	0.03
94810_at	Ewsh	Ewing sarcoma homolog	57.54	0.05	3.82	0.07	-5.37	0.01	1.72	0.39	-0.03	0.99
99929_at	Ext2	exostoses (multiple) 2	36.15	0.00	-1.99	0.18	-5.49	0.00	-3.92	0.01	5.70	0.00
92453_at	Eya4	eyes absent 4 homolog (Drosophila)	-0.72	0.05	0.11	0.93	-1.39	0.28	-0.86	0.50	-4.00	0.01
96501_at	F10	coagulation factor X	51.78	0.04	-1.85	0.34	-3.78	0.06	5.38	0.01	0.43	0.82
92509_at	F12	coagulation factor XII (Hageman factor)	100.18	0.02	1.79	0.09	-1.08	0.29	3.28	0.00	-0.33	0.74
102748_at	F5	coagulation factor V	103.24	0.01	3.04	0.05	4.33	0.01	3.75	0.02	0.73	0.61
92918_at	F7	coagulation factor VII	77.43	0.01	-2.74	0.23	-5.81	0.02	5.66	0.02	-4.29	0.07
161458_at	F7	coagulation factor VII	71.43	0.01	-4.31	0.07	-4.73	0.04	2.73	0.23	-5.95	0.01
102291_at	F9	coagulation factor IX	98.89	0.00	3.79	0.02	3.11	0.06	6.19	0.00	1.49	0.34
96795_at	Faah	fatty acid amide hydrolase	61.06	0.02	4.99	0.03	-0.69	0.75	0.85	0.69	6.40	0.01
97889_at	Fabp2	fatty acid binding protein 2, intestinal	68.09	0.00	19.71	0.00	23.11	0.00	9.01	0.09	30.62	0.00
99977_at	Fabp6	fatty acid binding protein 6, ileal (gastrotropin)	34.32	0.01	-21.82	0.00	-9.39	0.18	-14.53	0.05	3.35	0.63
104017_at	Facl4	fatty acid-Coenzyme A ligase, long chain 4	13.02	0.00	-1.13	0.64	-0.68	0.78	-0.87	0.72	-13.59	0.00
98588_at	Fah	fumarylacetoacetate hydrolase	127.80	0.04	1.45	0.17	0.67	0.52	1.66	0.12	2.72	0.02
96918_at	Fbp1	fructose bisphosphatase 1	138.23	0.00	0.72	0.46	2.75	0.01	1.83	0.07	4.70	0.00
97410_at	Fbs	fibrosin	19.77	0.05	10.11	0.08	-4.57	0.41	10.81	0.06	-10.41	0.07
96162_at	Fbxo15	f-box only protein 15	-4.01	0.03	4.02	0.00	0.43	0.70	0.02	0.99	0.16	0.89
94917_at	Fbxo8	f-box only protein 8	34.39	0.04	-3.78	0.16	-3.76	0.16	-5.29	0.06	-5.02	0.07
100056_at	Fbxw2	f-box and WD-40 domain protein 2	45.32	0.02	8.30	0.00	-0.72	0.74	-1.69	0.44	1.37	0.53
96799_at	Fbxw5	f-box and WD-40 domain protein 5	25.88	0.02	7.76	0.02	-3.22	0.29	-7.75	0.02	3.32	0.27
101793_at	Fcgr1	Fc receptor, IgG, high affinity I	-27.45	0.01	-10.42	0.02	12.56	0.01	9.30	0.04	-1.42	0.73
97533_at	Fcgrt	Fc receptor, IgG, alpha chain transporter	62.53	0.02	1.62	0.44	0.08	0.97	0.35	0.87	7.98	0.00

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
97518_at	Fdft1	farnesyl diphosphate farnesyl transferase 1	62.93	0.02	-11.94	0.15	-14.73	0.08	-8.48	0.30	-24.78	0.01
99098_at	Fdps	farnesyl diphosphate synthetase	95.72	0.00	-21.08	0.02	-18.05	0.04	-12.51	0.15	-26.04	0.01
160424_f_at	Fdps	farnesyl diphosphate synthetase	80.80	0.00	-22.50	0.01	-18.57	0.04	-11.66	0.17	-29.17	0.00
160062_i_at	Fdx1	ferredoxin 1	-1.34	0.02	3.34	0.19	-6.04	0.02	1.91	0.44	-5.81	0.03
92595_r_at	Fech	ferrochelatase	47.49	0.01	-1.55	0.54	3.54	0.17	-2.58	0.32	-9.36	0.00
160244_at	Fem1a	feminization 1 homolog a (C. elegans)	29.12	0.01	3.06	0.13	2.99	0.14	2.19	0.27	6.60	0.00
93674_at	Fgd1	faciogenital dysplasia homolog (human)	-6.80	0.05	6.14	0.01	-1.26	0.57	-1.92	0.40	3.77	0.10
100494_at	Fgf1	fibroblast growth factor 1	47.41	0.03	7.09	0.00	2.50	0.27	2.55	0.26	-0.87	0.70
94697_at	Fgr	Gardner-Rasheed feline sarcoma viral (Fgr) oncogene homolog	11.30	0.01	-9.88	0.03	-15.49	0.00	-0.83	0.85	-0.34	0.94
99148_at	Fh1	fumarate hydratase 1	90.28	0.04	-0.49	0.80	-2.05	0.30	6.34	0.00	-1.45	0.46
102628_at	Fhit	fragile histidine triad gene	25.05	0.03	-1.09	0.72	6.15	0.06	-4.32	0.17	7.97	0.02
92365_at	Figf	c-fos induced growth factor	3.38	0.02	0.52	0.78	1.28	0.50	-5.59	0.01	-4.56	0.02
93309_at	Fin14	fibroblast growth factor inducible 14	34.95	0.00	3.98	0.07	-2.07	0.33	-3.77	0.09	-12.28	0.00
99007_at	Flot2	flotillin 2	11.56	0.01	10.81	0.01	4.68	0.20	-1.96	0.58	9.48	0.01
162024_at	Fmn	formin	-14.67	0.02	-3.50	0.17	-7.74	0.01	0.20	0.94	-3.95	0.12
92852_at	Fn1	fibronectin 1	117.19	0.01	2.59	0.10	2.86	0.07	5.45	0.00	0.23	0.88
101422_at	Fnbp4	formin binding protein 4	18.95	0.00	-3.91	0.20	-8.09	0.01	-5.20	0.10	-10.57	0.00
98121_at	Fnta	farnesyltransferase, CAAX box, alpha	50.04	0.01	0.90	0.65	-8.36	0.00	-2.12	0.30	1.62	0.42
98306_g_at	Foxm1	forkhead box M1	23.26	0.05	-4.80	0.38	-5.56	0.31	-4.18	0.44	-16.38	0.01
160850_at	Fpgs	folylpolyglutamyl synthetase	78.52	0.01	-4.27	0.07	-7.02	0.01	-3.42	0.14	3.20	0.17
104708_at	Frap1	FK506 binding protein 12-rapamycin associated protein 1	39.30	0.02	4.99	0.01	1.79	0.30	1.65	0.34	3.82	0.03
103309_at	Frap1	FK506 binding protein 12-rapamycin associated protein 1	43.52	0.05	1.84	0.32	1.08	0.55	-3.27	0.08	4.80	0.02
92695_at	Frat1	frequently rearranged in advanced T-cell lymphomas	21.21	0.01	-3.32	0.04	0.83	0.59	-5.44	0.00	1.48	0.34
101407_at	Frda	Friedreich ataxia	21.23	0.00	-0.19	0.94	-0.70	0.79	5.41	0.05	13.81	0.00
94794_at	Fth	ferritin heavy chain	131.19	0.02	-3.92	0.03	-0.93	0.57	-4.26	0.02	2.55	0.13
161913_r_at	Fth	ferritin heavy chain	91.44	0.02	-5.80	0.03	4.57	0.08	-3.82	0.13	-4.46	0.08
162479_f_at	Ftl1	ferritin light chain 1	108.38	0.00	-4.71	0.00	-0.58	0.62	-3.78	0.00	-3.23	0.01
99872_s_at	Ftl1	ferritin light chain 1	143.45	0.00	-3.13	0.00	-1.64	0.06	-4.03	0.00	-0.16	0.85
99415_at	Fzd8	frizzled homolog 8 (Drosophila)	26.36	0.02	4.92	0.10	6.90	0.03	1.44	0.62	7.41	0.02
97531_at	G0s2	G0/G1 switch gene 2	45.51	0.01	-5.82	0.46	4.87	0.53	-7.63	0.33	30.87	0.00
103333_at	G6pc	glucose-6-phosphatase, catalytic	111.28	0.03	-5.52	0.23	-13.98	0.01	-6.56	0.15	-3.28	0.47
97430_at	G6pt1	glucose-6-phosphatase, transport protein 1	98.34	0.00	10.17	0.00	10.71	0.00	7.52	0.00	8.88	0.00
160714_at	Gab1	growth factor receptor bound protein 2-associated protein 1	16.83	0.01	3.38	0.06	-4.94	0.01	1.11	0.52	3.99	0.03
103934_at	Gabt3	gamma-aminobutyric acid (GABA-A) transporter 3	96.47	0.01	-2.73	0.07	-3.27	0.04	-4.26	0.01	0.11	0.94
100407_at	Gal	galanin	30.42	0.00	-9.83	0.00	4.15	0.06	-2.77	0.20	-1.92	0.37

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
103367_at	Galgt1	UDP-N-acetyl-alpha-D-galactosamine:(N-acetylneuraminyl)-galactosylglucosylceramide-beta-1, 4-N-acetylgalactosaminyltransferase	53.58	0.04	1.88	0.52	-7.62	0.02	-5.66	0.06	2.90	0.33
101333_at	Galnt4	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 4	7.06	0.04	1.07	0.56	4.27	0.03	4.74	0.02	-0.03	0.99
104616_g_at	Galt	galactose-1-phosphate uridyl transferase	61.65	0.00	-0.67	0.81	-11.96	0.00	-6.21	0.04	-1.20	0.67
101214_f_at	Gapd	glyceraldehyde-3-phosphate dehydrogenase	123.11	0.00	0.21	0.90	1.87	0.28	-0.34	0.84	8.01	0.00
94338_g_at	Gas2	growth arrest specific 2	45.76	0.01	-7.66	0.05	-11.49	0.00	-4.83	0.19	-5.31	0.15
104678_at	Gas7	growth arrest specific 7	12.97	0.03	-3.56	0.17	-3.44	0.19	-3.63	0.16	-6.90	0.01
102654_at	Gata1	GATA binding protein 1	17.45	0.05	-2.63	0.37	-8.85	0.01	0.96	0.74	-3.52	0.24
104698_at	Gata6	GATA binding protein 6	11.81	0.05	1.74	0.21	-0.03	0.98	-1.13	0.41	4.12	0.01
102402_at	Gbas	glioblastoma amplified sequence	48.51	0.01	-0.72	0.48	-1.92	0.07	-1.87	0.08	3.18	0.00
160628_at	Gcat	glycine C-acetyltransferase (2-amino-3-ketobutyrate-coenzyme A ligase)	62.08	0.00	-8.24	0.01	-12.44	0.00	-5.25	0.09	-11.32	0.00
162189_r_at	Gcdh	glutaryl-Coenzyme A dehydrogenase	3.94	0.03	-12.89	0.00	2.88	0.43	-0.80	0.83	2.51	0.49
103498_at	Gcgr	glucagon receptor	82.60	0.03	7.11	0.02	1.19	0.68	2.40	0.41	7.07	0.02
102313_at	Gch	GTP cyclohydrolase 1	66.54	0.03	-0.38	0.90	-7.04	0.04	-0.64	0.84	-8.99	0.01
102651_at	Gck	glucokinase	74.70	0.00	16.23	0.06	29.20	0.00	16.86	0.05	8.91	0.29
99649_at	Gclc	glutamate-cysteine ligase, catalytic subunit	73.14	0.00	-4.40	0.09	-9.42	0.00	-10.48	0.00	4.24	0.10
97917_at	Gcn5l1	general control of amino acid synthesis-like 1 (yeast)	54.24	0.01	-2.23	0.27	2.50	0.22	6.17	0.01	4.34	0.04
102095_f_at	Gcnt2	glucosaminyltransferase, I-branching enzyme	3.36	0.03	0.40	0.78	-2.97	0.05	2.89	0.06	-3.14	0.04
94192_at	Gdap10	ganglioside-induced differentiation-associated-protein 10	9.54	0.00	9.50	0.00	0.79	0.74	4.50	0.07	7.88	0.00
161753_f_at	Gdc1	glycerol phosphate dehydrogenase 1, cytoplasmic adult	15.92	0.01	4.14	0.18	3.23	0.30	5.58	0.08	10.96	0.00
92592_at	Gdc1	glycerol phosphate dehydrogenase 1, cytoplasmic adult	86.36	0.00	5.87	0.00	4.38	0.03	-0.87	0.64	6.78	0.00
97313_at	Gdi1	guanosine diphosphate (GDP) dissociation inhibitor 1	45.41	0.04	6.20	0.01	2.44	0.27	-0.52	0.81	-3.26	0.14
98984_f_at	Gdm1	glycerol phosphate dehydrogenase 1, mitochondrial	35.91	0.00	3.82	0.20	10.58	0.00	7.38	0.02	19.38	0.00
102993_at	Ggta1	glycoprotein galactosyltransferase alpha 1, 3	18.46	0.01	-9.63	0.00	-0.34	0.91	6.82	0.03	0.17	0.95
160530_at	Ghitm	growth hormone inducible transmembrane protein	80.11	0.01	-0.72	0.64	4.77	0.01	-0.95	0.54	3.98	0.02
99108_s_at	Ghr	growth hormone receptor	91.61	0.03	3.85	0.05	4.13	0.04	3.55	0.07	-1.36	0.48
100065_r_at	Gja1	gap junction membrane channel protein alpha 1	5.24	0.03	5.96	0.02	3.34	0.15	4.84	0.04	-0.26	0.91
100064_f_at	Gja1	gap junction membrane channel protein alpha 1	20.03	0.03	15.34	0.01	2.91	0.58	8.69	0.11	-6.03	0.26
93771_at	Gjb1	gap junction membrane channel protein beta 1	92.80	0.02	1.58	0.63	-1.95	0.55	-3.83	0.24	-11.50	0.00

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
160900_at	Gkap42-pending	42 kD cGMP-dependent protein kinase anchoring protein	12.78	0.01	2.19	0.19	-5.66	0.00	1.63	0.32	-2.81	0.10
161363_r_at	Glk	galactokinase	64.29	0.01	-9.79	0.00	3.53	0.18	-2.75	0.29	-1.46	0.57
97820_at	Glk	galactokinase	40.02	0.01	-0.11	0.97	-4.39	0.19	-5.07	0.13	11.98	0.00
99498_at	Glns	glutamine synthetase	62.01	0.00	2.68	0.54	5.24	0.24	13.92	0.00	13.93	0.00
104524_at	Gltp-pending	glycolipid transfer protein	25.88	0.01	-5.33	0.05	8.42	0.00	6.03	0.03	1.55	0.55
99141_at	Gm2a	GM2 ganglioside activator protein	77.55	0.00	-7.48	0.02	-9.92	0.00	-14.27	0.00	0.06	0.98
95364_at	Gna14	guanine nucleotide binding protein, alpha 14	0.26	0.00	6.08	0.05	7.77	0.02	13.01	0.00	4.39	0.15
161902_f_at	Gnao	guanine nucleotide binding protein, alpha o	3.27	0.05	-4.62	0.02	2.29	0.21	-0.55	0.76	3.25	0.08
100386_at	Gnaz	guanine nucleotide binding protein, alpha z subunit	16.90	0.01	-8.45	0.02	-6.20	0.08	-6.87	0.05	-6.00	0.09
96911_at	Gnb2	guanine nucleotide binding protein, beta 2	65.03	0.01	5.17	0.01	-2.90	0.11	-1.22	0.48	4.06	0.03
99340_at	Gnb2-rs1	guanine nucleotide binding protein, beta 2, related sequence 1	105.53	0.04	-1.31	0.40	-4.65	0.01	-2.22	0.17	-1.00	0.52
93080_at	Gng3lg	G protein gamma 3 linked gene	56.97	0.05	3.52	0.22	4.56	0.12	7.11	0.02	2.57	0.37
96828_at	Gnmt	glycine N-methyltransferase	135.48	0.00	-1.93	0.16	-2.02	0.14	-4.36	0.00	-4.36	0.00
100565_at	Gnpi	glucosamine-6-phosphate deaminase	31.73	0.01	-4.73	0.07	1.03	0.68	-7.87	0.01	6.16	0.02
100325_at	Gp49a	glycoprotein 49 A	3.86	0.00	-0.02	0.99	1.27	0.34	3.52	0.01	-5.34	0.00
104614_at	Gpc1	glypican 1	26.89	0.02	0.91	0.81	5.67	0.15	-0.89	0.82	14.06	0.00
160158_at	Gpc3	glypican 3	17.62	0.02	-3.88	0.03	-2.80	0.10	-2.68	0.12	-3.60	0.04
99441_at	Gphn	gephyrin	55.03	0.02	1.79	0.38	-2.45	0.24	-2.83	0.18	-6.60	0.00
100573_f_at	Gpi1	glucose phosphate isomerase 1	36.94	0.01	-1.56	0.72	-0.97	0.83	0.58	0.90	18.64	0.00
100574_f_at	Gpi1	glucose phosphate isomerase 1	94.59	0.01	-1.89	0.51	3.08	0.29	1.27	0.66	12.33	0.00
103252_at	Gpr37	G protein-coupled receptor 37	2.52	0.03	-3.10	0.06	-2.66	0.10	0.57	0.72	-3.82	0.02
101763_at	Gpr50	G-protein-coupled receptor 50	61.98	0.04	-5.55	0.03	5.33	0.04	-0.32	0.89	-3.34	0.17
102217_at	Gprk5	G protein-coupled receptor kinase 5	13.29	0.00	-11.34	0.00	-6.90	0.05	-11.50	0.00	-3.23	0.35
94897_at	Gpx4	glutathione peroxidase 4	69.97	0.02	-4.78	0.13	-7.83	0.02	-6.73	0.04	2.52	0.41
98965_at	Grcc3f	gene rich cluster, C3f gene	40.88	0.04	3.15	0.19	1.67	0.48	3.15	0.19	6.71	0.01
103993_at	Grcc9	gene rich cluster, C9 gene	26.04	0.03	7.05	0.01	-4.45	0.11	-4.13	0.13	3.27	0.23
95084_f_at	Grhpr	glyoxylate reductase/hydroxypyruvate reductase	110.73	0.00	0.49	0.67	0.61	0.60	6.73	0.00	4.86	0.00
95085_r_at	Grhpr	glyoxylate reductase/hydroxypyruvate reductase	13.44	0.04	0.94	0.66	7.42	0.00	0.76	0.72	0.16	0.94
101710_at	Gria4	glutamate receptor, ionotropic, AMPA4 (alpha 4)	1.54	0.05	-0.35	0.79	1.25	0.34	-3.96	0.01	1.54	0.25
104686_at	Grin1	glutamate receptor, ionotropic, NMDA1 (zeta 1)	3.98	0.02	-3.97	0.09	5.22	0.03	0.41	0.85	-5.33	0.03
93066_at	Grn	granulin	61.71	0.02	-1.94	0.30	-4.13	0.03	4.81	0.02	-1.92	0.30
160646_at	Gsr	glutathione reductase 1	52.82	0.00	-1.13	0.59	-6.28	0.01	-9.65	0.00	-2.75	0.20
101872_at	Gsta2	glutathione S-transferase, alpha 2 (Yc2)	43.27	0.00	-41.29	0.00	-44.99	0.00	-60.60	0.00	-28.85	0.02
93015_at	Gsta3	glutathione S-transferase, alpha 3	114.90	0.02	-4.53	0.03	-1.40	0.47	-6.04	0.01	-0.61	0.75

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
96085_at	Gsta4	glutathione S-transferase, alpha 4	42.82	0.00	-16.58	0.01	-28.17	0.00	-27.77	0.00	-16.91	0.01
102094_f_at	Gstm1	glutathione S-transferase, mu 1	135.88	0.00	-9.26	0.00	-9.04	0.00	-12.81	0.00	-3.88	0.05
93543_f_at	Gstm1	glutathione S-transferase, mu 1	146.79	0.00	-11.57	0.00	-12.41	0.00	-15.92	0.00	-4.76	0.03
93009_at	Gstm2	glutathione S-transferase, mu 2	49.12	0.00	-15.88	0.00	-15.92	0.00	-16.71	0.00	1.08	0.79
97682_r_at	Gstm3	glutathione S-transferase, mu 3	87.35	0.00	-15.34	0.00	-23.87	0.00	-15.63	0.00	-10.85	0.02
97681_f_at	Gstm3	glutathione S-transferase, mu 3	124.03	0.00	-17.41	0.00	-19.13	0.00	-23.65	0.00	-10.78	0.00
100631_r_at	Gstm5	glutathione S-transferase, mu 5	-1.58	0.00	38.68	0.00	11.91	0.16	-3.88	0.64	-3.44	0.68
104637_at	Gstm6	glutathione S-transferase, mu 6	66.83	0.00	-14.55	0.01	-14.21	0.01	-24.96	0.00	-12.42	0.02
104636_at	Gstm6	glutathione S-transferase, mu 6	38.97	0.00	-8.60	0.01	-14.35	0.00	-18.65	0.00	-8.13	0.02
97819_at	Gsto1	glutathione S-transferase omega 1	81.68	0.00	-5.16	0.00	-6.49	0.00	-9.96	0.00	-6.62	0.00
99583_at	Gstp2	glutathione S-transferase, pi 2	155.72	0.01	-1.09	0.57	-2.39	0.22	-2.91	0.14	-6.74	0.00
104603_at	Gstt2	glutathione S-transferase, theta 2	67.08	0.00	-15.68	0.01	-19.58	0.00	-22.98	0.00	-11.23	0.05
160350_at	Gstz1	glutathione transferase zeta 1 (maleylacetoacetate isomerase)	121.79	0.02	0.43	0.81	3.22	0.08	1.82	0.30	5.68	0.00
101444_at	Gt	gene trap ROSA 26 antisense, Philippe Soriano	26.53	0.01	5.23	0.00	4.18	0.02	1.15	0.47	0.39	0.80
102039_at	Gtf2h4	general transcription factor II H, polypeptide 4	42.13	0.02	-1.28	0.25	-3.52	0.00	-0.87	0.43	1.97	0.08
94295_at	Gtf2i	general transcription factor II I	41.78	0.00	4.76	0.01	-6.08	0.00	3.50	0.03	1.47	0.34
161683_r_at	Gtpbp1	GTP binding protein 1	46.63	0.01	-11.00	0.00	4.46	0.18	-5.78	0.09	1.13	0.73
99180_at	Gtpbp3-pending	GTP binding protein 3	53.11	0.00	3.21	0.26	2.10	0.46	0.71	0.80	-12.69	0.00
160161_at	Gtrgeo22	gene trap ROSA b-geo 22	21.05	0.01	3.09	0.39	-8.88	0.02	-0.33	0.93	11.38	0.00
95569_at	Guca2b	guanylate cyclase activator 2b (retina)	-19.31	0.00	-0.97	0.82	-3.96	0.37	23.26	0.00	-6.68	0.14
97538_at	Gus	beta-glucuronidase	23.86	0.03	1.75	0.35	-0.69	0.71	1.19	0.53	6.44	0.00
100597_at	Gyg1	glycogenin 1	6.36	0.03	1.73	0.38	-4.94	0.02	-0.95	0.63	4.90	0.02
97525_at	Gyk	glycerol kinase	56.91	0.02	7.62	0.02	1.05	0.72	1.20	0.68	8.28	0.01
98496_at	Gys1	glycogen synthase 1, muscle	29.23	0.03	-4.11	0.18	2.41	0.42	-8.13	0.01	-4.98	0.11
100609_at	H2-Bf	histocompatibility 2, complement component factor B	88.75	0.03	1.24	0.42	-0.20	0.90	5.44	0.00	-0.88	0.57
104429_at	H2-Ob	histocompatibility 2, O region beta locus	7.27	0.03	-3.67	0.15	-0.04	0.99	-3.31	0.19	7.22	0.01
93865_s_at	H2-T10	histocompatibility 2, T region locus 10	67.95	0.02	-0.96	0.69	0.54	0.82	6.77	0.01	6.10	0.02
101876_s_at	H2-T17	histocompatibility 2, T region locus 17	75.22	0.03	1.30	0.59	5.11	0.04	5.69	0.03	3.85	0.12
102692_s_at	H2-T3	histocompatibility 2, T region locus 3	-2.87	0.04	0.27	0.94	4.39	0.22	-10.02	0.01	5.42	0.13
94805_f_at	H2afx	H2A histone family, member X	85.51	0.03	2.10	0.64	2.01	0.65	8.43	0.07	13.92	0.01
100708_at	H3f3b	H3 histone, family 3B	77.06	0.01	3.42	0.11	2.80	0.19	2.63	0.22	-7.12	0.00
94245_at	H47	histocompatibility 47	51.82	0.04	-2.50	0.23	-1.02	0.62	-2.02	0.32	-6.11	0.01
95485_at	Hadhsc	L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain	95.96	0.00	3.48	0.12	4.69	0.04	2.12	0.34	10.23	0.00
92833_at	Hal	histidine ammonia lyase	95.57	0.00	-6.49	0.02	-8.03	0.00	-7.18	0.01	-7.96	0.00

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
103649_at	Hao3	hydroxyacid oxidase (glycolate oxidase) 3	2.10	0.01	0.04	0.99	1.56	0.53	2.33	0.35	10.05	0.00
100549_at	Hba-x	hemoglobin X, alpha-like embryonic chain in Hba complex	13.43	0.03	-0.74	0.64	5.60	0.00	0.04	0.98	1.82	0.26
94484_at	Hbs1l	Hbs1-like (S. cerevisiae)	52.67	0.02	-1.63	0.45	-1.87	0.38	2.61	0.23	-7.10	0.00
103458_at	Hc	hemolytic complement	110.47	0.01	1.39	0.68	-0.50	0.88	10.10	0.01	-10.50	0.01
94945_at	Hcarg-pending	hypertension-related, calcium regulated gene	-8.57	0.00	21.68	0.00	-11.31	0.06	4.49	0.43	16.31	0.01
161662_f_at	Hcngp-pending	transcriptional regulator protein	-16.82	0.03	-0.84	0.86	2.03	0.66	-13.87	0.01	9.70	0.05
94098_at	Hcrt	hypocretin	14.40	0.04	13.60	0.01	6.56	0.14	-0.01	1.00	0.74	0.86
92629_f_at	Hdgf	hepatoma-derived growth factor	88.31	0.00	-3.22	0.03	-1.29	0.36	-3.71	0.02	-4.53	0.00
92630_r_at	Hdgf	hepatoma-derived growth factor	70.69	0.04	-2.91	0.29	-3.77	0.18	-8.01	0.01	-2.09	0.45
99869_at	Hdgfrp1	hepatoma-derived growth factor, related protein 1	1.07	0.00	-14.56	0.00	-10.74	0.01	-1.28	0.74	-0.44	0.91
98599_at	Hdgfrp2	hepatoma-derived growth factor, related protein 2	11.49	0.01	9.18	0.00	-2.15	0.38	-0.40	0.87	-4.33	0.09
95057_at	Herpud1	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	111.21	0.00	10.02	0.00	13.32	0.00	8.47	0.01	-5.63	0.06
160887_at	Hes1	hairy and enhancer of split 1, (Drosophila)	37.58	0.03	10.73	0.02	3.42	0.42	3.69	0.39	9.70	0.03
97334_at	Hes6	hairy and enhancer of split 6, (Drosophila)	61.69	0.01	0.53	0.88	0.59	0.86	-0.45	0.89	-14.17	0.00
104182_at	Hgfac	hepatocyte growth factor activator	94.02	0.00	2.82	0.09	1.24	0.45	6.59	0.00	9.41	0.00
100286_at	Hgfl	hepatocyte growth factor-like	68.73	0.03	-1.48	0.38	-4.70	0.01	3.55	0.04	0.19	0.91
160447_at	Hiat1	hippocampus abundant gene transcript 1	40.17	0.02	-0.62	0.71	0.51	0.75	1.42	0.39	-6.13	0.00
103833_at	Hipk2	homeodomain interacting protein kinase 2	3.57	0.00	13.12	0.00	-10.12	0.01	1.78	0.64	7.46	0.06
103233_at	Hipk3	homeodomain interacting protein kinase 3	4.99	0.03	8.14	0.27	-21.45	0.01	-0.26	0.97	-13.24	0.08
92908_at	Hivep1	human immunodeficiency virus type I enhancer binding protein 1	9.12	0.01	2.04	0.32	-6.80	0.00	-0.12	0.95	-4.59	0.03
93095_at	Hmgb1	high mobility group box 1	47.44	0.00	4.37	0.00	4.11	0.00	4.15	0.00	4.44	0.00
161970_f_at	Hmgcl	3-hydroxy-3-methylglutaryl-Coenzyme A lyase	81.72	0.02	0.92	0.75	-2.76	0.35	0.83	0.78	10.84	0.00
104285_at	Hmgcr	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	26.73	0.03	5.50	0.55	-3.88	0.67	5.86	0.53	-32.75	0.00
92590_at	Hmgcs2	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2	93.27	0.00	4.92	0.13	3.24	0.31	4.67	0.15	14.79	0.00
96699_at	Hmgn1	high mobility group nucleosomal binding domain 1	92.08	0.00	-3.25	0.03	-5.05	0.00	-0.76	0.58	-1.97	0.16
92724_at	Hnrpa1	heterogeneous nuclear ribonucleoprotein A1	22.74	0.01	-1.08	0.63	-2.31	0.31	-1.57	0.48	-8.79	0.00
93118_at	Hnrpa2b1	heterogeneous nuclear ribonucleoprotein A2/B1	45.31	0.01	-0.09	0.97	1.46	0.54	-0.10	0.97	-10.47	0.00
96083_s_at	Hnrpdl	heterogeneous nuclear ribonucleoprotein D-like	57.50	0.01	1.48	0.43	-0.14	0.94	0.34	0.85	-8.15	0.00
93990_at	Hnrph1	heterogeneous nuclear ribonucleoprotein H1	56.44	0.00	-3.40	0.21	3.12	0.24	0.20	0.94	-16.62	0.00
93761_at	Hnrpu	heterogeneous nuclear ribonucleoprotein U	3.78	0.04	3.42	0.05	0.62	0.71	2.45	0.16	-3.94	0.03

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
104498_at	Homer1-pending	homer, neuronal immediate early gene, 1	-2.20	0.05	-0.80	0.60	2.90	0.07	-0.19	0.90	-4.20	0.01
160695_i_at	Homer2-pending	homer, neuronal immediate early gene, 2	25.77	0.03	5.74	0.01	-1.05	0.61	0.16	0.94	-4.55	0.04
92914_at	Hoxb7	homeo box B7	17.69	0.04	-5.43	0.02	4.04	0.06	-1.86	0.37	-1.26	0.54
92386_at	Hps4	Hermansky-Pudlak syndrome 4 homolog (human)	8.10	0.04	4.47	0.13	-8.31	0.01	-3.44	0.24	-0.10	0.97
160536_at	Hras1	Harvey rat sarcoma virus oncogene	44.45	0.02	-4.04	0.16	1.01	0.72	6.66	0.03	7.45	0.02
100954_at	Hrb	HIV-1 Rev binding protein	12.98	0.01	2.18	0.01	1.69	0.04	-0.49	0.53	-1.38	0.09
96048_at	Hrsp12	heat-responsive protein 12	100.10	0.03	-1.60	0.52	-3.82	0.13	-8.00	0.00	0.10	0.97
97515_at	Hsd17b4	hydroxysteroid (17-beta) dehydrogenase 4	107.12	0.00	3.68	0.02	3.63	0.02	0.60	0.68	7.36	0.00
92869_at	Hsd3b4	hydroxysteroid dehydrogenase-4, delta<5>-3-beta	1.52	0.01	2.78	0.00	-1.01	0.17	-0.75	0.30	-0.35	0.62
94795_at	Hsd3b5	hydroxysteroid dehydrogenase-5, delta<5>-3-beta	103.60	0.01	0.45	0.90	-0.78	0.83	-1.47	0.68	-15.59	0.00
98111_at	Hsp105	heat shock protein, 105 kDa	68.84	0.00	7.45	0.12	18.57	0.00	1.97	0.67	-18.45	0.00
93277_at	Hsp60	heat shock protein, 60 kDa	115.34	0.00	-1.61	0.18	2.62	0.03	-1.86	0.12	-6.55	0.00
100946_at	Hsp70-1	heat shock protein, 70 kDa 1	42.12	0.00	13.92	0.17	25.20	0.02	-10.63	0.29	-37.20	0.00
95359_at	Hsp84-1	heat shock protein, 84 kDa 1	122.33	0.01	3.18	0.13	3.54	0.09	-5.40	0.01	-3.76	0.07
161761_r_at	Hsp84-1	heat shock protein, 84 kDa 1	24.76	0.02	-7.38	0.01	0.01	1.00	-3.25	0.19	-4.26	0.09
100352_at	Hspa4	heat shock 70 kDa protein 4	18.05	0.02	5.93	0.02	4.47	0.07	-1.28	0.59	-5.04	0.05
101955_at	Hspa5	heat shock 70kD protein 5 (glucose-regulated protein, 78kD)	121.45	0.00	1.90	0.53	12.32	0.00	2.98	0.33	-8.20	0.01
96564_at	Hspa8	heat shock 70kD protein 8	97.45	0.00	6.26	0.01	9.59	0.00	5.64	0.02	-11.93	0.00
93747_at	Hspc121-pending	butyrate-induced transcript 1	105.21	0.00	1.73	0.22	2.24	0.11	3.16	0.03	4.92	0.00
103671_at	Htatip2	HIV-1 tat interactive protein 2, 30 kDa homolog (human)	28.40	0.00	-8.96	0.00	-12.73	0.00	-7.33	0.01	1.71	0.50
101140_at	Htr1a	5-hydroxytryptamine (serotonin) receptor 1A	12.81	0.03	-9.23	0.01	0.73	0.81	-6.33	0.05	1.32	0.67
92919_at	Htr3a	5-hydroxytryptamine (serotonin) receptor 3A	22.74	0.01	-2.51	0.60	-6.26	0.20	1.70	0.72	18.08	0.00
95323_at	Htr4	5 hydroxytryptamine (serotonin) receptor 4	20.10	0.04	-6.68	0.02	-2.83	0.28	3.54	0.18	-4.01	0.14
97181_f_at	Iap	intracisternal A particles	79.52	0.03	1.95	0.50	3.61	0.22	-3.75	0.20	-8.72	0.01
93013_at	Idb2	inhibitor of DNA binding 2	77.95	0.03	-4.30	0.16	7.55	0.02	-2.81	0.35	5.45	0.08
95693_at	Idh2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	57.95	0.00	-8.83	0.01	-10.66	0.00	-7.90	0.02	2.24	0.48
99882_at	Ids	iduronate 2-sulfatase	9.42	0.01	-5.88	0.01	0.23	0.90	3.37	0.09	-4.27	0.04
161281_f_at	Ier3	immediate early response 3	-3.57	0.01	0.16	0.92	-0.15	0.93	-0.32	0.85	-7.52	0.00
92773_at	Ier5	immediate early response 5	25.27	0.03	3.24	0.25	1.69	0.54	7.53	0.01	-5.79	0.05
160251_at	Ierepo4-pending	immediate early response, erythropoietin 4	59.96	0.00	-4.11	0.00	-0.04	0.97	1.56	0.16	-7.16	0.00

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
160092_at	Ifrd1	interferon-related developmental regulator 1	9.86	0.00	2.54	0.20	1.11	0.57	2.63	0.18	-10.79	0.00
95546_g_at	Igf1	insulin-like growth factor 1	119.60	0.01	-3.54	0.06	-0.57	0.75	0.66	0.71	-6.62	0.00
95117_at	Igf2r	insulin-like growth factor 2 receptor	16.61	0.01	-4.28	0.34	-11.82	0.01	-0.58	0.90	-13.08	0.01
103896_f_at	Igfbp1	insulin-like growth factor binding protein 1	102.19	0.00	-5.95	0.60	-16.52	0.16	24.21	0.04	-49.74	0.00
98627_at	Igfbp2	insulin-like growth factor binding protein 2	125.06	0.01	-10.16	0.10	-13.55	0.03	-13.44	0.03	-14.66	0.02
95082_at	Igfbp3	insulin-like growth factor binding protein 3	27.01	0.02	8.91	0.06	-4.11	0.36	1.86	0.68	14.11	0.00
93583_s_at	Igh-6	immunoglobulin heavy chain 6 (heavy chain of IgM)	41.64	0.04	-11.16	0.01	-1.99	0.59	-5.77	0.13	-2.27	0.54
94196_at	Ikbkg	inhibitor of kappaB kinase gamma	21.03	0.00	1.24	0.61	-7.76	0.00	-7.49	0.01	-6.00	0.02
93874_s_at	Il11ra2	interleukin 11 receptor, alpha chain 2	43.17	0.00	0.35	0.83	-6.27	0.00	-4.64	0.01	-4.34	0.01
98240_at	Il12rb1	interleukin 12 receptor, beta 1	-4.28	0.04	4.81	0.07	1.32	0.61	-7.52	0.01	-1.05	0.68
161037_at	Il15	interleukin 15	-1.76	0.00	-1.09	0.36	-2.63	0.04	-1.91	0.12	4.73	0.00
94755_at	Il1a	interleukin 1 alpha	8.74	0.04	4.35	0.10	-0.56	0.83	5.26	0.05	-5.49	0.04
93914_at	Il1r1	interleukin 1 receptor, type I	50.67	0.04	12.89	0.09	16.31	0.04	12.17	0.11	-9.39	0.21
102021_at	Il4ra	interleukin 4 receptor, alpha	25.31	0.03	6.98	0.05	-4.90	0.15	-2.03	0.54	8.41	0.02
162006_r_at	Immt	inner membrane protein, mitochondrial	29.99	0.03	-7.66	0.01	5.06	0.08	-3.07	0.28	-3.94	0.17
100277_at	Inhba	inhibin beta-A	15.81	0.02	-15.05	0.01	-8.56	0.09	1.52	0.76	7.11	0.16
160828_at	Inhbb	inhibin beta-B	-4.12	0.03	6.13	0.01	0.79	0.70	2.80	0.19	3.62	0.09
103986_at	Inhbc	inhibin beta-C	65.05	0.00	8.59	0.00	8.60	0.00	6.99	0.01	10.93	0.00
97153_at	Inhbe	inhibin beta E	19.16	0.00	5.66	0.22	6.24	0.18	6.67	0.15	23.14	0.00
94398_s_at	Inpp5b	inositol polyphosphate-5-phosphatase, 75 kDa	26.34	0.01	9.00	0.07	-7.66	0.12	3.54	0.46	16.32	0.00
93850_at	Iqgap1	IQ motif containing GTPase activating protein 1	2.92	0.05	-0.51	0.80	-1.84	0.35	1.04	0.60	6.31	0.00
99103_at	Irf3	interferon regulatory factor 3	31.47	0.01	0.39	0.83	-6.47	0.00	-2.08	0.27	-3.29	0.09
92440_at	Irf6	interferon regulatory factor 6	42.58	0.00	-4.25	0.09	-8.28	0.00	-10.04	0.00	-9.73	0.00
98824_at	Irs1	insulin receptor substrate 1	8.69	0.00	-1.11	0.38	-4.33	0.00	-2.39	0.07	-4.64	0.00
98834_at	Itga2	integrin alpha 2	1.01	0.04	3.80	0.25	8.50	0.02	4.34	0.19	4.21	0.20
98828_at	Itgam	integrin alpha M	-10.22	0.02	-13.91	0.02	-16.75	0.01	1.76	0.76	0.07	0.99
100123_f_at	Itgb1	integrin beta 1 (fibronectin receptor beta)	82.17	0.04	-3.86	0.12	-7.12	0.01	-1.21	0.61	-1.54	0.52
102353_at	Itgb2	integrin beta 2	7.51	0.03	0.05	0.98	-5.95	0.01	3.90	0.08	2.67	0.22
103305_at	Itgb4	integrin beta 4	-35.51	0.00	4.38	0.09	4.65	0.07	6.94	0.01	11.85	0.00
98014_at	Itih1	inter-alpha trypsin inhibitor, heavy chain 1	88.18	0.04	5.58	0.09	-3.25	0.31	8.43	0.01	1.99	0.53
100002_at	Itih3	inter-alpha trypsin inhibitor, heavy chain 3	121.43	0.00	2.15	0.48	0.49	0.87	15.38	0.00	-2.52	0.41
98467_at	Itih4	inter alpha-trypsin inhibitor, heavy chain 4	111.26	0.00	1.30	0.66	-2.32	0.44	14.22	0.00	2.36	0.43
103028_at	Itk	IL2-inducible T-cell kinase	15.51	0.04	-2.94	0.16	2.95	0.16	0.76	0.71	5.61	0.01
98922_at	Itm1	intergral membrane protein 1	19.40	0.04	-3.75	0.03	2.22	0.17	3.29	0.05	0.16	0.92
96283_at	Itm3-pending	integral membrane protein 3	39.54	0.02	5.23	0.12	1.59	0.63	4.12	0.21	11.02	0.00
104153_at	Ivd	isovaleryl coenzyme A dehydrogenase	76.37	0.00	-1.61	0.32	-3.08	0.07	-7.17	0.00	-6.60	0.00
104121_at	Jup	junction plakoglobin	34.62	0.01	6.65	0.01	-0.69	0.78	0.37	0.88	7.76	0.00

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
103787_at	Kcna1	potassium voltage-gated channel, shaker-related subfamily, member 1	-27.50	0.03	1.80	0.26	-2.82	0.08	2.18	0.17	3.97	0.02
101302_at	Kcnd1	potassium voltage-gated channel, Shal-related family, member 1	-8.76	0.01	-1.17	0.59	3.02	0.17	-7.85	0.00	2.07	0.34
98829_at	Kcnj12	potassium inwardly-rectifying channel, subfamily J, member 12	1.10	0.04	4.48	0.01	0.85	0.59	0.48	0.76	2.89	0.08
101188_at	Kcnj3	potassium inwardly-rectifying channel, subfamily J, member 3	3.73	0.02	-3.83	0.02	-2.17	0.16	-1.11	0.47	3.71	0.02
161796_r_at	Kcnq1	potassium voltage-gated channel, subfamily Q, member 1	20.19	0.02	-3.66	0.16	8.15	0.00	-3.57	0.17	-2.68	0.30
104265_at	Kdr	kinase insert domain protein receptor	25.17	0.03	0.36	0.92	-4.57	0.24	5.15	0.19	12.03	0.00
96938_at	Keg1	kidney expressed gene 1	93.50	0.00	-6.03	0.00	-0.55	0.77	-4.55	0.03	-12.70	0.00
99962_at	Kif2	kinesin heavy chain member 2	6.07	0.01	3.36	0.01	-0.84	0.49	3.37	0.01	-0.54	0.66
161275_at	Kif3a	kinesin family member 3a	-0.12	0.04	-1.61	0.12	-1.77	0.09	-1.57	0.13	1.95	0.06
100113_s_at	Kifap3	kinesin-associated protein 3	5.76	0.01	1.87	0.21	-4.10	0.01	-2.68	0.08	3.46	0.03
161604_r_at	Kifap3	kinesin-associated protein 3	0.52	0.04	-3.11	0.00	-0.49	0.61	0.44	0.65	1.13	0.25
160617_at	Klf13	Kruppel-like factor 13	52.37	0.02	4.18	0.19	4.84	0.13	10.11	0.00	-1.31	0.67
99622_at	Klf4	Kruppel-like factor 4 (gut)	2.08	0.01	2.44	0.08	-3.14	0.03	3.15	0.03	-2.19	0.11
101370_at	Kpna1	karyopherin (importin) alpha 1	34.22	0.02	3.01	0.03	2.55	0.06	-2.84	0.04	-0.17	0.89
96010_at	Kpna3	karyopherin (importin) alpha 3	52.53	0.04	3.59	0.02	0.46	0.75	1.92	0.21	3.27	0.04
100320_at	Kpna4	karyopherin (importin) alpha 4	0.31	0.01	5.40	0.01	2.61	0.15	-0.75	0.67	-3.61	0.05
93070_at	Kpnb3	karyopherin (importin) beta 3	22.75	0.01	4.05	0.00	2.21	0.05	-0.64	0.55	0.51	0.64
94270_at	Krt1-18	keratin complex 1, acidic, gene 18	81.04	0.03	-4.25	0.18	-7.85	0.02	-1.81	0.56	-6.81	0.04
98997_f_at	Krt1-24	keratin complex 1, acidic, gene 24	-2.68	0.04	10.89	0.00	-0.07	0.98	1.00	0.76	-3.83	0.25
97814_at	Krt1-3	keratin complex 1, acidic, gene 3	-1.65	0.01	1.05	0.86	-12.50	0.05	-8.47	0.17	-19.87	0.00
94317_at	Krt2-5	keratin complex 2, basic, gene 5	-4.10	0.01	0.53	0.80	-6.39	0.01	-3.46	0.11	-5.25	0.02
101009_at	Krt2-8	keratin complex 2, basic, gene 8	72.88	0.03	-7.24	0.06	-6.14	0.10	-7.56	0.05	-5.21	0.16
101376_at	Krtap6-1	keratin associated protein 6-1	19.09	0.04	-4.10	0.10	6.10	0.02	-3.80	0.12	-1.35	0.57
103729_at	Lama1	laminin, alpha 1	24.64	0.03	-1.57	0.68	7.69	0.05	-11.18	0.01	2.89	0.45
101590_at	Lamp2	lysosomal membrane glycoprotein 2	94.92	0.03	2.06	0.27	-0.85	0.64	-3.53	0.06	-5.02	0.01
97750_at	Lamr1	laminin receptor 1 (67kD, ribosomal protein SA)	94.84	0.00	-6.77	0.03	-11.02	0.00	-3.64	0.21	-1.50	0.60
96016_at	Lamr1	laminin receptor 1 (67kD, ribosomal protein SA)	36.99	0.01	4.06	0.13	-0.03	0.99	3.84	0.15	9.83	0.00
103656_at	Lancl1	LanC (bacterial lantibiotic synthetase component C)-like	42.53	0.00	-1.56	0.44	-11.35	0.00	-2.32	0.26	-4.38	0.04
93632_g_at	Lbcl1	lymphoid blast crisis-like 1	18.27	0.00	0.72	0.69	-0.97	0.60	-2.24	0.23	-8.16	0.00
161759_r_at	Lcat	lecithin cholesterol acyltransferase	-6.32	0.05	-27.56	0.01	-1.55	0.88	-14.31	0.16	13.84	0.18
161684_r_at	Lcn2	lipocalin 2	12.98	0.04	-3.78	0.03	-1.07	0.51	3.44	0.05	-2.51	0.14
160564_at	Lcn2	lipocalin 2	13.73	0.03	4.73	0.78	-24.10	0.16	55.10	0.00	0.23	0.99
96072_at	Ldh1	lactate dehydrogenase 1, A chain	127.83	0.00	8.66	0.00	4.68	0.02	6.39	0.00	13.76	0.00
102938_at	Lect2	leukocyte cell-derived chemotaxin 2	71.58	0.00	3.21	0.41	15.80	0.00	8.72	0.03	17.73	0.00

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
99669_at	Lgals1	lectin, galactose binding, soluble 1	27.28	0.00	-6.64	0.28	1.85	0.76	1.67	0.78	30.61	0.00
95706_at	Lgals3	lectin, galactose binding, soluble 3	-2.61	0.05	4.13	0.23	-2.80	0.42	9.63	0.01	4.25	0.22
103335_at	Lgals9	lectin, galactose binding, soluble 9	116.26	0.00	0.56	0.44	0.35	0.63	-2.35	0.00	3.69	0.00
101192_at	Lhx5	LIM homeobox protein 5	-1.92	0.02	1.00	0.45	-0.02	0.99	-1.15	0.39	-4.81	0.00
94176_at	Lhx6	LIM homeobox protein 6	15.92	0.04	2.28	0.35	1.47	0.55	3.32	0.18	7.47	0.01
104659_g_at	Lifr	leukemia inhibitory factor receptor	109.51	0.00	-0.96	0.88	-2.59	0.68	-9.74	0.14	-29.07	0.00
104658_at	Lifr	leukemia inhibitory factor receptor	117.61	0.00	1.27	0.82	-3.59	0.53	-7.83	0.18	-30.19	0.00
104657_at	Lifr	leukemia inhibitory factor receptor	11.90	0.02	-0.37	0.91	-2.17	0.53	-7.26	0.05	-11.44	0.00
102123_at	Lip1	lysosomal acid lipase 1	42.42	0.00	1.75	0.64	-3.08	0.42	-4.63	0.23	20.91	0.00
162274_f_at	Lisch7-pending	liver-specific bHLH-Zip transcription factor	67.51	0.00	-4.66	0.02	-0.60	0.76	6.60	0.00	-5.58	0.01
160270_at	Lman1	lectin, mannose-binding, 1	97.97	0.01	1.06	0.53	5.57	0.00	3.79	0.03	-2.62	0.13
102235_at	Lmyc1	lung carcinoma myc related oncogene 1	19.18	0.01	-0.08	0.97	-0.45	0.85	2.82	0.23	9.08	0.00
96269_at	LOC207933	similar to Isopentenyl-diphosphate delta-isomerase (IPP isomerase) (Isopentenyl pyrophosphate isomerase)	77.16	0.00	-17.31	0.10	-24.64	0.03	-15.06	0.15	-45.81	0.00
96825_at	LOC209039	tensin 2	42.52	0.00	10.27	0.00	1.16	0.62	-2.70	0.25	0.83	0.72
98896_at	LOC214987	hypothetical protein BC023107	7.42	0.04	17.33	0.06	-20.36	0.03	-10.74	0.24	-12.76	0.16
103580_at	LOC215751	similar to hypothetical protein BC014320	51.34	0.03	11.13	0.02	5.29	0.24	10.69	0.02	2.08	0.64
160622_at	LOC217721	similar to CG1358 gene product	3.05	0.05	1.05	0.53	-4.64	0.01	1.62	0.33	2.46	0.15
96841_at	LOC223775	similar to Serine/threonine-protein kinase pim-3	60.43	0.03	10.38	0.04	-1.76	0.72	5.90	0.23	-12.45	0.02
103418_at	LOC224052	similar to CG8142 gene product	5.29	0.04	-5.35	0.01	1.99	0.30	-0.01	1.00	-3.28	0.10
104694_at	LOC224598	similar to zinc finger protein 40	14.28	0.01	2.40	0.17	-0.23	0.89	-5.78	0.00	-4.12	0.02
95043_at	LOC226105	similar to CYTOCHROME P450 2C22 (CYPIIC22) (P450 MD) (P450 P49)	116.18	0.01	-1.60	0.75	-3.28	0.51	-3.88	0.44	-19.57	0.00
160130_at	LOC226757	similar to hypothetical protein FLJ21016	33.95	0.05	-5.10	0.01	1.47	0.38	1.15	0.49	1.26	0.45
96913_at	LOC231086	similar to hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit	91.96	0.02	2.86	0.15	2.05	0.30	0.91	0.64	6.52	0.00
100996_at	LOC55933	putative lysophosphatidic acid acyltransferase	6.66	0.05	4.41	0.01	-0.61	0.68	2.42	0.12	-0.36	0.81
103389_at	Lorsdh	lysine oxoglutarate reductase, saccharopine dehydrogenase	107.23	0.01	-1.66	0.28	0.04	0.98	-1.47	0.33	-5.74	0.00
98892_at	Lpin1	lipin 1	91.36	0.02	5.87	0.40	9.30	0.19	18.34	0.02	-17.23	0.02
162002_r_at	Lrp1	low density lipoprotein receptor-related protein 1	8.29	0.00	2.62	0.29	-12.22	0.00	1.44	0.56	-2.16	0.38
96186_at	Lrp10	low-density lipoprotein receptor-related protein 10	43.77	0.00	6.74	0.01	-8.25	0.00	-4.68	0.04	4.11	0.07
160952_r_at	Lrrc6	leucine-rich repeat-containing 6 (testis)	2.75	0.04	2.79	0.02	0.85	0.46	-0.10	0.93	-2.76	0.02

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
160818_at	Lrrfip2	leucine rich repeat (in FLII) interacting protein 2	31.14	0.02	0.33	0.93	-13.66	0.00	-0.13	0.97	0.45	0.90
160737_at	Lss	lanosterol synthase	36.43	0.00	-5.96	0.26	-9.56	0.08	-1.38	0.79	-26.20	0.00
160133_at	Ltbp3	latent transforming growth factor beta binding protein 3	32.21	0.02	-9.57	0.01	-6.74	0.06	1.66	0.62	-5.69	0.10
100771_at	Ly57	lymphocyte antigen 57	-7.89	0.03	-1.36	0.67	0.44	0.89	10.63	0.00	-4.13	0.21
160553_at	Ly6d	lymphocyte antigen 6 complex, locus D	11.46	0.02	1.58	0.64	5.18	0.13	-2.76	0.41	11.27	0.00
97207_f_at	Lypla1	lysophospholipase 1	97.16	0.01	0.57	0.64	2.13	0.09	-3.13	0.02	3.32	0.01
161774_f_at	Lypla1	lysophospholipase 1	94.53	0.04	-0.21	0.87	2.44	0.06	-2.85	0.03	2.33	0.08
95379_at	Mab21l2	mab-21-like 2 (C. elegans)	7.01	0.03	-2.08	0.26	1.97	0.28	-0.31	0.86	5.91	0.00
104220_at	Madh6	MAD homolog 6 (Drosophila)	29.77	0.00	-5.10	0.06	7.43	0.01	-4.98	0.07	6.85	0.02
103291_at	Magea2	melanoma antigen, family A, 2	-13.99	0.01	5.39	0.03	-6.88	0.01	-1.73	0.44	1.48	0.51
94289_r_at	Maged2	melanoma antigen, family D, 2	16.37	0.00	-1.95	0.34	-2.08	0.31	4.11	0.05	8.70	0.00
92270_at	Maged3	melanoma antigen, family D, 3	33.47	0.00	-11.64	0.00	3.16	0.38	-0.77	0.83	-11.19	0.01
104628_at	Man2a1	mannosidase 2, alpha 1	85.97	0.02	1.11	0.63	3.57	0.13	2.18	0.34	-7.37	0.00
99562_at	Man2b1	mannosidase 2, alpha B1	67.16	0.03	2.68	0.11	-1.62	0.33	2.30	0.17	4.74	0.01
92543_at	Map2k2	mitogen activated protein kinase kinase 2	28.43	0.04	-1.18	0.46	5.16	0.00	1.19	0.46	0.71	0.66
103021_r_at	Map3k1	mitogen activated protein kinase kinase kinase 1	10.50	0.04	-4.16	0.01	1.36	0.32	-1.71	0.21	-0.14	0.92
104272_s_at	Map3k4	mitogen activated protein kinase kinase kinase 4	22.32	0.04	-1.02	0.65	-2.58	0.26	-7.13	0.00	0.79	0.73
99978_s_at	Mapk14	mitogen activated protein kinase 14	63.97	0.03	0.34	0.82	3.77	0.02	3.48	0.03	1.07	0.47
104047_at	Mapk8	mitogen activated protein kinase 8	26.34	0.03	-0.11	0.93	-4.18	0.00	-0.26	0.82	0.65	0.57
102284_at	Masp1	mannan-binding lectin serine protease 1	54.12	0.01	-2.51	0.26	-0.49	0.82	3.26	0.15	-8.89	0.00
98481_at	Masp2	mannan-binding lectin serine protease 2	53.22	0.02	4.23	0.03	0.30	0.87	5.01	0.01	-1.89	0.30
104428_s_at	Matk	megakaryocyte-associated tyrosine kinase	19.81	0.04	6.38	0.23	16.29	0.01	0.85	0.87	-4.59	0.39
161776_at	Matn2	matrilin 2	-4.75	0.03	2.81	0.05	0.96	0.48	-0.32	0.81	4.06	0.01
96011_at	Matr3	matrin 3	16.85	0.00	2.13	0.20	2.23	0.18	1.39	0.40	-7.04	0.00
96012_f_at	Matr3	matrin 3	73.68	0.00	2.47	0.03	1.01	0.35	0.73	0.49	-4.57	0.00
104340_at	Mbd1	methyl-CpG binding domain protein 1	44.62	0.00	10.74	0.07	10.35	0.08	3.36	0.55	-24.30	0.00
101385_at	Mbd3	methyl-CpG binding domain protein 3	63.97	0.00	-5.28	0.00	0.01	1.00	-2.15	0.09	-1.98	0.11
93041_at	Mcmd4	mini chromosome maintenance deficient 4 homolog (S. cerevisiae)	4.28	0.03	1.19	0.56	2.86	0.17	-1.24	0.54	6.43	0.00
93356_at	Mcmd7	mini chromosome maintenance deficient 7 (S. cerevisiae)	17.59	0.00	0.00	1.00	-4.10	0.09	2.59	0.27	9.57	0.00
100891_at	Mcsp	mitochondrial capsule selenoprotein	5.64	0.03	1.25	0.60	8.15	0.00	1.32	0.59	2.66	0.28
100432_f_at	Mdfi	MyoD family inhibitor	31.78	0.01	-3.06	0.07	1.92	0.25	-1.97	0.23	-5.18	0.00
100433_r_at	Mdfi	MyoD family inhibitor	20.43	0.05	-4.77	0.18	-10.16	0.01	1.96	0.57	-2.54	0.47
99465_at	Mecp2	methyl CpG binding protein 2	0.48	0.02	0.42	0.84	-6.79	0.00	-3.19	0.14	-2.74	0.20
93852_at	Mef2a	myocyte enhancer factor 2A	20.80	0.00	6.92	0.00	0.09	0.96	4.19	0.04	-4.40	0.03
93417_at	Mef2b	myocyte enhancer factor 2B	28.05	0.02	5.72	0.09	1.17	0.72	4.21	0.20	-10.77	0.00

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
97282_at	Mela	melanoma antigen, 80 kDa	14.91	0.00	13.81	0.00	2.61	0.53	8.85	0.04	-9.02	0.04
102753_at	Men1	multiple endocrine neoplasia 1	-18.03	0.03	4.54	0.17	-6.59	0.05	3.93	0.23	-7.40	0.03
95405_at	Mesdc2	mesoderm development candiate 2	43.02	0.04	1.42	0.44	4.40	0.03	4.25	0.03	-0.76	0.68
94060_at	MGC11654	hypothetical protein MGC11654	20.29	0.05	0.43	0.77	-4.22	0.01	-1.73	0.24	1.68	0.25
99120_f_at	MGC11769	hypothetical protein MGC11769	66.76	0.03	2.19	0.41	-9.40	0.00	-0.50	0.85	-0.02	0.99
96754_s_at	MGC18745	hypothetical protein MGC18745	56.11	0.01	1.77	0.38	-1.44	0.48	-2.60	0.21	-8.32	0.00
98608_at	MGC18745	hypothetical protein MGC18745	54.51	0.04	-0.59	0.67	-1.74	0.23	-2.87	0.05	-3.62	0.02
96158_at	MGC27648	hypothetical protein MGC27648	48.50	0.01	-1.12	0.53	4.07	0.03	-0.25	0.89	-5.86	0.00
97116_at	MGC27770	hypothetical protein MGC27770	12.35	0.00	-3.88	0.10	-9.63	0.00	1.71	0.46	0.19	0.93
94016_at	MGC28623	hypothetical protein MGC28623	2.28	0.01	-6.88	0.03	0.29	0.92	-10.64	0.00	0.07	0.98
96626_at	MGC28978	hypothetical protein MGC28978	65.79	0.02	1.71	0.40	-2.05	0.32	-5.47	0.01	-4.62	0.03
161502_r_at	MGC29044	hypothetical protein MGC29044	18.11	0.00	-7.05	0.01	8.89	0.00	2.65	0.30	2.59	0.31
162055_f_at	MGC31450	hypothetical protein MGC31450	24.56	0.01	-1.43	0.57	9.31	0.00	4.46	0.09	-3.50	0.17
103511_at	MGC32512	hypothetical protein MGC32512	-3.28	0.03	6.88	0.14	-11.15	0.02	-10.25	0.04	-0.71	0.88
96774_at	MGC36305	hypothetical protein MGC36305	83.14	0.02	-3.10	0.12	-5.64	0.01	-4.06	0.05	-1.30	0.51
98569_at	MGC36388	hypothetical protein MGC36388	79.84	0.03	1.90	0.62	-11.46	0.01	0.31	0.94	8.26	0.04
101532_g_at	MGC36398	hypothetical protein MGC36398	117.84	0.00	2.59	0.27	7.32	0.00	3.13	0.19	8.82	0.00
101531_at	MGC36398	hypothetical protein MGC36398	125.24	0.00	1.82	0.29	4.21	0.02	4.15	0.02	7.19	0.00
94325_at	MGC36662	hypothetical protein MGC36662	74.07	0.03	-10.70	0.18	-14.54	0.07	-12.08	0.13	-18.32	0.03
102348_at	MGC37588	hypothetical protein MGC37588	34.98	0.01	10.01	0.00	-0.41	0.89	6.37	0.04	-1.43	0.62
95692_at	MGC38208	hypothetical protein MGC38208	61.91	0.01	-0.01	1.00	4.62	0.00	-0.03	0.98	-4.27	0.01
99619_at	MGC38847	hypothetical protein MGC38847	30.40	0.01	1.94	0.48	0.05	0.99	-1.37	0.62	-11.01	0.00
101470_at	MGC38950	hypothetical protein MGC38950	11.30	0.00	-7.43	0.00	0.62	0.70	0.32	0.84	1.70	0.30
160815_at	MGC41710	hypothetical protein MGC41710	21.17	0.03	2.10	0.38	6.47	0.01	3.85	0.12	3.48	0.15
161214_r_at	MGC47434	hypothetical protein MGC47434	31.02	0.05	1.56	0.47	3.07	0.16	5.51	0.02	-3.30	0.14
101485_at	MGC6664	hypothetical protein MGC6664	48.31	0.02	5.23	0.09	-5.98	0.06	-2.49	0.41	-7.51	0.02
97241_at	MGC6696	hypothetical protein MGC6696	67.54	0.04	1.05	0.63	-4.66	0.04	-5.39	0.02	-2.41	0.27
161434_r_at	MGC7221	hypothetical protein MGC7221	-2.85	0.02	-1.74	0.23	3.56	0.02	3.88	0.01	0.01	1.00
97365_at	MGC7221	hypothetical protein MGC7221	9.43	0.04	-1.29	0.45	2.38	0.17	-0.33	0.84	5.28	0.01
99512_at	MGC7843	hypothetical protein MGC7843	48.95	0.04	4.26	0.03	-4.84	0.02	-1.14	0.54	1.15	0.54
97511_at	Mgll	monoglyceride lipase	61.76	0.00	15.28	0.00	16.01	0.00	8.67	0.02	23.68	0.00
97510_at	Mgll	monoglyceride lipase	11.61	0.05	-5.51	0.04	2.56	0.31	-3.36	0.19	4.88	0.06
93026_at	Mgst1	microsomal glutathione S-transferase 1	134.44	0.03	-2.28	0.01	0.52	0.49	-0.44	0.56	-1.48	0.06
96258_at	Mgst3	microsomal glutathione S-transferase 3	32.96	0.03	-9.25	0.33	-16.99	0.08	-12.36	0.20	25.71	0.01
94848_at	Mif	macrophage migration inhibitory factor	-2.34	0.02	-3.58	0.04	-2.47	0.14	1.00	0.54	4.33	0.02

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
99640_at	Minpp1	multiple inositol polyphosphate histidine phosphatase 1	39.29	0.03	5.88	0.08	-3.86	0.23	3.43	0.29	8.28	0.02
101007_at	Mknk2	MAP kinase-interacting serine/threonine kinase 2	82.04	0.00	10.68	0.00	2.09	0.53	-0.15	0.96	-11.46	0.00
103622_at	Mlycd	malonyl-CoA decarboxylase	62.24	0.00	3.06	0.17	-6.67	0.01	-6.56	0.01	1.18	0.59
160964_at	MNCb-4137	hypothetical protein MNCb-4137	58.67	0.03	-10.68	0.00	3.40	0.27	0.99	0.75	-2.14	0.49
93991_at	Mor1	malate dehydrogenase, mitochondrial	102.87	0.01	-4.58	0.01	-2.85	0.07	-2.57	0.10	2.11	0.17
160805_s_at	Mpdu1	mannose-P-dolichol utilization defect 1	44.17	0.04	1.50	0.63	2.10	0.49	1.27	0.68	10.21	0.00
93887_at	Mpdz	multiple PDZ domain protein	26.77	0.02	3.61	0.05	-2.44	0.18	-1.92	0.28	-4.95	0.01
92926_at	Mpl	myeloproliferative leukemia virus oncogene	-0.51	0.00	-0.38	0.83	5.88	0.00	-0.01	1.00	-9.40	0.00
97803_at	Mpp1	membrane protein, palmitoylated (55 kDa)	58.20	0.00	2.95	0.20	3.08	0.19	9.76	0.00	12.67	0.00
96632_at	Mrgx-pending	MORF-related gene X	88.09	0.00	5.02	0.01	8.77	0.00	3.44	0.08	0.09	0.96
96633_s_at	Mrgx-pending	MORF-related gene X	63.00	0.01	0.87	0.76	10.86	0.00	2.66	0.36	-6.20	0.04
99140_at	Mrpl16	mitochondrial ribosomal protein L16	48.74	0.03	1.53	0.37	-0.54	0.75	-0.03	0.99	6.12	0.00
98120_at	Mrpl27	mitochondrial ribosomal protein L27	73.82	0.03	0.67	0.80	3.90	0.14	5.83	0.04	6.36	0.02
95653_at	Mrpl37	mitochondrial ribosomal protein L37	44.17	0.03	5.79	0.03	2.38	0.34	0.55	0.82	6.77	0.01
160488_at	Msh3	mutS homolog 3 (E. coli)	1.50	0.04	8.51	0.08	12.82	0.01	-1.25	0.78	3.54	0.44
94140_at	Msr1	macrophage scavenger receptor 1	10.30	0.02	-3.55	0.49	18.74	0.00	4.93	0.34	1.71	0.74
101526_at	Msx1	homeo box, msh-like 1	29.10	0.02	-6.36	0.05	5.30	0.10	-7.27	0.03	-4.72	0.14
100018_at	Mtf1	metal response element binding transcription factor 1	12.89	0.04	0.08	0.98	7.21	0.08	-1.87	0.64	-11.84	0.01
161470_r_at	Mtf2	metal response element binding transcription factor 2	4.87	0.00	-1.85	0.28	3.28	0.06	-5.52	0.00	-4.56	0.01
96199_at	Mtm1	X-linked myotubular myopathy gene 1	25.09	0.01	4.12	0.01	0.42	0.78	0.53	0.72	5.06	0.00
101190_at	Mtnr1a	melatonin receptor 1A	1.98	0.04	7.49	0.08	-2.28	0.57	5.65	0.17	10.16	0.02
94277_at	Mtx1	metaxin 1	39.71	0.04	-3.75	0.38	-10.49	0.02	3.53	0.41	9.12	0.04
160076_at	Mtx2	metaxin 2	48.88	0.01	0.95	0.33	-3.43	0.00	0.28	0.78	1.79	0.08
102918_at	Muc1	mucin 1, transmembrane	-6.64	0.03	-6.65	0.21	3.28	0.53	5.08	0.34	16.44	0.01
97680_at	Mug-ps1	murinoglobulin, pseudogene 1	147.57	0.02	4.33	0.00	1.58	0.26	2.49	0.08	0.91	0.51
95633_r_at	Mvk	mevalonate kinase	35.68	0.00	-7.15	0.01	-10.77	0.00	-0.75	0.76	-1.43	0.56
95632_f_at	Mvk	mevalonate kinase	-11.64	0.01	-2.51	0.65	-18.70	0.00	1.16	0.83	-15.60	0.01
160626_at	Myef2	myelin basic protein expression factor 2, repressor	16.98	0.05	1.90	0.50	1.72	0.54	3.57	0.21	-8.49	0.01
161545_r_at	Myh4	myosin, heavy polypeptide 4, skeletal muscle	5.64	0.02	-6.55	0.15	1.46	0.74	-4.49	0.31	15.02	0.00
93482_at	Mylk	myosin, light polypeptide kinase	68.06	0.04	0.36	0.85	6.12	0.00	2.19	0.25	-0.03	0.99
92382_at	Myo6	myosin VI	3.66	0.04	6.30	0.10	-6.54	0.09	-0.71	0.85	-8.90	0.02
160566_at	Myst1	MYST histone acetyltransferase 1	-7.76	0.02	-6.00	0.01	-4.77	0.04	1.55	0.47	-2.27	0.30
97860_at	Nap1l4	nucleosome assembly protein 1-like 4	36.53	0.05	-4.67	0.29	-4.22	0.34	-2.19	0.62	13.28	0.01
98887_at	Napa	N-ethylmaleimide sensitive fusion protein attachment protein alpha	36.04	0.02	7.81	0.07	-13.73	0.00	-4.77	0.26	-1.90	0.65

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
93246_at	Narg1	NMDA receptor-regulated gene 1	8.18	0.02	4.07	0.01	-0.55	0.70	3.76	0.02	0.12	0.94
95070_at	Nars	asparaginyl-tRNA synthetase	61.34	0.01	3.98	0.16	2.25	0.41	3.34	0.23	-9.56	0.00
101108_at	Nasp	nuclear autoantigenic sperm protein (histone-binding)	4.76	0.03	8.62	0.03	-1.70	0.65	-0.04	0.99	-10.27	0.01
94723_at	Nat1	N-acetyltransferase 1 (arylamine N-acetyltransferase)	3.82	0.04	-0.66	0.70	-1.27	0.47	1.66	0.34	5.76	0.00
92746_at	Nat2	N-acetyltransferase 2 (arylamine N-acetyltransferase)	28.37	0.01	3.69	0.11	1.62	0.47	2.41	0.28	8.75	0.00
104439_at	Nat6	N-acetyltransferase 6	60.19	0.04	-5.90	0.06	0.38	0.90	-5.11	0.10	6.67	0.03
103662_at	Ncf4	neutrophil cytosolic factor 4	-8.02	0.02	5.85	0.03	-6.30	0.02	-2.83	0.28	-4.14	0.12
97302_at	Nd1-pending	Nd1	46.35	0.00	4.03	0.06	11.14	0.00	8.68	0.00	1.26	0.54
160464_s_at	Ndr1	N-myc downstream regulated 1	27.95	0.00	-8.66	0.01	-14.00	0.00	-7.35	0.03	-6.05	0.07
96596_at	Ndrl	N-myc downstream regulated-like	29.26	0.00	-11.23	0.00	-18.97	0.00	-16.24	0.00	-8.91	0.02
101469_at	Nedd9	neural precursor cell expressed, developmentally down-regulated gene 9	1.93	0.05	-0.04	0.99	-0.14	0.96	1.38	0.65	-10.45	0.00
102827_at	Nek7	NIMA (never in mitosis gene a)-related expressed kinase 7	57.06	0.04	1.06	0.54	-4.22	0.02	-3.63	0.04	-1.50	0.39
161829_at	Nes	nestin	-23.87	0.03	1.84	0.52	0.66	0.82	3.50	0.23	-9.67	0.00
94223_at	Net1	neuroepithelial cell transforming gene 1	46.66	0.00	-4.82	0.11	-8.43	0.01	-9.58	0.00	-2.26	0.44
92717_at	Neurod1	neurogenic differentiation 1	6.43	0.04	2.26	0.14	-3.16	0.05	3.21	0.04	-1.15	0.44
93230_at	Neurod3	neurogenic differentiation 3	-17.70	0.01	-1.10	0.56	-3.22	0.10	-0.64	0.73	7.57	0.00
93073_at	Nfatc2	nuclear factor of activated T-cells, cytoplasmic 2	36.43	0.03	-6.25	0.01	3.38	0.11	0.97	0.63	-1.75	0.39
160535_at	Nfe2l1	nuclear factor, erythroid derived 2,-like 1	58.05	0.05	-2.47	0.30	-2.99	0.21	-6.15	0.02	3.39	0.16
98427_s_at	Nfkb1	nuclear factor of kappa light chain gene enhancer in B-cells 1, p105	27.88	0.01	9.60	0.00	-1.22	0.64	0.29	0.91	-5.30	0.05
95065_at	Nfs1	nitrogen fixation gene 1 (S. cerevisiae)	72.72	0.00	-0.99	0.44	-1.75	0.18	5.07	0.00	-3.12	0.02
94714_at	Ngfg	nerve growth factor, gamma	-2.14	0.02	-2.11	0.15	-0.33	0.82	0.78	0.58	-4.95	0.00
94236_at	Nisch	nischarin	70.86	0.04	1.97	0.34	-0.33	0.87	4.84	0.03	4.92	0.02
99873_at	Nkx2-6	NK2 transcription factor related, locus 6 (Drosophila)	-28.34	0.01	-6.32	0.07	-4.70	0.17	-1.60	0.63	10.84	0.00
92794_f_at	Nme1	expressed in non-metastatic cells 1, protein (NM23A) (nucleoside diphosphate kinase)	35.42	0.04	-3.90	0.15	-5.70	0.04	-0.29	0.91	-6.16	0.03
94982_f_at	Nme3	expressed in non-metastatic cells 3	50.58	0.00	4.86	0.06	-7.73	0.01	6.99	0.01	3.11	0.22
99009_at	Nnt	nicotinamide nucleotide transhydrogenase	64.92	0.03	3.22	0.18	3.95	0.11	1.69	0.48	6.56	0.01
92569_f_at	Nol5	nucleolar protein 5	11.57	0.00	0.79	0.74	3.33	0.17	2.55	0.29	-12.35	0.00
104766_at	Nola1	nucleolar protein family A, member 1 (H/ACA small nucleolar RNPs)	27.75	0.03	0.69	0.78	6.46	0.02	0.23	0.93	-6.43	0.02

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
93830_at	Nono	non-POU-domain-containing, octamer binding protein	64.46	0.02	-1.30	0.66	0.97	0.75	-2.38	0.43	-11.35	0.00
99999_at	Np220	nuclear protein 220	21.94	0.04	1.14	0.64	-1.91	0.43	1.93	0.43	-7.79	0.00
95390_at	Npas2	neuronal PAS domain protein 2	-14.13	0.02	0.56	0.77	-3.84	0.06	-6.11	0.00	0.19	0.92
98114_at	Npc1	Niemann Pick type C1	74.56	0.02	6.47	0.03	-3.58	0.20	4.44	0.11	5.51	0.05
160344_at	Npc2	Niemann Pick type C2	62.89	0.05	-1.88	0.41	-5.85	0.02	-4.11	0.08	-1.79	0.43
101634_at	Npm1	nucleophosmin 1	70.87	0.01	4.31	0.15	-1.30	0.66	-1.16	0.69	-10.86	0.00
101156_at	Npn2	neoplastic progression 2	2.32	0.02	1.09	0.35	3.37	0.01	-2.80	0.02	0.37	0.75
93134_at	Nptx1	neuronal pentraxin 1	12.11	0.05	-1.07	0.69	1.01	0.71	-8.61	0.00	-2.38	0.38
94350_f_at	Nqo1	NAD(P)H dehydrogenase, quinone 1	6.87	0.04	2.42	0.17	-0.45	0.80	-3.06	0.09	4.61	0.01
104381_at	Nr1h3	nuclear receptor subfamily 1, group H, member 3	67.17	0.00	4.11	0.02	0.86	0.60	2.41	0.15	8.87	0.00
104507_g_at	Nr1i3	nuclear receptor subfamily 1, group I, member 3	64.82	0.01	2.52	0.40	1.31	0.66	3.35	0.27	11.90	0.00
92190_at	Nr2c1	nuclear receptor subfamily 2, group C, member 1	8.12	0.00	2.60	0.24	-10.09	0.00	-3.57	0.11	-1.58	0.47
104554_at	Nr2f6	nuclear receptor subfamily 2, group F, member 6	69.27	0.00	3.04	0.10	-7.72	0.00	-3.53	0.06	1.98	0.27
161418_r_at	Nr5a1	nuclear receptor subfamily 5, group A, member 1	0.27	0.03	-6.48	0.02	4.58	0.08	-0.82	0.75	4.63	0.08
100700_s_at	Nr5a1	nuclear receptor subfamily 5, group A, member 1	10.84	0.05	2.77	0.40	5.09	0.13	7.57	0.03	-5.57	0.10
103654_at	Nsbp1	nucleosome binding protein 1	63.76	0.00	-0.26	0.89	6.98	0.00	0.27	0.89	-10.50	0.00
93868_at	Nsdhl	NAD(P) dependent steroid dehydrogenase-like	34.02	0.00	-12.79	0.04	-12.74	0.04	-6.56	0.28	-25.52	0.00
98631_g_at	Nsdhl	NAD(P) dependent steroid dehydrogenase-like	51.57	0.00	-16.70	0.01	-15.25	0.02	-6.45	0.30	-31.14	0.00
93740_at	Nsep1	nuclease sensitive element binding protein 1	114.39	0.04	-1.40	0.42	-2.34	0.19	-3.99	0.03	3.66	0.04
93202_at	Nt5e	5' nucleotidase, ecto	9.59	0.00	-7.17	0.00	-0.32	0.87	-2.14	0.29	-5.60	0.01
98884_r_at	Nudel-pending	nuclear distribution gene E-like	26.66	0.00	2.18	0.29	4.46	0.04	4.11	0.05	-6.71	0.00
94372_at	Nudt1	nudix (nucleoside diphosphate linked moiety X)-type motif 1	40.29	0.01	-0.26	0.93	0.65	0.82	-0.79	0.78	12.51	0.00
101977_at	Nudt3	nudix (nucleotide diphosphate linked moiety X)-type motif 3	48.52	0.05	-0.10	0.95	1.51	0.33	-1.36	0.38	4.82	0.00
98099_at	Nudt9	nudix (nucleoside diphosphate linked moiety X)-type motif 9	29.65	0.01	0.48	0.83	-3.65	0.11	5.80	0.02	7.09	0.00
103868_at	Nufip1	nuclear fragile X mental retardation protein interacting protein	0.52	0.02	-5.27	0.00	2.95	0.08	-0.14	0.93	1.25	0.45
102231_at	Oasis-pending	old astrocyte specifically induced substance	43.99	0.05	-2.57	0.24	5.38	0.02	-4.11	0.07	-0.89	0.68
92848_at	Oat	ornithine aminotransferase	115.89	0.02	-4.13	0.21	0.01	1.00	-4.51	0.17	-10.67	0.00
101013_at	Oaz1	ornithine decarboxylase antizyme	127.76	0.02	-0.21	0.78	-2.36	0.01	-1.52	0.06	0.74	0.33
101002_at	Oazi	ornithine decarboxylase antizyme inhibitor	75.18	0.00	7.06	0.00	9.17	0.00	5.67	0.00	-0.48	0.78
160668_at	Ogfr	opioid growth factor receptor	32.62	0.01	4.43	0.12	-9.50	0.00	4.47	0.11	-1.08	0.69

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
93369_at	Omd	osteomodulin	0.35	0.04	-0.52	0.69	1.88	0.15	3.86	0.01	-0.87	0.50
94828_at	Oprs1	opioid receptor, sigma 1	71.97	0.00	-4.44	0.10	-7.60	0.01	-8.52	0.00	1.75	0.50
104096_at	Orc4	origin recognition complex, subunit 4	30.31	0.04	6.24	0.00	-1.26	0.52	0.89	0.65	2.00	0.31
100894_at	Orc5	origin recognition complex, subunit 5 homolog (S. cerevisiae)	16.31	0.01	3.53	0.07	-0.95	0.61	1.46	0.43	6.39	0.00
95712_at	Orc6l	origin recognition complex, subunit 6-like (S. cerevisiae)	6.55	0.00	0.47	0.75	-0.27	0.86	0.92	0.55	6.86	0.00
96093_at	ORF11	open reading frame 11	50.63	0.01	-10.71	0.01	-7.48	0.04	-4.41	0.21	-6.34	0.08
94386_at	ORF60	open reading frame 60	43.30	0.05	2.82	0.11	-2.10	0.23	0.27	0.87	-4.65	0.01
100436_at	Orm1	orosomucoid 1	113.60	0.02	-4.92	0.34	-8.48	0.11	11.11	0.04	-12.71	0.02
100437_g_at	Orm1	orosomucoid 1	138.34	0.04	-5.47	0.28	-8.15	0.12	10.76	0.04	-10.18	0.05
94734_at	Orm2	orosomucoid 2	84.69	0.03	-14.07	0.17	-16.92	0.10	26.81	0.01	-12.08	0.23
93316_at	Osbpl1a	oxysterol binding protein-like 1A	62.92	0.00	3.13	0.21	6.43	0.01	4.21	0.09	-9.66	0.00
99489_at	Osp94	osmotic stress protein 94 kDa	19.66	0.00	0.52	0.78	7.58	0.00	-4.23	0.03	-5.10	0.01
102074_at	Otp	orthopedia homolog, (Drosophila)	14.94	0.01	-6.49	0.00	2.36	0.21	-0.12	0.95	-4.27	0.03
101712_at	P2rx7	purinergic receptor P2X, ligand-gated ion channel, 7	41.67	0.04	-7.75	0.05	1.04	0.78	-10.47	0.01	-1.51	0.69
92775_at	Pabpc4	poly(A) binding protein, cytoplasmic 4 (inducible form)	44.78	0.03	-0.37	0.87	5.30	0.03	3.32	0.16	-5.52	0.03
101476_at	Pabpn1	poly(A) binding protein, nuclear 1	57.53	0.02	-2.05	0.43	-4.44	0.10	-8.42	0.00	-0.16	0.95
95404_at	Pafah1b2	platelet-activating factor acetylhydrolase, isoform 1b, alpha2 subunit	20.19	0.03	9.34	0.00	1.27	0.65	2.64	0.35	-3.23	0.26
161890_f_at	Pap	pancreatitis-associated protein	1.61	0.03	-2.11	0.20	-2.66	0.12	1.66	0.31	4.52	0.01
161033_at	Papolb	poly (A) polymerase beta (testis specific)	26.61	0.03	-3.57	0.21	8.88	0.00	-2.83	0.31	-0.08	0.98
93298_at	Papss1	3'-phosphoadenosine 5'-phosphosulfate synthase 1	39.95	0.04	-6.30	0.03	3.42	0.22	0.31	0.91	6.14	0.03
96713_at	Papss2	3'-phosphoadenosine 5'-phosphosulfate synthase 2	80.17	0.00	-6.26	0.05	-2.57	0.40	-4.25	0.17	-15.55	0.00
96595_at	Pax1	paired box gene 1	10.20	0.05	-0.40	0.76	0.99	0.45	-1.63	0.22	-3.95	0.01
94461_at	Pbef-pending	pre-B-cell colony-enhancing factor	22.58	0.03	6.54	0.01	0.95	0.69	5.75	0.02	-0.46	0.85
94632_at	Pbsn	probasin	-2.47	0.02	1.61	0.22	4.10	0.00	-1.69	0.20	-1.72	0.19
94552_at	Pcbp1	poly(rC) binding protein 1	100.92	0.01	3.07	0.12	3.02	0.12	2.65	0.17	-6.51	0.00
160352_at	Pcbp4	poly(rC) binding protein 4	17.41	0.01	-7.63	0.00	-6.55	0.01	-0.37	0.87	-0.45	0.85
97756_s_at	Pcdha5	protocadherin alpha 5	-12.15	0.03	-1.53	0.37	2.16	0.21	-4.32	0.02	-3.72	0.04
102781_at	Pcee-pending	Paneth cell enhanced expression	68.89	0.00	-0.76	0.69	-0.32	0.87	-0.31	0.87	-10.71	0.00
160481_at	Pck1	phosphoenolpyruvate carboxykinase 1, cytosolic	130.81	0.01	3.49	0.05	2.18	0.21	-0.16	0.93	-5.60	0.00
96140_at	Pcm1	pericentriolar material 1	2.49	0.02	-5.15	0.01	-3.25	0.10	2.76	0.16	-3.45	0.08
104675_at	Pcsk4	proprotein convertase subtilisin/kexin type 4	-10.07	0.01	7.35	0.02	10.66	0.00	-0.26	0.93	0.35	0.91
101173_at	Pctp	phosphatidylcholine transfer protein	23.98	0.03	3.18	0.45	5.80	0.17	-12.43	0.01	5.26	0.22
93308_s_at	Pcx	pyruvate carboxylase	65.66	0.01	6.88	0.13	2.46	0.57	2.43	0.58	17.95	0.00
160412_at	Pdcd2	programmed cell death 2	18.13	0.02	0.83	0.66	0.53	0.78	2.14	0.26	6.64	0.00
103029_at	Pdcd4	programmed cell death 4	86.94	0.02	-3.22	0.07	-2.73	0.12	-4.60	0.01	-1.52	0.38
96252_at	Pdcd6ip	programmed cell death 6 interacting protein	62.40	0.01	1.74	0.39	0.66	0.74	-4.48	0.04	-6.58	0.00
160941_at	Pde8a	phosphodiesterase 8A	26.36	0.04	2.69	0.16	-2.89	0.13	-4.80	0.02	-2.18	0.25

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
96831_at	Pdir-pending	protein disulfide isomerase-related	57.48	0.01	0.26	0.94	-6.27	0.09	5.05	0.16	-12.25	0.00
92810_at	Pdk3	pyruvate dehydrogenase kinase, isoenzyme 3	0.12	0.03	4.08	0.00	-1.10	0.40	-1.21	0.35	-1.89	0.15
102049_at	Pdk4	pyruvate dehydrogenase kinase, isoenzyme 4	5.05	0.02	-8.53	0.02	-1.38	0.69	-9.39	0.01	4.74	0.18
100554_at	Pdlim1	PDZ and LIM domain 1 (elfin)	33.79	0.03	3.12	0.11	-2.00	0.30	-0.07	0.97	-5.96	0.01
98821_at	Pdx1	pancreatic and duodenal homeobox gene 1	-0.79	0.04	1.61	0.38	-2.47	0.18	-5.08	0.01	-2.37	0.20
100548_at	Pea15	phosphoprotein enriched in astrocytes 15	-8.56	0.05	21.69	0.01	-7.37	0.35	10.99	0.17	-6.32	0.42
94485_at	Peci	peroxisomal delta3, delta2-enoyl-Coenzyme A isomerase	87.77	0.03	5.75	0.08	0.06	0.99	-2.38	0.46	10.16	0.00
96765_at	Peg3	paternally expressed 3	29.05	0.05	13.80	0.02	9.54	0.10	6.10	0.28	-6.00	0.29
101368_at	Pem	placentae and embryos oncofetal gene	-9.09	0.01	10.17	0.00	1.67	0.55	-1.79	0.52	-4.51	0.12
93619_at	Per1	period homolog 1 (Drosophila)	7.76	0.03	13.67	0.09	1.36	0.86	23.54	0.01	-8.66	0.27
93694_at	Per2	period homolog 2 (Drosophila)	16.23	0.00	12.00	0.00	18.07	0.00	18.39	0.00	-2.16	0.55
97825_at	Perp-pending	p53 apoptosis effector related to Pmp22	71.93	0.00	6.90	0.01	5.57	0.02	4.84	0.04	18.17	0.00
103660_at	Pex11a	peroxisomal biogenesis factor 11a	60.57	0.00	-1.29	0.72	-3.47	0.35	-1.56	0.67	22.00	0.00
100027_s_at	Pex14	peroxisomal biogenesis factor 14	66.64	0.04	0.72	0.78	-5.33	0.05	-2.01	0.43	6.64	0.02
104318_at	Pex5	peroxin 5	49.86	0.05	0.66	0.70	-3.38	0.06	-2.48	0.15	3.88	0.03
99469_at	Pex6	similar to peroxisomal biogenesis factor 6	63.42	0.01	11.68	0.00	-2.52	0.46	-0.08	0.98	8.40	0.02
103297_at	Pfkfb1	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1	32.84	0.04	3.12	0.32	8.02	0.02	-0.30	0.92	6.68	0.04
160641_at	Pfkfb3	inducible 6-phosphofructo-2-kinase	18.42	0.00	1.21	0.46	1.83	0.27	4.95	0.01	-6.87	0.00
94438_at	Pfkm	phosphofructokinase, muscle	36.90	0.00	-6.22	0.00	-5.75	0.00	-4.06	0.03	0.99	0.56
93039_at	Pgcp-pending	plasma glutamate carboxypeptidase	42.42	0.04	2.94	0.11	-3.20	0.09	2.91	0.12	3.33	0.08
101388_at	Pgk2	phosphoglycerate kinase 2	-2.55	0.03	2.19	0.21	-5.30	0.01	0.91	0.60	2.57	0.15
95147_at	Pgls	6-phosphogluconolactonase	71.78	0.04	2.20	0.36	-2.68	0.27	-2.92	0.23	7.20	0.01
101585_at	Pgrmc1	progesterone receptor membrane component 1	125.99	0.00	-3.97	0.01	-3.39	0.02	-7.75	0.00	-0.42	0.76
98056_at	Phlda3	pleckstrin homology-like domain, family A, member 3	26.84	0.05	-2.35	0.34	3.95	0.11	-1.94	0.42	-6.49	0.01
93708_at	Pias3	protein inhibitor of activated STAT 3	14.46	0.00	-0.54	0.85	-3.75	0.19	4.87	0.10	11.65	0.00
161433_f_at	Piga	phosphatidylinositol glycan, class A	12.05	0.00	2.80	0.13	9.14	0.00	1.77	0.33	-3.10	0.10
92304_at	Piga	phosphatidylinositol glycan, class A	11.34	0.01	5.33	0.03	8.29	0.00	1.70	0.45	-1.15	0.61
100594_at	Pigq	phosphatidylinositol glycan, class Q	42.16	0.01	3.49	0.05	2.03	0.24	-0.43	0.80	5.47	0.00
162027_f_at	Pigq	phosphatidylinositol glycan, class Q	-25.74	0.01	11.26	0.00	0.52	0.88	10.64	0.01	1.51	0.66
96592_at	Pik3r1	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 1 (p85 alpha)	12.83	0.02	4.18	0.07	3.01	0.18	6.44	0.01	-1.72	0.43

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
102759_at	Pik3r2	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 2 (p85 beta)	0.04	0.03	1.54	0.75	-16.68	0.00	-6.07	0.22	-2.18	0.65
99384_at	Pim1	proviral integration site 1	-0.60	0.02	4.43	0.15	-1.98	0.51	6.23	0.05	8.43	0.01
103573_at	Pip5k1a	phosphatidylinositol-4-phosphate 5-kinase, type 1 alpha	8.00	0.00	-2.12	0.10	5.02	0.00	-2.05	0.11	-2.28	0.08
160409_at	Pitpn	phosphatidylinositol transfer protein	14.41	0.04	-1.56	0.52	6.20	0.02	-1.73	0.47	4.90	0.05
101461_f_at	Pja1	praja1, RING-H2 motif containing	88.19	0.04	-2.99	0.04	-2.92	0.04	-1.10	0.42	-2.13	0.13
98005_at	Pkia	protein kinase inhibitor, alpha	-3.57	0.01	4.63	0.00	-0.11	0.93	2.96	0.04	-1.27	0.35
101471_at	Pklr	pyruvate kinase liver and red blood cell	38.07	0.00	6.95	0.14	12.74	0.01	8.01	0.09	32.86	0.00
101472_s_at	Pklr	pyruvate kinase liver and red blood cell	30.07	0.00	2.66	0.56	13.86	0.01	2.73	0.55	18.32	0.00
104201_at	Plac1	placental specific protein 1	32.75	0.01	-3.02	0.21	7.26	0.01	-0.77	0.74	-6.45	0.01
92466_at	Plcb1	phospholipase C, beta 1	70.02	0.03	-4.32	0.13	2.95	0.30	-5.92	0.04	-6.64	0.03
161626_f_at	Plg	plasminogen	153.61	0.02	-3.00	0.03	1.82	0.17	3.45	0.02	-0.98	0.45
101064_at	Plrg1	pleiotropic regulator 1, PRL1 homolog (Arabidopsis)	40.54	0.03	-1.16	0.58	-4.56	0.04	3.17	0.15	5.18	0.02
95368_at	Plxna2	plexin A2	9.05	0.05	-4.27	0.07	-4.29	0.07	-4.81	0.04	0.08	0.97
97332_at	Pnkp	polynucleotide kinase 3'-phosphatase	23.55	0.00	2.67	0.32	-10.82	0.00	-8.27	0.01	4.27	0.12
92601_at	Pnliprp1	pancreatic lipase related protein 1	0.53	0.05	-2.95	0.09	2.22	0.20	-0.81	0.63	-4.30	0.02
94239_at	Pnn	pinin	7.94	0.01	3.81	0.13	4.24	0.09	2.97	0.23	-7.68	0.00
93290_at	Pnp	purine-nucleoside phosphorylase	90.50	0.00	-4.90	0.06	-6.51	0.02	-10.79	0.00	-10.09	0.00
162307_at	Polk	polymerase (DNA directed), kappa	-4.73	0.02	3.98	0.09	1.38	0.54	6.66	0.01	3.27	0.15
161668_f_at	Por	P450 (cytochrome) oxidoreductase	32.94	0.04	5.32	0.26	1.64	0.72	10.28	0.04	-10.97	0.03
93915_at	Pou2af1	POU domain, class 2, associating factor 1	0.73	0.02	-0.05	0.97	-1.06	0.42	-3.43	0.02	3.53	0.01
99386_at	Pou3f4	POU domain, class 3, transcription factor 4	-4.80	0.00	-1.20	0.37	-3.90	0.01	-4.36	0.00	2.40	0.09
94990_at	Pp6-pending	placental protein 6	6.61	0.05	4.05	0.44	-0.13	0.98	-2.21	0.67	17.14	0.00
102668_at	Ppara	peroxisome proliferator activated receptor alpha	45.51	0.00	10.87	0.00	6.39	0.05	8.70	0.01	21.05	0.00
94198_at	Ppard	peroxisome proliferator activator receptor delta	6.55	0.01	-1.80	0.38	-2.67	0.20	-7.43	0.00	3.52	0.10
101055_at	Ppgb	protective protein for beta-galactosidase	61.64	0.04	-2.19	0.35	-7.53	0.00	-0.18	0.94	1.18	0.61
101207_at	Ppia	peptidylprolyl isomerase A	138.59	0.00	-2.89	0.00	-1.47	0.12	-3.31	0.00	-1.49	0.11
97507_at	Ppicap	peptidylprolyl isomerase C-associated protein	34.59	0.03	6.76	0.04	1.69	0.59	7.48	0.03	5.28	0.10
95110_at	Ppil2	peptidylprolyl isomerase (cyclophilin)-like 2	21.31	0.02	3.56	0.03	-1.71	0.28	0.27	0.86	4.39	0.01
93933_at	Ppp1r3c	protein phosphatase 1, regulatory (inhibitor) subunit 3C	20.58	0.01	6.73	0.06	0.87	0.80	-7.49	0.04	9.56	0.01
92638_at	Ppp2ca	protein phosphatase 2a, catalytic subunit, alpha isoform	15.58	0.01	5.25	0.00	-1.54	0.27	-0.22	0.87	-1.56	0.26
99183_at	Ppp3r1	protein phospatase 3, regulatory subunit B, alpha isoform (calcineurin B, type I)	52.04	0.04	2.96	0.06	3.88	0.02	-1.72	0.26	-0.54	0.72
98426_at	Ppt2	palmitoyl-protein thioesterase 2	33.04	0.02	10.63	0.00	1.46	0.62	2.12	0.47	1.48	0.61

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
97055_s_at	Prdx1	peroxiredoxin 1	137.13	0.00	-2.66	0.00	-1.50	0.07	-1.37	0.10	-1.93	0.02
97758_at	Prdx1	peroxiredoxin 1	132.82	0.01	-2.80	0.00	-0.09	0.92	-1.20	0.16	-1.31	0.13
99608_at	Prdx2	peroxiredoxin 2	25.37	0.01	5.93	0.01	3.51	0.11	-0.03	0.99	6.61	0.01
96256_at	Prdx3	peroxiredoxin 3	78.33	0.00	-3.78	0.01	-2.83	0.03	-1.15	0.36	4.42	0.00
98146_at	Prei2	preimplantation protein 2	39.11	0.01	3.54	0.11	6.68	0.00	5.28	0.02	-0.26	0.90
161459_f_at	Prep	prolyl endopeptidase	1.38	0.00	-2.06	0.04	3.56	0.00	-0.58	0.54	2.58	0.01
160808_at	Prkab1	protein kinase, AMP-activated, beta 1 non-catalytic subunit	24.97	0.00	8.05	0.00	-2.62	0.06	1.74	0.19	7.47	0.00
96852_at	Prkar1a	protein kinase, cAMP dependent regulatory, type I, alpha	68.89	0.01	0.11	0.93	-4.12	0.00	-2.96	0.03	-2.13	0.11
93476_at	Prkdc	protein kinase, DNA activated, catalytic polypeptide	8.99	0.04	5.57	0.00	-0.46	0.78	-0.73	0.65	-0.98	0.55
98018_at	Procr	protein C receptor, endothelial	15.75	0.01	-5.27	0.01	6.56	0.00	-0.26	0.89	2.24	0.25
103452_at	Prodh2	proline dehydrogenase (oxidase) 2	88.22	0.01	3.89	0.27	3.26	0.35	4.15	0.24	14.37	0.00
93651_r_at	Prp2	proline rich protein 2	22.11	0.02	-38.92	0.00	-5.08	0.61	-3.27	0.75	2.28	0.82
102017_at	Prpf4b	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	2.04	0.01	2.54	0.15	3.06	0.09	1.26	0.47	-6.41	0.00
98382_f_at	Prpmp5	proline-rich protein MP5	-6.08	0.01	-4.75	0.13	8.43	0.01	-6.55	0.04	-6.90	0.03
92353_at	Prss18	protease, serine, 18	0.01	0.02	-8.53	0.03	-8.24	0.03	-0.49	0.89	-6.40	0.09
100909_at	Prss8	protease, serine, 8 (prostasin)	0.85	0.02	-16.02	0.01	-8.16	0.17	-11.85	0.05	-6.54	0.27
104541_at	Prtn3	proteinase 3	-0.08	0.02	-0.46	0.91	0.68	0.86	14.10	0.00	-6.66	0.10
161476_at	Psap	prosaposin	41.36	0.04	4.38	0.18	0.51	0.87	2.36	0.46	9.78	0.01
97114_at	Psap	prosaposin	81.88	0.03	4.58	0.03	-0.08	0.97	1.72	0.39	5.16	0.02
99930_s_at	Psen2	presenilin 2	79.51	0.00	-3.63	0.08	-6.57	0.00	-5.30	0.01	1.72	0.39
98557_f_at	Psmb4	proteasome (prosome, macropain) subunit, beta type 4	97.39	0.02	-1.49	0.11	-0.40	0.66	1.40	0.13	-2.69	0.01
93085_at	Psmb9	proteosome (prosome, macropain) subunit, beta type 9 (large multifunctional protease 2)	27.52	0.02	9.78	0.08	6.78	0.21	5.37	0.32	15.58	0.01
102970_at	Psmc3ip	proteasome (prosome, macropain) 26S subunit, ATPase 3, interacting protein	-5.80	0.04	-1.69	0.32	-1.59	0.35	-1.27	0.46	-5.19	0.01
95672_at	Psmc4	proteasome (prosome, macropain) 26S subunit, ATPase, 4	13.93	0.01	-7.29	0.03	7.84	0.02	-0.06	0.98	6.02	0.06
160305_at	Psmd11	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	56.55	0.00	-5.52	0.02	-7.80	0.00	-6.87	0.00	0.18	0.93
93971_f_at	Psmd12	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12	29.77	0.01	7.68	0.01	-6.17	0.02	2.94	0.24	-3.59	0.16
96698_at	Psmd5	proteasome (prosome, macropain) 26S subunit, non-ATPase, 5	49.10	0.02	-1.09	0.60	-6.27	0.01	-2.90	0.17	4.30	0.05
101510_at	Psme1	proteasome (prosome, macropain) 28 subunit, alpha	67.85	0.02	-3.74	0.13	-7.25	0.01	-3.64	0.14	-2.41	0.32
100588_at	Psme2	proteasome (prosome, macropain) 28 subunit, beta	71.96	0.01	-3.16	0.28	-10.52	0.00	5.73	0.06	1.32	0.65
160853_at	Ptdss2	phosphatidylserine synthase 2	5.74	0.05	0.49	0.90	-12.62	0.00	2.13	0.58	0.72	0.85
93542_at	Pter	phosphotriesterase related	65.07	0.01	-3.78	0.22	-4.40	0.16	6.50	0.04	9.05	0.01

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
102105_f_at	Ptgds	prostaglandin D2 synthase (21 kDa, brain)	19.53	0.00	-1.06	0.94	31.54	0.03	-57.08	0.00	-16.04	0.26
160765_at	Ptges2	prostaglandin E synthase 2	46.62	0.03	-1.53	0.57	-5.68	0.05	-7.75	0.01	0.38	0.89
161713_f_at	Ptgfr	prostaglandin F receptor	4.82	0.00	1.68	0.21	-1.63	0.22	-3.07	0.03	4.63	0.00
161982_at	Ptk2	PTK2 protein tyrosine kinase 2	10.36	0.00	0.03	0.98	0.35	0.73	-0.53	0.61	4.70	0.00
99599_s_at	Ptov1	prostate tumor over expressed gene 1	68.70	0.00	3.18	0.10	-5.44	0.01	-5.15	0.01	7.56	0.00
99600_at	Ptov1	prostate tumor over expressed gene 1	21.25	0.00	3.00	0.18	-4.05	0.08	-6.23	0.01	6.07	0.01
94489_at	Ptp4a1	protein tyrosine phosphatase 4a1	95.06	0.00	9.50	0.00	8.33	0.01	3.77	0.21	-10.99	0.00
160862_at	Ptp4a3	protein tyrosine phosphatase 4a3	6.88	0.00	8.11	0.00	-1.13	0.66	3.54	0.18	8.49	0.00
98385_at	Ptpn14	protein tyrosine phosphatase, non-receptor type 14	15.14	0.05	-8.27	0.02	3.49	0.28	0.96	0.76	5.68	0.08
103070_at	Ptpns1	protein tyrosine phosphatase, non-receptor type substrate 1	-19.41	0.02	4.71	0.16	-10.82	0.00	5.22	0.12	-0.81	0.80
160760_at	Ptprk	protein tyrosine phosphatase, receptor type, K	34.25	0.00	2.20	0.22	-2.22	0.21	5.50	0.00	6.62	0.00
103501_at	Pura	purine rich element binding protein A	58.37	0.01	-5.48	0.00	-4.60	0.01	-1.09	0.52	1.14	0.50
103047_at	Pxmp3	peroxisomal membrane protein 3, 35 kDa	51.53	0.01	2.54	0.27	6.82	0.01	2.77	0.22	4.56	0.05
93799_at	R74819	expressed sequence R74819	58.84	0.01	0.60	0.85	8.08	0.02	3.03	0.35	-9.87	0.01
161058_f_at	R74862	expressed sequence R74862	3.37	0.00	2.05	0.15	4.20	0.01	2.76	0.06	3.59	0.02
92882_at	Rab1	RAB1, member RAS oncogene family	53.97	0.04	2.10	0.44	8.70	0.00	0.73	0.79	2.27	0.40
101933_at	Rab10	RAB10, member RAS oncogene family	33.43	0.05	-5.34	0.22	5.11	0.24	-2.99	0.49	-12.00	0.01
92854_at	Rab11a	RAB11a, member RAS oncogene family	67.43	0.02	2.05	0.16	1.67	0.25	4.76	0.00	1.62	0.26
96238_at	Rab11a	RAB11a, member RAS oncogene family	18.04	0.02	2.00	0.28	-3.22	0.09	-4.43	0.02	3.72	0.05
98150_at	Rab11b	RAB11B, member RAS oncogene family	54.89	0.01	5.85	0.02	-7.52	0.00	-0.13	0.96	4.76	0.06
92329_at	Rab17	RAB17, member RAS oncogene family	15.05	0.03	-0.25	0.88	-5.31	0.01	-1.61	0.35	2.78	0.11
160731_at	Rab25	RAB25, member RAS oncogene family	22.15	0.00	-9.20	0.01	1.09	0.74	-7.69	0.03	9.63	0.01
160868_at	Rab3b	RAB3B, member RAS oncogene family	-22.39	0.01	12.10	0.01	-9.27	0.03	-0.26	0.95	5.44	0.19
97415_at	Rab3d	RAB3D, member RAS oncogene family	-8.32	0.04	12.72	0.01	-7.54	0.12	-2.79	0.55	6.90	0.15
94478_at	Rab5a	RAB5A, member RAS oncogene family	59.80	0.05	1.99	0.27	1.91	0.29	-4.65	0.02	-2.87	0.12
96059_at	Rab6	RAB6, member RAS oncogene family	39.96	0.00	3.03	0.17	1.18	0.58	2.89	0.18	9.70	0.00
160501_at	Rab6kifl	Rab6, kinesin-like	0.21	0.00	-8.98	0.00	-2.99	0.15	-4.05	0.05	-1.90	0.35
95077_at	Rabggtb	RAB geranylgeranyl transferase, b subunit	50.21	0.01	-1.56	0.49	-5.92	0.02	-3.73	0.11	-7.18	0.00
103944_at	Rad51l1	RAD51-like 1 (S. cerevisiae)	6.65	0.00	5.15	0.11	-1.38	0.66	7.84	0.02	19.26	0.00
101924_at	Rad51l3	RAD51-like 3 (S. cerevisiae)	7.46	0.01	4.12	0.00	2.28	0.08	-2.83	0.04	1.05	0.41
160466_at	Rae1	RAE1 RNA export 1 homolog (S. pombe)	26.84	0.03	-1.57	0.38	-5.74	0.00	0.80	0.65	2.57	0.16
102649_s_at	Raet1c	retinoic acid early transcript gamma	24.01	0.00	-15.79	0.01	-14.14	0.01	-22.10	0.00	-9.57	0.07
94264_at	Raf1	v-raf-1 leukemia viral oncogene 1	62.16	0.00	-0.30	0.82	-6.33	0.00	0.30	0.82	5.06	0.00

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
101163_at	Rag2	recombination activating gene 2	-2.29	0.01	2.98	0.09	1.08	0.52	2.13	0.21	-6.43	0.00
98602_at	Rangap1	RAN GTPase activating protein 1	48.54	0.02	3.98	0.10	6.62	0.01	-1.08	0.64	-4.80	0.05
100562_at	Rangnrf-pending	RAN guanine nucleotide release factor	-28.31	0.01	-6.78	0.08	13.44	0.00	-6.10	0.12	-4.27	0.27
93319_at	Rasa3	RAS p21 protein activator 3	14.97	0.03	-0.43	0.67	-0.44	0.66	2.75	0.01	-2.38	0.03
102821_s_at	Rasl2-9	RAS-like, family 2, locus 9	82.24	0.04	-2.45	0.14	-1.58	0.33	-4.72	0.01	-0.73	0.65
92647_at	Rbbp4	retinoblastoma binding protein 4	81.04	0.02	2.21	0.28	0.57	0.77	1.51	0.45	-7.35	0.00
99990_at	Rbbp6	retinoblastoma binding protein 6	56.59	0.00	-1.89	0.40	-6.06	0.01	-4.35	0.06	-9.90	0.00
162230_r_at	Rbbp9	retinoblastoma binding protein 9	-0.66	0.01	1.48	0.16	-1.18	0.25	-0.17	0.87	3.92	0.00
97293_at	Rbm10	RNA binding motif protein 10	11.72	0.02	0.14	0.94	4.79	0.02	-5.38	0.01	-1.75	0.38
97848_at	Rbmx	RNA binding motif protein, X chromosome	2.01	0.01	-0.03	0.98	-3.90	0.00	-2.97	0.02	-0.50	0.67
160192_at	Rbmxrt	RNA binding motif protein, X chromosome retrogene	17.27	0.04	2.15	0.11	-2.82	0.04	1.31	0.32	-2.56	0.06
101151_at	Rcvrn	recoverin	-19.82	0.05	-5.46	0.01	-2.85	0.15	-0.93	0.63	-2.09	0.29
98336_s_at	Recc1	replication factor C, 140 kDa	-14.14	0.04	1.22	0.53	-2.55	0.20	-6.17	0.00	1.09	0.58
98335_at	Recc1	replication factor C, 140 kDa	13.66	0.05	2.45	0.09	-2.01	0.16	-2.01	0.16	-2.76	0.06
96064_at	Reg3g	regenerating islet-derived 3 gamma	-5.20	0.04	2.31	0.17	-0.97	0.56	3.81	0.03	-3.65	0.04
96591_at	Reln	reelin	36.60	0.00	7.34	0.00	6.88	0.01	3.62	0.12	1.81	0.42
161269_i_at	Ren1	renin 1 structural	0.30	0.02	-1.05	0.26	0.79	0.40	1.04	0.27	3.27	0.00
160888_at	Reps1	RalBP1 associated Eps domain containing protein	7.45	0.01	4.08	0.07	-7.97	0.00	-2.62	0.22	2.10	0.33
102960_at	Rga	recombination activating gene 1 gene activation	25.57	0.05	3.46	0.07	0.40	0.83	-0.92	0.62	5.19	0.01
103384_at	Rgs10	regulator of G-protein signalling 10	-15.78	0.03	-6.78	0.02	-1.27	0.64	3.03	0.28	6.31	0.03
102650_at	Rgs11	regulator of G-protein signaling 11	-3.41	0.04	-11.04	0.08	6.59	0.28	-15.98	0.01	0.08	0.99
161609_at	Rgs16	regulator of G-protein signaling 16	36.84	0.00	9.33	0.16	24.06	0.00	19.84	0.01	14.79	0.03
94378_at	Rgs16	regulator of G-protein signaling 16	80.44	0.00	15.84	0.21	37.65	0.01	40.70	0.00	32.53	0.01
96180_at	Rgs5	regulator of G-protein signaling 5	1.35	0.05	5.52	0.02	2.06	0.36	4.29	0.07	2.20	0.33
98042_at	Risc-pending	retinoid-inducible serine caroboxypetidase	34.24	0.03	-2.95	0.21	-2.07	0.38	-5.57	0.02	-5.38	0.03
102083_at	Rit2	Ras-like without CAAX 2	28.92	0.02	-3.85	0.05	6.04	0.00	0.58	0.75	1.23	0.51
96038_at	Rnase4	ribonuclease, RNase A family 4	116.43	0.02	3.70	0.41	3.03	0.50	10.97	0.02	-12.18	0.01
96859_at	Rnf10	ring finger protein 10	84.39	0.02	0.89	0.49	0.18	0.89	-4.58	0.00	1.85	0.16
160205_f_at	Rnf11	ring finger protein 11	74.46	0.03	-3.05	0.04	-2.05	0.16	-2.00	0.17	3.10	0.04
101965_at	Rnf13	ring finger protein 13	63.57	0.03	0.58	0.72	1.09	0.50	-1.26	0.44	-5.74	0.00
97506_at	Rnf2	ring finger protein 2	15.88	0.01	7.68	0.08	-10.48	0.02	2.57	0.54	-11.20	0.01
161983_f_at	Rnh1	ribonuclease/angiogenin inhibitor 1	39.52	0.01	5.18	0.05	1.82	0.46	8.87	0.00	2.28	0.36
93267_at	Rnpc2	RNA-binding region (RNP1, RRM) containing 2	49.83	0.01	4.27	0.19	1.27	0.69	-2.07	0.51	-13.31	0.00
160746_at	Rock1	Rho-associated coiled-coil forming kinase 1	17.78	0.00	1.74	0.35	-2.21	0.24	-1.02	0.58	-8.75	0.00
100980_at	Rock1	Rho-associated coiled-coil forming kinase 1	26.75	0.03	-1.43	0.34	0.35	0.81	-1.69	0.26	-4.86	0.00

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
98504_at	Rock2	Rho-associated coiled-coil forming kinase 2	9.59	0.00	3.66	0.09	3.48	0.11	2.47	0.24	-8.56	0.00
99951_at	Rorc	RAR-related orphan receptor gamma	29.40	0.01	-1.81	0.51	2.47	0.37	3.27	0.24	11.60	0.00
98342_at	Rpl10	ribosomal protein 10	125.26	0.00	-2.02	0.03	-1.58	0.08	0.85	0.33	-2.97	0.00
99778_at	Rpl12	ribosomal protein L12	93.69	0.00	-5.48	0.02	-3.60	0.11	-4.38	0.05	-7.40	0.00
160476_f_at	Rpl18	ribosomal protein L18	78.81	0.01	-4.10	0.06	-7.90	0.00	0.38	0.86	0.28	0.89
96290_f_at	Rpl21	ribosomal protein L21	112.82	0.01	-5.70	0.00	-1.30	0.45	-0.55	0.75	-3.86	0.03
100729_at	Rpl26	ribosomal protein L26	112.81	0.03	-3.03	0.06	-2.29	0.15	2.27	0.15	-3.39	0.04
101573_f_at	Rpl27a	ribosomal protein L27a	118.71	0.01	-3.68	0.05	-4.36	0.02	0.19	0.91	-5.74	0.00
101680_at	Rpl27a	ribosomal protein L27a	97.81	0.02	-7.57	0.01	-6.82	0.02	-2.50	0.35	-2.03	0.45
100727_at	Rpl28	ribosomal protein L28	107.82	0.03	-3.97	0.10	-6.50	0.01	-1.72	0.46	-3.09	0.19
100734_at	Rpl3	ribosomal protein L3	96.27	0.00	-3.38	0.00	-3.81	0.00	1.22	0.26	-4.81	0.00
98119_at	Rpl30	ribosomal protein L30	122.80	0.01	-2.13	0.12	-0.98	0.47	-0.21	0.87	-5.00	0.00
160080_r_at	Rpl44	ribosomal protein L44	-11.71	0.01	-2.98	0.20	2.28	0.32	0.60	0.79	-8.85	0.00
101129_at	Rpl5	ribosomal protein L5	120.24	0.00	0.10	0.91	0.05	0.96	-1.45	0.10	-4.30	0.00
96962_at	Rpl6	ribosomal protein L6	114.75	0.00	-3.11	0.00	-2.60	0.02	-0.13	0.90	-3.24	0.00
97695_s_at	Rpl7	ribosomal protein L7	110.80	0.04	-0.83	0.62	-1.13	0.50	1.61	0.33	-5.24	0.00
96575_at	Rpl8	ribosomal protein L8	113.74	0.04	-1.69	0.19	-3.95	0.01	-0.69	0.58	-0.97	0.44
100694_at	Rplp1	ribosomal protein, large, P1	130.34	0.02	-5.39	0.02	-5.03	0.03	-2.39	0.27	-2.10	0.33
98085_f_at	Rpo1-1	RNA polymerase 1-1 (40 kDa subunit)	134.36	0.03	-4.51	0.03	-4.28	0.04	1.00	0.61	-3.64	0.08
161379_at	Rpo1-4	RNA polymerase 1-4 (194 kDa subunit)	-4.24	0.04	4.46	0.01	-0.26	0.87	3.52	0.04	-0.75	0.64
94767_at	Rps11	ribosomal protein S11	113.37	0.01	-1.05	0.53	-6.04	0.00	0.38	0.82	-2.72	0.11
99590_at	Rps17	ribosomal protein S17	103.10	0.03	-3.21	0.03	0.56	0.69	0.54	0.70	-3.70	0.01
98333_at	Rps18	ribosomal protein S18	127.82	0.00	-3.39	0.02	-4.54	0.00	-0.20	0.88	-5.87	0.00
100686_at	Rps2	ribosomal protein S2	132.38	0.01	-1.39	0.04	-1.09	0.10	-1.78	0.01	-0.88	0.18
98564_f_at	Rps26	ribosomal protein S26	111.91	0.01	-5.04	0.08	-6.27	0.03	-0.08	0.98	-7.79	0.01
93030_at	Rps27a	ribosomal protein S27a	98.37	0.01	-4.47	0.02	-4.66	0.02	0.87	0.62	-4.00	0.03
101137_at	Rps3	ribosomal protein S3	104.28	0.03	-2.14	0.22	-4.61	0.01	-3.37	0.06	-1.80	0.30
162498_r_at	Rps4x	ribosomal protein S4, X-linked	0.08	0.01	5.89	0.09	-2.31	0.49	13.70	0.00	0.91	0.79
99336_at	Rps5	ribosomal protein S5	103.36	0.00	-6.04	0.00	-5.96	0.00	-2.06	0.19	-8.74	0.00
97405_at	Rps6ka1	ribosomal protein S6 kinase polypeptide 1	23.74	0.03	-3.03	0.18	-0.04	0.98	-0.79	0.72	7.48	0.00
103825_at	Rps6kb2	ribosomal protein S6 kinase, 70kD, polypeptide 2	19.68	0.05	1.34	0.50	2.11	0.29	-5.66	0.01	-2.48	0.22
100732_at	Rps8	ribosomal protein S8	116.19	0.01	-4.88	0.01	-4.10	0.02	-1.07	0.53	-2.33	0.18
94394_at	Rras	Harvey rat sarcoma oncogene, subgroup R	19.24	0.02	0.98	0.77	-11.33	0.00	-1.91	0.57	-4.68	0.17
100612_at	Rrm1	ribonucleotide reductase M1	-12.10	0.03	-4.00	0.28	-12.18	0.00	1.95	0.59	1.16	0.75
96778_at	Rrr-pending	regulator for ribosome resistance homolog (S. cerevisiae)	14.06	0.00	0.30	0.89	-1.47	0.51	2.01	0.36	-10.76	0.00
102797_at	Rsdr1-pending	retinal short-chain dehydrogenase/reductase 1	57.00	0.01	-2.32	0.45	-3.98	0.20	-10.46	0.00	5.88	0.07
101584_at	Rsu1	Ras suppressor protein 1	36.86	0.05	2.65	0.36	8.29	0.01	1.27	0.66	4.12	0.16
160484_at	Rtn4	reticulon 4	48.75	0.00	3.18	0.47	2.63	0.55	10.06	0.03	20.42	0.00
92237_at	Rxrg	retinoid X receptor gamma	-6.27	0.04	2.95	0.49	-1.18	0.78	7.22	0.10	12.70	0.01
99464_at	Rxrip110	retinoid X receptor interacting protein 110	34.83	0.01	3.49	0.06	5.27	0.01	1.62	0.37	-3.37	0.07
100003_at	Ryr1	ryanodine receptor 1, skeletal muscle	3.09	0.01	-4.19	0.01	2.77	0.06	-3.16	0.03	-2.09	0.14
92539_at	S100a10	S100 calcium binding protein A10 (calpactin)	76.83	0.01	-4.50	0.25	2.19	0.57	-2.65	0.50	14.51	0.00
162428_i_at	S100a15	S100 calcium binding protein A15	41.06	0.02	-4.04	0.15	6.18	0.04	-7.20	0.02	3.32	0.24
92242_at	Saa4	serum amyloid A 4	71.43	0.01	19.42	0.01	12.56	0.09	22.27	0.01	-5.41	0.45

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
102193_at	Sah	SA rat hypertension-associated homolog	20.68	0.04	-0.72	0.62	0.69	0.63	-4.91	0.00	-1.04	0.48
104072_at	Sap	serum amyloid P-component	76.02	0.01	-10.41	0.17	-18.27	0.02	23.63	0.00	-9.52	0.21
161339_f_at	Sars2	seryl-aminoacyl-tRNA synthetase 2	-3.43	0.02	3.00	0.18	-0.40	0.85	-4.60	0.05	6.47	0.01
104147_at	Sas	sialic acid synthase	41.57	0.00	-8.55	0.00	-7.20	0.01	-7.84	0.01	5.01	0.08
160388_at	Sc4mol	sterol-C4-methyl oxidase-like	61.11	0.00	-13.76	0.07	-16.33	0.03	-10.18	0.17	-37.94	0.00
102768_i_at	Sc5d	sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae)	56.79	0.03	-5.11	0.23	-3.51	0.40	-4.29	0.31	-13.14	0.00
99127_at	Sca10	spinocerebellar ataxia 10 homolog (human)	74.81	0.00	3.52	0.00	0.10	0.93	2.62	0.03	3.25	0.01
160795_at	Scamp1	secretory carrier membrane protein 1	12.14	0.01	0.07	0.98	-8.79	0.00	0.38	0.89	-6.74	0.02
104365_at	Scamp2	secretory carrier membrane protein 2	25.23	0.00	0.19	0.88	-1.00	0.46	2.38	0.09	8.09	0.00
100095_at	Scarb1	scavenger receptor class B, member 1	93.56	0.00	11.30	0.00	6.87	0.06	7.77	0.04	10.44	0.01
94058_r_at	Scd1	stearoyl-Coenzyme A desaturase 1	18.38	0.01	-1.82	0.55	-8.96	0.01	-1.78	0.56	9.53	0.00
98302_at	Scn10a	sodium channel, voltage-gated, type X, alpha polypeptide	-1.99	0.00	2.51	0.03	-2.07	0.07	4.32	0.00	-5.77	0.00
93278_at	Scp2	sterol carrier protein 2, liver	129.29	0.03	0.06	0.96	3.96	0.00	0.69	0.53	-0.54	0.62
104069_at	Scr59-pending	serine-rich spermatocytes and round spermatid protein, 59kDa	44.16	0.02	-3.62	0.01	-0.95	0.42	-1.70	0.16	1.90	0.12
92755_f_at	Sct	secretin	57.86	0.01	-0.11	0.97	7.02	0.05	-1.62	0.63	-12.24	0.00
92578_at	Scye1	small inducible cytokine subfamily E, member 1	44.03	0.01	-1.95	0.37	0.07	0.97	0.14	0.95	-9.50	0.00
96033_at	Sdc1	syndecan 1	43.32	0.02	-3.83	0.12	-8.55	0.00	-1.73	0.47	-0.08	0.97
95104_at	Sdc2	syndecan 2	69.64	0.01	2.26	0.12	-3.53	0.02	-0.55	0.69	-4.22	0.01
162078_at	Sdh1	sorbitol dehydrogenase 1	20.79	0.05	5.24	0.06	4.23	0.12	5.67	0.04	-0.98	0.71
160373_i_at	Sdpr	serum deprivation response	23.88	0.04	-2.14	0.30	-5.58	0.01	-4.10	0.06	0.04	0.99
96758_s_at	Sec14l2	SEC14-like 2 (S. cerevisiae)	91.17	0.01	7.29	0.01	-0.76	0.75	-3.38	0.16	6.43	0.01
96759_r_at	Sec14l2	SEC14-like 2 (S. cerevisiae)	57.86	0.01	5.12	0.01	-0.14	0.94	1.99	0.30	6.47	0.00
98944_at	Sec23b	SEC23B (S. cerevisiae)	62.25	0.01	0.82	0.71	9.98	0.00	1.25	0.58	-0.83	0.71
99350_at	Sec63	SEC63 (S. cerevisiae)	25.97	0.01	2.58	0.28	-2.75	0.25	4.55	0.07	-7.59	0.00
162030_r_at	Selenbp1	selenium binding protein 1	38.29	0.02	1.82	0.57	-6.09	0.07	-1.72	0.59	10.14	0.00
104692_at	Selp	selectin, platelet	-12.65	0.01	5.42	0.02	-1.38	0.51	-6.54	0.00	-1.65	0.43
96097_at	Sema3e	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3E	-36.60	0.01	-5.42	0.22	-13.96	0.00	-9.83	0.03	3.05	0.48
92460_at	Sema4f	sema domain, immunoglobulin domain (Ig), TM domain, and short cytoplasmic domain	58.72	0.03	-6.14	0.10	8.94	0.02	-0.84	0.82	-7.05	0.06
98609_at	Sept9	septin 9	61.63	0.00	-4.20	0.07	-0.84	0.70	-4.28	0.06	11.47	0.00
103094_at	Serf1	small EDRK-rich factor 1	14.61	0.02	-7.26	0.09	13.01	0.00	4.79	0.25	-4.13	0.32
102816_at	Serpina3m	serine (or cysteine) proteinase inhibitor, clade A, member 3M	81.04	0.00	3.18	0.34	12.05	0.00	12.59	0.00	4.98	0.15
104374_at	Serpina3n	serine (or cysteine) proteinase inhibitor, clade A, member 3N	101.80	0.01	12.58	0.07	4.57	0.49	23.82	0.00	4.95	0.45

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
96227_at	Serpina6	serine (or cysteine) proteinase inhibitor, clade A, member 6	99.05	0.03	3.35	0.27	5.33	0.08	3.41	0.26	8.21	0.01
99081_at	Serping1	serine (or cysteine) proteinase inhibitor, clade G, member 1	126.93	0.01	2.68	0.07	0.81	0.56	4.90	0.00	-2.08	0.15
96777_at	Sf3b1	splicing factor 3b, subunit 1, 155 kDa	28.04	0.02	2.02	0.27	-1.64	0.37	2.04	0.27	-6.11	0.00
99620_at	Sfpq	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	5.09	0.03	0.13	0.92	0.41	0.75	1.60	0.23	-4.39	0.00
97890_at	Sgk	serum/glucocorticoid regulated kinase	36.21	0.01	-2.36	0.56	-13.55	0.00	-4.99	0.22	-7.80	0.06
96127_at	Sgpl1	sphingosine phosphate lyase 1	34.39	0.05	-0.38	0.85	-6.72	0.00	-1.49	0.46	0.24	0.91
93806_at	Sh3bgrl	SH3-binding domain glutamic acid-rich protein like	70.26	0.00	2.51	0.17	3.01	0.11	6.51	0.00	3.78	0.05
93275_at	Sh3d2b	SH3 domain protein 2B	16.49	0.04	-1.17	0.79	6.89	0.13	-2.52	0.57	13.32	0.01
99158_at	Sh3d3	SH3 domain protein 3	41.11	0.01	2.55	0.20	-1.23	0.53	3.55	0.08	6.31	0.00
103813_at	Sh3yl1	Sh3 domain YSC-like 1	6.70	0.01	0.52	0.75	-5.29	0.00	-0.43	0.79	-4.22	0.02
103894_at	Shkbp1	Sh3kbp1 binding protein 1	69.15	0.03	-6.60	0.01	-2.18	0.32	0.06	0.98	-3.73	0.10
102930_at	Si	silver	0.14	0.04	13.93	0.02	12.31	0.04	-1.58	0.77	-3.23	0.56
99847_at	Siat4a	sialyltransferase 4A (beta-galactosidase alpha-2,3-sialytransferase)	40.53	0.01	-5.34	0.01	-5.12	0.02	-4.99	0.02	0.14	0.94
95599_at	Siat4c	sialyltransferase 4C (beta-galactosidase alpha-2,3-sialytransferase)	56.47	0.01	4.67	0.11	6.35	0.03	8.21	0.01	-1.10	0.70
92403_at	Siat7e	sialyltransferase 7 ((alpha-N-acetylneuraminyl 2,3-betagalactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltransferase) E	0.96	0.03	-3.72	0.01	-2.98	0.04	1.26	0.37	0.95	0.49
100369_at	Siat7f	sialytransferase 7 ((alpha-N-acetylneuraminyl 2,3-betagalactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialytransferase) F	-14.81	0.01	6.69	0.17	-13.03	0.01	-5.09	0.29	14.06	0.01
98596_s_at	Siat9	sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase)	86.42	0.02	8.42	0.07	7.62	0.10	12.49	0.01	-4.13	0.36
162007_i_at	Sipa1	signal-induced proliferation associated gene 1	10.16	0.05	-4.89	0.07	0.10	0.97	-2.76	0.29	-6.74	0.02
160869_at	Sirt3	sirtuin 3 (silent mating type information regulation 2, homolog) 3 (S. cerevisiae)	58.96	0.02	6.38	0.04	5.52	0.07	3.43	0.25	6.50	0.04
99111_at	Skd3	suppressor of K+ transport defect 3	33.62	0.01	0.59	0.64	0.46	0.72	2.00	0.13	4.73	0.00
104719_at	Slc12a7	solute carrier family 12, member 7	45.90	0.01	6.37	0.03	-2.98	0.27	8.71	0.00	1.61	0.54
103918_at	Slc15a2	solute carrier family 15 (H+/peptide transporter), member 2	3.50	0.05	2.43	0.24	-5.28	0.02	3.36	0.11	1.41	0.49
100491_at	Slc16a2	solute carrier family 16 (monocarboxylic acid transporters), member 2	60.78	0.00	6.63	0.02	3.30	0.20	1.46	0.56	16.85	0.00

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
162219_f_at	Slc16a2	solute carrier family 16 (monocarboxylic acid transporters), member 2	25.89	0.00	5.75	0.09	-1.06	0.75	11.16	0.00	16.65	0.00
101623_at	Slc16a8	solute carrier family 16 (monocarboxylic acid transporters), member 8	13.82	0.04	-0.39	0.82	3.23	0.08	-4.21	0.02	-2.94	0.10
96078_g_at	Slc17a1	solute carrier family 17 vesicular glutamate transporter), member 1	9.76	0.00	-1.24	0.23	0.02	0.98	5.69	0.00	3.62	0.00
103065_at	Slc20a1	solute carrier family 20, member 1	26.33	0.00	14.67	0.00	14.60	0.00	11.56	0.00	3.48	0.32
100916_at	Slc22a1	solute carrier family 22 (organic cation transporter), member 1	102.61	0.00	2.09	0.24	4.72	0.01	3.87	0.04	10.64	0.00
92497_at	Slc22a4	solute carrier family 22 (organic cation transporter), member 4	-8.55	0.02	0.23	0.85	-3.83	0.00	-1.87	0.12	1.37	0.25
104267_at	Slc23a1	solute carrier family 23 (nucleobase transporters), member 1	30.72	0.04	-1.96	0.26	3.04	0.09	-0.46	0.79	4.64	0.01
99112_at	Slc25a10	solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter), member 10	56.37	0.02	-3.15	0.58	-3.35	0.55	-10.05	0.09	18.85	0.00
95695_at	Slc25a20	solute carrier family 25 (mitochondrial carnitine/acylcarnitine translocase), member 20	79.15	0.01	-0.09	0.97	3.96	0.10	3.32	0.16	8.85	0.00
93084_at	Slc25a4	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4	11.22	0.02	0.82	0.68	-5.00	0.02	-0.27	0.89	5.51	0.01
94797_at	SLC26A1	sulfate anion transporter-1	49.25	0.01	6.80	0.10	-6.24	0.12	-0.16	0.97	12.99	0.00
100967_at	Slc27a2	solute carrier family 27 (fatty acid transporter), member 2	126.20	0.02	5.23	0.01	3.40	0.06	2.29	0.19	0.79	0.64
97957_at	Slc27a4	solute carrier family 27 (fatty acid transporter), member 4	20.42	0.04	3.59	0.25	1.68	0.59	0.03	0.99	10.12	0.00
103357_at	Slc2a2	solute carrier family 2 (facilitated glucose transporter), member 2	96.21	0.02	2.47	0.55	8.30	0.06	9.02	0.04	10.24	0.02
162385_i_at	Slc2a4	solute carrier family 2 (facilitated glucose transporter), member 4	1.16	0.03	-2.50	0.07	0.71	0.59	-1.50	0.25	-3.66	0.01
102683_at	Slc30a3	solute carrier family 30 (zinc transporter), member 3	57.82	0.02	-5.99	0.02	5.52	0.03	-1.93	0.42	-3.71	0.13
94470_i_at	Slc30a5-pending	solute carrier family 30 (zinc transporter), member 5	45.42	0.01	3.34	0.22	9.40	0.00	5.53	0.05	-3.28	0.22
93304_at	Slc3a1	solute carrier family 3, member 1	29.79	0.01	2.49	0.59	-8.94	0.07	16.06	0.00	-3.94	0.40
98457_at	Slc4a4	solute carrier family 4 (anion exchanger), member 4	17.83	0.02	0.73	0.82	-2.18	0.51	0.79	0.81	12.17	0.00
161201_r_at	Slc9a1	solute carrier family 9 (sodium/hydrogen exchanger), member 1	6.88	0.01	-42.07	0.00	-8.96	0.47	-26.24	0.04	11.03	0.37
92471_i_at	Slfn2	schlafen 2	1.58	0.04	5.76	0.22	-7.53	0.12	5.94	0.21	11.87	0.02
95411_at	Smap-pending	small acidic protein	52.72	0.02	-1.17	0.45	0.71	0.64	-5.76	0.00	0.95	0.54

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
161414_f_at	Smarcd2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2	2.54	0.01	13.57	0.01	-9.51	0.04	7.97	0.09	4.50	0.32
96945_at	Snap23	synaptosomal-associated protein, 23kD	23.50	0.03	1.37	0.49	7.00	0.00	0.17	0.93	1.23	0.53
93846_at	Snn	stannin	8.45	0.00	-7.63	0.01	-10.36	0.00	2.70	0.33	-0.61	0.82
97429_at	Snrk	SNF related kinase	42.84	0.01	10.47	0.00	-0.61	0.85	2.26	0.48	-8.90	0.01
162026_r_at	Snrpb2	U2 small nuclear ribonucleoprotein B	-5.91	0.00	-3.33	0.56	-13.98	0.02	-17.22	0.01	14.23	0.02
94550_at	Snx1	sorting nexin 1	30.89	0.03	4.85	0.28	-8.52	0.06	4.80	0.28	11.24	0.02
103489_at	Soc-pending	socius	5.18	0.03	0.10	0.98	-1.90	0.56	6.83	0.05	-9.86	0.01
160320_at	Sorbs1	sorbin and SH3 domain containing 1	41.32	0.00	-0.13	0.95	-1.70	0.40	5.17	0.02	7.71	0.00
93698_at	Sox13	SRY-box containing gene 13	53.37	0.04	-5.59	0.01	-0.02	0.99	2.77	0.16	-2.22	0.26
104408_s_at	Sox18	SRY-box containing gene 18	15.26	0.03	-2.85	0.23	-0.02	0.99	-7.29	0.01	3.99	0.10
100009_r_at	Sox2	SRY-box containing gene 2	2.63	0.02	3.19	0.00	0.26	0.77	0.46	0.60	0.64	0.46
92487_at	Sox7	SRY-box containing gene 7	24.96	0.02	-5.98	0.01	3.67	0.07	-2.71	0.17	1.48	0.45
101848_g_at	Sp100	nuclear antigen Sp100	0.84	0.02	3.89	0.02	-4.22	0.02	-2.12	0.19	-0.22	0.89
96192_at	Sp3	trans-acting transcription factor 3	30.80	0.02	0.51	0.70	-1.60	0.23	-4.00	0.01	-2.64	0.06
97017_f_at	Sparc	secreted acidic cysteine rich glycoprotein	33.48	0.05	-6.31	0.03	3.01	0.28	-2.26	0.41	-5.59	0.05
99655_at	Spc18-pending	signal peptidase complex (18kD)	70.39	0.00	2.64	0.16	7.14	0.00	5.88	0.00	-0.66	0.71
96630_at	Spink3	serine protease inhibitor, Kazal type 3	10.91	0.01	6.76	0.37	23.13	0.01	8.86	0.24	-17.61	0.03
103345_at	Spna2	alpha-spectrin 2, brain	33.87	0.02	1.62	0.67	-12.62	0.00	-6.01	0.13	-4.94	0.21
97519_at	Spp1	secreted phosphoprotein 1	55.65	0.02	12.38	0.07	9.05	0.18	20.24	0.01	2.84	0.67
97886_at	Spr	sepiapterin reductase	73.06	0.01	6.61	0.08	-4.80	0.19	-4.83	0.19	12.79	0.00
94322_at	Sqle	squalene epoxidase	46.44	0.01	-16.32	0.11	-12.71	0.20	-5.17	0.60	-34.50	0.00
101995_at	Sqstm1	sequestosome 1	93.82	0.00	-2.18	0.16	-5.48	0.00	-6.63	0.00	-1.28	0.40
93264_at	Srebf1	sterol regulatory element binding factor 1	87.76	0.00	17.29	0.02	10.84	0.13	19.57	0.01	18.88	0.01
92540_f_at	Srm	spermidine synthase	36.83	0.00	2.10	0.46	13.28	0.00	2.14	0.45	-2.80	0.33
101037_at	Ssh3bp1	spectrin SH3 domain binding protein 1	-2.49	0.01	2.33	0.48	13.96	0.00	-2.04	0.53	-3.17	0.34
104595_at	Stag2	stromal antigen 2	30.91	0.03	0.90	0.49	-3.61	0.01	-0.39	0.76	-2.81	0.04
92213_at	Star	steroidogenic acute regulatory protein	9.72	0.01	0.05	0.99	-12.33	0.01	-11.56	0.01	4.23	0.31
94331_at	Stat6	signal transducer and activator of transcription 6	34.85	0.01	1.95	0.27	-5.04	0.01	0.28	0.87	-5.12	0.01
100952_at	Stim1	stromal interaction molecule 1	40.86	0.03	8.19	0.02	-1.28	0.70	-7.50	0.03	3.73	0.27
93680_at	Stk10	serine/threonine kinase 10	10.61	0.00	-1.79	0.18	6.50	0.00	2.29	0.09	2.78	0.04
98456_at	Stk19	serine/threonine kinase 19	22.08	0.00	-1.10	0.53	2.78	0.12	-6.64	0.00	-9.33	0.00
101437_at	Stk2	serine/threonine kinase 2	7.98	0.04	-5.01	0.01	3.42	0.07	0.42	0.81	-0.57	0.75
98775_at	Stk3	serine/threonine kinase 3 (Ste20, yeast homolog)	1.27	0.04	5.06	0.01	-1.20	0.51	0.48	0.79	-3.45	0.07
94292_at	Strap	serine/threonine kinase receptor associated protein	62.02	0.02	0.37	0.82	1.27	0.44	-0.86	0.60	-6.19	0.00
100878_at	Strn3	striatin, calmodulin binding protein 3	29.48	0.04	1.60	0.51	-4.65	0.06	0.21	0.93	-6.84	0.01
96076_at	Stx5a	syntaxin 5A	55.72	0.02	-1.05	0.65	7.57	0.00	1.85	0.43	4.96	0.04

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
99146_at	Stx6	syntaxin 6	2.90	0.01	6.55	0.00	-0.92	0.58	1.65	0.32	0.93	0.57
160064_at	Stx7	syntaxin 7	30.93	0.04	-5.07	0.01	2.57	0.19	-0.32	0.87	3.28	0.10
101398_at	Stxbp2	syntaxin binding protein 2	17.09	0.02	4.68	0.16	-10.71	0.00	-4.18	0.20	-0.55	0.86
92855_at	Sui1-rs1	suppressor of initiator codon mutations, related sequence 1 (S. cerevisiae)	79.55	0.02	1.31	0.50	-2.99	0.13	-0.43	0.82	-6.79	0.00
100585_at	Supt4h	suppressor of Ty 4 homolog (S. cerevisiae)	-6.95	0.01	-4.22	0.01	0.19	0.90	-4.91	0.00	-1.57	0.30
100094_at	Supt5h	suppressor of Ty 5 homolog (S. cerevisiae)	37.93	0.00	2.25	0.34	-1.50	0.52	-3.81	0.11	-10.50	0.00
96663_at	Surf6	surfeit gene 6	4.30	0.04	4.40	0.00	-0.36	0.78	-0.18	0.89	-1.27	0.33
160143_r_at	Sycp3	synaptonemal complex protein 3	0.60	0.02	1.00	0.33	-0.10	0.92	-1.33	0.20	-3.43	0.00
96734_at	Synj2bp	synaptojanin 2 binding protein	60.44	0.01	-0.15	0.88	0.95	0.36	-1.65	0.12	-3.87	0.00
104269_at	Syt5	synaptotagmin 5	-26.71	0.04	-11.03	0.01	-1.08	0.77	-3.04	0.42	6.28	0.10
100364_at	Syt6	synaptotagmin 6	11.48	0.01	-7.67	0.01	-1.65	0.51	-6.32	0.02	-2.41	0.34
160162_at	Tagln2	transgelin 2	31.61	0.02	-2.06	0.57	0.92	0.80	2.09	0.56	13.65	0.00
96326_at	Tat	tyrosine aminotransferase	138.74	0.03	1.98	0.29	-1.15	0.53	-0.80	0.66	-6.43	0.00
98087_at	Tbk1	TANK-binding kinase 1	30.08	0.00	-0.14	0.93	2.02	0.20	1.36	0.38	-8.17	0.00
102250_at	Tccr	T cell cytokine receptor	52.80	0.04	-9.82	0.00	-1.04	0.73	1.21	0.69	-3.96	0.21
102344_s_at	Tcea3	transcription elongation factor A (SII), 3	35.95	0.02	6.89	0.01	-0.42	0.87	4.89	0.07	5.18	0.06
95536_at	Tceb3	transcription elongation factor B (SIII), polypeptide 3 (110kD)	42.08	0.02	0.72	0.72	-0.81	0.68	1.44	0.47	-7.31	0.00
101008_at	Tcerg1	transcription elongation regulator 1 (CA150)	7.61	0.03	1.83	0.14	-0.46	0.70	-1.59	0.20	-3.75	0.01
103050_at	Tcf21	transcription factor 21	10.01	0.02	4.48	0.02	-1.24	0.49	-0.79	0.66	5.24	0.01
160780_at	Tcf3	transcription factor 3	28.38	0.00	5.41	0.02	-8.09	0.00	0.65	0.76	-1.61	0.45
93736_at	Tcn2	transcobalamin 2	64.17	0.00	-1.74	0.52	-8.29	0.01	-2.09	0.44	9.40	0.00
101006_at	Tcp1-rs1	t-complex protein 1, related sequence 1	43.95	0.03	-6.81	0.12	-10.99	0.02	-5.41	0.21	-6.15	0.16
99798_at	Tcrb-J	T-cell receptor beta, joining region	3.85	0.00	-3.47	0.07	-2.29	0.22	1.23	0.50	-7.33	0.00
103387_at	Tctex3	t-complex testis-expressed 3	25.59	0.03	-0.93	0.66	-3.94	0.08	-5.96	0.01	-2.57	0.23
160117_at	Tef	thyrotroph embryonic factor	66.82	0.00	17.78	0.00	11.75	0.02	11.77	0.02	2.18	0.64
94104_at	Tert	telomerase reverse transcriptase	25.77	0.00	-5.90	0.00	0.01	0.99	-0.39	0.77	-4.44	0.00
94007_at	Tex189	testis expressed gene 189	97.62	0.03	1.00	0.47	1.50	0.28	-0.28	0.84	-4.67	0.00
102315_at	Tex292	testis expressed gene 292	22.50	0.01	2.14	0.17	1.59	0.31	0.86	0.58	-5.67	0.00
94383_at	Tfpi2	tissue factor pathway inhibitor 2	69.15	0.01	-9.25	0.00	-4.63	0.08	-0.12	0.96	1.04	0.68
93728_at	Tgfb1i4	transforming growth factor beta 1 induced transcript 4	43.25	0.00	19.44	0.01	7.12	0.27	-0.27	0.97	25.99	0.00
92877_at	Tgfbi	transforming growth factor, beta induced, 68 kDa	27.61	0.00	6.17	0.00	2.32	0.24	6.47	0.00	5.44	0.01
94702_at	Tgfbr2	transforming growth factor, beta receptor II	-0.30	0.01	-2.49	0.09	-1.98	0.17	-4.16	0.01	-2.75	0.06
100404_at	TgN737Rpw	transgene insert site 737, insertional mutation, polycystic kidney disease	55.53	0.02	-11.48	0.01	-8.28	0.04	-3.36	0.38	-3.84	0.31
99143_at	Tgoln2	trans-golgi network protein 2	81.16	0.01	-1.16	0.44	-2.26	0.14	-0.60	0.69	5.99	0.00
160469_at	Thbs1	thrombospondin 1	1.17	0.02	5.89	0.03	1.80	0.47	2.88	0.26	-7.12	0.01
103869_at	Thbs3	thrombospondin 3	8.55	0.00	3.47	0.13	4.76	0.04	0.64	0.77	-12.18	0.00
99076_at	Thra	thyroid hormone receptor alpha	46.48	0.00	11.14	0.00	7.72	0.03	9.51	0.01	0.06	0.98

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
160306_at	Thrsp	thyroid hormone responsive SPOT14 homolog (Rattus)	94.24	0.01	8.27	0.37	33.23	0.00	23.51	0.02	5.77	0.53
103795_f_at	Timd2	T-cell immunoglobulin and mucin domain containing 2	34.71	0.05	2.45	0.38	1.63	0.56	4.86	0.09	7.52	0.01
94012_at	Timm13a	translocase of inner mitochondrial membrane 13 homolog a (yeast)	28.41	0.04	-17.80	0.00	-8.43	0.14	2.35	0.67	0.52	0.93
93348_at	Timm22	translocase of inner mitochondrial membrane 22 homolog (yeast)	14.33	0.00	1.65	0.32	-7.45	0.00	2.21	0.19	6.19	0.00
101464_at	Timp1	tissue inhibitor of metalloproteinase 1	44.51	0.02	-6.87	0.01	1.69	0.47	-1.34	0.57	-5.80	0.02
160519_at	Timp3	tissue inhibitor of metalloproteinase 3	29.28	0.00	-0.35	0.80	-0.73	0.61	-3.39	0.03	-5.65	0.00
96081_at	Tk1	thymidine kinase 1	49.39	0.02	-4.45	0.16	-4.94	0.12	-6.59	0.05	-7.48	0.03
101964_at	Tkt	transketolase	66.48	0.01	-4.93	0.09	-5.07	0.08	-7.31	0.02	7.11	0.02
102425_at	Tle1	transducin-like enhancer of split 1, homolog of Drosophila E(spl)	41.37	0.00	4.72	0.06	-5.22	0.04	-3.05	0.21	-8.88	0.00
100014_at	Tlk2	tousled-like kinase 2 (Arabidopsis)	11.01	0.02	3.82	0.02	-3.42	0.03	1.86	0.23	-2.07	0.18
97893_at	Tlp	TATA box binding protein-like protein	9.29	0.00	-1.12	0.39	-6.19	0.00	-1.80	0.17	-3.35	0.02
161315_i_at	Tm4sf1	transmembrane 4 superfamily member 1	7.10	0.02	-2.31	0.11	3.42	0.02	2.45	0.09	-2.42	0.10
98129_at	Tmsb10	thymosin, beta 10	20.16	0.02	1.88	0.49	-4.85	0.09	-4.90	0.09	7.42	0.01
93917_at	Tnfsf12	tumor necrosis factor (ligand) superfamily, member 12	25.15	0.01	-0.72	0.57	1.72	0.19	5.03	0.00	1.64	0.21
97113_at	Tnfsf6	tumor necrosis factor (ligand) superfamily, member 6	-6.15	0.04	-0.29	0.87	-2.24	0.21	3.51	0.06	-4.41	0.02
98318_at	Tnfsf7	tumor necrosis factor (ligand) superfamily, member 7	-13.56	0.02	25.31	0.00	4.51	0.53	9.83	0.18	-4.86	0.50
100492_at	Tnnt2	troponin T2, cardiac	61.55	0.03	1.79	0.72	-6.60	0.20	-7.47	0.15	14.71	0.01
160533_r_at	Tnp1	transition protein 1	36.38	0.00	-2.75	0.20	-6.25	0.01	-0.62	0.77	7.38	0.00
95694_at	Top1	topoisomerase (DNA) I	63.37	0.00	3.62	0.05	3.87	0.04	6.36	0.00	-6.14	0.00
93849_at	Tpk1	thiamin pyrophosphokinase	0.62	0.00	10.36	0.00	4.20	0.11	2.81	0.27	2.38	0.35
160532_at	Tpm1	tropomyosin 1, alpha	41.08	0.03	-4.69	0.08	0.33	0.90	7.90	0.01	-3.09	0.24
100605_at	Tpm2	tropomyosin 2, beta	-4.29	0.02	20.96	0.01	5.67	0.40	-13.60	0.05	0.00	1.00
160499_at	Tra1	tumor rejection antigen gp96	128.05	0.02	-0.63	0.77	7.21	0.00	2.22	0.30	-3.81	0.08
95010_at	Traf3	Tnf receptor-associated factor 3	19.84	0.05	-1.37	0.34	4.01	0.01	1.62	0.26	1.58	0.27
162407_at	Traip	TRAF-interacting protein	20.51	0.05	1.49	0.79	-4.53	0.42	-15.98	0.01	-9.00	0.12
160724_at	Trfp	Trf (TATA binding protein-related factor)-proximal protein homolog (Drosophila)	12.94	0.04	6.28	0.00	0.95	0.60	0.08	0.96	-1.30	0.48
95602_at	Trpc4ap	transient receptor potential cation channel, subfamily C, member 4 associated protein	71.20	0.00	3.45	0.01	1.90	0.14	3.55	0.01	7.37	0.00
97953_g_at	Tsc2	tuberous sclerosis 2	27.60	0.00	4.36	0.00	-3.12	0.03	-1.68	0.20	3.25	0.02
97951_s_at	Tsc2	tuberous sclerosis 2	41.83	0.00	3.47	0.01	-2.93	0.03	-5.51	0.00	4.82	0.00
95350_at	Ttr	transthyretin	117.23	0.00	-0.55	0.70	0.29	0.84	5.30	0.00	6.48	0.00
93538_at	Ttrap-pending	Traf and Tnf receptor associated protein	18.92	0.03	1.82	0.46	-5.95	0.02	-3.70	0.14	4.96	0.05
100343_f_at	Tuba1	tubulin, alpha 1	78.19	0.01	-3.79	0.14	-0.19	0.94	1.85	0.46	9.40	0.00

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
98759_f_at	Tuba2	tubulin, alpha 2	89.00	0.01	-4.51	0.03	-2.72	0.17	2.36	0.23	5.61	0.01
160420_r_at	Tuba3	tubulin, alpha 3	-4.66	0.00	1.63	0.14	-6.49	0.00	-1.76	0.11	-0.75	0.48
101543_f_at	Tuba6	tubulin, alpha 6	97.91	0.03	-4.32	0.11	-1.16	0.65	2.26	0.39	8.02	0.01
94835_f_at	Tubb2	tubulin, beta 2	75.39	0.00	-19.81	0.00	-12.58	0.02	-17.12	0.00	12.60	0.02
160462_f_at	Tubb3	tubulin, beta 3	62.68	0.00	-19.82	0.00	-10.83	0.02	-12.75	0.01	9.58	0.03
94788_f_at	Tubb5	tubulin, beta 5	67.56	0.00	-13.17	0.00	-5.22	0.01	-7.45	0.00	10.19	0.00
94789_r_at	Tubb5	tubulin, beta 5	27.85	0.04	-17.74	0.29	-41.52	0.02	-37.00	0.04	3.05	0.85
99985_at	Txnrd1	thioredoxin reductase 1	59.64	0.05	1.16	0.51	-2.40	0.18	3.22	0.08	-4.22	0.02
160437_at	Txnrd2	thioredoxin reductase 2	32.31	0.02	-0.89	0.69	-5.99	0.01	-3.24	0.15	5.20	0.03
100397_at	Tyrobp	TYRO protein tyrosine kinase binding protein	13.59	0.02	4.02	0.31	-0.70	0.86	10.75	0.01	10.69	0.01
102817_at	U2af1-rs1	U2 small nuclear ribonucleoprotein auxiliary factor (U2AF), 35 kDa, related sequence 1	15.46	0.02	-0.99	0.68	-0.52	0.83	0.42	0.86	-9.01	0.00
162396_at	Ube1y1	ubiquitin-activating enzyme E1, Chr Y 1	-2.52	0.02	4.28	0.00	0.94	0.41	-0.23	0.84	0.27	0.81
93069_at	Ube2d2	ubiquitin-conjugating enzyme E2D 2	33.90	0.03	4.48	0.00	1.60	0.26	1.30	0.35	-0.87	0.53
160164_at	Ube2v1	ubiquitin-conjugating enzyme E2 variant 1	61.25	0.05	-0.41	0.89	-9.58	0.00	-1.42	0.63	2.26	0.44
161725_r_at	Ube2v2	ubiquitin-conjugating enzyme E2 variant 2	-12.87	0.04	-4.84	0.01	-3.24	0.09	2.45	0.19	-1.06	0.56
96701_at	Uble1b	ubiquitin-like 1 (sentrin) activating enzyme E1B	41.85	0.01	2.07	0.19	-0.28	0.86	1.87	0.23	-6.15	0.00
97304_at	Ubp1	upstream binding protein 1	54.39	0.01	0.67	0.63	-0.32	0.82	-4.49	0.00	-4.13	0.01
96244_at	Uchl1	ubiquitin carboxy-terminal hydrolase L1	10.52	0.04	-12.37	0.03	-4.49	0.41	-11.48	0.04	-8.11	0.15
100091_at	Ugalt2	UDP-galactose translocator 2	87.09	0.03	-0.15	0.94	2.68	0.23	-0.09	0.97	7.67	0.00
96623_at	Ugcg	UDP-glucose ceramide glucosyltransferase	21.66	0.01	7.12	0.01	-2.41	0.36	2.15	0.42	-8.99	0.00
102322_at	Ugdh	UDP-glucose dehydrogenase	93.88	0.00	-10.82	0.00	-8.18	0.00	-10.46	0.00	-10.91	0.00
99580_s_at	Ugt1a6	UDP glycosyltransferase 1 family, polypeptide A6	130.50	0.00	-3.13	0.05	-4.73	0.00	-5.36	0.00	-2.34	0.13
96796_f_at	Ugt2b5	UDP-glucuronosyltransferase 2 family, member 5	135.31	0.00	-2.89	0.00	-1.44	0.10	-5.46	0.00	-3.41	0.00
102332_at	Ulk1	Unc-51 like kinase 1 (C. elegans)	55.88	0.01	7.23	0.00	2.39	0.28	4.62	0.05	4.45	0.05
94381_at	Umpk	uridine monophosphate kinase	32.54	0.04	3.09	0.42	1.87	0.62	-1.16	0.76	12.52	0.00
102792_at	Ung	uracil-DNA glycosylase	47.14	0.05	-4.89	0.25	9.67	0.03	8.32	0.06	-3.24	0.44
161325_at	Upp	uridine phosphorylase	53.69	0.02	-8.94	0.02	-3.59	0.30	-4.70	0.18	-8.45	0.02
93655_at	Usf1	upstream transcription factor 1	90.30	0.05	0.36	0.92	1.43	0.69	-10.04	0.01	-6.85	0.07
95024_at	Usp18	ubiquitin specific protease 18	20.80	0.04	2.18	0.34	-2.85	0.21	6.35	0.01	2.87	0.21
92821_at	Usp2	ubiquitin specific protease 2	35.42	0.00	5.41	0.13	13.60	0.00	12.63	0.00	0.65	0.85
92820_at	Usp2	ubiquitin specific protease 2	29.71	0.00	8.00	0.28	17.84	0.02	13.26	0.08	24.10	0.00
95337_at	Uty	ubiquitously transcribed tetratricopeptide repeat gene, Y chromosome	8.79	0.02	2.88	0.05	3.40	0.02	-2.24	0.12	1.69	0.23
100679_at	V2r16	vomeronasal 2, receptor, 16	-1.11	0.05	0.65	0.73	-3.97	0.05	0.49	0.79	4.90	0.02
102317_at	Vamp4	vesicle-associated membrane protein 4	21.22	0.00	2.10	0.14	-0.30	0.82	0.43	0.75	-6.23	0.00
92998_at	Vav2	Vav2 oncogene	18.06	0.02	7.49	0.00	-2.33	0.27	-0.62	0.77	-0.95	0.65

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
101509_at	Vbp1	von Hippel-Lindau binding protein 1	34.34	0.03	1.34	0.35	3.96	0.01	3.06	0.04	-0.27	0.85
92558_at	Vcam1	vascular cell adhesion molecule 1	10.35	0.00	6.50	0.01	1.37	0.52	9.15	0.00	1.06	0.62
92559_at	Vcam1	vascular cell adhesion molecule 1	2.06	0.03	2.43	0.02	-0.25	0.80	2.62	0.01	-0.21	0.83
94963_at	Vcl	vinculin	52.50	0.03	4.90	0.06	1.80	0.46	1.89	0.44	-6.79	0.01
161255_at	Vdac2	voltage-dependent anion channel 2	-8.01	0.02	7.22	0.01	1.50	0.52	4.58	0.06	1.04	0.65
103520_at	Vegfa	vascular endothelial growth factor A	37.66	0.03	3.57	0.27	3.63	0.26	6.05	0.07	-8.85	0.01
100084_at	Vil2	villin 2	5.57	0.04	-0.14	0.96	0.93	0.73	3.15	0.25	-8.85	0.00
104165_at	Vnn1	vanin 1	53.19	0.00	9.11	0.28	16.72	0.06	8.49	0.32	36.05	0.00
96847_at	Vps28	vacuolar protein sorting 28 (yeast)	71.51	0.00	3.98	0.12	-10.04	0.00	3.07	0.22	8.96	0.00
92995_at	Vsnl1	visinin-like 1	-5.37	0.03	6.61	0.00	1.25	0.54	-2.25	0.28	1.58	0.44
98549_at	Vtn	vitronectin	128.89	0.05	2.61	0.15	-0.24	0.89	5.01	0.01	-1.69	0.34
104390_at	W91701	expressed sequence W91701	43.45	0.02	-3.00	0.10	-6.01	0.00	-1.42	0.42	1.07	0.54
102931_at	Wap	whey acidic protein	-4.65	0.03	-1.26	0.75	-8.14	0.05	-2.02	0.61	-11.29	0.01
98606_s_at	Wars	tryptophanyl-tRNA synthetase	37.58	0.00	0.52	0.77	4.83	0.01	2.72	0.14	9.56	0.00
98605_at	Wars	tryptophanyl-tRNA synthetase	38.15	0.04	-4.97	0.04	4.71	0.05	0.06	0.98	4.49	0.07
98617_at	Wbp11	WW domain binding protein 11	43.20	0.02	5.26	0.04	-0.79	0.75	-7.36	0.01	-2.62	0.29
95643_at	Wdr6	WD repeat domain 6	8.71	0.00	10.28	0.01	-14.07	0.00	3.41	0.38	2.56	0.51
101458_at	Wee1	wee 1 homolog (S. pombe)	5.24	0.00	2.43	0.29	6.70	0.01	8.09	0.00	1.03	0.65
103824_at	Wfs1	Wolfram syndrome 1 homolog (human)	18.06	0.03	4.90	0.02	3.65	0.08	2.14	0.29	-3.29	0.11
98862_at	Wnt10a	wingless related MMTV integration site 10a	9.47	0.03	-4.25	0.06	-1.80	0.41	5.70	0.02	2.28	0.30
103490_at	Wnt11	wingless-related MMTV integration site 11	-1.48	0.02	-3.53	0.02	0.18	0.90	3.30	0.03	2.06	0.15
103415_at	Wrnip	Werner syndrome homolog (human) interacting protein	36.90	0.00	-6.52	0.01	-7.15	0.01	-5.76	0.02	-2.70	0.24
94821_at	Xbp1	X-box binding protein 1	84.25	0.04	-0.58	0.88	7.20	0.08	6.20	0.13	-9.76	0.02
97950_at	Xdh	xanthine dehydrogenase	55.02	0.04	5.38	0.05	5.28	0.05	4.56	0.09	-2.39	0.36
160583_at	Xlkd1	extra cellular link domain-containing 1	5.64	0.03	2.80	0.31	5.47	0.06	0.11	0.97	-7.58	0.01
92384_at	Xpa	xeroderma pigmentosum, complementation group A	25.64	0.04	-1.69	0.53	-7.23	0.01	-5.67	0.05	-1.69	0.53
160520_at	Yap	yes-associated protein, 65 kDa	61.35	0.01	2.74	0.24	5.39	0.03	-0.93	0.68	-7.24	0.00
103933_at	Ysg2	yolk sac gene 2	21.04	0.03	5.19	0.03	-3.02	0.20	2.91	0.22	5.32	0.03
95716_at	Ywhag	3-monooxgenase/tryptophan 5-monooxgenase activation protein, gamma polypeptide	85.60	0.04	1.02	0.53	4.80	0.01	0.75	0.64	2.92	0.08
104080_at	Ywhaz	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	51.77	0.00	0.43	0.80	-1.25	0.47	-4.54	0.01	-6.30	0.00
92444_f_at	Zfp1	zinc finger protein 1	19.68	0.02	3.21	0.08	3.83	0.04	2.75	0.13	3.89	0.04
92443_i_at	Zfp1	zinc finger protein 1	5.54	0.04	11.44	0.03	-8.23	0.11	1.07	0.83	10.28	0.05
160588_at	Zfp131	zinc finger protein 131	20.38	0.01	0.26	0.88	1.63	0.34	-3.58	0.05	-6.51	0.00
98285_at	Zfp146	zinc finger protein 146	2.98	0.02	-1.36	0.52	0.40	0.85	-0.20	0.92	-8.27	0.00
102275_at	Zfp185	zinc finger protein 185	-10.80	0.00	-2.26	0.46	-8.74	0.01	-4.87	0.12	10.86	0.00
161881_f_at	Zfp259	zinc finger protein 259	32.05	0.00	-7.46	0.01	0.38	0.88	0.68	0.78	-8.83	0.00
104002_at	Zfp275	Zinc finger protein 275	18.28	0.01	1.41	0.70	-8.67	0.03	5.41	0.15	-10.55	0.01
102309_at	Zfp326	zinc finger protein 326	14.43	0.02	4.84	0.03	0.71	0.73	0.37	0.86	-6.40	0.01

Name	Symbol	Description	INT00	pANY	WK02	pWK02	WK04	pWK04	Wk08	pWK08	WK12	pWK12
95244_at	Zfp40	zinc finger protein 40	3.12	0.05	0.35	0.76	1.99	0.09	0.58	0.61	3.19	0.01
95522_i_at	Zfp68	Zinc finger protein 68	24.03	0.00	-2.08	0.06	-0.84	0.42	-2.26	0.04	-4.10	0.00
92990_at	Zfp93	zinc finger protein 93	2.67	0.05	4.65	0.05	-4.33	0.06	-3.81	0.10	-1.22	0.58
94101_at	Zfp98	zinc finger protein 98	-9.87	0.01	-2.64	0.19	-6.62	0.00	1.57	0.43	4.08	0.05
97974_at	Zfpm1	zinc finger protein, multitype 1	61.77	0.00	0.88	0.66	-9.65	0.00	-4.39	0.04	-0.25	0.90
96707_at	Zipro1	zinc finger proliferation 1	49.41	0.00	-1.15	0.35	-3.84	0.00	-1.75	0.16	-7.10	0.00
95156_g_at	Zrfp1-pending	zinc ring finger protein 1	6.94	0.01	4.33	0.04	-5.78	0.01	-1.26	0.53	-4.08	0.05
95157_at	Zrfp1-pending	zinc ring finger protein 1	-8.96	0.02	-0.34	0.92	-12.90	0.00	5.25	0.15	0.97	0.78

APPENDIX C

Trend Analysis: Genes that are signifcantly up-regulated (P < 0.01)

Name	TREND	Sequence Description	Biological Process
Cyp2b9	5.09	cytochrome P450, 2b9, phenobarbitol inducible, type a	monooxygenase
Anxa2	3.33	annexin A2	actin binding
Lgals1	3.32	lectin, galactose binding, soluble 1	sugar binding
Tubb2	2.78	tubulin, beta 2	GTP binding/microtubule-based process
Tubb3	2.54	tubulin, beta 3	microtubule-based process/movement
Dhodh	2.45	dihydroorotate dehydrogenase	pyrimidine nucleotide biosynthesis/dihydroorate dehydrogenase
Pex11a	2.26	peroxisomal biogenesis factor 11a	peroxisome organization and biogenesis
Pklr	2.20	pyruvate kinase liver and red blood cell	glycolysis
Tubb5	1.99	tubulin, beta 5	microtubule-based process/movement
Gpi1	1.91	glucose phosphate isomerase 1	glycolysis/gluconeogenesis
Lip1	1.83	lysosomal acid lipase 1	lipid metabolism/lysosome
Rtn4	1.81	reticulon 4	morphogenesis
Rad51l1	1.66	RAD51-like 1 (S. cerevisiae)	DNA repair/binding, ATPase
Hdgfrp1	1.49	hepatoma-derived growth factor, related protein 1	cell differentiation
Frda	1.47	Friedreich ataxia	metal ion homeostasis
Slc16a2	1.44	solute carrier family 16 (monocarboxylic acid transporters), member 2	integral plasma membrane protein/transport
Decr1	1.44	2,4-dienoyl CoA reductase 1, mitochondrial	fatty acid metabolism
Zfp185	1.43	zinc finger protein 185	nucleic acid binding
Pias3	1.41	protein inhibitor of activated STAT 3	DNA binding
Scd1	1.36	stearoyl-Coenzyme A desaturase 1	fatty acid biosynthesis
Sept9	1.32	septin 9	cytokinesis/cortical organization
Tcn2	1.31	transcobalamin 2	metal ion transport
Gdm1	1.25	glycerol phosphate dehydrogenase 1, mitochondrial	glycerol metabolism
Eno1	1.24	enolase 1, alpha non-neuron	glycolysis
Cstb	1.23	Mus musculus cystatin B (Stfb) gene, complete cds.	cysteine protesase inhibitor
Sas	1.22	sialic acid synthase	N-acetylneuraminic acid phosphatase synthase
Alad	1.22	aminolevulinate, delta-, dehydratase	heme biosynthesis
Rorc	1.20	Mus musculus nuclear orphan receptor RORgamma (RORC) gene, exon 11 and complete cds.	regulation of transcription
Htatip2	1.20	HIV-1 tat interactive protein 2, 30 kDa homolog (human)	apoptosis/dehydrogenase/reductase
Arhd	1.16	ras homolog D (RhoD)	GTP binding/GTPase
Maged2	1.15	melanoma antigen, family D, 2	cell growth and/or maintenance
Tnp1	1.15	transition protein 1	cell growth and/or maintenance
Nudt1	1.14	nudix (nucleoside diphosphate linked moiety X)-type motif 1	purine nucleoside triphosphate catabolism
Mcmd7	1.13	mini chromosome maintenance deficient 7 (S. cerevisiae)	DNA binding/ATP binding/ ATPase
Dusp12	1.11	dual specificity phosphatase 12	protein tyrosine/serine/threonine phosphatase
Agt	1.08	Mus musculus angiotensinogen precursor, gene, exon 5 and complete cds.	serine protease inhibitor
Mpp1	1.07	membrane protein, palmitoylated (55 kDa)	signal transduction
Perp-pending	1.05	p53 apoptosis effector related to Pmp22	induction of apoptosis
Ctsg	1.05	M.musculus serine proteinase gene.	peptidase
Apoc2	1.00	M.musculus APOC2 gene, complete CDS ,and exons 2 and 3.	lipid metabolism
Sorbs1	0.93	sorbin and SH3 domain containing 1	cell adhesion/glucose uptake/insulin receptor signaling
Hao3	0.93	hydroxyacid oxidase (glycolate oxidase) 3	fatty acid metabolism
Nudt9	0.93	nudix (nucleoside diphosphate linked moiety X)-type motif 9	hydrolayze
Neurod3	0.91	Mus musculus neurogenic basic-helix-loop-helix protein (neuroD3) gene, complete cds.	regulation of transcription
Zfp98	0.90	zinc finger protein 98	DNA binding
Anxa4	0.87	annexin A4	lipid binding
Scamp2	0.84	secretory carrier membrane protein 2	transport
Ext2	0.82	exostoses (multiple) 2	cell growth and/or maintenance
Prdx3	0.79	peroxiredoxin 3	antioxidant
Hgfac	0.78	hepatocyte growth factor activator	peptidase
Raf1	0.77	v-raf-1 leukemia viral oncogene 1	protein kinase/ATP binding
Ttr	0.77	Mus musculus gene for prealbumin, complete cds and exon 4.	thyroxine binding

APPENDIX D

Trend Analysis: Genes that are significantly down-regulated (p < 0.01)

Name	TREND	Sequence Description	Biological Process
Dnajb1	-5.92	DnaJ (Hsp40) homolog, subfamily B, member 1	heat shock protein
Acr	-3.95	preproacrosin	peptidase
Gstm5	-3.87	glutathione S-transferase, mu 5	glutathione conjugation reaction
Egfr	-3.55	epidermal growth factor receptor	transmembrane receptor protein tyrosine kinase
Mbd1	-3.44	methyl-CpG binding domain protein 1	DNA modification/methylation
Hsp105	-3.03	heat shock protein, 105 kDa	heat shock protein
Dnaja1	-2.97	DnaJ (Hsp40) homolog, subfamily A, member 1	heat shock protein
Lifr	-2.96	leukemia inhibitory factor receptor	integral membrane protein
gag protein	-2.81	Mouse endogenous retrovirus truncated gag protein, complete cds, clone del env-1 3.1.	cell growth and/or maintenance
Brd2	-2.30	Mus musculus DNA sequence from clone 11KLT on chromosome 17. Contains mouse RING3 gene, CpG Island.	protein kinase
Cgef2-pending	-2.12	cAMP-regulated guanine nucleotide exchange factor II	cell growth and/or maintenance
Cryac	-2.08	crystallin, alpha C	heat shock protein
Bag3	-2.04	Bcl2-associated athanogene 3	apoptosis/anti-apoptosis
Ptp4a1	-2.01	protein tyrosine phosphatase 4a1	protein tyrosine phosphatase
Mknk2	-1.98	MAP kinase-interacting serine/threonine kinase 2	protein kinase
Hspa8	-1.85	Mouse U14 snRNA (intron 5 of hsc70 gene).	heat shock protein
Bysl	-1.82	bystin-like	cell communication
Mela	-1.78	melanoma antigen, 80 kDa	peptidase/nucleotidyltransferase
Cacna1a	-1.70	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	ion transport
Rnpc2	-1.67	RNA-binding region (RNP1, RRM) containing 2	transcription factor binding
Herpud1	-1.64	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	cell growth and/or maintenance
Thbs3,Muc1,GeneY	-1.59	Mus musculus thrombospondin 3 (Thbs3) gene, partial cds and mucin 1 (Muc1) gene, complete cds.	cell communication
Igk-V20	-1.58	Mouse VK gene for kappa light chain variable region and J4 sequence	immune response
Snrk	-1.55	SNF related kinase	protein kinase
Gtpbp3-pending	-1.50	GTP binding protein 3	nucleotide binding/hydrolase/GTPase
Srr	-1.49	Mus musculus, Similar to hypothetical protein FLJ10534, clone MGC:28320 IMAGE:4014819, mRNA, complete cds	pyruvate metabolism
Hsd3b5	-1.49	hydroxysteroid dehydrogenase-5, delta<5>-3-beta	lipid metabolism
Sct	-1.47	secretin	peptid hormone/receptor binding
Fin14	-1.46	fibroblast growth factor inducible 14	cell proliferation
Hnrph1	-1.42	heterogeneous nuclear ribonucleoprotein H1	nucleic acid binding
Cyp2a4	-1.39	cytochrome P450, 2a4	oxireductase
Amd2	-1.36	M.musculus gene for S-adenosylmethionine decarboxylase.	cell proliferation
Hspa5	-1.36	heat shock 70kD protein 5 (glucose-regulated protein, 78kD)	heat shock protein
Osbpl1a	-1.30	oxysterol binding protein-like 1A	lipid transport
Cast	-1.30	calpastatin	protease inhibitor/calpain inhibitor
Nol5	-1.29	nucleolar protein 5	cell growth
Adrm1	-1.28	adhesion regulating molecule 1	cell communication
Nsbp1	-1.25	nucleosome binding protein 1	regulation of transcription
Ugcg	-1.22	UDP-glucose ceramide glucosyltransferase	glucosyltransferase
Ccr4	-1.22	carbon catabolite repression 4 homolog (S. cerevisiae)	rhythmic behavior
Dby	-1.22	DEAD (aspartate-glutamate-alanine-aspartate) box polypeptide, Y chromosome	nucleic acid binding
Ell2	-1.22	ELL-related RNA polymerase II, elongation factor	transcription
Cebpa-rs1	-1.21	CCAAT/enhancer binding protein alpha (C/EBP), related sequence 1	regulation of transcription
Epha3	-1.19	Eph receptor A3	ephrin receptor/protein kinase
Supt5h	-1.18	suppressor of Ty 5 homolog (S. cerevisiae)	chromatin modeling
Ifrd1	-1.18	interferon-related developmental regulator 1	differentiation
Facl4	-1.17	fatty acid-Coenzyme A ligase, long chain 4	fatty acid metabolism
Nfkb1	-1.17	nuclear factor of kappa light chain gene enhancer in B-cells 1, p105	apoptosis/transcription factor
Rock2	-1.16	Rho-associated coiled-coil forming kinase 2	protein kinase/ATP binding
Mpl	-1.10	myeloproliferative leukemia virus oncogene	cell growth and/or maintenance
C4,CYP21OH-A,slp,G11,NG6,SKI,Bf,C2	-1.07	Mus musculus major histocompatibility locus class III region: complement C4 (C4) and cytochrome P450 hydroxylase A (CYP21OH-A) genes, complete cds; slp pseudogene, complete sequence; NG6, SKI, and complement factor B (Bf) genes, complete cds; and compleme	kinase/helicase
Tle1	-1.04	transducin-like enhancer of split 1, homolog of Drosophila E(spl)	cell growth and/or maintenance
Hnrpa2b1	-1.03	heterogeneous nuclear ribonucleoprotein A2/B1	cell growth and/or maintenance
Hdgfrp2	-1.02	hepatoma-derived growth factor, related protein 2	cell differentiation
Osp94	-0.94	osmotic stress protein 94 kDa	ATP binding