

DISSERTATION

*FRANCISELLA TULARENSIS*: HOST-PATHOGEN RESPONSES TO  
INFECTION AND DRUG TARGET IDENTIFICATION

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## ABSTRACT

### *FRANCISELLA TULARENSIS*: HOST-PATHOGEN RESPONSES TO INFECTION AND DRUG TARGET IDENTIFICATION

The pathobiology of the host and pathogen responses to *Francisella tularensis* infection and disease progression were poorly understood when I started my graduate career. To address this, we have employed an integrative biological approach consisting of monitoring of the host transcriptional response to infection and dissemination, and determining the transcriptionally active and essential genes required for *F. tularensis* infection and disease progression. Drug therapies for *F. tularensis* that control the dissemination of the bacterium from the lungs to the spleen, liver, and kidneys are associated with positive clinical outcome. Therefore the studies focused on the host response were designed to address the hypothesis that host responses to *F. tularensis* strains of varying virulence will differ and the differences will shed light on why the host is unable to contain infection with highly virulent strains of *Francisella* in the lungs. We utilized the *F. tularensis* mouse model of pulmonary infection, the highly virulent Type A *F. tularensis* strain Schu4, and the less virulent Type B live vaccine strain (LVS) to study the host response to infection and identification of

essential bacterial genes. This model and these strains provide a means for comparative analysis of virulence in a defined and rapidly adaptable model of disease progression. Bacterial burden and organ pathology was used to monitor disease progression, and the host transcriptional response to *F. tularensis* infection was used as a guide for the bacterial studies. We found that dissemination and pathology in the spleen was significantly greater in mice infected with *F. tularensis* Schu4 compared to *F. tularensis* LVS and there was altered apoptosis, antigen presentation, and production of inflammatory mediators that explain the differences in pathogenicity of *F. tularensis* Schu4 and LVS. We then designed experiments to address the hypothesis that genes actively transcribed during infection could be used to define the genes essential for the bacteria to cause disease. We identified active metabolic pathways utilized by *F. tularensis* during the infection, and the essential genes necessary for the bacteria to cause infection including those encoding components in isoprenoid biosynthesis, fatty acid biosynthesis, and aromatic amino acid biosynthesis. Together, these studies allowed for the identification of host diagnostic markers and *F. tularensis* therapeutic targets required for the establishment of infection in the lungs and dissemination to secondary sites of infection. Importantly, this information promises to guide the development of diagnostics, chemotherapeutics and therapeutic vaccines that are relevant to clinical stages of disease.

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## LIST OF ABBREVIATIONS

2D-PAGE: Two Dimensional Poly Acrylamide Gel Electrophoresis

ANOVA: Analysis of Variance

BSA: Bovine Serum Albumin

BSL: Bio-safety Level

°C: Degrees Centigrade

CDC: Centers for Disease Control

cDNA: Complementary DNA

CFU: Colony Forming Units

CSU: Colorado State University

Cy3: Cyanine 3

Cy5: Cyanine 5

DC: Dendritic Cell

$\Delta$ CT : Delta Count Threshold

DEG: Database of Essential Genes

DNA: Deoxyribonucleic Acid

FAD: Flavin Adenine Dinucleotide

FASII: Fatty Acid Synthesis Type II

FPI: *Francisella* Pathogenicity Island

g: Gram

mg: Milligram

μg: Microgram

GC: Guanine Cytosine

GEO: Gene Expression Omnibus

IgA: Immunoglobulin A

IgG: Immunoglobulin G

IgM: Immunoglobulin M

lfn: Interferon

i.n.: Intranasal

IS: Insertional Sequence

Kb: Kilobase Pairs

kDa: Kilo Dalton

L: Liter

mL: Milliliter

μL: Microliter

LPS: Lipopolysaccharide

LVS: Live Vaccine Strain

MALDI: Matrix Assisted Laser Desorption/Ionization

Mb: Megabase Pairs

MHC: Major Histocompatibility Complex

MLVA: Multi Loci Variable Number of Tandem Repeat Analysis

MPL: Monophosphorylated Lipid A

mRNA: Messenger RNA

MS: Mass Spectrometry

NLR: NOD Like Receptor

NOD: Nucleotide Oligomerization Domain

ORF: Open Reading Frame

PAGE: Polyacrylamide Gel Electrophoresis

PBMC: Peripheral Blood Mononuclear Cell

PBS: Phosphate Buffered Saline

PFGE: Pulse Field Gel Electrophoresis

PI: Isoelectric Point

QRT-PCR: Quantitative Real Time Polymerase Chain Reaction

RPKM: Reads Per Kilobase Per Million Reads

RNA: Ribonucleic Acid

rRNA: Ribosomal RNA

SOLiD: Supported Oligo Ligation Detection

SNP: Single Nucleotide Polymorphism

SDS: Sodium Dodecyl Sulfate

SSC: Saline Sodium Citrate

T2S: Type II Secretion

TfP: Type IV Pili

TLR: Toll Like Receptor

TNF: Tumor Necrosis Factor

UTP: Uridine Triphosphate

UV: Ultra Violet

## DEDICATION

I dedicate this work to my beautiful fiancé; your love and encouragement made me strive to be the best scientist I could be.

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## CHAPTER 1

### General Overview of *Francisella tularensis*

#### 1.1: Background

##### **1.1.1 History**

*Francisella* was discovered in 1911 in Tulare County, California isolated from rodents suffering from a “plague” like disease [1, 2]. Edward Francis characterized *Bacterium tularensis* [1] and theorized that tularemia was the cause of many previously unknown diseases in other outbreaks in rodents dating back to the early 19<sup>th</sup> century [2]. Outbreaks in the United States, Norway, and Japan were all thought to be caused by *Francisella* [2]. The first human case positively identified as *Francisella* was reported from Ohio in 1914 [3].

##### **1.1.2 Taxonomy**

Initially classified as *Bacterium tularensis*, it was eventually renamed in honor of Edward Francis for his contributions to the study of the bacterium [2]. Originally thought to belong to the *Pasturella* genus, it was not until the 1960's that DNA hybridization provided experimental evidence that demonstrated that

*Francisella* was not closely related to *Pasturella* [4]. Through 16s rRNA sequencing it was shown that *Francisella* belonged to the gamma-proteobacteria subclass with no close relationship to other bacteria in the subclass and warranted its own genus designation [5]. *Francisellaceae* remains the only recognized genus in its class, which is further substantiated by a unique fatty acid composition and high lipid content [6, 7].

Subspecies were determined primarily by different clinical presentations, varying severity of disease, and geographical distribution of *Francisella* cases [6]. *Francisella* isolates found in only North America demonstrated greater virulence in rabbits and a more severe form of tularemia in humans and thus designated as a separate sub-species, *F. tularensis* sub-species *tularensis* [8, 9]. Isolates found in North America, Europe, and Asia that showed less virulence in animals and a less severe form of disease in humans, were given the classification of sub-species *holarctica* [8, 9]. Further distinction of sub-species found primarily in ticks from Central Asia and the former Soviet Union were given the designation as sub-species *mediasiatica* based on the origin of isolates and their unique biochemical properties [7]. An isolate from Utah in the 1950's was found to be closely related to *Francisella* but it was not until the 1980's that it was determined there was only 75% genomic relatedness between the isolate and the other three sub-species [8, 11, 12]. This led to the designation of the isolate as sub-species *novicida*, which was less fastidious in its growth requirements and less virulent than the other three sub-species [12]. Currently, there are four sub-species of *Francisella tularensis*; *tularensis*, *holarctica*, *mediasiatica*, and *novicida* [8].

Human and animal infections are primarily due to subspecies *tularensis* and subspecies *holarctica*, which are commonly referred to as type A and type B, respectively [8, 16]. Isolates from both type A and B demonstrate subtle differences in both virulence and geographical location that warrant further taxonomical designation [9, 17]. Type A and B isolates from North America have been further differentiated into two clades, 1 and 2 [17, 18]. Type A has additionally been separated into sub-clades A1a and A1b, based on MLVA, PFGE, and SNP analysis [18-21].

### **1.1.3 Epidemiology**

Worldwide distribution of *Francisella* has been difficult to accurately define due to the amount of resources necessary to survey wildlife and vector reservoirs in endemic and outbreak regions. A breakthrough in *Francisella* epidemiology came in 1959 by Olsufiev *et al.* when it was determined that there were two subspecies of distinct virulence that tended to result from different geographical locations [6]. The subspecies were dubbed *tularensis* and *holarctica*. It was observed that subspecies *tularensis* had significantly higher virulence in mammals and infections typically resulted from contact with rabbits whereas infections with subspecies *holarctica* resulted from contact with lakes, ponds, streams, and aquatic mammals such as beavers [6]. *Francisella* has endemic foci in Europe and North America where infections of animals and human are more common, and ticks isolated from these regions harbor the bacteria more often [2]. In Europe, foci in Finland and Sweden have been identified [9]. Foci in

Russia, Turkmenistan, and Kazakhstan have long been documented and studied extensively by the former Soviet Union [10]. Studies were conducted due to the prevalence of tularemia in the region. However, since 1990 cases have dramatically decreased to just a few hundred a year [2].

Figure 1

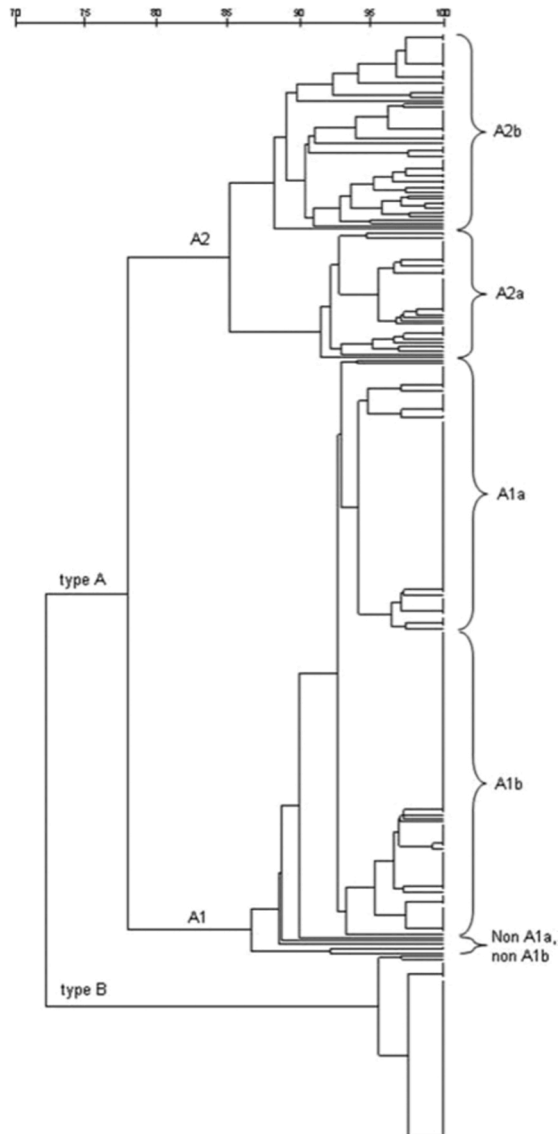


Figure 1: Adapted from Kugeler *et al.* 2009. Dendrogram depicting 363 isolates of *Francisella tularensis* from humans and animals (302 type A and 61 type B isolates) genotyped by PFGE. Clusters corresponding to type A, type B, and A1, A2, A1a, A1b, A2a, and A2b genotypes are indicated.

The majority of cases in the United States are reported in Arkansas, Missouri, South Dakota, and Oklahoma [11, 12]. The distribution of subspecies and clades in the United States was originally described by Kugeler *et al.*, and as



more isolates are sequenced, new distinctions provide a clearer picture of the epidemiology of *F. tularensis* that correlates more closely with geographical distribution of strains in the United States [13].

#### **1.1.4 Ecology**

Identification of *F. tularensis* reservoirs and vectors was first undertaken by the Soviets in the mid 1900's [14]. Using epidemiological data, the Soviets identified two main environmental foci associated with human tularemia, swamp-floodland and grassland-meadow environments [14]. Soviet research from 1930-1960 led to the identification of numerous naturally infected arthropods, mammals, and insects as reservoirs that coincided with human infections [14]. Many efforts to control the population of natural reservoirs in endemic areas included poisoning of rodents, fumigation of burrows, and controlled hunting of wild rabbits [14]. In conjunction with data from research conducted in the United States, the "deer fly" was identified as an important vector in the USSR, thus tularemia is also commonly referred to as deer fly fever [14].

In the United States two thirds of human tularemia cases were believed to be associated with contact with cottontail rabbits [11]. Tularemia was thought to be a problem mostly in the eastern United States, but spread west due to the transport of cottontails to the west for sport [15]. As the ecology of *Francisella* was studied further, it was determined that tick bites were also an important source of human tularemia. It was estimated that between 1938 and 1948, 56% of the human tularemia cases in Arkansas were due to tick bites, while 31% of

infections were the result of contact with contaminated rabbits [11]. Due to the higher rate of infection in trappers and hunters, aquatic mammals were also determined to be an ecological reservoir of *Francisella* in the United States [16]. Contaminated water sources were deemed the precursor to zoonotic infections of muskrats and beavers that led to infection of humans [16]. This infection cycle has been associated with *F. tularensis* subspecies *holarctica* in both the United States and Russia [14, 16].

In Europe and Scandinavia similar ecology of *F. tularensis* has been described, however, with a stronger emphasis on mosquito born infections due to contaminated water sources as the reservoir for human infection [17]. Epidemiology data show that human outbreaks strongly correlate with nearby contaminated water sources and mosquito populations [17]. Similar conclusions were drawn by researchers in Europe suggesting that contaminated water sources were the site of infection of mosquitoes during their larval stages [17].

### **1.1.5 Evolution**

Original methods of determining *Francisella* sub-species and taxonomical relationship were through phenotypic analysis of colony morphology and grouping of isolates by clinical manifestations [18]. MLVA, PFGE, Real time PCR, and whole genome sequencing have since been employed to create a more defined understanding of *Francisella* sub-species and their relatedness [5, 13, 18-26]. The study of the evolution of *Francisella* has provided unique insight into the transformation of a relatively harmless environmental bacterium into a host-

dependent highly virulent pathogen [18]. This was aided by the fact that many highly related strains and sub-species with significant differences in virulence have been well characterized. *Francisella* is a desirable model for the study of bacterial evolution due to the many subtle differences in isolate virulence that represent the various stages of genome decay and host-restriction that occur over time [30, 32].

The evolution of *Francisella tularensis* sub-species has been the subject of much study for diagnostic purposes and has shed light on the many subtypes and evolutionary steps that *Francisella tularensis* has undergone. Type A and B strains (Discussed in 1.2 Taxonomy) have distinct genomic arrangements that differentiate them molecularly in addition to the virulence differences observed in humans [21, 29, 33, 34]. Both type A and B *Francisella tularensis* have a high level of pseudogenes interrupting numerous biochemical pathways, indicating genomic decay as a result of host-restriction [19, 35]. Examination of SNPs between sequenced strains revealed that type B strains differ very little while type A strains show a high level of diversity [21, 29, 30, 36]. Unique SNP patterns have also been determined among type A strains, resulting in the designations of AI and AII. Due to further analysis based on virulence differences and more recently on genomic sequence, AIa and AIb have now been defined and accepted as separate clades [13, 27, 36] (Further discussed in 1.2 Taxonomy).

### **1.1.6 *Francisella* as a Bioweapon**

*Francisella* has been considered a potential biological weapon since the years leading up to World War II [37, 38]. Japan began studying numerous biological weapons, including tularemia, in 1937 and tested them on prisoners of war [38]. In 1942, the United States and Britain agreed to use biological weapons only in retaliation, but both countries continued stockpiling large arsenals of biological weapons [38]. The United States' main bioweapons facility was based out of Fort Detrick in Maryland, where botulism and anthrax was the primary focus, but brucellosis, tularemia, and glanders were also studied [38].

It has been suggested that shortly before the battle of Stalingrad a large outbreak of pneumonic tularemia along the German-Soviet front was the result of a Soviet intentional release of *F. tularensis* [38]. The author that suggested this attributes the large number of Soviet cases to a sudden change in wind direction. However, others have proposed that the outbreak was a result of an endemic source that arose from deteriorating sanitation caused by the war time conditions [38]. The Soviet Union studied biological weapons extensively, even creating vaccine and antibiotic resistant strains of many different pathogens including tularemia [38].

As tularemia cases dropped drastically in the United States by the 1980's the CDC removed it from the list of notable diseases. However, in 2001 a renewed interest in studying tularemia was revived after the intentional distribution of anthrax spores immediately after the September 11<sup>th</sup> terrorist attacks in 2001 [37]. The CDC continues to classify *F. tularensis* as a category A

select agent due to its high infectivity, less than 10 cells to cause fatal infection, and its ease of dispersal as an aerosol [37]. It has been estimated that dispersal over a population of 5 million people could render 250,000 people extremely ill and cause approximately 19,000 fatalities [37].

## 1.2: Physiology

### 1.2.1 *Metabolism*

As an intracellular pathogen, *F. tularensis* has evolved to depend highly on nutrients available in the biological niche that it occupies. Intracellular pathogens encounter a number of different carbon and nitrogen sources as well as minute and fluctuating concentrations of iron, magnesium, and manganese [39]. There have been very few studies that aim to classify the complicated regulation and utilization of different metabolic pathways in *F. tularensis* both *in vitro* and *in vivo*. Initial studies to define growth requirements were done empirically and identified amino acid supplements necessary for growth *via* pathway interruption by pseudogenes, most important of which was a cysteine supplement required for growth [31]. Rapid growth *in vitro* requires many carbon, vitamin, and amino acid supplements [31]. However, growth can be achieved on a simple amino acid solution derived from protease treated animal tissue (LCK unpublished results). In murine macrophages, microarray analysis of *F. tularensis* Schu4 required the expression of genes associated with amino acid metabolism, *de novo* nucleotide synthesis, metabolism of vitamins and cofactors, translation and protein biosynthesis, and carbohydrate metabolism including glycolysis and the pentose phosphate pathway [40]. The study highlighted the need for multiple amino acids for active intracellular growth by expression of genes involved in specific amino acid biosynthetic pathways as well as the expression of five of eight encoded oligopeptide transporters [40],

Figure 2

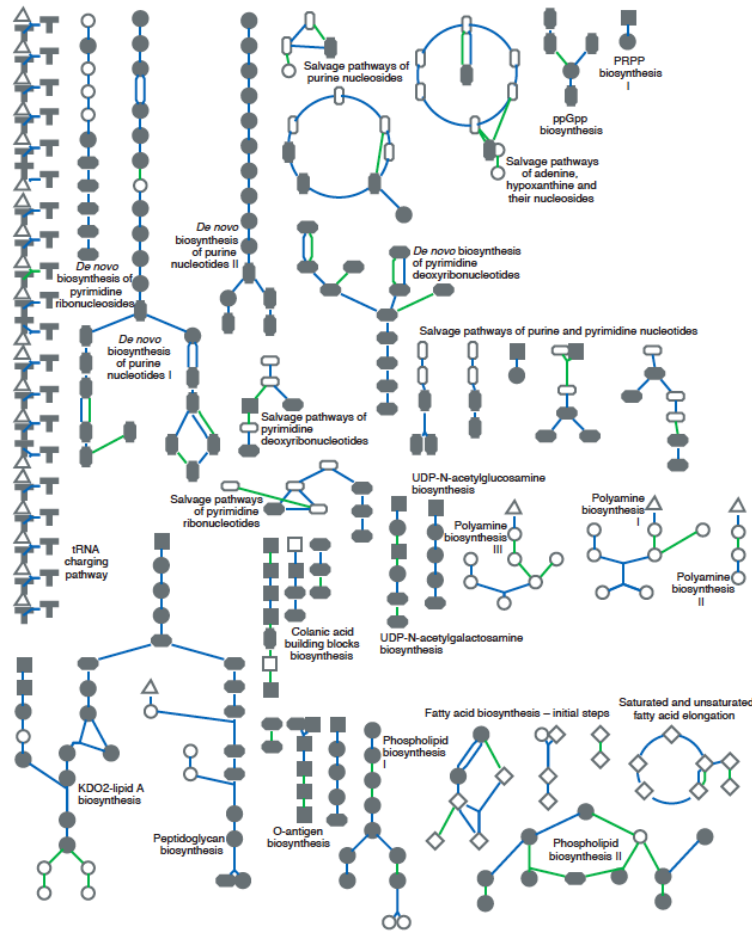


Figure 2: Adapted from Larsson et al, 2005 [19]. Metabolic pathways in *F. tularensis* Schu4. Grey indicates genes present; white indicates holes in metabolic pathways. Using prediction software to identify genes involved in small molecule metabolism, genes encoding 350 different enzymes were identified. This analysis resulted in 390 gaps in 137 predicted metabolic pathways, which is 54% of known metabolic pathways.

consistent with the many interrupted pathways throughout the *Francisella* genome as shown in figure 3 [18]. These observations are consistent with the earliest studies to determine growth requirements of *F. tularensis in vitro* [31].

### 1.2.2 Cell Envelope

Bacterial cell envelopes are a complex layered structure of molecules designed to protect the cell and allow it to interact with the biological niche in which it resides [41, 42]. In the case of bacterial pathogens it is particularly

important that the cell is able to interact with its host and evade the many defenses designed to combat and kill the pathogen [41, 42]. *Francisella* is a facultative intracellular gram-negative bacterium and possesses some novel characteristics that set it apart from other gram-negatives [43, 44]. Gram-negative bacteria are traditionally surrounded by a lipopolysaccharide (LPS) rich outer membrane, a thin cell wall composed of peptidoglycan, and a lipid bi-layer inner membrane [45]. In contrast, gram-positive bacteria which have no outer membrane and a thick cross linked layer of peptidoglycan as the cell wall with a lipid bi-layer inner membrane [42]. Both gram-positive and gram-negative bacteria can have a polysaccharide capsule that surrounds the outermost surface of the cell that aids in host evasion and protection from the environment [42]. *Francisella* possesses all of the structural components aforementioned including a polysaccharide capsule. However, the LPS of *Francisella* is unique and poorly immunogenic unlike most gram-negative LPS [44].

Bacterial LPS consists of a lipid A subunit that anchors the molecule in the outer membrane, a polysaccharide core, and an oligo or poly saccharide O-antigen [41, 45]. *Francisella* LPS has been characterized in the sub-species *novicida*, *mediasiatica*, *holarctica*, and *tularensis*, with both lab strains and clinical isolates [43, 44, 46]. The structure of the *Francisella* lipid A and polysaccharide core are identical for all of the sub-species but the structure of the O-antigen differs between pathogenic and environmental strains [43, 44, 46, 47]. The O-antigen genes are identical between sub-species *holarctica* and *tularensis* [47], whereas the sub-species *novicida* has fewer genes in the same gene



cluster encoding O-antigen modification enzymes [48]. This difference has been hypothesized to be an important difference in virulent versus environmental strains but needs further study [44]. The O-antigen of *Francisella* has been shown to protect the bacteria from antimicrobial peptides, serum opsonization, and complement killing [44, 49, 50]. These observations were made by knocking out genes in the *wbt* operon, specifically *wbtA*, which led to the absence of O-antigen on the cell surface [51].

As previously mentioned, *Francisella* is poorly immunogenic which has been attributed to a dephosphorylated glucosamine on the glycosyl dimer in the lipid A anchor [42-44]. This same phenomenon has been shown in *Salmonella*, which contains a monophosphorylated lipid A (MPL) with poorly immunogenic properties [52]. The lipid A of *Francisella* is also unique in that it is tetra-acylated with carbon chains of 16-18 carbons in length [43, 53, 54]. In contrast, common gram-negative bacterial lipid A molecules are hexa-acylated with carbon chains of 12-14 carbons in length [42].

The capsule of *Francisella* remains the most poorly understood component of the surface structure [44]. A study published in 1988 showed that LVS treated with acridine orange resulted in rough colony morphology variants that were deemed capsule deficient [55]. The cells lacked the ability to grow intracellularly within macrophages and were susceptible to the binding of IgG immunoglobulins to leading complement protein C3 deposition and complement susceptibility [55]. Another study showed that lyophilized LVS resulted in the spontaneous occurrence of rough colonies when the cells were grown on

synthetic media [56]. The rough variants showed similar infection defects as the previous studies with capsule deficient colonies, but it was observed that sub-culturing on synthetic media resulted in reversion to smooth colony morphology [56]. In addition, after several passages the cells became increasingly encapsulated and showed higher virulence in mice demonstrating the importance of the capsule to the infectious cycle of *Francisella* [56]. There has been debate however, about whether or not there are aberrations in the O-antigens of the rough colony variants that would also explain differences in virulence [57, 58]. Recently, a knockout mutant of a putative capsule biosynthetic gene *capB* was described [57, 58]. The study did not comment on colony morphology of the mutants but did confirm that the O-antigen was intact and protected against serum killing [57, 58]. The mutant showed lower bacterial burden in mice and 100% protection against challenge with lethal doses of wild type LVS and Schu4 [57, 58]. This study demonstrated the importance of the characterization and understanding of the *Francisella* capsule and the genes associated with its construction and maintenance.

For the construction and maintenance of the surface components of the bacterial cell, the ability to secrete proteins and molecules to the cell surface is important [59]. In addition, bacteria secrete enzymes for the conversion of molecules into nutrients taken from the milieu of the biological niche in which the bacteria grow [59]. The *Francisella* genome encodes genes that have homology to both Type IV pili (Tfp) and a Type II Secretion System (T2S), although data suggests that protein secretion is carried out through a mechanism that more

closely resembles Tfp based secretion [19, 59, 60]. The majority of the studies designed to characterize *Francisella* secretion used the environmental strain *novicida* [61-64]. Due to the fact that orthologs for Tfp in pathogenic strains contain mutations, they have been designated as pseudogenes [19]. Although the gene interruptions do not explicitly rule out functionality in strains of higher virulence, researchers have focused on *novicida* due to this and further study to characterize functionality in these strains is needed.

### **1.2.3 Iron Uptake**

Many bacterial pathogens require iron for full virulence and iron acquisition is particularly important for intracellular pathogens due to the scarcity of free iron within host cells [65]. Consequently, host mechanisms for combating infection include the sequestration of free iron throughout the body upon recognition of infection [65] with the exception of the phagosome where iron is released via iron sequestering proteins in a pH dependent manner as the phagosome becomes increasingly acidified [65, 66]. This mechanism allows cells to acquire iron in a controlled fashion. Thus, many bacterial pathogens have developed highly efficient strategies for acquiring iron within acidified phagosomes through the use of siderophores and dedicated transport systems for iron uptake [65, 66].

Iron acquisition in *Francisella* has been studied extensively in multiple sub-species and therefore is well characterized. In the 1960's, a secreted protein from *Francisella* with characteristics of a siderophore was discovered to be essential for full virulence and promoted growth in highly dilute cultures [67].

Years later, Fortier *et al.* showed that *Francisella* LVS was unable to replicate outside of host cells without the presence of iron and only replicated within an acidified phagosome where iron was freely available [68]. In 2006, Sullivan *et al.* characterized the siderophore produced by *Francisella* and identified the FslA protein as responsible for its production [69]. Bioinformatic analysis was used to identify the *fsIABCD* operon and the *feoB* (ferrous iron transporter) locus suggesting little iron uptake machinery encoded in the *Francisella* genome [69-71]. The lack of iron uptake machinery coupled with the absence of the ubiquitous genes *tonB*, *exxB*, and *exbD*, normally present in gram-negative bacteria for binding and uptake of siderophores, suggest that *Francisella* mechanisms for siderophore uptake may be unique [69]. In addition, they showed the *fsIA* locus was iron regulated and its deletion resulted in the inability of *Francisella* to grow in iron-depleted conditions [69]. Later, two genes downstream of the *fsIABCD* operon were found to be co-transcribed with the operon and designated *fsIE* and *fsIF* [70, 71]. Recently shown was a knockout of *fsIE* defective in the uptake of iron bound siderophore molecules, representing a novel iron uptake mechanism found only in *Francisella* to date [70, 71]. The entire *fsIABCDEFG* operon is under the control of the ferric uptake regulator (*fur*) protein that binds a Fur box region in the promoter region of *fsIA* [70, 71]. In reduced iron conditions the Fur protein is deferrated and loses its DNA binding capability resulting in the activation of the siderophore production and binding operon *fsIABCDEFG* [70, 71]. Identification of other Fur dependent genes has led to a more complete understanding of the genes in the *Francisella* genome

responsible for iron metabolism [70]. This approach led to the characterization of the 58-kDa ferric uptake protein FupA [72]. FupA was shown to work in tandem with FslE during siderophore uptake [70, 71]. Interestingly, the *fupA* locus in LVS is disrupted and was hypothesized as a prime candidate for the basis of LVS attenuation [70, 71]. This hypothesis was further supported by the expression of a functional *fupA* in LVS that increased its virulence in mice [71]. Additional studies have shown that the disrupted *fupA* gene in LVS is active though likely at a less efficient rate than the homologue in virulent strains of *Francisella* [71]. Much of the work characterizing *Francisella* siderophore production and uptake was performed using the LVS strain. However, many studies have also been conducted in the highly virulent lab strain Schu4 and homologues for all genes identified in LVS have been annotated in the Schu4 genome as well.

#### **1.2.4 Genomics**

Since 1995 there has been a substantial effort to sequence and categorize the full genomes of microbes in order to develop a clearer understanding of evolutionary relationships, minimal coding capacity, and to decipher the molecular basis of biology behind the interaction of bacteria with their biological niches [73]. In the case of bacterial pathogens, full genome sequencing has been useful in the development of diagnostic tools for detection in developing novel protein derived vaccine candidates that can be cloned only if the sequence is known [74]. This has been particularly true in the *Francisella* field where molecular diagnostics based on genome differences were developed to discern

*Francisella* strains down to the sub-clade level [25, 27, 36]. These diagnostics continue to develop and are important for informing therapeutic intervention strategies and characterizing strains responsible for outbreaks.

The first *Francisella* genome to be sequenced was the highly virulent lab strain Schu4 by Larsson *et al* in 2005 [19]. To date there are over 15 complete genomes of *Francisella* published with many more in the works [75]. All *Francisella* genomes sequenced to date are less than 2 Mb [76]. Studies comparing full genomes to understand the evolution of *Francisella* have indicated a high level of genomic rearrangements and decay that resulted in an increase in virulence [19-21, 24, 29, 30, 35, 36, 77-81]. A study comparing a 1.1 Mb region shared by all sequenced *Francisella* genomes revealed 97.7% average nucleotide identity between environmental and pathogenic strains [32]. Among pathogenic subspecies, the average nucleotide identity was 99.2% [32]. Importantly, there is a significant difference in the severity of disease between the subspecies [34, 37, 82] leading researchers to hypothesize that comparison of *Francisella* genomes of high and low virulence could lead to insight into the molecular basis of pathogenesis [19-21, 29, 30, 35, 78-81]. Many studies have approached this question by comparing genomes of *Francisella*, however to relatively little outcome.

There are several important features of the *Francisella* genome that led to major discoveries in the field. First, a 30 kb region of sequence found to be duplicated in pathogenic strains of *Francisella*, while the environmental parent strain contains only one copy [19, 29]. The regions shared characteristics of

pathogenicity islands found in other pathogenic bacteria, mainly a significantly different GC content from that of the rest of the genome and structural/coding similarities to virulence loci found in the *Vibrio* and *Pseudomonas* genus [83-86]. Therefore genes within the region became a focus of many groups trying to understand the basis of pathogenesis in *Francisella*. A four-gene operon was found to encode protein products essential for intracellular growth and through the knockout of these genes, pathogenesis of the bacteria was reduced significantly leading to their designation as intracellular growth locus genes (*IglA-D*) [83, 84]. Another important feature found while comparing the known *Francisella* genomes was the distribution and location of insertional sequence (IS) elements found throughout the *Francisella* genome [29, 30]. IS elements have been shown to be the primary site of genomic rearrangement events throughout the evolution of the bacteria [29, 30]. The IS elements have been instrumental in the taxonomical designation of the different subspecies of *Francisella* as genomic rearrangements tend to be conserved among the subspecies [21, 29, 30, 35, 36] and were recently found to differ among isolates of subspecies *tularensis* clade A1 leading to the reclassification of the clade into two different clades, A1a and A1b [30]. The clades only differ by 3 IS elements yet show a significant difference in virulence [27, 30]. In mice, A1b strains cause significantly faster time to death [27] while in humans A1b caused death in 24% of patients compared to 4% for A1a [13, 88]. Recently transcriptional activity was shown to originate from IS elements and continuing into the downstream open reading frames during exposure of *Francisella* to intracellular conditions [87].

Future studies that continue to examine the significance of IS element position and transcriptional activity offer a promising avenue for deciphering virulence differences between subspecies.

### **1.2.5 Proteomics**

Two primary approaches have been employed to characterize the proteomes of bacteria. The first is the development of comprehensive 2-Dimensional (2D) PAGE databases taken from whole cell lysates [88]. This approach suffers from a significant disconnect between proteins identified and proteins encoded in the genome [88], but this approach continues to benefit from advances in protein isolation/separation strategies and more importantly by the improvements in MS technology and analysis [88]. Separation strategies have improved by focusing on certain subsets of proteins in cell compartments that may contain groups of proteins that require more unique chemical isolation strategies [88]. The best example of this application is the preferential isolation of cell wall/membrane associated and secreted proteins whose characterization can inform hypotheses about host and pathogen interactions [88]. The second main strategy used in bacterial proteomic studies is the use of comparative studies to examine differences in protein production between strains of high and low virulence [88]. Similar to genomic strategies comparing coding capacity differences, this strategy can be used to identify pathogenesis determinants that vary between strains of differing virulence at the protein level [88]. The most sophisticated example of this approach is the examination of differentially



produced proteins in conditions that mimic *in vivo* conditions and in particular, proteins isolated from macrophages or tissues during infection [88]. Importantly, the combination of the two approaches are essential for studying genes with no characterized function or are annotated as pseudogenes yet are still produced and may play a role during infection.

Figure 3 shows a whole genome ontology analysis of 8 proteobacteria [18]. The figure highlights the high proportion of cell envelope dedicated genes in *Francisella* compared to the other pathogens, indicating the importance of this functional subset of genes to the infectious cycle of the bacterium. There is also Type II and VI secretion machinery in the *Francisella* genome and the presence of signal sequences at the N-termini of a large number of proteins further indicates the importance of the cell envelope to the bacterium's interaction with its host [18]. In addition, a study by Hubalek *et al.* that aimed to create a comprehensive *F. tularensis* Schu4 2D-PAGE proteomic database showed approximately 34% of the proteins identified were annotated as membrane proteins, whereas statistically, the expected result for bacteria would normally be 20% of the genome encoding membrane proteins [88, 89].

Proteomic studies in *Francisella* have primarily utilized comparative approaches in hopes of identifying virulence determinants that are different between strains of high and low virulence [90-93]. In addition, proteomic subsets such as outer membrane proteins, secreted proteins, glycoproteins, and immuno-reactive proteins have been characterized in various *Francisella* strains [88-93]. One of the most comprehensive studies compared the proteomes of 13 strains of

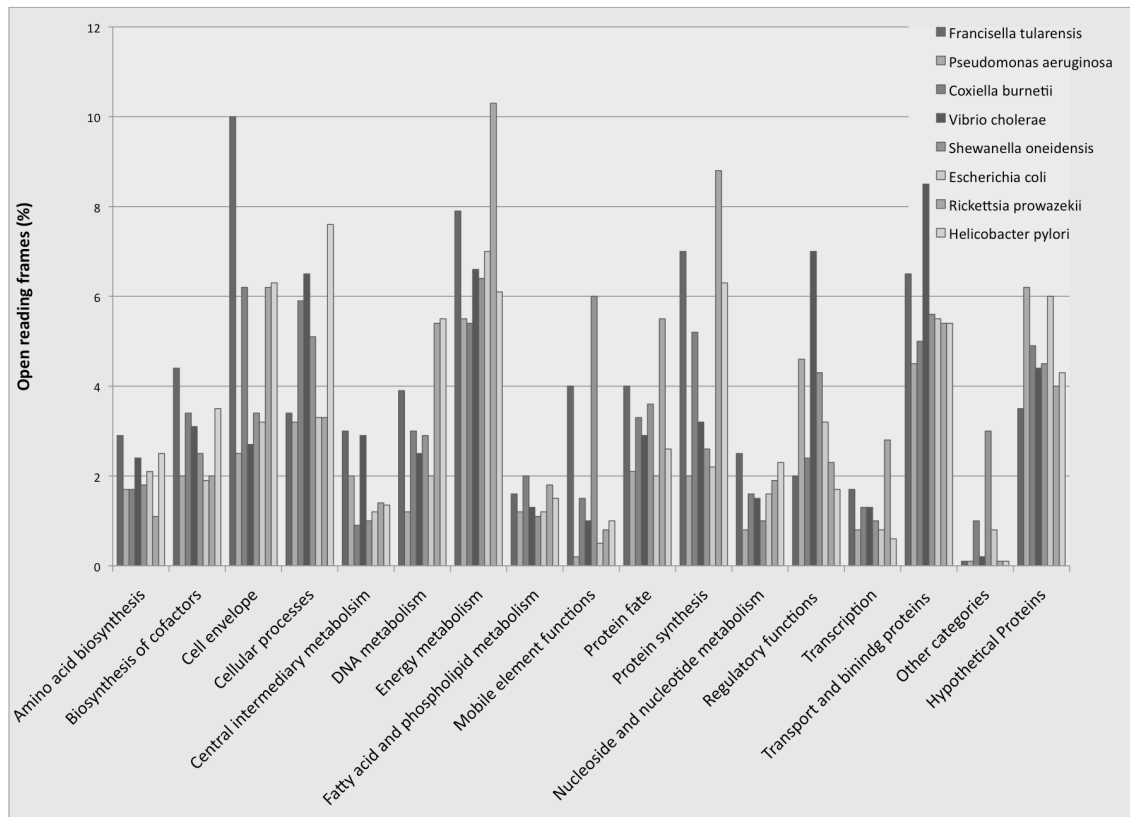


Figure 3: Figure adapted from Keim et al. [18] Gene ontology percentages for 8 pathogenic bacteria. The bar graph highlights the large amount of genes encoded by *Francisella* that fall into the functional category of cell envelope.

*Francisella* of varying virulence from 3 different sub-species [92]. The study utilized 2D PAGE and MALDI to compare the proteomes of each strain grown in synthetic media and identified proteins unique/absent, proteins at higher/lower abundance, and proteins with charge/mass/PI shifts distinct to each strain [92]. Of particular interest were proteins either unique to, or produced at a higher abundance in highly virulent strains compared to the other strains [92]. Many of the proteins identified in strains of high virulence were annotated as putative outer membrane proteins, indicating a potential role in virulence and host

interaction [92]. A highly informative study with significant implications to my work performed in 2006 by Twine *et al.* identified proteins produced *in vivo* during infection using the mouse model [94]. *Francisella* FSC033 proteins were isolated from mouse spleens and identified by mass spectrometry [94]. The study identified 78 proteins that were differentially produced *in vivo* compared to *in vitro* grown *Francisella* [94]. Additionally, the study highlighted the unique proteomic profile necessary for adaptation to growth in host tissues, and was important for identifying novel vaccine candidates and clinically relevant drug targets. There remains a large amount of information still unknown about the *Francisella* proteome and what subtle differences exist between strains of differing virulence due to their highly similar genomic coding capacity.

### **1.2.6 Pathogenicity**

The mechanisms of pathogenesis utilized by *Francisella* have been extensively studied in order to decipher the extreme virulence of the pathogen. These studies have led to significant advancements in the regulation and expression of numerous virulence genes and pathways. Traditional molecular methods to study gene function in *Francisella* was problematic due to the inability of the bacterium to replicate and retain non-native plasmids [60]. Thus, discovery of a native plasmid in the environmental strain *novicida* [95] led to significant progress in the study of virulence mechanisms used by highly pathogenic strains of *Francisella*. Initial work was primarily executed in *novicida* and focused on genes also present in pathogenic strains [60]. Genetic

engineering of the native *Francisella* plasmid has since made it possible to utilize the highly pathogenic strains of *Francisella* for further studies [96].

The initial breakthrough came when transposon mutants of *F. novicida* defective for growth in macrophages were isolated by Baron *et al.* [97]. The mutation was mapped to a gene that shared a 20% resemblance to SspA, a stringent response transcriptional regulator from *E. coli* [97]. The SspA protein was shown to interact with RNA polymerase to regulate expression of stationary-phase genes during nutrient starvation [98]. The gene was named MglA (macrophage growth locus A) and is expressed as a bi-cistronic transcript with MglB, also shown to be required for intracellular growth [97, 99]. The ability of *Francisella* to escape the phagosome into the cytosol is critical to its virulence, a study performed by Mariathasan *et al.* showed that MglA mutants were unable to escape the phagosome and are thus exposed to the low pH of the mature phagosome and killed [99]. A bacterial 2-hybrid experiment demonstrated that MglA interacts with RNA polymerase along with another SspA homologue identified during the study [99]. SspA was subsequently shown to form a complex with MglA and is required for positive regulation of virulence genes. A study by Brotcke *et al.* showed expression of MglA positively regulates over 100 genes [100], including those located on the *Francisella* pathogenicity island. Most of these genes however, have no assigned role or function indicating the need for further study to clearly understand mechanisms of *Francisella* pathogenesis.

The 30 kilobase *Francisella* pathogenicity island (FPI) contains two operons and a total of 16 genes, most of which are required for intracellular growth [84]. 8 of these genes share homology to the recently described Type VI secretion system from *Pseudomonas aeruginosa* and *Vibrio cholerae* [85, 86]. Further study is needed to confirm these genes are indeed part of a secretion system since preliminary evidence is solely based on bioinformatics. The most studied gene within the FPI is intracellular growth locus C (*IgIC*), which was first identified as the most up-regulated protein found during infection of macrophages [101]. *IgIC* was shown to be required for intracellular growth in macrophage, amoeba, and for virulence in mice [102-105]. Studies to identify the function of the *IgIC* protein have demonstrated its importance for phagosomal escape and the prevention of phagosome-lysosome fusion [104]. It has additionally been hypothesized that *IgIC* also plays a role in cytosolic growth, macrophage apoptosis, and disruption of TLR signaling. However, it is unclear if these are secondary roles of the protein or polar effects of the gene knockout [106-108].

As previously mentioned, the *Francisella* genome encodes a relatively large amount of genes annotated as cell surface components and therefore suggested that the cell surface of *Francisella* is highly important for its virulence [59]. The novel structure of *Francisella* LPS, presence of a capsule, and genes encoding Type IV pili have all been evaluated for a potential role in pathogenesis [59]. The Type IV pili genes encoded in the *Francisella* genome share homology with those of *Neisseria meningitidis* and *Pseudomonas aeruginosa* and are also arranged in a similar fashion [109]. Bacterial pili machinery are commonly

associated with adhesion to host cells, biofilm formation, and motility, whereas Type IV pili have been shown to be involved in protein secretion [110]. The *Francisella* capsule is the most poorly understood of the pathogen's surface components. Disruption in the capsule biogenesis gene locus *capB*, has been central for deciphering the role of capsule production for *Francisella* infection [57]. (Discussed in 1.8 Cell Envelope)

The study of *Francisella* virulence has benefited from numerous transposon mutagenesis studies that led to the discovery of several genes necessary for causing disease [111-123]. The initial studies were performed in sub-species *novicida* but subsequent studies have utilized the technique on *holarctica* and *tularensis* sub-species. Of note was a transposon mutagenesis study that used the highly virulent Schu4 strain where murine hepatic cells were infected with the mutants and 18 individual clones with transposon insertions were found defective for intracellular growth [115]. One mutant, a purine auxotroph, was successfully utilized as a vaccine in mice that protected against infection with homologous challenge of wild type Schu4. While transposon mutagenesis studies have been extremely informative, it is important to note that the technique relies on insertional bias of transposons and therefore is not considered a comprehensive assay for determining genes essential to infection.

### 1.3: Host Response to Infection

Mammals have developed many mechanisms for combating bacterial and viral pathogens [127]. In addition to mechanical barriers such as the skin and mucosal membrane, there are conserved molecular mechanisms of non-specific microbial resistance that recognize general molecular signatures of pathogens and recruit immune cells capable of direct killing to the site of infection [127]. The initial innate response to microbes leads to an adaptive immune response through the generation of specific antibodies and the ability to recognize the pathogen if encountered again [127]. Bacteria have also evolved mechanisms to evade and subvert both the innate and adaptive responses designed to defend against infection [128]. Response to *Francisella* infection has been thoroughly studied to characterize both the innate and adaptive response to infection. This research is particularly important for a bacterium of such extreme virulence for the generation of a vaccine that would protect humans in case of outbreak or intentional release. In general the immune response to *Francisella* is thought to be weak and incapable of protecting the host from infection with highly virulent strains through the pulmonary route [129-131]. Attempts to develop both live attenuated vaccines as well as vaccines from *Francisella* derived molecular components have been hampered by the bacteria's poorly immunogenic properties and poor cross reactivity between sub-species of differing virulence [132].

### **1.3.1 Innate Immune Response to *Francisella tularensis***

This section describes the research conducted to characterize the innate immune response to pulmonary infection with *Francisella*, as this is the most relevant model that mimics clinical presentation of severe human disease in animal models [133]. As the primary defense mechanism in the lungs is macrophages, it is also important to include analyses utilizing *ex vivo* studies that examine the macrophage response to *Francisella* infection. Macrophages can clear the lung of up to  $10^5$  CFU of bacteria within 2 hours through phagocytosis of the bacteria [134]. Like many pulmonary pathogens, *Francisella* has taken advantage of this defense mechanism by directly infecting macrophages in the lungs [135, 136]. The fact that *Francisella* targets macrophages has led to some debate on whether or not macrophages play a role in immunity against *Francisella* infection, however, TLR2 deficient mice are significantly more susceptible to infection suggesting some innate and immunostimulatory response to the bacterium after initial infection of alveolar macrophages [137, 138]. Dendritic cells (DCs) have also been shown to be important sites of *Francisella* infection and replication [139]. DCs are normally highly effective at ingesting bacteria and presenting antigen to naïve T-Cells, thus activating an effective T-Cell mediated immune response [127]. DCs isolated from mice infected with LVS showed abnormal activation and secretion of the anti-inflammatory cytokine TgfB1 and evidence of bacterial replication within the cytoplasm [139]. This study demonstrated the ability of *Francisella* to dampen the host immune response and replicate within cells that are important for recognition and



response to infection [139]. Studies have also shown a significant delay in response to infection when monitoring transcriptional response in mouse lungs over the course of infection with type A *Francisella* [140, 141].

The uptake of *Francisella* into macrophages likely relies on the deposition of serum proteins on the surface of the bacterium due to the enhanced uptake of bacteria after treatment with complement containing serum [142]. It has also been shown that *Francisella* is ingested *via* a looped-coil mechanism that has only been observed in the *Francisella* infection model, suggesting the interaction of the host and pathogen is dependent on bacterial mechanisms that result in unique uptake of the bacteria [143]. Alternative proteins responsible for the unique uptake of *Francisella* have yet to be characterized, however the recent discovery of Type VI secretion machinery encoded in the *Francisella* genome offers promise for determining candidates for host cell manipulation [60, 85, 86]. *Francisella* has been shown to escape the phagosome into the cytosol within 60 minutes of ingestion where it is likely that the cells recognize the bacterium through interaction of unknown bacterial products and TLR2/TLR6 heterodimers [135, 137, 138]. This mechanism was shown *in vitro* in *Francisella* infected dendritic cells [107], as well as TLR2 knockout mice infected with *Francisella*, but there is evidence that *Francisella* interferes with downstream TLR signaling after TLR2 recognition [108, 129]. A study performed in macrophages treated with *Francisella* cell wall extracts and subsequently treated with highly toxic *E. coli* LPS showed no secretion of inflammatory cytokines by the treated cells,

indicating the ability of *Francisella* to interfere with innate mechanisms of bacterial recognition [129].

By far the most extensively studied innate immune response to *Francisella* is activation of the host inflammasome. The inflammasome is a multi-protein complex that is activated by nucleotide oligomerization domain (NOD-like receptors (NLRs)) that recognize intracellular pathogen components [144]. Upon binding of bacterial components, a cascade of protein oligomerization results in the activation of caspase-1, which leads to the secretion of pro-inflammatory cytokines and cellular apoptosis [144]. The eukaryotic inflammasome has been characterized through the study of many intracellular pathogens including *Salmonella* [145], *Shigella* [146], *Legionella* [147], and *Listeria* [148]. Recently a group found that macrophages lacking the absent in melanoma 2 protein (Aim-2) do not undergo inflammasome activation after infection with *Francisella*; suggesting the Aim-2 protein is required for intracellular recognition of *Francisella* [149, 150]. There is also evidence that the ultimate consequence of inflammasome activation, caspase-1 mediated cytokine release and cellular apoptosis, is interrupted *in vivo* due to a delay in apoptosis until late infection with highly virulent strains until immediately before death [140, 141].

The innate immune response to *Francisella* was studied in many different models with various strains of the bacteria. While results vary between the studies, the overall understanding is that highly virulent strains of *Francisella* avoid the innate immune response in the lungs, leading to dissemination of the bacteria to secondary sites of infection. Thus, there has been substantial effort

to engineer effective vaccines for *Francisella* to provide people immune memory in the case of an intentional release or laboratory or military personnel that are more likely to come in to contact with the bacteria.

### **1.3.2 Adaptive Immune Response and Vaccines**

In order to mount a protective adaptive response to infection the host must be able to survive the initial exposure to the pathogen long enough to produce antibodies and cells that develop memory of the pathogen. In general, a strong protective immunity does develop in both humans and animal models after survival of initial challenge with virulent strains of *Francisella*, however survival after infection with virulent strains is extremely inconsistent [37, 151]. Due to high antibody titers found in humans up to 11 years after survival of the initial infection, baseline antibody titers for laboratory researchers are commonly taken prior to work with the pathogens so that laboratory exposure can be diagnosed accurately [151]. In order to study the adaptive immune response to *Francisella* researchers have utilized less virulent and mutant strains so that host infection models used can consistently survive the initial infection and mount a protective response [152].

A live vaccine strain developed through the attenuation of a type B *holarctica* isolate via repeated passage through mice, and therefore retains its virulence in mice but not in humans, has been a valuable research tool for studying pathogenesis in BSL-2 laboratories [153-156]. The vaccine has been available for laboratory researchers and military personnel, although the genetic

basis of attenuation is poorly understood and different lots of the vaccine have showed mixed efficacy for both humans and animals which has prevented its licensing and use for the general public [157].

As previously mentioned, attenuated and mutated strains were most commonly studied in order to characterize the adaptive response to *Francisella*. LVS, *novicida*, and mutants of these strains were the most useful for these purposes [131-135]. In addition, there have been auxotrophic mutants and virulence factor mutants of highly virulent strains that showed efficacy against homologous challenge with wild type strains of highly virulent sub-species [47, 95, 96, 136-138, 158]. LVS and *novicida* strains that protect against homologous challenge tend to show inconsistent results when vaccinated animals are challenged with highly virulent strains. Therefore there is increased need for the development of a type A derived vaccine [130]. Transposon mutants of the Schu4 strain of *F. tularensis* passaged through immortalized hepatic cells identified 18 mutants deficient for intracellular survival, of which, 7 showed transposon insertion in genes of the purine biosynthesis pathway [115]. This led to the development of a purine auxotroph of Schu4 that showed 100% protective efficacy in mice against a lethal dose of wild type Schu4 [115, 124-126]. While this research has shows promise for the development of a live vaccine strain of *Francisella* that is derived from a type A strain, there has been little follow up on these original studies. Likewise, several studies have identified genes that are required for virulence that when mutated, are effective live vaccines in the mouse model [132, 159]. Yet, there has been a tendency to utilize information derived

from these studies to learn more about the bacteria's virulence rather than the development of a new vaccine strain for clinical trials.

Studies have identified cells and molecular requirements for a proper protective response to lethal challenge with *Francisella*. As previously mentioned, the majority of data about the adaptive immune response to *Francisella* relies mostly on attenuated strains due to the lethality of type A strains in animal and human models of infection. Effective vaccination in humans with LVS results in a very specific and long lasting IgM, IgA, and IgG antibody memory for up to 11 years [151]. The contribution of antibodies was also confirmed by protecting naive mice from type B infection through passive transfer of anti-type B antibodies [160]. Protection has been shown to rely on CD4 and CD8+ T-Cells [161, 162]. Depletion of either cell population resulted in the inability to control secondary lethal infection with LVS while wild type mice survived the same challenge [161, 162]. In contrast, natural infection and vaccination with type A subunit preparations primarily generates CD4+ and CD8+ memory T-cells rather than a strong antibody response [151, 163]. Interestingly, it was shown that low dose of type A infection in mice results in thymic atrophy and depletion of T-Cells, indicating that *Francisella* may avoid the cell mediated response by active T-Cell depletion [162]. The adaptive response is difficult to study as animal models die rapidly after infection with type A *Francisella*, and are unable to develop an adaptive response [133].

### **1.3.3 Global Transcriptional Response**

Pertinent to my project were several studies aimed to characterize the global host transcriptional response to *Francisella* and decipher the molecular mechanisms responsible for the host interaction with the pathogen. The focus of these studies was to understand the inability of the host to combat highly infectious strains as well as how the host survives infection with less virulent strains. The first studies were performed by Andersson *et al.* where one experiment examined the response to *Francisella* using the mouse model, while another used a human model of natural infection [140, 164, 165]. The first experiment monitored the murine transcriptional response to the type A clinical isolate FSC033 in whole lung homogenates over the course of infection with the main results demonstrating an overall delay in transcriptional response [140]. Interferon induced genes were active, however not until 4 days post infection [140]. In addition, the mean time to death was 5 days post infection, indicating the inability for the mice to mount a proper response to control the infection [140].

Using a mouse macrophage model the same group examined the transcriptional response to LVS [164]. An initial interferon-gamma and TNF-alpha mediated response was observed, however this response was subsequently down regulated after 4 hours of infection [164]. The initial recognition of the attenuated strain by mouse macrophages may explain the virulence difference observed in humans. Other studies have identified the interferon-gamma mediated immune response as necessary for survival of initial infection with *Francisella* with various strains of the bacteria [166-170]. In

addition, a study has shown that in human macrophages LVS infection induces significant cytokine production, while in mouse macrophages similar cytokine production was not observed [164, 171].

The third study conducted by Andersson *et al.* analyzed the transcriptional response of peripheral blood monocytes (PBMCs) from patients infected during an outbreak in an endemic area of Sweden [165]. Type B *holarctica* strains are endemic to the area and responsible for the outbreak. The patients all survived and recovered with the transcriptional response dominated by interferon-gamma mediated inflammatory response 2-3 days after infection [165]. Throughout patient monitoring however, there was generally a very modest overall response to infection [165]. A similar experiment conducted by Fuller *et al.* examined the transcriptional response of PBMCs of patients after vaccination with LVS [172]. The major finding of the study was a significant increase in DC activation with antigen processing and presentation 18-48 hours post infection with a subsequent down-regulation of these pathways [172]. Another study utilizing human PBMCs infected with LVS *in vitro* showed a strong interferon-gamma mediated response with a large increase in pro-apoptotic genes [173]. The difference between *in vitro* and *in vivo* models of infection has been noted before and may represent a significant issue when deriving information from cell culture models of *Francisella* infection studies.

The final studies conducted by Butcher and Cremer *et al.* used an *in vitro* model of infection of human PBMCs with both Schu4 and *F. novicida* comparing the host response to the two strains of *Francisella* [174, 175]. The first of two

studies noted a higher degree of inflammation induced by Schu4 initially while *F. novicida* induced these gene pathways later and in a more sustained fashion, indicating a down-regulation of the initial pro-inflammatory response by the more virulent strain [175]. The second study showed the autophagy pathway up-regulated by *F. tularensis* Schu4, possibly indicating a mechanism for the strain of higher virulence to escape continued activation of intracellular microbial recognition receptors that sense free living bacteria in the host cell cytoplasm [174]. Overall, the global transcriptional response indicates the importance of interferon-gamma signaling for mounting a protective response to *Francisella*, and a general down-regulation and evasion of the inflammatory response by highly virulent strains of the bacteria, particularly in the *in vivo* models of infection.



## 1.4: Tularemia

The worldwide incidence of tularemia is poorly understood and likely underestimated due to under reporting and misdiagnosis [37]. Cases were the highest in the years following World War II and have steadily declined since [37]. In a seven-year period between 1985 and 1992, there was an average of 171 cases a year in the United States with a fatality rate of 1.4%. Cases in the United States are sporadic while in Europe and Asia airborne outbreaks infecting hundreds of individuals have been reported [37].

### **1.4.1 Clinical Manifestations**

The clinical manifestations of tularemia depend on the route of infection. Ulceroglandular, glandular, oculoglandular, oropharyngeal, and pneumonic forms of tularemia have all been reported and studied in detail [37]. The most common forms of tularemia results from contact with infectious material and the bite of an infected tick [38]. The most common clinical manifestation is ulceroglandular tularemia and usually results when the bacteria disseminate from the site of infection (tick bite or contact with an open sore) to the regional lymph node [37]. The sore becomes suppurative and necrotic with significant edema surrounding the sore. The regional lymph node becomes inflamed, closely resembling the “bubos” observed in bubonic plague infection caused by *Yersinia pestis* [37].

In the case of contact with aerosolized *Francisella*, manifestations of tularemia would affect the eyes, upper digestive tract, and respiratory system. Cases of ocular and oropharyngeal tularemia have been observed and also lead

to glandular tularemia in the regional lymph nodes [37]. By far the most deadly form of tularemia is when the disease is contracted through the pulmonary route [37]. The disease closely resembles symptoms of the common cold or the flu and is not readily detectable through a chest x-ray [37]. The bacteria initially infect macrophages in the lungs and rapidly disseminates to the regional lymph nodes, blood, spleen, kidneys, and liver [37]. Monkeys infected *via* aerosol with Schu4 showed significant inflammation throughout the respiratory system within day 3 post-inoculation [176]. Upon dissemination, chemotherapeutic intervention strategies are extremely aggressive to treat the disease and prevent relapse [177, 178]. The largest reported outbreak of pulmonary tularemia was in a farming community in Sweden in 1966 and 1967 and affected over 600 people [179]. The strain responsible for the outbreak was from the less deadly *holarctica* subspecies and the majority of patients suffered high fever, chest pains, and flu like symptoms [179]. Although many patients complained of pneumonia like symptoms, the primary radiological finding was enlarged hilar lymph nodes but no fluid accumulation in the lungs [179]. Since the description of *Francisella* as an emerging pathogen in 2001 many molecular tools for diagnosis have been developed to rapidly confirm tularemia positive patients and type the strain to inform therapeutic treatment and patient prognosis.

### **1.4.2 Treatment of Tularemia**

When treating a disease that is caused by a pathogen of such extreme virulence, it is important that the infection is completely resolved before cessation of antibiotic treatment so there is no chance of relapse. Relapse was an issue during early studies of antimicrobials to combat *Francisella*. There have been many studies characterizing antimicrobial compounds against *Francisella*. Currently, the aminoglycoside family of antibiotics is used and effective against most cases of tularemia [37]. Streptomycin and gentamicin are the preferred antibiotics for the treatment of tularemia due to their bactericidal activity that clears the host of infection, thus significantly reducing relapse [37]. Tetracycline, doxycycline, and chloramphenicol have shown a higher rate of relapse when treating tularemia and therefore not considered first line therapeutics for treatment [37]. Use of these antibiotics is recommended for longer periods and commonly augmented with streptomycin or gentamicin to prevent relapse [37]. In addition to aminoglycosides, the fluoroquinolone ciprofloxacin was shown to have bactericidal activity against *Francisella* both *in vitro*, and in animals and is considered to be a frontline therapeutic, although it is still recommended that the treatment be augmented with an aminoglycoside especially in the case of infection with a type A strain of *Francisella* [37].

### **1.4.3 How Does *Francisella* Kill?**

One of the essential questions in the pathobiology of pulmonary intracellular pathogens is how respiratory infection leads to death. As previously mentioned, the mammalian respiratory system can clear up to  $10^5$  CFU of bacteria within 2 hours [134]. The ability of intracellular pathogens to evade clearance and disseminate to other areas of the body is essential to the pathogens' virulence, however it remains unclear as to how the pathogens actually kill their hosts. Organ congestion, toxin production, and uncontrolled cytokine response induced during systemic infection have all been implicated as mechanisms that bacterial pathogens induce death [180]. Evidence leading to these conclusions is commonly anecdotal. The term multi-organ failure is used to describe death caused by a viral pathogen and is often a general description for death caused by bacterial pathogens because of the inability to identify a single cause of death [180]. This event is characterized by break down of the endothelial structures throughout the body, organs, and blood vessels, leading to multiple organs ceasing function simultaneously [180]. What is important to gain from this is the understanding of critical phases of disease that can be targeted for therapeutic intervention. As previously mentioned, dissemination from the lungs is associated with poor outcome of disease with pulmonary pathogens. The lung can clear a large amount of material, so drugs designed to combat dissemination have positive outcomes on survival. Patients seek treatment at all stages of disease, therefore it is important to also examine disseminated disease as a landmark for therapeutic intervention. The bacterial metabolic profile likely

differs in tissues outside the lungs and thus will produce unique proteins for survival in those tissues. The identification of these metabolic capacities at different points of disease represent novel drug targets to combat the pathogen at the disseminated disease state. Finally, the identification of the host response near death also provides a unique stage of disease where therapeutic intervention can be used to combat the overwhelming release of compounds that results in multiple organ failure. Targeting the host during infection to boost defenses is not a new concept and can be adapted during the late stages of tularemia to avoid a catastrophic response that leads to death.

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## CHAPTER 2:

### Therapeutic Development using Host and Pathogen Responses

#### 2.1: Background

It was thought that the discovery of antibiotics would eradicate infectious disease, but it very shortly became understood that this would not be the case. As early as 1940, Abraham and Chain identified a bacterial enzyme able to hydrolyze beta-lactam rings and postulated that the enzyme could result in problems with penicillin as an antibacterial therapeutic [1]. A steady rise in antibiotic resistance has not reciprocated a steady rise in the development of new antibiotics to combat resistance. A shocking example of the constant need for novel antibiotics is linezolid, the only oxazolidinone on the market at the time, released in 2000 as a drug of “last resort” to treat infection with multi drug resistant gram-positive pathogens. Resistant strains were identified early the following year, demonstrating the rapid ability for bacterial pathogens to develop resistance to antibiotics [2]. The idea that the discovery of a compound that would globally eliminate infectious bacterial diseases is intrinsically flawed due to the laws of natural selection [3, 4]. Therefore novel therapeutics will need to be continuous development as diseases continue to persist and emerge.

### ***2.1.1 Drug Discovery Strategies and Evolution***

The primary strategy for developing drug targets and inhibitors has been described as a pipeline, with the idea of placing a target into one end and receiving an inhibitor at the other end through a series of high throughput, regimented steps to provide the most potent inhibitor for the least amount of cost and effort. In theory, the pipeline should provide a streamline, cost effective strategy for development of antibacterial drugs, however the reality is that it is time consuming and expensive to go from drug target to clinical therapeutic.

The 4 main targets of current antibacterials are the inhibition of cell wall and macromolecular synthesis, inhibition of DNA replication, inhibition of transcription, and inhibition of translation. These biochemical pathways are intuitively essential for bacteria to survive and cause infection. Many of the inhibitors targeting these pathways were derived from natural products and therefore remain a primary focus of antibiotic development leading to multiple and extreme drug resistance that the medical community has no answer to. The need for novel new drug targets is clear. Targeting virulence proteins, alternative biochemical pathways, and new targets within already exploited pathways need to be a priority to combat the growing threat of extremely resistant bacteria. Future studies are needed to identify new targets for inhibitors that act on other essential pathways in bacteria. Targeting virulence proteins for chemical inhibition can present problems when trying to develop broad-spectrum inhibitors. However general virulence protein systems such as Type III secretion, quorum

sensing, and two component signal transduction systems present targets that can treat many clinically relevant bacteria [5-9].

Several groups have studied alternative biochemical pathway inhibition with varying success. As this has been a goal for many years in the drug discovery field, biochemical pathways unique to bacteria and absent in mammals have been well described [10]. Cell division [11], lumazine/riboflavin biosynthesis [12], the isoprenoid biosynthesis pathway [13, 14], and phosphotransferase systems [10, 15] are all examples of biochemical pathways that have been identified as candidates for novel inhibitors. Enzymes in these pathways must fit criteria for further consideration such as drugability, essentiality, and whether or not the enzyme is at a metabolic “choke point,” [16-19]. Drugability refers to the enzymes binding properties at the active site and allosteric regions that bind co-factors or regulatory molecules that can be mimicked [18, 19]. To comprehensively study an enzyme’s drugability, a crystal structure of the protein is most desirable. Computational folding of novel proteins remains an extremely difficult process and does not yet represent a feasible mechanism for obtaining structural information from an enzyme that has not been crystallized. In the event that there is closely or distantly related orthologs or paralogs from other bacteria that have been crystallized, computer software is available to build homology models and create a virtual crystal structure for analysis of an enzyme’s drugability. A metabolic “choke point” is a point in a metabolic pathway that a unique substrate is acted upon or synthesized so that redundant enzymes from other pathways cannot complete the particular step in the pathway [10, 16,



19]. This criterion usually translates into an enzyme's essentiality for growth. In addition, enzymes that have products that feed into many different pathways ("load points") tend to be good candidates due to their essentiality to multiple biochemical pathways. Identifying "load point" enzymes relies on known biochemical pathways and enzyme interaction. Unfortunately, most bacterial genomes encode 30-40% of genes that have no known function. To prioritize the classification and functional characterization of unknown genes, studies to identify any given gene's essentiality to growth and the infection process are needed.

### **2.1.2 *In vitro* Potency Versus *In vivo* Efficacy**

One of the main issues facing the drug development field is translation from *in vitro* drug potency into drug efficacy in *in vivo* models. There are many potential reasons for this disconnect. Bioavailability of active compounds at the site of infection is often a problem due to serum binding of the drug, metabolic breakdown, and accumulation of the drug in physiologically irrelevant areas of the body. In addition, little is known about the metabolic requirements of bacterial pathogens during infection and *in vivo* efficacy relies on the drug target being produced during infection. This problem is most effectively dealt with through the use of alternative chemical formulations that more efficiently shuttle the compounds to the site of infection in their active form. The process of therapeutic development and formulation of compounds for better bioavailability

will be far more effective when augmented with studies that identify which genes are expressed and the most essential genes to the infection process.

## 2.2: Novel Target Development

### **2.2.1 Gene Essentiality in Drug Discovery**

One of the promising expectations of whole genome sequencing was the determination of a minimal gene set necessary for a bacterial cell to survive. While there is still much debate and discussion about the minimal gene set for a bacteria to merely survive, the study of bacterial pathogens is concerned with the minimal gene set necessary to cause disease. Comparative genomics using related strains of low and high virulence provides little insight into more complex mechanisms of virulence such as genome organization that affects transcriptional regulation. This has been the case in the *Francisella* field where strains of significantly different virulence share as much as 97% of their genome sequence [20]. The primary difference between these strains is the organization and orientation of the genomic sequence [20]. Therefore, study of the minimal gene set necessary to cause infection has relied on functional studies to determine genes essential to the infection process on a whole genome scale. Essentiality of bacterial genes has primarily been determined through insertion mutation libraries where genes that do not accumulate insertions are essential for bacterial survival. This technique has been extremely informative for identifying essential genes for survival as well as defining virulence factors in *Francisella*, however there are intrinsic biases that leave many essential genes unidentified. In addition to sequence bias of insertional elements [21], many strategies employ an outgrowth step that requires selection on synthetic media that can also bias the studies. A selection free method uses PCR amplification to synthesize a

cDNA library primed from the transposon sequence. The cDNA library is fluorescently labeled and hybridized to a full genome microarray to determine genes with transposon insertion [21]. This technique however cannot account for insertions that cause polar effects in non-coding regions of the genome that modify gene expression or protein functionality. Therefore, new methods for the global identification of essential genes and candidates for inhibition by novel chemotherapeutics must be developed.

Gene essentiality studies can also suffer from biases introduced when determining genes essential for growth *in vitro* as opposed to genes essential for growth *in vivo*. This dilemma was addressed in *Francisella* by using recovery assays that use a library of mutants to infect a cell line or animal model and recover bacteria that cause wild type disease [22, 23]. Genes that have mutations in the recovery pool are considered non-essential for infection, while genes with no insertional mutations are considered essential for the bacteria to cause infection. This assay in particular suffers from biases introduced by polar mutations that cause problems downstream with gene regulation and expression of open reading frames on the same cistron. A method for creating a mutant clone library without any of the aforementioned biases has yet to be described.

### **2.2.2 Bacterial Gene Expression in Drug Discovery**

Ever since the advent of microarrays, researchers have been trying to examine the transcriptional profile of pathogens grown in host infection models. Little advancement in the field can be attributed to the problem of separating and

isolating the bacterial RNA from the host RNA. In addition, amplification of the bacterial RNA is necessary due to the low abundance of RNA recovered introducing quantification error. Many different strategies for isolating the bacterial RNA have been attempted, including sheared genomic DNA as hybridization capture probes and chemical degradation of host RNA that preferentially destroys macrophage cells and RNA, leaving the bacteria intact [24-26]. The latter method has been effective for studying bacterial gene expression in *ex vivo* macrophage models for many bacterial infection models [27-30]. It is important to recognize that gene expression studies provide a simple “snap-shot” of genes being expressed at the moment of RNA isolation. Chemical degradation of host cells and RNA and subsequent centrifuge isolation of bacterial cells is very likely to affect the gene expression profile of the bacteria before the RNA is stabilized. Although *ex vivo* macrophage studies have been informative there are more complicated cellular interactions during *in vivo* infection that need to be defined. Numerous studies have characterized bacterial gene expression during *in vivo* infection. The first study isolated Group A *Streptococcus* RNA from bacteria swabbed from the pharyngeal tract of infected monkeys [31]. Analysis of both host and pathogen RNA correlated host and pathogen gene expression to identify pathways activated during the disease interaction. Two studies have examined the *in vivo* expression profile of *M. avium* subs. *paratuberculosis* isolated from the intestinal tracts of both sheep and cows [32, 33]. The most recent study used sheared *M. tuberculosis* genomic DNA as capture probes to isolate *M. tuberculosis* RNA from the lungs of infected

mice and sequenced the captured material using Illumina next generation sequencing technology. While this analysis takes advantage of the depth of coverage a next generation sequencing study provides, it still relies on outdated methods for capturing bacterial RNA from tissues and was published with focus on the technique rather than what the metabolic requirements of the bacteria are during the infection process.

### **2.2.3 Host Response in Drug Discovery**

In addition to developing novel methods for determining bacterial targets there has been an increased effort to understand the host response to infection in order to augment the host defenses to combat infections. By examining the host response, or lack thereof, drugs can be used to increase the chance of the host to mount a proper response to infection [34]. *Francisella* is generally thought of as a bacterium able to evade the host response in the lungs where it escapes to secondary organs, resulting in massive cytokine production and rapid death [35]. Importantly, *Francisella* is susceptible to many existing chemotherapeutics [35], however timely diagnosis is necessary to keep inhaled *Francisella* from spreading throughout the body. Administration of immunomodulatory drugs will vary depending on the state of disease, particularly in the case of pulmonary pathogens that disseminate to cause bacteremia throughout the body [34]. If properly characterized, there are distinct opportunities for therapeutic interventions to effectively treat primary and acute pulmonary tularemia. Previous studies using *Mycobacteria* have used strains of differing

virulence in order to understand the host response for the control of an infection [36]. *Francisella* has well defined strains of differing virulence that can be used to compare the host response to attenuated and highly virulent *Francisella*. Strains attenuated for dissemination from the lungs during pulmonary infection are prime candidates for comparing host response with highly virulent strains of *Francisella*. Identification of the important host events that lead to the control or dissemination of the infection will help define the landmarks of infection for various therapeutic intervention strategies. Once disseminated from the lungs, treatment must be potent enough to eliminate the bacteria completely from the body to prevent death and relapse. *Francisella* can cause acute disease with less than 50 live cells and therefore relapse has been an issue with effectively treating tularemia [35].

## 2.3: A look back

### **2.3.1: *The state of the field at the beginning***

Study of *Francisella* and the other select agents increased dramatically following the anthrax attacks of late 2001. Pathogens of extreme virulence have long been known for their capacity as bioweapons, however decommissioning of bioweapon programs and relatively low clinical significance led to a poor understanding of many of the select agents. Funding for the study of select agent presented an opportunity for many research groups to utilize methods to characterize more clinically relevant pathogens on poorly understood select agents. This led to a striking increase in the number of publications characterizing virulence mechanisms, animal models, vaccine studies, and genome sequences for select agents in the last decade. I joined Dr. Slayden's lab in February 2007 where the focus of the lab was novel therapeutic development against tuberculosis with a new grant to translate tools developed in the lab for the study of select agents.

The goal of my research has been to use existing and novel methods to identify genes essential to the infection process, while also monitoring host response to infection to identify landmarks for effective targeting of bacteria throughout the disease process. For highly pathogenic pulmonary pathogens such as *Francisella*, dissemination from the lungs to secondary sites of infection represents a key point in the infection where therapeutic efficacy drops dramatically. This observation was made in many models of infection, including



*Francisella*. Due to this observation, it was important to identify the host response during dissemination to *Francisella* strains of low and high virulence to understand host mechanisms responsible for the control of infection. The knowledge of the host response to *Francisella* was limited and primarily stemmed from studies aimed at characterizing highly immunogenic proteins for vaccine development. Importantly, there had been no studies at the time that characterized the global response to dissemination in *Francisella* strains of both high and low virulence.

After successful completion and publication of my first project, the next question to address was, what genes are active during the infection that may differ from those expressed in culture. Primarily, can the disconnect between *in vitro* potency and *in vivo* efficacy be explained by the fact that certain drug targets simply are not produced during the infection? For a bacterial protein to be classified as a candidate for drug targeting, it is important that the protein is not only essential for survival *in vitro* but also active and essential *in vivo*, during infection. The first step to understanding gene essentiality for the infection process is to examine the genes expressed by the bacteria during the infection. No group had previously been able to capture and label bacterial RNA isolated from host tissues for use on microarrays without extensive amplification steps to achieve sufficient material for study. The advent of next generation sequencing promised to make the identification of nucleic acid at extremely low abundance much more feasible. Using this technique, I was able to determine differences in gene expression not only between *F. tularensis* grown culture but tissue and time

dependent differences that reflect the adaptive response of the bacteria during early and late stages of the infection.

The next question to address was which of the genes expressed during infection were indeed essential and how do we comprehensively approach this question without having to engineer hundreds of mutant strains of bacteria. Dr. Slayden and I hypothesized that if subjected to saturation mutagenesis, a population of bacteria that survived mutagenic treatment would only have disruptive mutations in genes that were non-essential to the bacteria's survival. As previously mentioned, there are many biases introduced during insertional mutagenesis studies and we attempting to avoid those biases. Using a chemical mutagen, insertional biases are removed and by sampling a large population of bacteria, a genome wide examination of essential genes becomes relatively simple and fast. By using the next generation sequencing technology available at CSU the entire genome of *Francisella* can be examined for mutations with a high degree of confidence. This remains the only study to use these methods for identification of bacterial genes essential for survival and virulence.

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## CHAPTER 3

### Genetic identification of unique immunological responses in mice infected with virulent and attenuated *Francisella tularensis*

This chapter was adapted from the published work:

Kingry, L.C., et al., *Genetic identification of unique immunological responses in mice infected with virulent and attenuated Francisella tularensis*. *Microbes Infect*, 2011. **13**(3): p. 261-75.

#### **3.1 Introduction**

*F. tularensis* Schu4 and LVS were selected for these studies because of the known difference in virulence associated with these strains, which provides a model with which to assess differences in host interaction and response genes [1-5]. Schu4 and LVS belong to the *F. tularensis* subspecies *tularensis* and *holarctica* respectively [6, 7]. Subspecies *tularensis*, referred to as type A, represents the most virulent of the *Francisella* subgroups whereas subspecies *holarctica*, referred to as type B, tends to be less deadly in humans [8]. LVS is the vaccine strain of *F. tularensis*, which was derived from a less virulent type B isolate [7]. While *F. tularensis* LVS retains its virulence in mice, lethal infection requires challenge with greater than  $10^3$  CFU by the pulmonary route, whereas challenge with Schu4 causes a consistent lethal infection with fewer than  $10^2$



CFU [2, 4]. In addition time-to-death in the murine pulmonary infection model differs, with Schu4 infection typically resulting in death by 120 hours post infection, while LVS infected mice survive up to 14 days following infection [2, 4, 9, 10]

To understand how infection with virulent *F. tularensis* leads to a rapidly disseminating and lethal infection, studies have been performed in a variety of different infection models. *In vitro* studies aimed at characterizing the transcriptional response to *F. tularensis* using multiple cell types have revealed some insights into the host pathogen interaction [11-14]. Andersson *et al.* examined the whole lung transcriptional response to infection with type A *Francisella* isolate FSC033, and found limited host gene expression in the first 4 days of infection, suggesting a subversion of host recognition and delayed immune responses until immediately before death [11]. Schu4 mutant strains have also been used to assess host-pathogen interactions [15-18]. The mutant bacterial strains are generally less virulent in mouse models of infection. However, studies with mutant strains of *F. tularensis* have not yet been employed to study the overall host response to infection. Rather, they have been more instrumental in assessing the role of specific bacterial components in establishing infection leading to pathology in the lung.

Monitoring bacterial growth and dissemination along with pathology and *in vivo* transcriptional profiling of the host response to infection has provided important advances in understanding the host-pathogen interaction for organisms such as *Listeria* [19], *Mycobacteria* [20], and *Yersinia* [21]. Therefore, we believe

this is also an appropriate technique for assessing the host response to infection in the *F. tularensis* mouse model of infection. We have previously shown that *F. tularensis* dissemination from the lung to the spleen directly correlates with disease outcome. Therefore we have designed these studies to address the hypothesis that the host response to strains of high and low virulence that cause significant different disease outcomes, will differ. By identifying the host response to disseminated infection with *F. tularensis* strains of differing virulence we aimed to mechanistically understand the hosts inability to contain highly virulent strains of *F. tularensis* in the lung. In the present study, bacterial burden was monitored, pathology was assessed, and global gene expression was examined throughout the course of infection with *F. tularensis*, comparing infection with the Schu4 and LVS strains in a murine model. Here we report significant differences in pathology and regulation of expression of host immune response genes following infection with the Schu4 and LVS strains of *F. tularensis*.

## **3.2 Materials and Methods**

### **3.2.1 Bacterial strains**

*F. tularensis* Schu4 and LVS were provided by Dr. J. Petersen (Centers for Disease Control, Fort Collins, CO). Schu4 and LVS were cultured in modified Mueller-Hinton broth at 37 °C with constant shaking overnight, supplemented with 10% glycerol and aliquoted into 1 ml samples, frozen at -80 °C, and thawed just before use. Frozen stocks were titered by enumerating viable bacteria from serial dilutions plated on modified Mueller-Hinton agar as previously described [22]. The number of viable bacteria in frozen stock vials varied <5% over a 10-month period.

### **3.2.2 Mice**

Six week-old female C57BL/6 mice were purchased from Jackson Laboratories, Bar Harbor, Maine. All mice were housed in sterilized micro-isolator cages in the laboratory animal resources facility or in the Rocky Mountain Regional Biocontainment Laboratory BSL-3 facility at Colorado State University (Fort Collins, CO) and provided water and food *ad libitum*. All research involving animals was conducted in accordance with the Animal Care and Use Committee approved animal guidelines and protocols.

### **3.2.3 Murine models of infection**

Mice were infected with either *F. tularensis* Schu4 or *F. tularensis* LVS via intranasal (i.n.) or aerosol routes as described previously [23, 24] depending on

the objective of the study. For pathology, qRT-PCR, and bacterial burden studies mice were infected via intranasal route. Mice were anesthetized with ketamine-xylazine (100mg/kg-10mg/kg) and a 10  $\mu$ L inocula was administered to each of the nares in sequential droplets allowing mice to inhale the fluid (20  $\mu$ L total). Infected mice were monitored for morbidity twice daily and were euthanized at pre-determined endpoints. For global transcriptional profiling, mice were exposed to *F. tularensis* Schu4 or *F. tularensis* LVS by exposure in a Glas-Col Inhalation Exposure System (Glas-Col, Inc, Terre Haute, IN). Exposure was conducted by aerosolizing approximately  $3.5 \times 10^7$  CFU in a volume of 5 cubic feet over a period of 30 min, followed by a 20 minute period of cloud decay.

#### **3.2.4 Histopathology.**

C57BL/6 mice (n = 4 per group per time point) were infected i.n. with the *F. tularensis* Schu4 strain ( $10^2$  CFU) or the *F. tularensis* LVS strain ( $10^4$  CFU) and then sacrificed at 48 and 120 hours after exposure. Lung and spleen tissues were removed, divided and placed in 10% neutral buffered formalin for histopathology or in sterile PBS for bacterial quantification. Organs for histopathological examination were fixed, imbedded in paraffin, sectioned, and stained with hematoxylin and eosin.

#### **3.2.5 Bacterial quantification**

Samples of lung and spleen tissues were homogenized in 5 mL sterile PBS using a stomacher (Teledyne Tekmar, Mason, OH). Bacterial CFU per mL

of organ homogenate were determined by plating serial 10-fold dilutions of organ homogenates on modified Mueller-Hinton agar and incubating at 37 °C for 72 hours. qRT-PCR was carried out on RNA samples from the lungs using a 16s primer set and approach adapted from Cole *et al.* [25]. Relative detection of 16s molecules was determined using the  $\Delta$ CT method.

### **3.2.6 RNA Isolation and amplification**

RNA was stabilized and recovered from mouse organs by the addition of TRIzol reagent and organic partitioning. Total RNA was extracted from the TRIzol by the addition of chloroform (1:1) to achieve a bi-phase separation, then precipitated by the addition of isopropanol and subjected to Dnase treatment, and purified using a Qiagen RNeasy kit (Valencia, CA). Messenger RNA was converted to cDNA using poly(T) primers and amplified in the presence of modified dUTPs using the AminoAllyl Message Amplification Kit (Ambion, Foster City, CA). Indirect labeling of cDNA for hybridization was conducted by conjugating Cy3 dye with modified dUTPs in a subsequent reaction.

### **3.2.7 Microarray Scanning and Analysis**

Full mouse genome version 4.0.3 (Operon Biotechnology, Huntsville, AL) cDNA spotted microarrays were obtained from the Genomics Proteomics Core of the Rocky Mountain Regional Center of Excellence (<http://www.rmrce.colostate.edu/>). The 70mer oligonucleotide cDNAs were printed on polyamine coated slides (ArrayIt Corporation, Sunnyvale, CA) and post-processed by

UV cross linking and blocking with 10% BSA and 3X SSC at 42 °C. Dye coupled cDNA, was combined with yeast tRNA (10 mg/mL), and hybridization buffer (formamide, 20X SSC and 10% SDS) and heated. Single channel (Cy3) hybridization was carried out in triplicate for each sample. Slides were scanned using the Genepix 4000B (Molecular Devices, Sunnyvale, CA) fluorescent scanner and analyzed using Genepix Pro 6.0 software. Background fluorescence was corrected for by subtracting background from foreground intensity values. Technical replicates were averaged before normalizing to the global mean intensity values from the entire data set. Log transformation, t-test, ANOVA, principal component analysis and Benjamini and Hochberg false discovery correction were applied to the data using the Genesifter software (Geospiza, Seattle, WA). Genes considered to be differentially expressed were induced or repressed by 1.5 fold or higher and had a p-value of 0.01 or lower. Clustering was conducted using Cluster software [26] ([http://rana.lbl.gov/eisen/?page\\_id=42](http://rana.lbl.gov/eisen/?page_id=42)). Functional enrichment analysis was conducted using the DAVID Bioinformatics Database [27, 28] (<http://david.abcc.ncifcrf.gov/>). Response to each strain was then compared to controls to examine changes in expression of genes during the progression of the infections. The complete dataset is available through the Gene Expression Omnibus (GEO) database using accession # GSE22203.

### **3.2.8 qRT-PCR**

Quantitative real time PCR was used to assess bacterial burden in infected tissues, validate microarray data, and monitor molecular markers of disease. Briefly, cDNA synthesis from total RNA was carried out using First Strand cDNA Synthesis Kit (Invitrogen, Carlsbad, CA). Briefly, 1 mg of total RNA was combined with random hexamer and oligo (dT) primers and heated in 10ml total volume for 5 minutes. 10  $\mu$ L of buffered enzyme mix (2  $\mu$ L 10X buffer, 4  $\mu$ L  $MgCl_2$  (6 mM), 2  $\mu$ L DTT (0.1 M), 1  $\mu$ L RNase out, and 1  $\mu$ L Superscript<sup>tm</sup>) was added and incubated at 25 °C for 10 minutes, 50 °C for 50 minutes, and 85 °C for 5 minutes. Platinum SYBR Green qPCR Supermix-UDG (Invitrogen, Carlsbad, CA) was combined with gene specific primers (5nmol) and 50ng of template (cDNA) and run in triplicate on an IQ5 thermocycler (Bio-Rad, Hercules, CA). The transcripts encoding 18S rRNA, GapDH, and  $\beta$ -actin were used to monitor consistency in biological replicates. Other genes described in the text were employed to confirm the expression trends identified by microarray analysis. Resulting data from each condition was compared to controls in an independent fashion using the  $\Delta$ CT method.

### **3.3 Results**

#### **3.3.1 Dissemination and pathology in the lung and spleen following infection**

To assess possible differences in dissemination to the spleen, and pathology between *F. tularensis* strains Schu4 and LVS, mice were infected by the intranasal route. The intranasal route of infection was chosen for the dissemination and pathology studies in order to facilitate equalizing the bacterial burden in the lungs at the 48h time point. To accomplish this, it was necessary to accurately administer higher challenge doses of *F. tularensis* LVS than for *F. tularensis* Schu4. In addition, we also employed a higher intranasal challenge dose of *F. tularensis* LVS because there was minimal lung pathology noted when mice were subjected to low-dose aerosol challenge with *F. tularensis* LVS (data not shown). Accordingly, by assuring that mice had equivalent bacterial burdens at the appropriate time points after infection, we were able to directly compare the efficiency of bacterial dissemination from the lungs and the associated organ pathology.

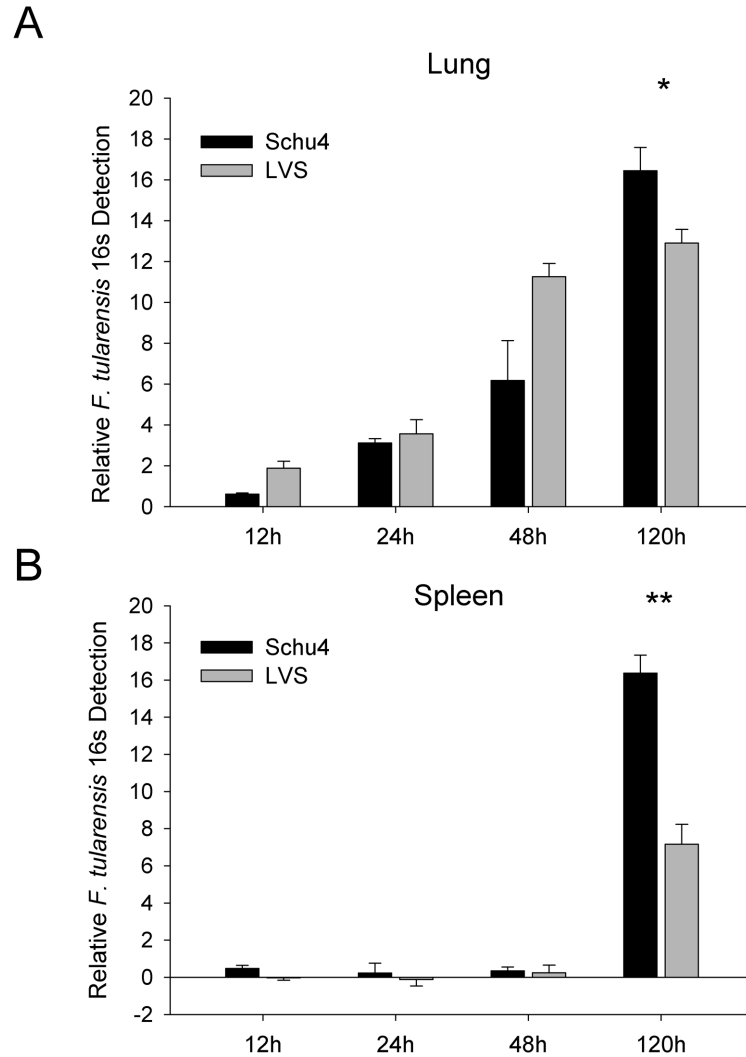
Bacterial load in lung and spleen tissue at different times of infection was determined by molecular detection of *F. tularensis* 16S RNA and confirmed by direct plating of organ homogenates for *F. tularensis* colony detection. At 24 hours after inoculation, the bacterial load of Schu4 and LVS in the lungs was similar based on 16S RNA (Figure 1A) and colony counting. For example, the lungs contained  $4.4 \pm 0.30 \text{ Log}_{10} \text{ CFU}$  Schu4 and  $4.9 \pm 0.30 \text{ Log}_{10} \text{ CFU}$  LVS at 24 hours of infection. In contrast, by 120 hours of infection, there was a



significantly higher bacterial load in the lungs of mice infected with Schu4 ( $8.6 \pm 0.09 \text{ Log}_{10} \text{ CFU Schu4}$  versus  $7.3 \pm 0.49 \text{ Log}_{10} \text{ CFU LVS}$ ). Although the bacterial load in the spleen was relatively low, Schu4 was detectable by 16S RNA as early as 24 hours after infection, while LVS was not detectable by 16S RNA until 48 hours after infection (Figure 1B). At 120 hours after infection, Schu4 and LVS were detected in the spleen, though the splenic bacterial burden was significantly ( $p < 0.001$ ) higher in Schu4 infected mice ( $8.3 \pm 0.26 \text{ Log}_{10} \text{ CFU Schu4}$  versus  $5.8 \pm 0.28 \text{ Log}_{10} \text{ CFU LVS}$ ). Overall, Schu4 demonstrated greater growth in the lungs, quicker dissemination to the spleen, and more rapid growth in the spleen compared to LVS. This observation is consistent with the known, more rapid disease progression and virulence of Schu4 compared to LVS [2, 4]. Further these data suggest that rapidity of dissemination to secondary sites is related to the extent of infection in the lungs. Spleen tissues from *F. tularensis* Schu4 and LVS infected mice collected 48 hours after infection were histologically unremarkable and indistinguishable from spleens of uninfected animals (Figure 2A, B). By 120 hours after infection (Figure 2C), spleens from *F. tularensis* LVS infected mice had mild lymphocyte depletion of the white pulp and multifocal accumulations of granulocytes and macrophages in the red pulp, with little evidence of necrosis. In contrast, spleens from *F. tularensis* Schu4 infected mice had almost complete destruction of parenchymal structures due to diffuse severe necrosis, fibrin-deposition and massive lymphocyte depletion. The marked increase in spleen pathology in *F. tularensis* Schu4 infected mice was

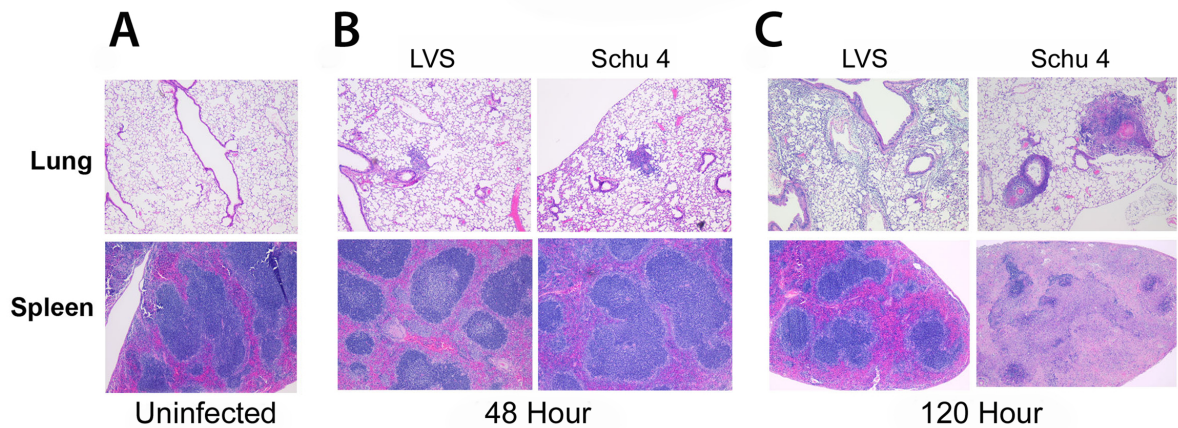
the most notable histological difference between infections caused by the two strains of bacteria.

Figure 1



**Figure 1.** Time-course of lung and spleen bacterial burden in mice infected with *F. tularensis* Schu4 and LVS. C57BL/6 mice (n = 4 per group) were inoculated i.n. with lethal doses of *F. tularensis* Schu4 ( $10^2$  CFU) or LVS ( $10^4$  CFU), as described in Methods. Lung and spleen tissues were collected 12, 24, 48 and 120 hours after infection and homogenized in TRIzol or PBS for isolation or total RNA or CFU enumeration, error bars represent standard deviation of all 4 samples. (A) *F. tularensis* 16s rRNA detection in the lungs of mice infected with Schu4 and LVS. (B) *F. tularensis* 16s rRNA detection in the spleens of mice infected with Schu4 and LVS. Data show similar growth trends through 48 hours in the lung, whereas 120 hours post infection Schu4 shows statistically significantly higher numbers in both the lung and spleen. Data from each time point was subjected to students T-test, (\*)= $p < 0.01$ , (\*\*)= $p < 0.001$ .

Figure 2



**Figure 2.** Time-course of lung and spleen pathology in mice infected with *F. tularensis* Schu4 and LVS. C57BL/6 mice (n = 4 per group) were inoculated i.n. with lethal doses of *F. tularensis* Schu4 ( $10^2$  CFU) or LVS ( $10^4$  CFU), as described in Methods. Lung and spleen tissues were collected 48 hours or 120 hours after infection and processed with hematoxylin and eosin staining for histopathological examination. (A) Histology from the lung and spleen of control (uninfected) mice. (B) Histology from the lung and spleen 48 hours post-infection with Schu4 or LVS. (C) Histology from the lung and spleen 120 hours post-infection with Schu4 or LVS. Pathological changes at 48 hours after infection were mild in both the lungs and spleen and indistinguishable between *F. tularensis* Schu4 and LVS infected mice. At 120 hours after infection, more severe lesions were noted in the lungs and especially the spleens of *F. tularensis* Schu4 infected mice, compared to LVS infected mice. Image magnification was 40X for all images displayed.

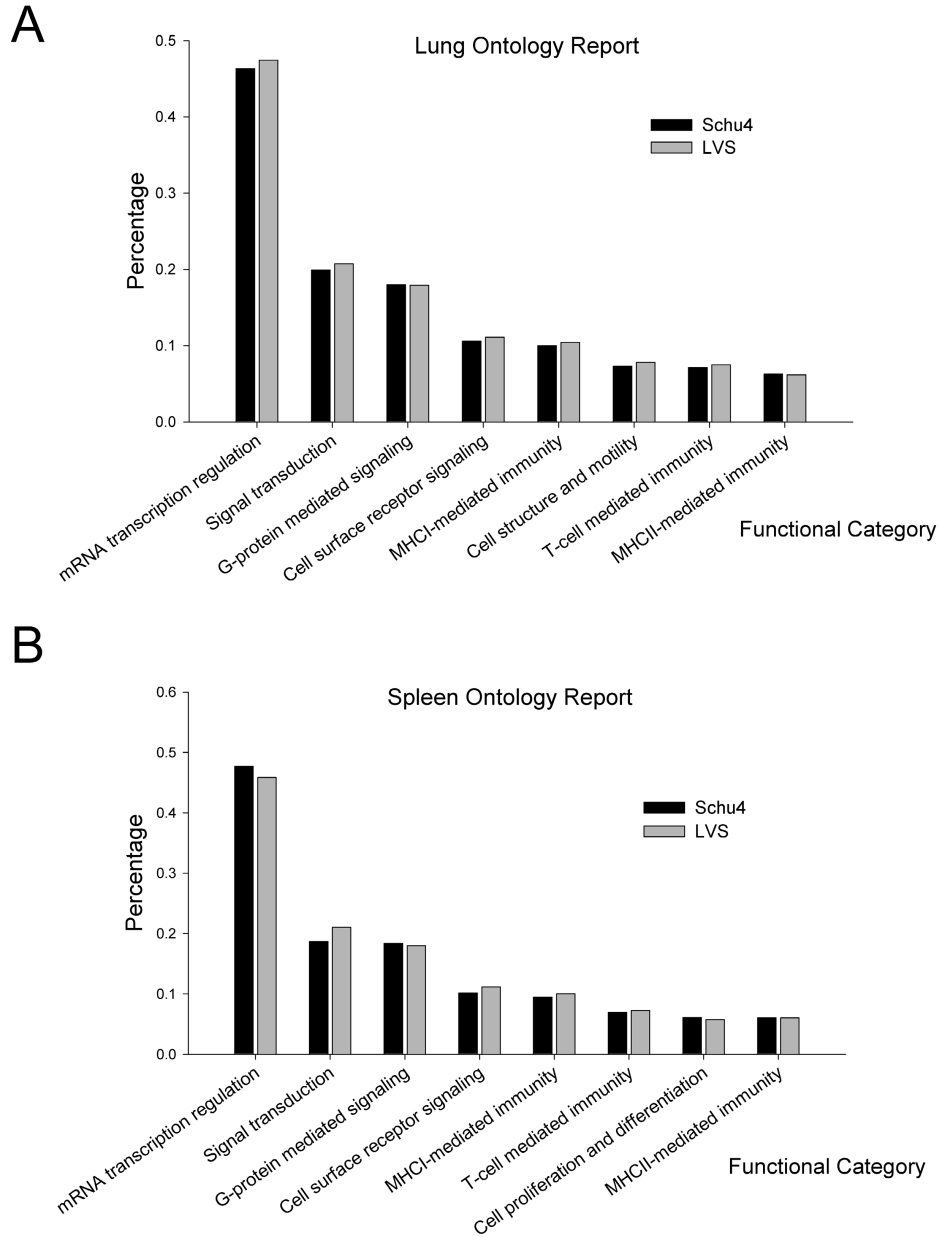
### 3.3.2 Common trends in the host response to *F. tularensis* Schu4 and LVS infection

Whole genome transcriptional profiling of lungs and spleen tissues collected at 12, 24, 48, and 120 hours of infection from mice infected *via* aerosol with Schu4 or LVS was conducted to investigate the global host response to infection with each bacterium. Low dose aerosol inoculation was used for the transcriptional studies in mice because this route is believed to more closely

approximate human infection by inhalation of *F. tularensis* than other routes of infection. Genes that were considered to be differentially regulated had a variance <0.01 (ANOVA) and were up or down-regulated > 1.5 fold compared to uninfected mice. The complete dataset is available through the Gene Expression Omnibus (GEO) Accession # GSE22203.

The total number of differentially expressed genes in the lung and spleen paralleled the bacterial burden. Infection with Schu4 resulted in differential regulation of 3,958 and 5,442 genes in lungs and spleen respectively, compared to uninfected mice. A similar range of differences in global responses was also observed in LVS infected mice, which resulted in 2,230 differentially regulated genes in the lungs and 9,388 differentially modulated open reading frames in the spleen. Global gene expression response data from all time points of infection with Schu4 and LVS were interrogated to identify ontologies and pathways that were over-represented in the host response to infection (Figure 3A and 3B). Genes associated with inflammation, host-pathogen interactions, cellular activation/differentiation, host antimicrobial activity, and leukocyte receptor signaling constituted the majority of the host response to infection with both strains of *F. tularensis* (Table 1).

Figure 3



**Figure 3. Functional enrichment of global transcriptional response data.** C57BL/6 mice (n = 2 per group) were inoculated via aerosol with lethal doses of *F. tularensis* Schu4 or LVS ( $10^4$  CFU), as described in Methods. Total RNA from the lung and spleen tissues was collected 12, 24, 48 and 120 hours post infection, converted to cDNA, labeled and hybridized on full mouse genome microarrays. (A) Ontology analysis showing select functional categories relevant to infection in the lung in response to infection with Schu4 or LVS. (B) Ontology analysis showing select functional categories relevant to infection in the spleen in response to infection with Schu4 or LVS. Genes with a p-value < 0.01 and differentially regulated > 1.5 fold were used for clustering and ontology analysis.

**Table 1: Genes with similar expression patterns in *F. tularensis* Schu4 and LVS infection**

**Lung**

Gene ID	Annotation	Accession	<i>Schu4</i> Infection				<i>LVS</i> Infection			
			12h	24h	48h	120h	12h	24h	48h	120h
<b>I. Inflammatory Response</b>										
Ccl25	Chemokine (C-C motif) ligand 25	NM_009138	-	1.94	-	-	-	2.47	-	-
Chi31	Chitinase 3-like 1	NM_007695	3.92	3.84	4.03	-	2.54	-	-	-
Chi34	Chitinase 3-like 4	NM_145126	-	-	-	2.33	-	2.87	-	-
Csf2	Colony stimulating factor 2 (granulocyte-macrophage)	NM_009969	-	-	-1.57	-	-	-	-1.60	-
Cxcl14	Chemokine (C-X-C motif) ligand 14	NM_019568	-	-	-1.97	-1.58	-	-	-	2.48
Cxcr7	Chemokine (C-X-C motif) receptor 7	NM_007722	-1.50	-2.18	-	-	-	-2.59	-	-
Il10ra	Interleukin 10 receptor, alpha	NM_008348	-	-1.73	-	-	-	-1.98	-	-
Il10rb	Interleukin 10 receptor, beta	NM_008349	-	-	-	-3.35	-	-1.81	-	-
Il18bp	Interleukin 18 binding protein	NM_010531	-	-	-	3.34	-	-	-	3.07
Il1b	Interleukin 1 beta	NM_008361	-3.22	-2.32	-	-2.18	-	-2.95	-2.46	-
Il33	Interleukin 33	NM_133775	-2.13	-1.80	-	-3.36	-	-2.01	-	-
Il9r	Interleukin 9 receptor	NM_008374	-	-	-	-2.46	-	-1.85	-	-
<b>II. Cellular Activation/Differentiation</b>										
Cd109	CD109 antigen	NM_153098	-	-	-2.24	-	-	-	-	-
Cd2	CD2 antigen	NM_013486	-	-	2.16	-	-	2.06	-	2.03
Cd55	CD55 antigen	NM_010016	-	-2.67	-	-	-	-2.20	-	-
Cd63	Cd63 antigen	NM_007653	-	3.09	2.72	-	-	-	2.16	-
<b>III. Antimicrobial Activity</b>										
Mmp8	Matrix metalloproteinase 8	NM_008611	-	-	-	3.60	-	-	-	1.64
Timp1	Tissue inhibitor of metalloproteinase 1	NM_011593	-	-	-	2.61	-	-	-	3.86
<b>IV. Leukocyte Receptors</b>										
Klra22	Killer cell lectin-like receptor subfamily A, member 22	NM_053152	-	-	-1.36	-2.38	-	-	-	1.94
<b>V. Cell Signaling</b>										
Ptger1	Prostaglandin E receptor 1 (subtype EP1)	NM_013641	-	-	-	2.59	-	-	2.43	-

**Spleen**

Gene ID	Annotation	Accession	Schu4 Infection				LVS Infection			
			12	24	48	120	12	24	48	120
<b>I. Apoptosis</b>										
<i>Aifm1</i>	Apoptosis-inducing factor, mitochondrion-associated 1	NM_012019	-	-	-1.82	-3.97	-	-1.78	-1.82	-3.08
<i>Bnip2</i>	BCL2/adenovirus E1B interacting protein 1, NIP2	NM_016787	-1.74	-2.28	-1.83	-3.01	-	-1.75	-1.66	-2.55
<i>Bnip3l</i>	BCL2/adenovirus E1B interacting protein 3-like	NM_009761	-	-	-	-3.11	-	-	-	-3.58
<i>Casp7</i>	Caspase 7	NM_007611	1.70	-	-	-	-	-	1.77	-
<i>Pdcd2</i>	Programmed cell death 2	NM_008799	-	-	-	-2.36	-	-	-	-2.37
<b>II. Inflammatory Response</b>										
<i>Ccl21b</i>	Chemokine (C-C motif) ligand 21b	NM_011124	-	-	-	-3.11	-	-	-	-2.00
<i>Ccr2</i>	Chemokine (C-C motif) receptor 2	NM_009915	-	-2.47	-	-3.87	-	-1.69	-	-2.51
<i>Ccr6</i>	Chemokine (C-C motif) receptor 6	NM_009835	-	-	-	-3.67	-	-	-	-2.34
<i>Ccr8</i>	Chemokine (C-C motif) receptor 8	NM_007720	-	2.22	-	1.76	-	-	-	1.79
<i>Cx3cr1</i>	Chemokine (C-X3-C) receptor 1	NM_009987	-	-	-	-4.28	-	-	-	-2.39
<i>Cxcl3</i>	Chemokine (C-X-C motif) ligand 3	NM_203320	-	-	-	2.38	-	-	-	2.21
<i>Il10</i>	Interleukin 10	NM_010548	-	-	2.65	-	-	-	1.72	-
<i>Il10rb</i>	Interleukin 10 receptor, beta	NM_008349	-1.83	-	-	-3.44	-	-	-	-3.69
<i>Il17a</i>	Interleukin 17A	NM_010552	-	-	-	-2.68	-	-1.97	-	-1.96
<i>Il18bp</i>	Interleukin 18 binding protein	NM_010531	-	-	-	2.84	-	-	-	1.58
<i>Il18rap</i>	Interleukin 18 receptor accessory protein	NM_010553	-	-1.61	-	-1.54	-	-	-1.74	-
<i>Il1b</i>	Interleukin 1 beta	NM_008361	-	-	-	1.75	2.03	-	-	-2.10
<i>Il22</i>	Interleukin 22	NM_016971	-	-	-	3.24	-	-	-	2.78
<i>Il3</i>	Interleukin 3	NM_010556	-	-	-	3.41	-	-	-	2.37
<i>Tgfb1</i>	Transforming growth factor, beta 1	NM_011577	-	-	1.83	-	-	-	-	1.75
<b>III. Cellular Activation/Differentiation</b>										
<i>Cd163</i>	CD163 antigen	NM_053094	-	-	-	-2.27	-	-	-	-1.74
<i>Cd300a</i>	CD300A antigen	NM_170758	-	-	-	-3.31	-	-	-	-2.12
<i>Cd34</i>	CD34 antigen	NM_133654	1.87	-	2.43	2.72	-	-	2.42	2.46
<i>Cd37</i>	CD37 antigen	NM_007645	-	2.01	-	-	-	-	2.99	-
<i>Cd48</i>	CD48 antigen	NM_007649	-	-	-	-1.73	-	-	-	-1.74
<i>Cd63</i>	Cd63 antigen	NM_007653	-	-	-	3.61	-	-	1.84	-
<i>Cd74</i>	CD74 antigen	NM_010545	-	2.84	-	-	-	-	2.66	-
<i>Cd79b</i>	CD79B antigen	NM_008339	-	1.64	-	-	-	-	-	-2.01
<i>Cd83</i>	CD83 antigen	NM_009856	-	1.67	-	-	-	1.77	1.61	-
<i>Cd86</i>	CD86 antigen	NM_019388	-	-1.74	-	-2.58	-	-	-	-3.04
<i>Cd97</i>	CD97 antigen	NM_011925	-	-	-	-1.74	-	-	-	-1.97
<b>IV. Antimicrobial Activity</b>										
<i>Adamts1</i>	A disintegrin-like and metalloproteinase thrombospondin type 1 motif, 1	NM_009621	-	-	-	3.58	-	-	-	2.22

C9	Complement component 9	NM_013485	-1.55	-	-	-2.65	-	-1.68	-1.52	-1.99
F5	Coagulation factor V	NM_007976	-	-1.74	-	-3.14	-	-	-2.05	-
<b>V. Leukocyte Receptors</b>										
<i>H2-Ab1</i>	Histocompatibility 2, class II antigen A, beta 1	NM_207105	-	3.02	-	-	-	-	4.07	-
<i>H2-BI</i>	Histocompatibility 2, blastocyst	NM_008199	-	-	-	2.55	-	-	2.03	-
<i>H2-M10.2</i>	Histocompatibility 2, M region locus 10.2	NM_177923	-	-	-	-1.82	-	-2.39	-	-
<i>H2-M3</i>	Histocompatibility 2, M region locus 3	NM_013819	-	-	-	3.81	-	-	2.84	3.31
<i>H2-Q8</i>	Histocompatibility 2, Q region locus 8	NM_207648	-	-	-	2.75	-	-	1.98	2.30
<i>Klra1</i>	Killer cell lectin-like receptor, subfamily A, member 1	NM_013793	-1.90	-3.63	-	-3.82	-2.53	-2.45	-1.67	-3.69
<i>Klra10</i>	Killer cell lectin-like receptor subfamily A, member 10	NM_008459	-	-2.88	-	-2.77	-2.48	-2.07	-	-
<i>Klra21</i>	Killer cell lectin-like receptor subfamily A, member 21	NM_010650	-	-2.18	-	-2.16	-2.75	-	-	-1.87
<i>Klra22</i>	Killer cell lectin-like receptor subfamily A, member 22	NM_053152	-	-2.10	-	-3.82	-	-	-	-3.72
<i>Klra18</i>	Killer cell lectin-like receptor subfamily A, member 18	NM_053153	-	-	2.99	3.12	-	-	-	2.14
<i>Klre1</i>	Killer cell lectin-like receptor family E member 1	NM_153590	-	-2.83	-	-	-1.82	-2.91	-1.90	-3.95
<i>Pecam1</i>	Platelet/endothelial cell adhesion molecule 1	NM_008816	-	-	-	1.82	-	-	-	1.54
<b>VI. Signaling</b>										
<i>Irf2</i>	Interferon regulatory factor 2	NM_008391	-	-	1.66	3.12	-	-	-	2.79
<i>Lck</i>	Lymphocyte protein tyrosine kinase	NM_010693	-	-	-	-3.93	-	-	-	-4.10
<i>Ltc4s</i>	Leukotriene C4 synthase	NM_008521	-	-	-	3.72	-	-	-	3.87
<i>Ptger1</i>	Prostaglandin E receptor 1 (subtype EP1)	NM_013641	-	-	2.37	-	-	-	-	3.94

Table 1: C57BL/6 mice (n = 2 per group) were inoculated via aerosol with lethal doses of *F. tularensis* Schu4 or LVS (10<sup>4</sup> CFU), as described in Methods. Total RNA Lung and spleen tissues were collected 12, 24, 48 and 120 hours post infection, converted to cDNA, labeled and hybridized on full mouse genome microarrays. Genes with a p-value < 0.01 and differentially regulated > 1.5 fold were mined for genes common to each infection that fell into the categories of inflammatory response, cellular activation/differentiation, antimicrobial activity, leukocyte receptors, and cell signaling.

Infection with either strain resulted in the down-regulation of *Il-1β* expression immediately following infection in the lungs. *Il-1β* is a potent inflammatory cytokine and its suppression may be a key mechanism in *Francisella* infection. Upregulation of *Tgfβ1* and *Ptger1* expression was noted



48 hours post infection in Schu4 infected mice, and expression of these immunosuppressive cytokines may be key to the rapid dissemination of Schu4. For example, *Tgfβ1* and *Ptger1* have both been shown to play a role in the suppression of host defenses in the lungs of LVS infected mice and in human dendritic cells infected with Schu4 [29, 30]. There was also altered expression of several MHC genes and the killer cell lectin-like receptor family genes, including (*Ly49/Klra*) and *H2-Ab1*, *H2-BI*, *H2-M10.2*, *H2-M3*, *H2-Q8*. The *Ly49/Klra* killer cell lectin-like receptors have been shown to be vital for recognition and activation/inhibition of natural killer cells [31, 32]. The fact that Schu4 and LVS infection both decreased the expression of these receptors adds further evidence to the notion that *F. tularensis* evades the host innate immune response by suppressing key mediators of this response.

### **3.3.3 Differences in host response to infection with Schu4 and LVS**

Although the overall host response to infection with *F. tularensis* Schu4 and LVS is similar, unique host transcriptional responses to infection with Schu4 or infection with LVS infection were identified. Further inspection of the transcriptional response to Schu4 revealed notable differences in the transcription of immunologically important genes relative to their expression in LVS-infected mice. These differentially expressed genes included genes encoding components involved in apoptosis, antimicrobial activity, inflammatory response, cellular activation and differentiation, leukocyte receptors, and cell signaling (Table 2, See Appendix I for full list of genes uniquely expressed).

Genes associated with apoptosis and antimicrobial activity had different expression patterns in Schu4 as compared to LVS and uninfected mice. For example, expression of the pro-apoptotic genes *Bad*, *Bnip2*, *Bnip3l*, *Pdcd2*, *Pdcd4* and *Pdcd6*, and the anti-apoptotic genes *Bcl2* was repressed in Schu4 infected lungs compared to LVS-infected lungs. Similarly, in the spleen there was also repression of *apitd1*, *Bclaf1* and *Casp6* expression. Inhibition of apoptosis has been shown to be an important mechanism for replication and survival during infection of other bacteria such as *C. burnetii* [33-35].

The antimicrobial activity response in the lungs of *F. tularensis* Schu4 infected mice was dominated by altered expression of *Adam2* and *Adam9*, cathepsin D, L, S and Z, thrombomodulin, thrombospondin 1 and 2, and *Timp3*. In the spleen, *Adam15*, *Defb1*, and *Defb21* showed increased expression, while cathepsin B, D and E had significantly reduced expression. The transcriptional response of these genes indicated a reduction in tissue remodeling and breakdown, intracellular protein metabolism, and breakdown of antigenic proteins for MHC-II presentation. Defensins are intrinsically antimicrobial but the isoforms induced during infection have been shown to have little effect on *Francisella* using human alveolar cells *in vitro* [36].

The transcription of *CD4*, *CD52*, *CD74* (Ii, Invariant chain), and B lymphocyte markers *CD37* and *CD79B* (*Igb*) involved in cellular activation and differentiation were uniquely upregulated in Schu4 infection. The increased expression of these particular components involved in MHC-II antigen presentation is consistent with augmented cell-mediated immunity. As antigen

presentation is a tightly regulated process [37], these data in addition to the cathepsin data above may implicate *F. tularensis* induced alterations in processing and presentation of antigens during infection with *F. tularensis* Schu4.

There were also important differences in the molecular mediators of the inflammatory response in mice infected with Schu4 compared to LVS infected mice. Expression of the genes for *IL-13*, *IL-13Ra2*, *CCL2*, *CCL6*, *CCL22*, and *CXCL10* were only induced in the lungs of Schu4 infected mice. Upregulated expression of *IL-13* is important because of its role as a Th2 related cytokine, which can be associated with downregulation of Th1 immunity. Upregulation of the chemokine genes suggests that Schu4 infection may lead to increased recruitment of monocytes. A similar trend of altered expression of cytokines and chemokines, specifically *IL-13*, *CCL3*, *CCR3*, *CCR5*, interferon activated genes, prostaglandin D2 synthase 2, prostacyclin I2, prostaglandin reductase 2, and several Ly6-family genes was observed in the spleen of Schu4 infected mice, albeit at later time points of infection. Interferon activated gene families as well as prostaglandin signaling has been shown to be involved in the response to virulent *Francisella* [9, 38]. We found similar involvement of these pathways in response to Schu4 infection in the mouse spleen. Interestingly, the expression of the T-helper 2 type interleukin *IL-13*, *anti-inflammatory cytokines IL-10 and TGFb*, and the down regulation of the proinflammatory cytokines *IL-18* and interferon alpha suggest a disruption in the activation of the protective defenses in Schu4 infection compared to LVS infection.

**Table 2: Unique genes differentially expressed in response to *F. tularensis***

**Schu4 discussed in the text**

**Lung**

Gene ID	Annotation	Accession	Hours Post-Infection			
			12	24	48	120
<b>I. Apoptosis</b>						
Anxa5	Annexin A5	NM_009673	-	3.49	3.79	-
Bad	Bcl-associated death promoter	NM_007522	-	-	-	-2.55
Bbc3	Bcl-2 binding component 3	NM_133234	2.34	-	-	2.69
Bcl2	B-cell leukemia/lymphoma 2	NM_177410	-	-1.96	-2.34	-
Bclaf1	BCL2-associated transcription factor 1	NM_153787	1.93	-	-	-
Bnip1	BCL2/adenovirus E1B interacting protein 1, NIP1	NM_172149	-	1.58	1.77	-
Bnip2	BCL2/adenovirus E1B interacting protein 1, NIP2	NM_016787	-2.20	-	-	-4.24
Bnip3l	BCL2/adenovirus E1B interacting protein 3-like	NM_009761	-	-	-	-3.56
Pdcd2	Programmed cell death 2	NM_008799	-1.85	-2.07	-1.94	-
Pdcd4	Programmed cell death 4	NM_011050	-	-	-	-3.34
Pdcd6	Programmed cell death 6	NM_011051	-	-	-	-2.76
<b>II. Inflammatory Response</b>						
Ccl2	Chemokine (C-C motif) ligand 2	NM_011333	-	-	-	3.67
Ccl22	Chemokine (C-C motif) ligand 22	NM_009137	-	1.93	2.04	-
Ccl6	Chemokine (C-C motif) ligand 6	NM_009139	-	-	1.86	-
Ccr6	Chemokine (C-C motif) receptor 6	NM_009835	-	-	-	-3.27
Cxcl10	Chemokine (C-X-C motif) ligand 10	NM_021274	-	-	-	1.84
Ifna1	Interferon alpha 1	NM_010502	-	-	-	-3.15
Il13	Interleukin 13	NM_008355	-	1.80	-	-
Il13ra2	Interleukin 13 receptor, alpha 2	NM_008356	2.11	-	-	-
Il18	Interleukin 18	NM_008360	-	-1.56	-	-
Il1r2	Interleukin 1 receptor, type II	NM_010555	-	-	-	2.28
Sdf2	Stromal cell derived factor 2	NM_009143	-	-	-	-1.96
Tgfr2	Transforming growth factor, beta receptor II	NM_009371	-	-	-	-3.14
Tnfrsf8	Tumor necrosis factor receptor superfamily, member 8	NM_009401	-	-	-	-2.79
<b>III. Cellular Activation/Differentiation</b>						
Cd164	CD164 antigen	NM_016898	-	-	-	-2.94
Cd209a	CD209a antigen	NM_133238	-	-	-	-3.66
Cd37	CD37 antigen	NM_007645	-	2.47	3.92	-
Cd4	CD4 antigen	NM_013488	-	-	-	3.93
Cd52	CD52 antigen	NM_013706	-	-	2.73	-
Cd74	CD74 antigen	NM_010545	-	3.47	-	-
Cd79b	CD79B antigen	NM_008339	-	-	2.99	-
Cd99l2	Cd99 antigen-like 2	NM_138309	-	-	2.01	-
<b>IV. Antimicrobial Activity</b>						
-	complement component 8, gamma subunit	XM_130127	-	-	-	3.12
Adam2	A disintegrin and metallopeptidase domain 2	NM_009618	-2.06	-	-3.09	-3.05
Adam9	A disintegrin and metallopeptidase domain 9 (meltrin gamma)	NM_007404	-	-	-	-2.99
Arg1	Arginase 1, liver	NM_007482	-	-	-	1.69
C1qc	Complement component 1, q subcomponent, C chain	NM_007574	-	2.12	2.60	-
C9	Complement component 9	NM_013485	-	-	-	-2.26
Ctsd	Cathepsin D	NM_009983	-	-2.41	-1.85	-
Ctsl	Cathepsin L	NM_009984	-	-	-	-2.92
Ctss	Cathepsin S	NM_021281	-	2.36	2.51	-
Ctsz	Cathepsin Z	NM_022325	-	1.52	1.58	-
F11r	F11 receptor	NM_172647	-	-	-	-2.21
F2r	Coagulation factor II (thrombin) receptor	NM_010169	1.60	-	-	-
F2rl2	Coagulation factor II (thrombin) receptor-like 2	NM_010170	-	-1.72	-	-

F5	Coagulation factor V	NM_007976	-1.63	-	-	-2.29
Oasl1	2-5 oligoadenylate synthetase-like 1	NM_145209	-	-	-	2.07
Thbd	Thrombomodulin	NM_009378	-	-	-	-3.04
Thbs1	Thrombospondin 1	NM_011580	-	-	-	1.84
Thbs2	Thrombospondin 2	NM_011581	-	-	-	-2.36
Timp3	Tissue inhibitor of metalloproteinase 3	NM_011595	-	2.22	1.86	-

#### V. Leukocyte Receptors

Fcgr1a	Fc receptor, IgE, high affinity I, alpha polypeptide	NM_010184	-	-	-	2.71
Fcgr2	Fc receptor, IgG, alpha chain transporter	NM_010189	-	2.61	2.90	-
H2-Ab1	Histocompatibility 2, class II antigen A, beta 1	NM_207105	-	-	2.86	-
H2-D1	Histocompatibility 2, T region locus 23	NM_010398	-	2.59	3.30	-
H2-DMa	Histocompatibility 2, class II, locus DMA	NM_010386	-	-	2.70	-
H2-K1	Histocompatibility 2, Q region locus 1	NM_010390	-	-	-2.54	-
H2-Ke2	H2-K region expressed gene 2	NM_010385	-	-	1.61	-
H2-Q7	Histocompatibility 2, Q region locus 7	NM_010394	-	2.45	-	-
Icam2	Intercellular adhesion molecule 2	NM_010494	-	3.68	3.88	-
Klra17	Killer cell lectin-like receptor, subfamily A, member 17	NM_133203	-	-	-1.51	-
Pecam1	Platelet/endothelial cell adhesion molecule 1	NM_008816	-	-	2.64	-
Tlr11	Toll-like receptor 11	NM_205819	-	-1.64	-2.23	-
Tlr5	Toll-like receptor 5	NM_016928	1.90	-	-	-
Tlr9	Toll-like receptor 9	NM_031178	-	-	-2.75	-

#### VI. Cell Signaling

Ifi204	Interferon activated gene 204	NM_008329	-2.10	-	-	-
Il1rap	Interleukin 1 receptor accessory protein	NM_134103	-	-	-	-1.54
Irak3	Interleukin-1 receptor-associated kinase 3	NM_028679	-	-	-1.99	-
Irak4	Interleukin-1 receptor-associated kinase 4	NM_029926	-	-	-	2.66
Irf2	Interferon regulatory factor 2	NM_008391	-	-	-	1.63
Irf4	Interferon regulatory factor 4	NM_013674	-	-	2.08	-
Irf9	Interferon regulatory factor 9	NM_008394	-	-	1.89	-
Ptger3	Prostaglandin E receptor 3 (subtype EP3)	NM_011196	-	-	-	-1.51
Ptgr1	Prostaglandin F receptor	NM_008966	-	-	-	-2.43
Ptgis	Prostaglandin I2 (prostacyclin) synthase	NM_008968	2.60	-	-	-
Ptgr2	Prostaglandin reductase 2	NM_029880	-	-	-	-2.25
Tbrg1	Transforming growth factor beta regulated gene 1	NM_025289	-	-	2.86	-
Traf5	Tnf receptor-associated factor 5	NM_011633	-	-	-	-3.10
Traf7	Tnf receptor-associated factor 7	NM_153792	-	-	2.16	-
Trap1	TNF receptor-associated protein 1	NM_026508	-	2.12	2.19	-

#### Spleen

Gene ID	Annotation	Accession	Hours Post Infection			
			12	24	48	120
<b>I. Apoptosis</b>						
<i>Apitd1</i>	Apoptosis-inducing, TAF9-like domain 1	NM_027263	-	-	-	-1.99
<i>Bclaf1</i>	BCL2-associated transcription factor 1	NM_153787	-	-	-	-2.43
<i>Casp6</i>	Caspase 6	NM_009811	-	-	-	-1.54
<i>Fadd</i>	Fas (TNFRSF6)-associated via death domain	NM_010175	2.45	1.95	-	2.25
<i>Faim</i>	Fas apoptotic inhibitory molecule	NM_011810	-	-	-	-3.18
<i>Pdcd4</i>	Programmed cell death 4	NM_011050	-	-	-	-2.69
<b>II. Inflammatory Response</b>						
<i>Ccl3</i>	Chemokine (C-C motif) ligand 3	NM_011337	-	-	-	3.01
<i>Ccr1</i>	Chemokine (C-C motif) receptor 1	NM_009912	-	-	-	-1.50
<i>Ccr11</i>	Chemokine (C-C motif) receptor 1-like 1	NM_007718	-	-	-	-4.21
<i>Ccr3</i>	Chemokine (C-C motif) receptor 3	NM_009914	-	-	2.94	-
<i>Ccr5</i>	Chemokine (C-C motif) receptor 5	NM_009917	-	-	1.63	-
<i>Cx3cl1</i>	Chemokine (C-X3-C motif) ligand 1	NM_009142	-	-	-	-1.94
<i>Cxcl11</i>	Chemokine (C-X-C motif) ligand 11	NM_019494	-	-	-	4.13
<i>Cxcl13</i>	Chemokine (C-X-C motif) ligand 13	NM_018866	-	-	-	3.09

<i>Cxcl14</i>	Chemokine (C-X-C motif) ligand 14	NM_019568	-	-	-	-2.98
<i>Cxcr6</i>	Chemokine (C-X-C motif) receptor 6	NM_030712	-	-	-	-2.69
<i>Ifnb1</i>	Interferon beta 1, fibroblast	NM_010510	-	-	-	2.20
<i>Il10ra</i>	Interleukin 10 receptor, alpha	NM_008348	-	-	-	-1.57
<i>Il13</i>	Interleukin 13	NM_008355	-	-	-	2.07
<i>Il13ra2</i>	Interleukin 13 receptor, alpha 2	NM_008356	-	-	-	-1.96
<i>Il18r1</i>	Interleukin 18 receptor 1	NM_008365	-	-	-	-2.09
<i>Il1f9</i>	Interleukin 1 family, member 9	NM_153511	-	-	-	2.60
<i>Il1r2</i>	Interleukin 1 receptor, type II	NM_010555	-	-	1.53	-
<i>Il2rb</i>	Interleukin 2 receptor, beta chain	NM_008368	-	-	-	-2.21
<i>Il9r</i>	Interleukin 9 receptor	NM_008374	-	-	-	-1.69
<i>Lta</i>	Lymphotoxin A	NM_010735	-	-	1.50	-
<i>Ltbp3</i>	Latent transforming growth factor beta binding protein 3	NM_008520	-	-	-	2.70
<i>Tgfb2</i>	Transforming growth factor, beta receptor II	NM_009371	-	-1.69	-	-3.55
<i>Tnfrsf1a</i>	Tumor necrosis factor receptor superfamily, member 1a	NM_011609	-	-	2.38	-
<i>Vegfc</i>	Vascular endothelial growth factor C	NM_009506	-	-	1.55	-
<i>Xcl1</i>	Chemokine (C motif) ligand 1	NM_008510	-	-	-	-2.54

### III. Cellular Activation/Differentiation

<i>Cd247</i>	CD247 antigen	NM_031162	-	-	-	-2.18
<i>Cd274</i>	CD274 antigen	NM_021893	-	-	-	1.82
<i>Cd300c</i>	CD300C antigen	NM_199225	-	-	-	-2.79
<i>Cd300e</i>	CD300e antigen	NM_172050	-	-	-	-3.91
<i>Cd300lb</i>	CD300 antigen like family member B	NM_199221	-	-	-	3.72
<i>Cd320</i>	CD320 antigen	NM_019421	-	-	-	-2.10
<i>Cd3d</i>	CD3 antigen, delta polypeptide	NM_013487	-	-	-	-3.05
<i>Cd3eap</i>	CD3E antigen, epsilon polypeptide associated protein	NM_145822	-	-	-	2.54
<i>Cd3g</i>	CD3 antigen, gamma polypeptide	NM_009850	-	-	-	-1.78
<i>Cd44</i>	CD44 antigen	NM_009851	-	-	-	-3.15

### IV. Antimicrobial Activity

-	complement factor properdin	XM_135820	-	-	-	-2.88
<i>Adam15</i>	A disintegrin and metallopeptidase domain 15	NM_009614	-	-	-	1.96
<i>Arg1</i>	Arginase 1, liver	NM_007482	-	-	-	3.09
<i>C2</i>	Complement component 2 (within H-2S)	NM_013484	-	-	-	1.98
<i>C6</i>	Complement component 6	NM_016704	-	-	-	-3.02
<i>Ctsb</i>	Cathepsin B	NM_007798	-	-	-	-2.63
<i>Ctsd</i>	Cathepsin D	NM_009983	-	-	-	-1.86
<i>Ctse</i>	Cathepsin E	NM_007799	-	-	-	-2.16
<i>Ctsw</i>	Cathepsin W	NM_009985	-	-	-	-3.14
<i>Defb1</i>	Defensin beta 1	NM_007843	-	-	-	2.64
<i>Defb21</i>	Defensin beta 21	NM_207276	-	1.51	-	-
<i>Gzmb</i>	Granzyme B	NM_013542	-	-1.71	-	-
<i>Igj</i>	Immunoglobulin joining chain	NM_152839	-	-	-	-3.23
<i>Mmp13</i>	Matrix metallopeptidase 13	NM_008607	-	-	-	1.96
<i>Mmp14</i>	Matrix metallopeptidase 14 (membrane-inserted)	NM_008608	-	-	-	2.49
<i>Ncf1</i>	Neutrophil cytosolic factor 1	NM_010876	-	-	-	-1.99
<i>Nos2</i>	Nitric oxide synthase 2, inducible, macrophage	NM_010927	-	-	-1.52	-2.44
<i>Oas1d</i>	2-5 oligoadenylate synthetase 1D	NM_133893	-	-	-	1.62
<i>Oas2</i>	2-5 oligoadenylate synthetase 2	NM_145227	-	-	-	2.41
<i>Oasl2</i>	2-5 oligoadenylate synthetase-like 2	NM_011854	-	-	-	-1.86
<i>Socs1</i>	Suppressor of cytokine signaling 1	NM_009896	1.58	-	1.84	-
<i>Timp3</i>	Tissue inhibitor of metalloproteinase 3	NM_011595	-	-	-	2.53
<i>Tslp</i>	Thymic stromal lymphopoietin	NM_021367	-	-	-	-3.34

### V. Leukocyte Receptors

<i>H2-D1</i>	Histocompatibility 2, T region locus 23	NM_010398	-	-	-	2.18
<i>H2-Ke2</i>	H2-K region expressed gene 2	NM_010385	-	-	-	3.53
<i>H2-Ke6</i>	H2-K region expressed gene 6	NM_013543	-	-	-	-2.88
<i>H2-M11</i>	Histocompatibility 2, M region locus 11	NM_177635	-	-	-	-2.20
<i>H2-T22</i>	Histocompatibility 2, T region locus 10	NM_010399	-	-	-	1.62
<i>H2-T22</i>	Histocompatibility 2, T region locus 10	NM_010397	-	-	-	3.20
<i>Ilgav</i>	Integrin alpha V	NM_008402	-	-	-	2.45

<i>Jam3</i>	Junction adhesion molecule 3	NM_023277	-	-	2.36	-
<i>Klra16</i>	Killer cell lectin-like receptor, subfamily A, member 16	NM_013794	-	-3.20	-	-3.30
<i>Klrd1</i>	Killer cell lectin-like receptor, subfamily D, member 1	NM_010654	-	-2.15	-	-3.42
<i>Ltb4r1</i>	Leukotriene B4 receptor 1	NM_008519	-	-	1.69	-
<i>Ly6a</i>	Lymphocyte antigen 6 complex, locus A	NM_010738	-	-	-	2.35
<i>Ly6e</i>	Lymphocyte antigen 6 complex, locus E	NM_008529	-	2.77	-	3.19
<i>Ly6f</i>	Lymphocyte antigen 6 complex, locus F	NM_008530	-	-	-	2.64
<i>Ly6g6e</i>	Lymphocyte antigen 6 complex, locus G6E	NM_027366	-	-	-	-3.92
<i>Ly6i</i>	Lymphocyte antigen 6 complex, locus I	NM_020498	-	-	-	2.67
<i>Ly6k</i>	Lymphocyte antigen 6 complex, locus K	NM_029627	-	-	-	3.09
<i>Lyve1</i>	Lymphatic vessel endothelial hyaluronan receptor 1	NM_053247	-	-	-	2.52
<i>Marco</i>	Macrophage receptor with collagenous structure	NM_010766	-	-2.87	-	-
<i>Mrc1</i>	Mannose receptor, C type 1	NM_008625	-	-	-	-1.67
<i>Mrc1</i>	Mannose receptor-like precursor	NM_181549	-	-	-	2.38
<i>Scarb2</i>	Scavenger receptor class B, member 2	NM_007644	-	-	-	-1.70
<i>Tlr11</i>	Toll-like receptor 11	NM_205819	-	-	-	-2.16

## VI. Signaling

<i>Cd2bp2</i>	CD2 antigen (cytoplasmic tail) binding protein 2	NM_027353	-	-	-	4.22
<i>Ifi202b</i>	Interferon activated gene 202B	NM_008327	-	-	-	4.16
<i>Ifi204</i>	Interferon activated gene 204	NM_008329	-1.69	-1.86	-2.24	-
<i>Ifi205</i>	Interferon activated gene 205	NM_172648	-	-	-	3.51
<i>Ifi27</i>	Interferon, alpha-inducible protein 27	NM_029803	-	-	-	2.57
<i>Ifi35</i>	Interferon-induced protein 35	NM_027320	-	-	-	4.15
<i>Ifitm2</i>	Interferon induced transmembrane protein 2	NM_030694	-	-	1.58	4.09
<i>Ifitm3</i>	Interferon induced transmembrane protein 3	NM_025378	-	-	-	3.32
<i>Il6st</i>	Interleukin 6 signal transducer	NM_010560	-	-1.51	-	-2.24
<i>Irf2bp1</i>	Interferon regulatory factor 2 binding protein 1	NM_178757	-	-	-	-1.95
<i>Isg20</i>	Interferon-stimulated protein	NM_020583	-	-	-	3.59
<i>Prnd</i>	Prion protein dublet	NM_023043	-	-	-	-3.13
<i>Ptgds2</i>	Prostaglandin D2 synthase 2, hematopoietic	NM_019455	-	-	-	-1.90
<i>Ptgis</i>	Prostaglandin I2 (prostacyclin) synthase	NM_008968	-	-	-	-4.02
<i>Ptgr2</i>	Prostaglandin reductase 2	NM_029880	-	-	-	-2.72
<i>Tnfaip1</i>	Tumor necrosis factor, alpha-induced protein 1 (endothelial)	NM_009395	-	1.65	-	1.60
<i>Tnfaip8l1</i>	Tumor necrosis factor, alpha-induced protein 8-like 1	NM_025566	-	-	-	3.05
<i>Tnfaip8l2</i>	Tumor necrosis factor, alpha-induced protein 8-like 2	NM_027206	-	-	-	-1.89
<i>Tnfrsf13c</i>	Tumor necrosis factor receptor superfamily, member 13c	NM_028075	-	-	-	-2.43
<i>Traf3</i>	Tnf receptor-associated factor 3	NM_011632	-	-	-	3.31
<i>Traf3ip3</i>	TRAF3 interacting protein 3	NM_153137	-	-	-	-2.20
<i>Vezf1</i>	Vascular endothelial zinc finger 1	NM_016686	-	-	-	-2.46

Table 2: C57BL/6 mice (n = 2 per group) were inoculated via aerosol with lethal doses of *F. tularensis* Schu4 or LVS (10<sup>4</sup> CFU), as described in Methods. Total RNA Lung and spleen tissues were collected 12, 24, 48 and 120 hours post infection, converted to cDNA, labeled and hybridized on full mouse genome microarrays. Genes with a p-value < 0.01 and differentially regulated > 1.5 fold were mined for genes unique to Schu4 infection that fell into the categories of inflammatory response, cellular activation/differentiation, antimicrobial activity, leukocyte receptors, and cell signaling.

### 3.3.4 Validation of transcriptional trends by qRT-PCR

To confirm the transcriptional response of select immunological genes during *F. tularensis* infection, quantitative real-time PCR (qRT) was performed on lung and spleen tissue from independent infections (Table 3). Analysis revealed that the trends identified by global microarray analysis were 85% and 62%

concordant with qRT data in the lung and spleen, respectively. The lower concordance noted in the spleen is attributed to temporal differences in dissemination. The expression of the 12 key pro-inflammatory and anti-inflammatory markers in the lung and spleen was limited in the initial 24 hours of infection. However, 48 hours post infection with LVS shows activation of cytokine and chemokine expression not seen until 120 hours post infection with Schu4. The genes significantly up-regulated as determined by qRT in the lungs during Schu4 infection included the pro-inflammatory chemokines *CCL4*, *CXCL1* and *CXCL10*; the pro-inflammatory cytokines *IL-6* and *IL-12a*; the gene for inducible nitric oxide, *Nos2*; and the gene for a type I interferon, *IFN- $\beta$* . A similar trend in the differential expression of these genes was observed in the spleen of Schu4-infected mice at 120 hours. This trend in transcriptional activity indicates a delayed and reduced host response to infection with Schu4 and is consistent with a lack of host recognition or active mechanism of host-response suppression by the Schu4, consistent with previous reports [22, 30, 39].



**Table 3: Relative expression values of inflammatory markers from lung and spleen of mice infected with *F. tularensis* Schu4 and LVS**

	Lung							
	<i>Schu4</i>				LVS			
	12 hours	24 hours	48 hours	120 hours	12 hours	24 hours	48 hours	120 hours
Tnfa	-0.88±1.09	-0.25±0.45	-0.29±0.25	2.51±1.53	0.44±0.30	-0.69±0.68	0.51±0.30	-0.95±0.19
lfn-γ	-7.72±0.09	-7.01±1.72	-0.81±0.45	1.79±0.39	-7.31±0.29	-7.32±0.11	1.25±0.38	4.22±0.47
lfn-β	-3.80±0.99	-1.92±1.07	-2.69±1.00	4.61±0.58	-4.18±0.95	-2.66±0.80	2.45±0.25	3.03±0.44
Tgfb1	0.97±0.33	1.38±0.57	1.02±0.13	1.84±0.63	0.40±0.66	2.09±0.40	1.39±0.21	1.72±0.34
Cxcl1	0.69±0.98	2.35±0.43	1.70±0.88	2.85±0.94	2.19±0.69	1.11±1.30	4.12±0.47	5.29±0.21
Cxcl10	-0.90±0.55	-0.81±0.50	0.74±0.87	7.74±0.21	-0.34±0.38	-0.75±0.88	5.78±1.03	9.07±0.40
Ccl4	-1.20±1.17	0.00±0.52	-0.51±0.52	1.78±0.55	-1.17±0.43	-1.57±0.87	2.21±0.45	4.38±0.29
Il-1β	-1.64±0.63	-0.55±1.14	1.00±0.71	-0.24±0.51	-2.42±0.43	-2.48±0.65	2.93±0.81	3.8±0.26
Il-6	-2.17±0.81	-0.23±1.05	1.84±1.05	4.30±0.43	-2.32±0.83	-1.00±1.17	4.64±1.16	5.50±0.71
Il-10	1.21±1.08	-2.46±0.82	-0.67±0.84	4.28±0.89	-1.06±1.10	-1.94±0.89	1.60±0.35	4.36±0.30
Il-12a	0.68±1.91	1.57±0.63	1.51±0.16	4.67±0.88	0.72±0.75	0.91±1.65	3.89±0.22	5.15±0.35
Nos2	0.57±1.16	0.61±0.16	1.94±0.27	3.78±0.43	0.04±0.76	0.77±0.47	2.73±0.33	7.58±0.51

	Spleen							
	<i>Schu4</i>				LVS			
	12 hours	24 hours	48 hours	120 hours	12 hours	24 hours	48 hours	120 hours
Tnfa	0.55±0.41	0.26±0.44	-1.81±0.33	3.23±0.18	2.03±0.42	0.79±0.45	-0.06±0.88	-2.52±0.16
lfn-γ	-6.93±0.83	-7.89±0.86	0.47±0.43	-1.19±0.55	-5.72±0.62	-6.69±0.25	1.76±0.38	3.28±0.30
lfn-β	-3.94±0.46	-4.25±1.22	-4.53±1.10	3.36±0.24	-3.51±1.75	-3.16±1.22	0.69±0.61	-1.98±0.73
Tgfb1	-1.27±0.25	-0.26±1.37	-1.50±0.51	3.68±0.81	1.53±0.54	-0.94±0.49	0.36±0.21	1.77±0.23
Cxcl1	-1.27±0.67	-0.26±0.39	-1.50±0.31	3.68±0.45	0.35±0.52	-0.94±0.98	0.36±0.93	1.77±0.84
Ccl4	-0.44±0.79	-1.04±1.03	-0.27±0.80	2.69±0.34	0.33±0.57	-0.19±0.59	0.61±0.94	1.63±0.47
Il-1β	-0.20±0.73	-0.05±0.36	1.29±0.65	1.40±0.28	-0.28±0.57	-0.81±0.43	2.00±0.62	2.53±0.82
Il-6	-6.04±2.26	-4.68±1.96	-4.79±1.40	2.23±0.43	-4.02±1.57	-3.21±1.18	-1.51±1.74	0.81±1.23
Il-10	0.03±0.44	-0.10±0.98	-1.05±0.87	3.63±0.41	2.08±0.51	0.32±0.53	0.98±0.35	2.97±0.35
Il-12a	-1.28±0.74	1.39±0.58	-1.48±0.76	0.46±0.40	-1.28±0.74	-1.39±0.58	-0.13±0.20	0.22±0.24
Nos2	0.34±0.50	0.50±0.37	-0.10±0.39	4.85±0.48	0.78±0.86	0.27±0.67	0.21±0.40	4.76±0.57

Table 3: C57BL/6 mice (n = 4 per group) were inoculated i.n. with lethal doses of *F. tularensis* Schu4 ( $10^2$  CFU) or LVS ( $10^4$  CFU), as described in Methods. Quantitative real time PCR was used to validate microarray data, and monitor molecular markers of disease. Data was monitored for consistency by the housekeeping genes 18S rRNA, GapDH, and β-actin. Data from each condition was compared to controls using the ΔCT method.

### **3.4 Discussion:**

A critical question in understanding *F. tularensis* pathobiology is to determine which critical host responses are altered during the first 4-5 days following infection. Whole genome microarrays are an established post-genomic approach that allows the assessment of global host responses in an unbiased fashion. In the present study, we coupled whole genome microarray analysis with analysis of tissue pathology and organ bacterial burden to gain a more complete understanding of disease progression and host response to infection with a fully virulent and a less virulent strain of *F. tularensis*. By means of this combined approach we were able to identify important host response differences to infection with the two strains of *F. tularensis*.

Quantification of bacterial burden in the lungs revealed that Schu4 had increased growth compared to LVS, such that by 120 hours the bacterial load of Schu4 in the lungs significantly exceeded that of mice infected with the LVS strain. In addition, *F. tularensis* Schu4 demonstrated increased dissemination to the spleen, as indicated by detection within 48 hours of infection and significantly increased bacterial burden in the spleen at later time points following infection. Tissue damage was markedly more severe in the spleen following infection with Schu4, particularly at later time points of infection. Notably, both Schu4 and LVS established similar levels of infection in the lung, but eventually the Schu4 infection progressed to more severe pulmonary pathology, presumably due to more rapid replication and avoidance of host immune responses. Efficient dissemination appears to be an important distinction and hallmark of infection

with highly virulent strains of *F. tularensis* [10, 40, 41]. Importantly, the correlation between controlled dissemination and survival has been observed in drug development studies that indicate that drug efficacy is related to control of dissemination to secondary organs such as the spleen [41].

Rapid dissemination is an important determinant of disease outcome and likely relies on the initial recognition and control of pathogen replication at the site of infection. A study conducted by Chiavolini *et. al* showed the importance of the initial inflammatory response in determining survival following *F. tularensis* infection. For example, survival was predicted by the induction of several inflammatory genes before day 7 of infection with LVS in mice [40]. Since replication of Schu4 was actually higher in the spleens of infected mice than replication of LVS, it is likely that the decrease in cytokine gene expression in the lungs of Schu4 infected mice reflects either failure to activate immune responses, or active immune suppression.

The results of the global analyses of the host response to infection with *Francisella* Schu4 or LVS strains indicate highly virulent strains are capable of subverting the host innate immune response and cell mediated immunity. In the present study, these altered responses included apoptosis, antigen processing and presentation, the inflammatory response, and leukocyte receptor signaling. The down regulation of multiple host defense mechanisms by *F. tularensis* is consistent with results reported in previous studies [9, 11-14, 22, 30, 39]. In addition, the transcriptional response to Schu4 and *F. tularensis* subspecies *novicida* in human monocytes found that reported that there was less

inflammatory gene activation by Schu4 as compared to the less virulent *F. novicida* strain [13].

In addition, we found *F. tularensis* Schu4 versus LVS induced changes in novel gene subsets, particularly *IL-13*, cathepsins, and most strikingly, the killer cell lectin-like receptor family (*Ly49/Klre1*). Studies have shown interferon activated macrophages treated with IL-13 have a reduced capacity to inhibit the growth of intracellular bacteria [42]. A previous transcriptional profiling study showed the increased expression of interferon-activated genes four days after infection in the lungs of mice infected with type A FSC033 [9]. Moreover, the killer cell lectin-like receptors have been shown to be vital for recognition and activation/inhibition of natural killer cells [31, 32]. Evidence that infection with *F. tularensis* Schu4 decreased the expression of these receptors further highlights the immuno-evasive activity of *Francisella* Schu4 compared to the less virulent *F. tularensis* LVS. Furthermore, expression of the prostaglandin E1 receptor (*Ptger1*) confirms recent reports implicating prostaglandin signaling as an important mechanism of *Francisella* manipulation of the host-response to infection [29, 38, 43].

Our studies also confirm previous studies and indicate that dissemination to secondary sites of infection leading to multi-organ damage and failure are key contributing factors to mortality from *F. tularensis* infection. We have also identified gene expression patterns that may reflect immune responses to bacterial dissemination from the lung to spleen tissues. These data may also be useful for facilitating the development of diagnostics for monitoring treatment

efficacy, the success of chemotherapeutic or vaccine strategies. For example, gene expression correlates of host evasion during early infection combined with gene expression signatures of dissemination provide a panel of genes that can be used to assess disease progression and severity that can be used as checkpoints of therapeutic efficacy. In addition, as high throughput RNA sequencing becomes more readily available, biomarkers can be correlated to *in vivo* transcriptional data from the pathogen in an attempt to decipher complex host-pathogen interactions. Importantly, the expression of markers that are associated with differences between the infections caused by Schu4 and LVS will be useful for assessing immune response to immunotherapeutic drugs. These studies therefore provide a foundation for continued research in this area that will ultimately provide unique opportunities that can be exploited for the development of protective vaccines and effective chemotherapeutics with enhanced efficacy and that prevent relapse of disease.

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## CHAPTER 4

### Transcriptional response of *Francisella tularensis* to growth in the lung and spleen of infected mice

#### 4.1 Introduction:

The mouse model of pulmonary tularemia resembles the clinical outcome of human disease when inhaled; the bacteria disseminate rapidly from the lungs to the liver and spleen resulting in death if left untreated [1-5]. With the rise of antibiotic resistance and the potential threat of *Francisella* as a bioweapon engineered to resist common antibiotic treatments, it is important to develop novel therapeutics to combat bacterial pathogens [1]. Development relies on the translation of *in vitro* potency of lead chemotherapeutics to *in vivo* efficacy, which is primarily dependent on the essentiality of the drug target to the infection process [6]. Comparing genes active during the infection process and those active during growth *in vitro* can inform the therapeutic development process by identifying target availability in the two growth conditions. Furthermore, the identification of pathogen transcriptional activity during infection has been a goal for scientists since the advent of the microarray.

There have been several studies using microarrays that have aimed at identifying global bacterial transcription during infection of macrophage and other

cell lines with intracellular pathogens such as *Mycobacteria*, *Listeria*, *Shigella*, *Yersinia*, and *Francisella* [7-11]. These studies while informative, to understanding the aspects of the intracellular lifestyle of these pathogens, are limited to a single cell type in an *ex vivo* model which cannot recapitulate *in vivo* growth conditions that are tissue specific. The challenge of the identification and quantification of nucleic acid at extremely low abundance has largely been overcome with next generation sequencing. RNA isolated from infected tissue for the purpose of analyzing bacterial transcription still suffers from a high degree of complexity with the majority of material being host message and ribosomal RNA. By employing a method of RNA depletion steps, we have been able to identify the metabolic requirements of *F. tularensis* during infection by examining the bacterial genes expressed in host tissues over the course of infection. Poly-A tailed RNA and rRNA, from the host and bacteria, was depleted through hybridization with biotinylated nucleic acid probes, captured with avidin coated metallic beads, and removed from the sample with magnetic separation. Thus, the resulting sample is enriched for bacterial transcripts and prepared for sequencing using SOLiD protocols for library preparation and sequencing.

Development of antimicrobials for inhibition of targets within essential metabolic pathways requires that the target be expressed during the infection. Thus we hypothesized that identification of genes expressed by *F. tularensis* during infection will help determine genes essential to the infection process. Using the mouse model of pulmonary tularemia and SOLiD next generation sequencing, we have identified active *Francisella* transcripts 48 hours post

infection in the lung, 96 hours in the lung and spleen, and at mid log phase of *in vitro* growth. Gene lists were compared to determine genes unique to each organ and stage of disease as well as genes unique to *in vivo* and *in vitro* growth conditions. The results of this study highlight the complexity of the adaptive transcriptional response of *Francisella* during infections as well as demonstrating a method to identify novel drug targets and target availability.

## **4.2 Materials and Methods:**

### **4.2.1 Bacterial strains.**

*F. tularensis* Schu4 was provided by Dr. J. Petersen (Centers for Disease Control, Fort Collins, CO). Schu4 was cultured in modified Mueller-Hinton broth at 37°C with constant shaking overnight, supplemented with 10% glycerol and aliquoted into 1 ml samples, frozen at -80°C, and thawed just before use. Frozen stocks were titered by enumerating viable bacteria from serial dilutions plated on modified cystein heart agar supplemented with 10% hemaglobin. The number of viable bacteria in frozen stock vials varied <5% over a 10-month period.

### **4.2.2 Mice.**

Six week-old female Balb/C mice were purchased from Jackson Laboratories, Bar Harbor, Maine. All mice were housed in sterilized micro-isolator cages in the laboratory animal resources facility or in the Rocky Mountain Regional Biocontainment Laboratory BSL-3 facility at Colorado State University (Fort Collins, CO) and provided water and food *ad libitum*. All research involving animals was conducted in accordance with animal care and use guidelines and animal protocols were approved by the Animal Care and Use Committee at Colorado State University.

### **4.2.3 Infections.**

Mice were anesthetized with 100/10 mg/kg ketamine/xylazine and inoculated intranasally with 20 µl drop wise in alternating nares. The inoculum

was plated in order to ensure a consistent dose of 25-50 CFU per mouse. Mice were monitored for clinical symptoms and sacrificed at pre-determined endpoints for harvesting of lung and spleen tissue. Organs were halved and homogenized in either PBS for bacterial quantification or TRIzol reagent for RNA isolation.

#### ***4.2.4 Bacterial quantification.***

Samples of lung and spleen tissues were homogenized in 1 mL sterile PBS using a stomacher (Teledyne Tekmar, Mason, OH). Bacterial CFU per mL of organ homogenate were determined by plating serial 10-fold dilutions of organ homogenates on modified cysteine heart agar supplemented with 10% hemoglobin and incubated at 37°C for 72 hours.

#### ***4.2.5 Isolation of bacterial transcripts and library preparation for SOLiD sequencing.***

Organs harvested from infected mice were homogenized in TRIzol (Invitrogen, Carlsbad, CA) and frozen at -80°C overnight. Samples were thawed and nucleic acid was isolated by organic partition. Samples were treated with DNase (Fermentas, Burlington, Ontario) for 30 minutes at 37°C and purified by phenol/chloroform/isoamyl alcohol (25:24:1) extraction and ammonium acetate precipitation. 20 µg of total RNA was used for removal of ribosomal RNA using mouse/human and bacterial Ribominus kits (Invitrogen, Carlsbad, CA). Host transcripts were removed using poly(dT) Dynabeads (Invitrogen, Carlsbad, CA) and the resulting material was purified by phenol/chloroform/isoamyl alcohol



(25:24:1) extraction and ammonium acetate precipitation to yield bacterial messenger RNA. Sequencing libraries were prepared using the Applied Biosciences Whole Transcriptome Kit. Briefly, bacterial RNA was fragmented using RNAase III, adapters were ligated to the fragmented RNA and converted into cDNA through a 15 cycle PCR amplification with adapter specific primers. Emulsion PCR was performed to attach template cDNA to beads that are deposited on a glass slide for sequencing.

#### **4.2.6 Data analysis.**

Raw read files were uploaded to NextGene data analysis server (Soft Genetics, State College, PA) for advanced analysis. Data from transcript runs was pooled by time point and organ (3 mice per time point and organ). Raw reads were mapped to the *F. tularensis* Schu4 gene bank reference file and expression reports for each organ and time point were exported in text format. Global means for each expression report were calculated using RPKM values and genes that fell below the global mean were removed to remove background noise and potential DNA contamination. Expression reports of active transcripts were compared between time point and growth condition to determine genes common and unique to each condition. Functional enrichment analysis was conducted using the DAVID Bioinformatics Database [12, 13].

#### **4.2.7 Quantitative Reverse Transcription Real Time PCR.**

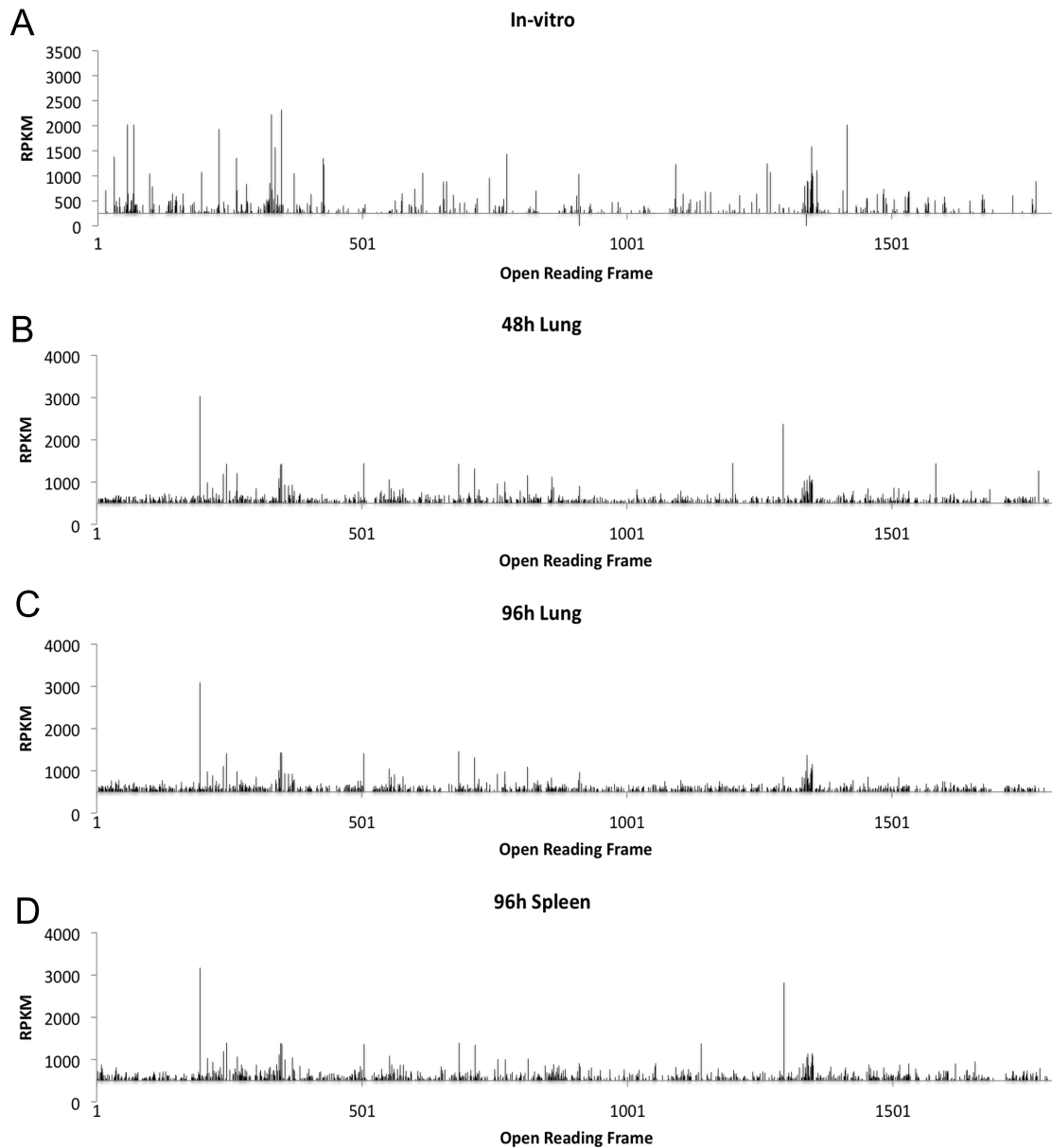
cDNA synthesis from total RNA from the lungs and spleens of infected mice was performed using First Strand cDNA Synthesis Kit (Invitrogen, Carlsbad, CA). Platinum SYBR Green qPCR Supermix-UDG (Invitrogen, Carlsbad, CA) was combined with gene specific primers (5nmol) and 50ng of template (cDNA) and run in triplicate on an IQ5 thermocycler (Bio-Rad, Hercules, CA). Data was normalized to transcripts encoding *F. tularensis* 16s rRNA. Data was compared to material taken from uninfected samples using the  $\Delta$ CT method.

### 4.3 Results:

#### 4.3.1 Global transcriptional profiling of *Francisella tularensis* from infected tissues

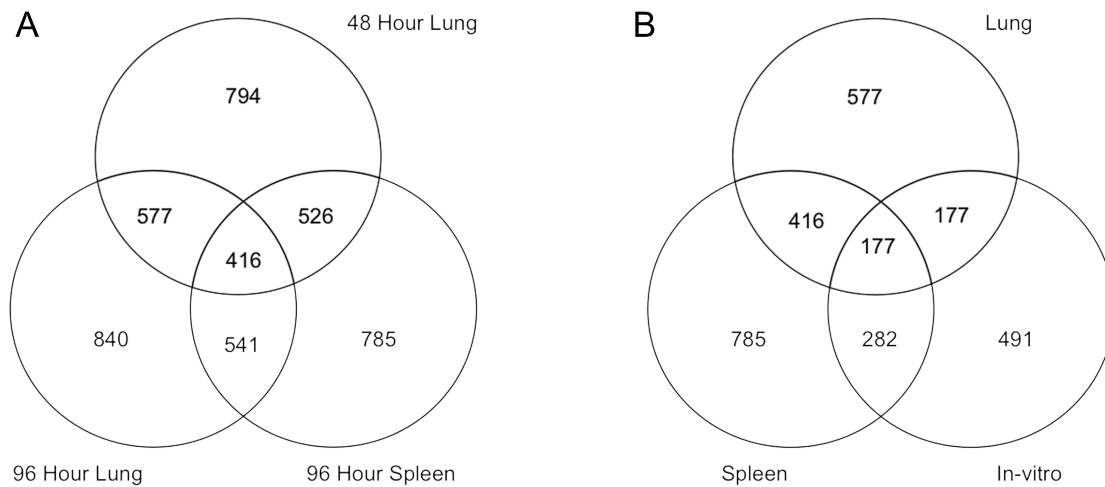
Gene expression using next generation sequencing is quantified using RPKM values that describe sequence reads for each individual open reading frame relative to overall number of sequence reads and gene length [14]. Genes considered to be active had RPKM values higher than the global mean RPKM of each condition in an effort to differentiate active genes from background noise and potential genomic DNA contamination. Figure 1 shows expression profiles of each condition (Figure 1 A-D). Full lists of active genes in each growth condition can be found in Appendix III-VI. Comparison of active genes from each condition showed 62-72% overlap between gene expression in the lung and the spleen with only 416 genes expressed that were common to each time point and organ (Figure 2A). The overlap between expression profiles of *in vivo* and *in vitro* growing *F. tularensis* was extremely low with only 177 genes commonly expressed in each condition. Interestingly, the limiting factor between *in vivo* and *in vitro* *F. tularensis* expression was the difference of genes expressed in the lung (Figure 2B). The difference has important implications for *in vitro* drug screening and the translation between *in vitro* potency and *in vivo* efficacy when developing therapeutics for pulmonary pathogens.

Figure 1



**Figure 1:** RPKM values for active *F. tularensis* transcripts were graphed based on the genomic position of each open reading frame. (A) *F. tularensis* Schu4 active transcripts from mid-logarithmic growth (.3 OD) n=3 biological replicates (B) *F. tularensis* Schu4 active transcripts 48 hours post infection in the lung (C) *F. tularensis* Schu4 active transcripts 96 hours post infection in the lung (D) *F. tularensis* Schu4 active transcripts 96 hours post infection in the spleen, n=3 mice per organ per time point.

Figure 2



**Figure 2:** Venn diagrams comparing the expression reports between (A) time point and organ, and (B) organ and *in vitro* growth.

#### **4.3.2 Metabolic requirements for growth of *Francisella tularensis* *in vitro* and *in vivo***

Genome coverage of expressed open reading frames from *in vitro* was lower than *in vivo*, 27% compared to 40-45% respectively, likely due to the freely available nutrients in broth culture and the need for intracellularly growing *F. tularensis* to utilize biochemical pathways and virulence mechanisms to survive host defenses.

To identify and compare biochemical pathways expressed in each growth condition, gene lists were subjected to ontology analysis using the DAVID bioinformatic database [12, 13]. Biochemical pathways active throughout all of the time points of the infection included nucleotide metabolism, oxidative phosphorylation, membrane transport, metal ion binding, and protein

biosynthesis. Comparison of the 416 genes active throughout the infection and the 491 genes active *in vitro* showed similar trends for metabolic requirements for growth, however *in vivo* growing bacteria had a greater number of genes with multiple ontological classifications resulting in a more evenly distributed metabolic profile (Figure 3). *In vitro* grown *Francisella* transcribed a more specific gene set with more genes having only one ontological classification (Figure 3). This is likely due to *in vivo* growing bacteria needing a broad gene set to survive, relying on proteins with overlapping metabolic functions to minimize energy consumption and waste, whereas *in vitro* grown *Francisella* can afford a more specialized gene set due to freely available nutrients in the culture media. Differences in the less abundant metabolic pathways including ubiquinone biosynthesis, FAD biosynthesis, and DNA repair show the adaptive response to intracellular growth relies heavily on energy maintenance, cofactor biosynthesis, and DNA damage response to combat host defense strategies.

To examine biochemical pathways unique to each condition, ontology analysis was conducted on unique gene lists from each growth condition and time point of infection. Genes expressed in the lung unique to each time point had similar ontological classification that only differed in percentage as the infection progressed (Figure 3). Enrichment of genes involved in metal binding, porphyrin biosynthesis, and molecular breakdown (hydrolase as opposed to transferase activity) in the spleen reflects the metabolic adaptations necessary for growth in the spleen as opposed to the lung. Interestingly, there were no genes uniquely expressed *in vitro* that were not expressed during any of the *in vivo* time points or tissues. Genes active in all conditions include the biochemical

Figure 3

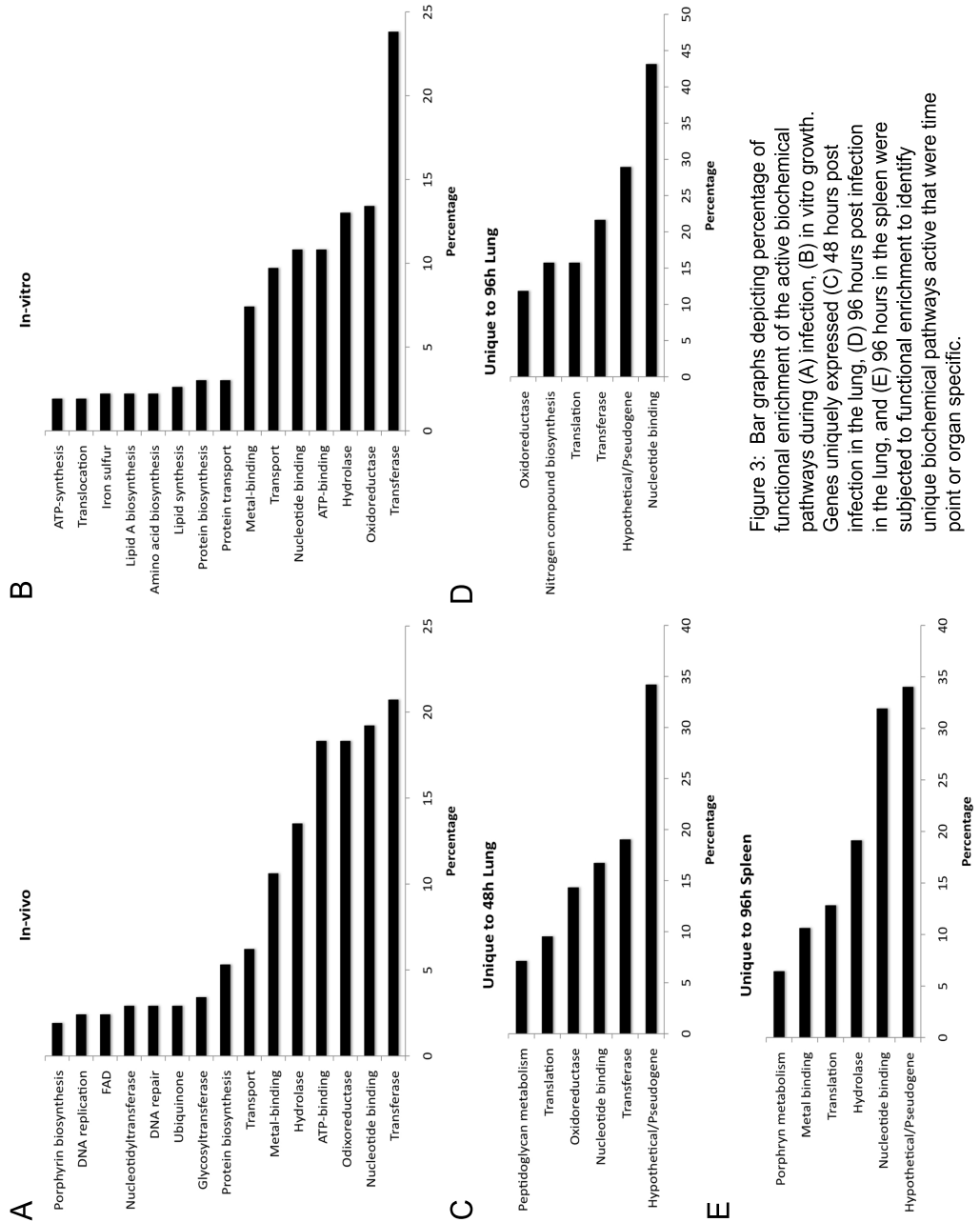


Figure 3: Bar graphs depicting percentage of functional enrichment of the active biochemical pathways during (A) infection, (B) in vitro growth. Genes uniquely expressed (C) 48 hours post infection in the lung, (D) 96 hours post infection in the lung, and (E) 96 hours in the spleen were subjected to functional enrichment to identify unique biochemical pathways active that were time point or organ specific.

pathways for replication, translation, fatty acid biosynthesis, and general cellular maintenance.

### ***Identification of genes essential to *F. tularensis* infection***

Genes expressed during infection in both the lung and the spleen were compared to the Database of Essential Genes (DEG) to identify genes that have been established as essential in *Francisella* and other species of bacteria through transposon mutagenesis studies [16, 17]. The database contains gene sequences for over 5,000 prokaryotic genes deemed essential from mutagenesis studies from 14 different prokaryotic species. Amino acid sequences of genes expressed during *Francisella* infection were blasted against the database using the BlastP algorithm and considered essential if their E-value fell below  $10^{-4}$ . Of the 416 genes expressed in both the lung and spleen of infected mice, 326 were considered to be essential to the bacteria. The 326 essential genes were then blasted against the human genome to determine genes essential to the bacteria with no significant homology to human genes in order to determine candidate genes for therapeutic targeting and inhibition. Genes with an E-value greater than  $10^{-4}$  and less than 40% coverage of human genes were considered as candidate drug targets. Of the 326 genes determined to be essential, 152 showed no significant homology to human genes and can be considered as candidate drug targets (Table 1).



**Table 1: Active open reading frames common to each time point and organ during infection with significant homology to proteins in the Database of Essential Genes (DEG) and no significant homology to human proteins**

Gene	Symbol	Annotation
FTT0011		Restriction endonuclease, pseudogene
FTT0013c		Hypothetical lipoprotein
FTT0018		Secretion protein
FTT0023c		Lipase/acyltransferase
FTT0056c		Protein transport
FTT0058	<i>atpB</i>	ATP synthase A chain
FTT0105c		Transporter AcrB/AcrD/AcrF family
FTT0106c		Efflux protein, RND family, MFP subunit
FTT0112		Transcriptional regulator
FTT0113	<i>deoB</i>	Phosphopentomutase
FTT0122	<i>oppA</i>	Periplasmic oligopeptide-binding protein
FTT0128		Hypothetical protein
FTT0142	<i>rplJ</i>	50s Ribosomal subunit
FTT0185	<i>ddlB</i>	D-alanine--D-alanine ligase B
FTT0187	<i>ftsA</i>	Cell division protein
FTT0189	<i>lpxC</i>	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase
FTT0200		Hypothetical protein
FTT0209c		Periplasmic solute binding family protein
FTT0212c	<i>wrbA</i>	Trp repressor binding protein
FTT0214		Transport protein, pseudogene
FTT0215	<i>priA</i>	Primosomal protein N
FTT0234c		Hypothetical protein
FTT0238	<i>aroE1</i>	Shikimate 5-dehydrogenase
FTT0239	<i>murC</i>	UDP-N-acetylmuramate--alanine ligase
FTT0240		Tetrapyrrole methyltransferase family protein
FTT0245	<i>usp</i>	Universal stress protein
FTT0265		ABC transporter, membrane protein
FTT0269		Carbonic anhydrase, family 3
FTT0278c	<i>cydB</i>	Cytochrome d terminal oxidase, polypeptide subunit II
FTT0279c	<i>cydA</i>	Cytochrome d terminal oxidase, polypeptide subunit I
FTT0281	<i>cyoA</i>	Cytochrome O ubiquinol oxidase subunit II
FTT0289c		Hypothetical lipoprotein
FTT0291		Hypothetical protein
FTT0308		Hypothetical protein
FTT0370c	<i>yjeE</i>	Nucleotide binding protein
FTT0406	<i>cadA</i>	Lysine decarboxylase
FTT0467	<i>ostA1</i>	Organic solvent tolerance protein
FTT0478c	<i>recJ</i>	Single stranded DNA specific exonuclease
FTT0480c	<i>xasA</i>	Gamma-aminobutyric acid antiporter
FTT0496		Hypothetical protein
FTT0509c		Hypothetical protein
FTT0544	<i>phnA</i>	Phosphonoacetate hydrolase
FTT0555		Hypothetical membrane protein
FTT0564	<i>potI</i>	Polyamine transporter, ABC transporter

FTT0569c		Hypothetical membrane protein
FTT0570		Hypothetical lipoprotein
FTT0580		Hypothetical protein
FTT0581	<i>coaD</i>	Phosphopantetheine adenylyltransferase
FTT0583	<i>fopA</i>	Outer membrane protein
FTT0586		Hypothetical protein
FTT0595c	<i>rubA</i>	Rubredoxin
FTT0622c		Hypothetical membrane protein
FTT0637	<i>thrC1</i>	Threonine synthase, pseudogene
FTT0647c		Hypothetical protein
FTT0658	<i>ruvA</i>	Holliday junction DNA helicase, subunit A
FTT0686c		Proton dependent oligopeptide transport protein
FTT0701	<i>kdsA</i>	2-dehydro-3-deoxyphosphooctonate aldolase
FTT0734		Hypothetical membrane protein, pseudogene
FTT0735		Mandelate racemase, pseudogene
FTT0742		Hypothetical lipoprotein
FTT0745c		Hypothetical protein
FTT0781c		Hypothetical protein
FTT0792		Glycosyl transferase group 1 family
FTT0808	<i>spoT</i>	Guanosine-3,5-bis 3-pyrophosphohydrolase ppGpp synthase
FTT0814c		Hypothetical protein
FTT0834	<i>aroQ</i>	Chorismate mutase
FTT0838	<i>tolR</i>	TolR protein, cell wall
FTT0840	<i>tolB</i>	TolB protein, cell wall
FTT0841		Hypothetical lipoprotein
FTT0861c		Type IV pili fiber building block protein
FTT0865		Hypothetical protein, pseudogene
FTT0868c		Arsenical resistance operon repressor
FTT0882		Mannose-6-phosphate isomerase, pseudogene
FTT0884c	<i>aspC1</i>	Aspartate transaminase
FTT0910		Hypothetical protein
FTT0918		Hypothetical protein
FTT0942c	<i>folK</i>	2-amino-4-hydroxy-6-hydroxymethylidihydropteridine pyrophosphokinase
FTT0986		Hypothetical protein
FTT1029	<i>dacD</i>	D-alanyl-D-alanine carboxypeptidase
FTT1058c		Radical SAM superfamily protein
FTT1059c	<i>dnaB</i>	Replicative DNA helicase
FTT1062c	<i>rpsF</i>	30S ribosomal protein S6
FTT1075		Transcriptional regulator
FTT1114c	<i>secF</i>	Preprotein translocase, subunit F, membrane protein
FTT1115c	<i>secD</i>	Preprotein translocase, subunit D, membrane protein
FTT1117c		Isochorismatehydrolase family protein
FTT1129c		Hypothetical protein
FTT1140		Hypothetical protein
FTT1143		Hypothetical protein
FTT1183c		Hypothetical lipoprotein
FTT1202		LysR transcriptional regulator
FTT1214c		Haloacid dehalogenase-like hydrolase family protein
FTT1215c	<i>queA</i>	S-adenosylmethionine:tRNA ribosyltransferase-isomerase

FTT1247		ABC transporter, membrane protein
FTT1255c		Transcriptional regulator araC family protein
FTT1256	<i>emrB</i>	Major facilitator superfamily (MFS) transport protein
FTT1257	<i>emrA1</i>	HlyD family secretion protein
FTT1276	<i>mgIB</i>	Macrophage growth locus, subunit B
FTT1286		Choloylglycine hydrolase family protein,pseudogene
FTT1295c	<i>glk</i>	Glucose kinase
FTT1304c	<i>murB</i>	UDP-N-acetylenolpyruvoylglucosamine reductase
FTT1313c	<i>greA</i>	Transcriptional elongation factor
FTT1329	<i>gpml</i>	2,3-bisphosphoglycerate-independent phosphoglycerate mutase
FTT1344	<i>pdpA</i>	Hypothetical protein
FTT1345	<i>pdpB</i>	Hypothetical protein
FTT1347		Hypothetical protein
FTT1349		Hypothetical protein
FTT1350		Hypothetical protein
FTT1351		Hypothetical protein
FTT1352		Hypothetical protein
FTT1354		Hypothetical protein
FTT1356c	<i>iglD</i>	Intracellular growth locus, subunit D
FTT1357c	<i>iglC</i>	Intracellular growth locus, subunit C
FTT1358c	<i>iglB</i>	Intracellular growth locus, subunit B
FTT1359c	<i>iglA</i>	Intracellular growth locus, subunit A
FTT1373	<i>fabH</i>	3-oxoacyl-[acyl carrier protein] synthase III
FTT1379c		Hypothetical protein, pseudogene
FTT1390	<i>panC</i>	Pantoate-beta-alanine ligase
FTT1392		Transcriptional regulator
FTT1402c		Hypothetical protein
FTT1418c	<i>nusB</i>	N utilisation substance protein B
FTT1419		Hypothetical lipoprotein
FTT1423c		Hypothetical membrane protein
FTT1461c	<i>wbtD</i>	Galacturonosyl transferase
FTT1479c		Hypothetical protein
FTT1503	<i>xerC</i>	Integrase/recombinase XerC
FTT1507		Hypothetical protein
FTT1508c	<i>relA</i>	GTP pyrophosphokinase
FTT1510c		Aromatic amino acid transporter of the HAAAP family
FTT1537c		Hypothetical protein
FTT1539c		Hypothetical protein
FTT1543		Two component response regulator
FTT1550		Hypothetical protein
FTT1591		Lipoprotein
FTT1602		Hypothetical lipoprotein
FTT1609		ABC transporter, membrane protein
FTT1645		Hypothetical membrane protien
FTT1649		Transglutaminase-like superfamily domain protein,pseudogene
FTT1656c		Hypothetical protein
FTT1679	<i>rpsT</i>	30S ribosomal protein S20
FTT1681c	<i>lpcA</i>	Phosphoheptose isomerase
FTT1684		Transcriptional regulator
FTT1724c	<i>tolC</i>	Outer membrane protein tolC precursor

FTT1726	<i>yegQ</i>	Protease yegQ
FTT1736c	<i>kdpD</i>	Two component sensor protein kdpD
FTT1746		Regulatory protein recX
FTT1753	<i>tdcD</i>	Propionate kinase
FTT1754	<i>pta</i>	Phosphate acetyltransferase
FTT1757c		Major facilitator superfamily (MFS) transport protein, pseudogene
FTT1768c		Chitinase
FTT1776c		Hypothetical membrane protein
FTT1783		Major facilitator superfamily (MFS) transport protein

**Table 1:** Amino acid sequences of genes expressed during *Francisella* infection were blasted against the database of essential genes using the BlastP algorithm and considered essential if their E-value fell below  $10^{-4}$ . Genes with an E-value greater than  $10^{-4}$  and less than 40% coverage of human genes were considered as candidate drug targets.

## Discussion:

In this study we identified the full transcriptome of the pulmonary bacterial pathogen *Francisella tularensis* during early and late stages of disseminated disease. Comparison of bacterial transcriptomes from the lung and spleen reveal the differential growth requirements necessary in each organ. Gene lists were subjected to ontology analysis to identify metabolic pathways necessary for bacterial survival in each condition and time point of infection. *Francisella* expression profiles throughout disease remained relatively similar with subtle differences in carbohydrate metabolism, protein biosynthesis, metal binding, and cofactor biosynthesis in the late stages of disease. During infection, *Francisella* necessitated transcriptional activity of 15-20 percent more of the encoded, annotated open reading frames in order to survive within host tissues as compared to *in vitro* growth. Expression trends were validated with quantitative RT-PCR, at high confidence revealing the sensitivity of next generation sequencing for transcriptional profiling of pathogen RNA isolated from host tissues. In addition to providing a greater understanding of the pathobiology of *Francisella* during the disease process, a total of 152 genes were identified as active, essential, and candidate drug targets with no significant homology to human proteins. In addition, we have compared *in vivo* grown bacteria with bacteria grown *in vitro* and noted only a small amount of overlap, 177 genes commonly expressed in all growth conditions. This has important implications on the traditional *in vitro* screening method of testing new chemotherapeutics as *in vitro* potency may be misleading when the biochemical pathways utilized during infection are so different than those expressed *in vitro*. The broad distribution of

genes expressed by *F. tularensis* during infection may be advantageous for the bacteria to rapidly adapt its metabolic flux around target pathways.

The sequencing of the *F. tularensis* Schu4 genome determined there were many “broken” metabolic pathways that seemed to be missing genes needed to synthesize many essential nutrients, leading the bacteria to rely on host nutrients available in the intracellular environment [18]. The conclusion was drawn that the purine and shikimate metabolic pathways could represent pathways that if disrupted, would lead to auxotrophic mutants for live vaccine candidates [18]. Indeed, throughout infection the expression of genes involved in *de novo* nucleic acid synthesis and aromatic amino acid biosynthesis were active at each time point. Two transposon mutagenesis studies that have confirmed mutants in pyrimidine and purine biosynthesis lead to attenuated phenotypes of *F. tularensis* Schu4 [19, 20], resulting in subsequent vaccination studies using a rationally developed purine auxotroph of *F. tularensis* Schu4 [21]. Our data indicate the activity of the shikimate-5-dehydrogenase (FTT0238) is active at all time points during infection and was on the list of 152 candidate drug targets predicted bioinformatically (Table 1). Interestingly, of the two transposon mutation studies in *F. tularensis* Schu4, this gene was never identified as essential however, a transposon study in *F. tularensis* LVS found the gene essential for efficient replication in murine macrophages [22]. There has been no further work to characterize the essentiality of FTT0238 in *F. tularensis* Schu4, which represents a gene in an established and essential metabolic pathway for a novel broad-spectrum antimicrobial drug target or a knockout vaccine candidate. In addition, there have been previous studies to test the antimicrobial efficacy of

inhibitors of bacterial dehydroquinate dehydratase (FTT0471), an enzyme upstream of shikimate dehydrogenase in the aromatic amino acid biosynthesis pathway, which was active in the spleen 96 hours post infection [23].

Another important finding of this study is a novel method of analyzing and deciphering disease mechanisms of *F. tularensis*. A common theme to expressed gene sets throughout the infection was the activity of hypothetical proteins, 30-35% of genes at each time point whose function remains undefined, often due to their inactivity during any laboratory manufactured growth condition. By developing short lists of hypothetical proteins unique to growth in specific organs at specific time points of disease, this more informed approach at studying *Francisella* virulence may lead to a better understanding of the disease.

Metabolic requirements for intracellular growth were previously shown to rely on *de novo* nucleotide synthesis, metabolism of vitamins and co-factors, protein biosynthesis, cell division, and carbohydrate metabolism [11]. We confirm these findings (Appendix III-VI) while also observing the activity of fatty acid metabolism, energy metabolism, and numerous transport and secretion genes (Appendix IV-VI). The necessity of bacterial pathogens to assemble and maintain cell membrane and cell wall components through the FASII system during infection is well documented and remains an important drug target for the development of novel chemotherapeutics [24]. Furthermore, the ability of the bacteria to sense and manipulate the surrounding environment through transport and secretion is highly important for an intracellular pathogen such as *Francisella*. We and other groups have previously demonstrated the evasion of host defenses by *F. tularensis* that is categorized by a dampened host response that does not

recognize the bacteria until late in the infection [5, 25, 26]. The abundance of transport and secretion genes expressed during infection provides evidence of an active mechanism used by the bacteria to manipulate the host response. This is the first report to identify the importance of these systems and specific genes active during the infection process of a gram-negative bacteria throughout early and late stages of disease, revealing the complexity of the pathogen-host interaction on a global scale.

Iron acquisition is a necessity for many intracellular pathogens and we have shown the *Francisella fsl* operon, found to encode a siderophore production pathway [27, 28], was active both early and late during infection in the lung. Activity of the *fsl* operon was not observed in the spleen, however iron is likely more abundant in the red pulp of the spleen where red blood cells are recycled. Previous studies show the importance of limiting dissemination to a positive outcome of disease for pulmonary pathogens [5, 29]. Targeting bacterial virulence mechanisms such as iron uptake machinery in bacterial infections is a relatively new theme in therapeutic development [6, 30] and disruption of iron uptake has shown *in vivo* efficacy in the mouse model of pulmonary tularemia [31]. Here we provide evidence of the activity of the iron uptake pathway of *F. tularensis* throughout infection in the lung, establishing the iron uptake pathway as a prime target to limiting growth in the lung and preventing dissemination.

The common dependence of *F. tularensis* on translation and protein biosynthesis during the infection likely explains the efficacy of aminoglycoside and tetracycline classes of antibiotics in the treatment of human infection. While this explains the activity of current lead therapeutics, the rapid emergence of



antibiotic resistance of clinical pathogens and the potential weaponization of priority agents requires the identification of novel broad-spectrum bacterial inhibitors. Using the transcriptionally active genes found throughout *Francisella* infection, we used a bioinformatic approach to determine genes for potential drug targets. Of the 415 genes expressed at every time point, 152 genes were found to have significant homology to genes in the Database of Essential Genes and no significant homology to human genes. The methods described in this study will allow researchers to expand the use of this technique to identify drug targets common to multiple agents.

The full potential of next generation sequencing technologies is far from realized however, the sensitivity of the technique provides endless opportunity for exploring research avenues thus far unattainable. One of the advantages of using next generation is that detection of transcripts does not rely on hybridization of sample to predetermined features. This allows for the detection of non-coding sequence that is transcribed, such as small regulatory RNAs and 5' un-translated regions (UTRs). Postic *et al* identified 24 putative small regulatory RNAs encoded in the *F. tularensis* LVS genome using a bioinformatic approach and experimentally validated the expression of 2 of the small regulatory RNAs [32]. All 24 small RNAs are encoded in the Schu4 genome and we observed the activity of 2 of the small RNAs during infection and 2 of the small RNAs *in vitro*. Although two small regulatory RNAs expressed during infection were only predicted bioinformatically, this report validates the expression of the non-coding RNAs and may represent transcriptional regulators important for virulence. One of the active small RNAs *in vitro* was the experimentally validated *ftrA*, shown to

negatively regulate the *de novo* nucleotide biosynthesis gene *pyrF* [32]. The essentiality of nucleotide biosynthesis for *F. tularensis* infectivity has been shown previously [19, 21] and the activity of *ptrA* *in vitro* may reflect a decreased need for *de novo* nucleotide biosynthesis in rich culture media.

Current studies in our laboratory are underway to define bacterial transcription during infection using *Mycobacteria*, *Burkholderia*, and *Yersinia*. In addition, studies are underway to functionally validate essential genes using a chemical saturation mutagenesis approach to eliminate transposon insertional bias and determine the minimal gene set required for *Francisella* infection by sequencing the recovered population and mapping genes that tolerate mutations.

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## CHAPTER 5

### 5.1 Final Discussion

#### **5.1.1 Genetic identification of unique immunological responses to *Francisella tularensis***

The ability of a host organism to respond effectively to a pulmonary infection relies on containment of the bacteria in the lungs and limiting dissemination to secondary organs. In addition, we have observed that antimicrobials that show efficacy in animals limit dissemination and lower bacterial burdens in secondary organs correlate with a positive disease outcome. We hypothesized that by comparing the host response to infection with the highly virulent lab strain *F. tularensis* Schu4 and the live vaccine strain LVS, we would be able to identify unique responses that provide mechanistic answers for the differing disease outcomes as well as identifying molecular correlates of disease progression. In addition to defining the molecular differences of disease, there was no study to date that characterized the differences between *F. tularensis* Schu4 and LVS in pathology and bacterial burden using the pulmonary route of infection. Importantly, this study provided us with landmarks of the disease process to be used in the future studies focused on bacterial gene expression throughout the infection. It was important that we identified key time points of the infection to properly isolate bacteria at different stages of infection such as early disease in the lung and late disease characterized by dissemination to secondary organs.

The goals in this study were to inform downstream studies of bacterial response during infection as well as identify molecular markers of bacterial dissemination to be used as a method to monitor therapeutic efficacy. As our group continues to develop chemotherapeutics to target priority pathogens with the main goal of containing the bacteria in the lung, molecular targets defined and tools developed from this study will be increasingly valuable in monitoring disease progression. In addition, by comparing the response to strains of low and high virulence, we identified a much larger set of genes that were modulated in response to *F. tularensis* LVS early in the infection as well as during dissemination. As strategies evolve for the therapeutic augmentation of the host response to better protect the host as well as inform the development of novel vaccines, this information can aid in mechanistically defining the protective immune response required for host survival.

The late stages of fatal infection caused by *Francisella* are characterized by expression of multiple potent cytokine and chemokine effectors that lead to multiple organ failure. The observation that multiple pro-apoptotic genes were expressed in response to *F. tularensis* LVS and not in response to Schu4 suggests that highly virulent strains of *Francisella* may interfere with apoptosis of host cells in order to avoid recognition and disseminate from the lung. There are multiple groups within our research consortium that aim to improve recognition of *Francisella* by the host with combinatorial administration of pro-inflammatory molecules and adjuvants with antimicrobial therapy with positive results. To test the hypothesis that disruption of apoptosis pathways during *Francisella* infection aids in the evasion of the host response and dissemination from the lungs, the



expression of the genes identified in my first study should be examined for expression in response to wild-type infection and in response to animals infected with highly virulent *Francisella* and treated with the combinatorial therapy. In order to determine the bacterial mechanism behind the alteration of host apoptotic pathways by *Francisella* is *via* a passive mechanism such as a cell wall component or active mechanism such as a secreted protein a simple exposure of host cells to heat killed bacteria or culture filtrate mixture could be employed. By monitoring the expression of apoptotic genes in response to the two treatments conclusions could be drawn about a bacterial mechanism. Cell wall fractions and culture filtrate fractions could be analyzed *via* mass spec to identify genes to be knocked out in order to identify specific bacterial genes responsible for disrupting host apoptotic pathways.

This study provided many significant advances to the field of *Francisella* pathobiology. It was the first study to directly compare and identify the differences in organ pathology caused by *F. tularensis* Schu4 and LVS during pulmonary infection. Additionally, it was the first study to compare molecular responses to infection from whole tissue with the Schu4 and LVS strains of *Francisella*. Furthermore, it was the first study to monitor the host transcriptional response to disseminated *Francisella* by examining the whole tissue response of the spleen during dissemination. The severe tissue damage caused by Schu4 in both the lung and the spleen coupled with the minimal transcriptional response when compared to LVS, reflected ability of Schu4 to evade host responses while rapidly spreading throughout the body and kill its host. Most importantly, the study provided us with a clear understanding of the timing of disease progression

and presented a framework to design subsequent experiments to monitor the bacterial response to infection.

### ***5.1.2 Transcriptional response of Francisella tularensis to growth in the lung and spleen of infected mice***

With our knowledge of the kinetics of dissemination determined by my first study we wanted to know what the bacterial transcriptional response was during infection. By defining the active transcriptional profile of *F. tularensis* in both the lung and the spleen, we hoped to identify the most clinically relevant drug targets for the development of novel therapeutics. In addition, we needed to identify metabolic requirements that were unique to each organ and time point so that genes expressed at all time points and in all organs could be prioritized as drug targets. The study was designed to assess *Francisella* transcription 48 hours post infection in the lungs, and 96 hours in the lung and spleen to monitor growth requirements early in the infection and during the latter stages of disseminated infection. In addition, message RNA from *F. tularensis* actively growing in culture was used for comparison to message RNA harvested from tissue. This comparison was particularly important to understand the differences in metabolic requirements that have implications in the translation of *in vitro* potency to *in vivo* efficacy. For proper translation, a drug target must be expressed and essential for growth in both the culture flask and during the infection.

This study was significant for several reasons. First, the utilization of next generation sequencing to capture the transcriptional profile of bacteria within host tissues is one of the first of its kind. Secondly, this was the first study to describe

tissue specific transcriptional adaptations of any bacteria. In addition, next generation sequencing is not limited by hybridization of material to predetermined sequence such as arrays, therefore the detection of RNA from regions of the genome previously thought to be non-coding sequence has important implications on annotation strategies as well as transcriptional regulation by small regulatory RNAs. Furthermore, the method outlined to capture and enrich for bacterial mRNAs from host tissue can be used on any model system and when transcriptional profiles of many pathogens begin to be published, broad spectrum antimicrobials can be developed for the most clinically relevant drug targets commonly expressed by bacterial pathogens. Finally, the expression of genes during the infection does not specifically imply essentiality for the disease process. A bioinformatic approach was used in this study to identify essential genes found to be transcriptionally active, however, experimental validation is needed to truly define the genes essential to the disease process. The experimental approaches used to validate predicted essential genes are discussed below in section 5.2.2.

There are steps that need to be taken to address the hypothesis that if particular pathways identified are inhibited the bacteria will die, thus establishing this experimental approach as a viable way to identify clinically relevant drug targets. Knockouts of essential genes both predicted and experimentally validated through mutagenesis studies should not be possible. There were several pathways identified in this study as metabolic choke points in *Francisella* that groups have developed inhibitors for such as aromatic amino acid biosynthesis, isoprenoid biosynthesis, fatty acid biosynthesis, and iron uptake. A

full study could be undertaken to first, determine the inhibitors affinity for the gene product encoded in the *Francisella* genome to test for cross reactivity between the *Francisella* homologue and the organism the drug was developed for. Second, the *in vitro* potency could be tested *via* MIC assays and finally, the drug could be tested for *in vivo* efficacy using the mouse model. This would establish the fact that the gene in question is indeed expressed during the infection, and the gene product is essential for the bacteria to cause infection, thus validating the approach as a viable method to determine clinically relevant drug targets.

## 5.2 Future Directions

### **5.2.1 Small regulatory RNA expression and function in *F. tularensis*.**

Small regulatory RNAs are found to be increasingly important for the regulation of transcription in many bacterial pathogens [1]. In *Francisella*, there have been over 20 small regulatory RNAs proposed by sequence analysis [2]. Our data suggest many previously un-annotated regions of sequenced being expressed may represent small regulatory RNA expression. Very little work has been done to characterize the function of small RNAs in *Francisella* and this represents an area of research in its infancy for many bacterial pathogens that can be exploited efficiently with technological capabilities at CSU. Addressing the question of which non-coding regions of sequence are expressed as RNA, constitute small regulatory RNAs, and which genes they regulate would have significant impact on the field of RNA biology and bacterial functional genomics.

### **5.2.2 Gene essentiality in *F. tularensis*.**

Experimental approaches to define gene essentiality have relied primarily on the disruption of genes based on insertional properties of mobile DNA elements and outgrowth on selective media. For prokaryotes, mobile DNA elements known as transposons have been used for their efficiency of movement throughout the genome [3]. Many classes of transposons have been studied and the sequence recognition site necessary for homologous recombination into the genome defines their utility for gene essentiality studies [3]. By relying on

sequence recognition, no matter how stringent, an inherent bias for transposition exists that does not allow for transposon mutagenesis saturation. In addition, in order to select for clones that have transposon insertions, an antibiotic selection marker is commonly engineered into the insertion sequence [3]. The expression of the antibiotic resistance marker therefore, must be inserted downstream of an active promoter. Downstream identification of genes with transposon insertions are biased only towards genes transcriptionally active in a given condition and cannot identify insertions in regulatory and promoter elements that may be essential to viability. In addition, it is generally understood that during homologous recombination of mobile DNA elements, genomic rearrangements at either end of the sequence insertion can frequently occur causing polar effects on genes adjacent to the actual gene containing the insertion [4]. Other polar effects such as insertional events that disrupt the expression of distal genes located on the same cistron are another source of bias introduced by traditional transposon mutagenesis studies [5]. Several transposon mutagenesis in the *Francisella* field have been informative for deciphering the unique disease process caused by the pathogen [4-8], however, in order to truly identify genes essential to a given growth condition new mutational strategies need to be developed.

The sequencing of the *Francisella* genome led researchers to believe that *de novo* nucleotide synthesis and aromatic amino acid biosynthesis are metabolic chokepoints essential to viability of the bacteria [9, 10]. Using transposon mutagenesis, both nucleotide biosynthesis and aromatic amino acid biosynthesis were identified as essential to *Francisella* viability and pathogenesis

and a purine auxotroph was engineered in the Schu4 strain in an attempt to develop a vaccine using the highly virulent Type A subspecies [4, 5, 11, 12]. Transposon mutagenesis studies in *Francisella* have primarily been used to identify virulence mechanisms due to the bacteria's high virulence and unique pathogenesis. In addition, the majority of these studies identified relatively few genes as essential and commonly excluded auxotrophic mutants from analysis to focus on deciphering virulence mechanisms. A bacterial pathogen's virulence is dependent on its ability to survive and replicate within a host organism. Mechanisms of pathogenesis stem from the ability to acquire and synthesize nutrients, therefore deciphering *Francisella* virulence must not only focus on unique virulence mechanisms, but any gene that is essential for the bacteria to infect the host. To address which genes are essential for *Francisella* to cause disease, we hypothesized that treatment of the bacteria with a chemical mutagen and sequencing the population of bacteria that survive treatment, we can identify genes unable to tolerate mutations that disrupt coding sequence and are therefore essential to survival. The initial studies that I conducted confirm that chemical mutagenesis is non-biased and saturating. Treatment for 60 minutes with mitomycin C resulted in a mutation frequency of one SNP every 168 base pairs resulting in 10,722 SNPs throughout the genome, with 9,079 of those resulting in non-synonymous amino acid changes. Nonsense mutations resulting in premature stop codons occurred in 258 annotated open reading frames. The selection media post treatment was a nutrient rich synthetic media so that the highest amount of mutations could be characterized, however, this led to many interruptions in genes that are generally accepted as essential. By treating the

bacteria with a chemical mutagen and infecting mice with the resulting population, the recovered bacteria that were still able to cause disease should show mutations only in genes non-essential to the disease process upon sequencing. This addresses the question of which genes are essential to *Francisella* infection, as well as addresses the aforementioned biases that tend to result from sequence based insertional strategies used in the past. These studies are currently underway.



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## APPENDIX

Appendix I: Global transcriptional data from the lungs of infected mice were compared to uninfected mice, log transformed, and subjected to ANOVA and Benjamini and Hochberg false positive correction. Genes that were differentially regulated by 1.5 fold or more with a variance less than 0.05 were considered significant. Genes of interest are discussed in depth in Chapter 3.

**Appendix A1: Genes uniquely expressed in the lungs of infected mice in response to infection with *Schu4* and *LVS***

Other ID	Gene Name	Gene ID	<i>Schu4</i> Infection								
			12	Direction	24	Direction	48	Direction	120	Direction	
M300007673	M300007673	-	-	-	-	-	-	1.8	Down	-	-
NM_080837	DNA segment, Chr 17, Wayne State University 104, expressed	D17Wsu104e	-	-	1.7	Up	2.1	Up	-	-	
NM_198001	RIKEN cDNA 1110008P14 gene	1110008P14	-	-	2.7	Up	2.9	Up	-	-	
M300008593	M300008593	-	2.1	Up	-	-	-	-	-	-	
NM_138659	Pre-mRNA processing factor 8	Prpf8	-	-	3.0	Up	3.7	Up	-	-	
NM_174990,	M400004812	-	-	-	2.2	Up	2.2	Up	-	-	
NM_175048	Protein tyrosine phosphatase, non-receptor type 6	Ptpn6	-	-	1.9	Up	-	-	-	-	
NM_013545	DEAH (Asp-Glu-Ala-His) box polypeptide 40	Dhx40	1.7	Down	-	-	-	-	-	-	
NM_026191	Eukaryotic translation initiation factor 6	Eif6	-	-	2.4	Up	3.0	Up	-	-	
NM_010579	Potassium inwardly-rectifying channel, subfamily J, member 8	Kcnj8	1.9	Up	-	-	-	-	-	-	
NM_008428											

NM_007638	Chaperonin subunit 7 (eta) V-maf musculoaponeurotic fibrosarcoma oncogene	Cct7	2.1	Up	-	-	-	-	-	-
NM_010755	family, protein F (avian) Leucine-rich repeat, immunoglobulin-like and transmembrane domains 1	Maff	-	-	1.5	Up	-	-	-	-
NM_146245	SAP30-like	Lrit1	-	-	-	-	1.7	Down	-	-
XM_203577	M400018877	-	-	-	-	-	1.7	Up	-	-
M400018877	M400018877	-	-	-	-	-	1.5	Down	-	-
NR_000040	thymidylate synthase, pseudogene	-	-	-	-	-	2.2	Down	-	-
NM_013705	Zinc finger protein 30	Zfp30	-	-	-	-	1.5	Down	-	-
NM_172453	PIF1 5-to-3 DNA helicase homolog (S. cerevisiae)	Pif1	-	-	-	-	1.5	Down	-	-
NM_144800	Metastasis suppressor 1	Mtss1	-	-	-	-	2.1	Up	-	-
NM_024176	Dr1 associated protein 1 (negative cofactor 2 alpha)	Drap1	-	2.7	Up	-	-	4.3	Up	-
M400002294	M400002294	-	-	-	-	-	-	1.6	Down	-
	Ras association (RalGDS/AF-6) domain family member 1	Rassf1	-	-	2.9	Up	-	2.6	Up	-
NM_019713	M400014858	-	-	-	-	-	-	1.9	Down	-
		A730011L01								
NM_177394	RIKEN cDNA A730011L01 gene	Rik	-	-	-	-	1.6	Down	-	-
NM_205819	Toll-like receptor 11	Tlr11	-	-	1.6	Down	-	2.2	Down	-
M400003725	M400003725	-	-	-	1.7	Up	-	-	-	1.5
XM_147082	gene model 520, (NCBI)	-	-	-	-	-	-	-	-	1.5
NM_008303	Heat shock protein 1 (chaperonin 10)	Hspe1	-	-	-	-	-	-	-	1.5
NM_028416	Kringle containing transmembrane protein 2	Kremen2	-	-	-	-	-	-	-	1.5
NM_025493	RIKEN cDNA 1700018B24 gene	-	-	-	-	-	-	-	-	1.5
NM_028821	Dynein, axonemal, light chain 1	Dnalc1	-	-	-	-	-	-	-	1.5
NM_010221	FK506 binding protein 10	Fkbp10	-	-	-	-	1.7	Up	-	1.5
M400015437	M400015437	-	-	-	-	-	-	-	-	1.5
NM_011196	Prostaglandin E receptor 3 (subtype EP3)	Ptger3	-	-	-	-	-	-	-	1.5
NM_029083	DNA-damage-inducible transcript 4	Ddit4	-	-	-	-	1.5	Down	-	1.5
M400010795	M400010795_90	-	-	-	2.8	Up	-	-	-	1.5
M400005665	M400005665	-	-	-	-	-	-	-	-	1.5
M400010453	M400010453	-	-	-	-	-	-	-	-	1.5
XM_283202	M400003910	-	-	-	-	-	-	-	-	1.5
NM_011948	Mitogen-activated protein kinase kinase kinase 4	Map3k4	-	-	-	-	1.0	Up	-	1.5
NM_020515	Olfactory receptor 140	Olf140	-	-	-	-	1.6	Down	-	1.5
M400010096	M400010096	-	-	-	-	-	-	-	-	1.5
M400017666	M400017666	-	-	-	-	-	-	-	-	1.5
XM_146411	zinc finger protein 791	-	-	-	-	-	-	-	-	1.5
M300000918	M300000918	-	-	-	-	-	-	-	-	1.5
NM_009426	Thyrotropin releasing hormone	Trh	-	-	-	-	-	-	-	1.5
XM_485947	M400006313	-	-	-	-	-	-	-	-	1.5
NM_175411,										
NM_194257	M400003692	-	-	-	-	-	-	-	-	1.5
M400008558	M400008558	-	-	-	-	-	1.6	Down	-	1.5

XM_143327	gene model 414, (NCBI)	-	-	-	2.1	Up	-	-	1.5	Up
NM_134103	Interleukin 1 receptor accessory protein	Il1rap	-	-	-	-	-	-	1.5	Down
M400001633	M400001633	-	-	-	-	-	-	-	1.5	Up
M300020990	M300020990	-	-	-	-	-	-	-	1.5	Down
NM_029017	Mitochondrial ribosomal protein L47	Mrpl47	-	-	-	-	-	-	1.5	Down
XM_358393	M400003385	-	-	-	-	-	-	-	1.5	Down
NM_011314	Serum amyloid A 2	Saa2	-	-	1.7	Up	-	-	1.5	Up
M400001060	M400001060	-	-	-	-	-	-	-	1.5	Down
NM_139300	Myosin, light polypeptide kinase	Mylk	-	-	-	-	-	-	1.5	Up
NM_153540	Expressed sequence C85492	C85492	-	-	-	-	-	-	1.5	Up
XM_487217	M400009936	-	-	-	-	-	-	-	1.5	Up
NM_146247	CDNA sequence BC024814	BC024814	-	-	-	-	-	-	1.6	Down
M400010305	M400010305	-	-	-	-	-	-	-	1.6	Down
XM_128932	solute carrier family 27 (fatty acid transporter), member 6	-	-	-	-	-	-	-	1.6	Down
M400006343	M400006343	-	-	-	-	-	-	-	1.6	Down
NM_027033,										
NM_145692	M400000870	-	-	-	-	-	-	-	1.6	Down
XM_128189	patatin-like phospholipase domain containing 5	-	-	-	-	-	1.4	Down	1.6	Down
NM_134115	Serine/threonine kinase 38	Stk38	-	-	-	-	-	-	1.6	Down
NM_008413	Janus kinase 2	Jak2	-	-	-	-	-	-	1.6	Down
NM_022313	Era (G-protein)-like 1 (E. coli)	Eral1	-	-	-	-	-	-	1.6	Down
NM_023219	Solute carrier family 5 (neutral amino acid transporters, system A), member 4b	Slc5a4b	-	-	-	-	-	-	1.6	Down
NM_199042	THAP domain containing, apoptosis associated protein 1	Thap1	-	-	-	-	-	-	1.6	Down
NM_020618	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1	Smarca1	-	-	1.7	Up	-	-	1.6	Down
M300005757	M300005757	-	-	-	-	-	-	-	1.6	Up
NM_007730	Collagen, type XII, alpha 1	Col12a1	-	-	-	-	-	-	1.6	Up
NM_025793	Wdr45 like	Wdr45l	-	-	-	-	-	-	1.6	Down
NM_146834	Olfactory receptor 101	Olf101	-	-	-	-	-	-	1.6	Up
NM_028780	Transmembrane 9 superfamily member 1	Tm9sf1	-	-	-	-	-	-	1.6	Down
NM_023731	Coiled-coil domain containing 86	Ccdc86	-	-	-	-	-	-	1.6	Down
NM_027307	Golgi membrane protein 1	Golm1	-	-	-	-	-	-	1.6	Down
XM_128090	La ribonucleoprotein domain family, member 4	-	-	-	-	-	-	-	1.6	Down
NM_011720	Wingless related MMTV integration site 8b	Wnt8b	-	-	-	-	2.8	Down	1.6	Down
M400013404	M400013404	-	-	-	-	-	-	-	1.6	Down
M400017026	M400017026	-	-	-	-	-	-	-	1.6	Up
NM_008923	Protein kinase, cAMP dependent regulatory, type I beta	Prkar1b	-	-	-	-	1.8	Down	1.6	Down
M200001442	M200001442	-	-	-	-	-	-	-	1.6	Down
M300009963	M300009963	-	-	-	-	-	-	-	1.6	Down
NM_010266	Guanine deaminase	Gda	-	-	-	-	-	-	1.6	Down
NM_024239	Stam binding protein	Stampb	-	-	-	-	-	-	1.6	Down
NM_027869	Polyribonucleotide nucleotidyltransferase 1	Pnpt1	-	-	-	-	-	-	1.6	Down

XM_484816	M200006929	-	-	-	1.8	Up	1.1	Up	1.6	Down
		1810030N24								
NM_025471	RIKEN cDNA 1810030N24 gene	Rik	-	-	-	-	-	-	1.6	Down
NM_029352	Dual specificity phosphatase 9	Dusp9	-	-	-	-	-	-	1.6	Up
	Potassium channel tetramerisation domain containing									
NM_027782	6	Kctd6	-	-	-	-	-	-	1.6	Down
NM_021498	Polymerase (DNA directed), epsilon 3 (p17 subunit)	Pole3	-	-	-	-	-	-	1.6	Up
NM_027790	Dehydrogenase/reductase member 2	Dhrs2	-	-	-	-	-	-	1.6	Up
NM_177130	Glycosyltransferase 28 domain containing 2	Glt28d2	-	-	-	-	-	-	1.6	Down
NM_009221	Synuclein, alpha	Snca	-	-	2.9	Up	-	-	1.6	Down
NM_024266	Ribosomal protein S25	Rps25	-	-	-	-	-	-	1.6	Down
M400008398	M400008398	-	-	-	-	-	-	-	1.6	Down
M400003249	M400003249	-	-	-	-	-	-	-	1.6	Down
NM_007828	Death-associated kinase 3	Dapk3	-	-	-	-	-	-	1.6	Down
NM_130890	Calpain 8	Capn8	-	-	-	-	-	-	1.6	Down
NM_026916	RIKEN cDNA 4930579G22 gene	-	-	-	-	-	-	-	1.6	Down
XM_129726	WD repeat domain 75	-	-	-	-	-	-	-	1.6	Down
NM_008156	Glycosylphosphatidylinositol specific phospholipase D1	Gpld1	-	-	-	-	-	-	1.6	Up
NM_008391	Interferon regulatory factor 2	Irf2	-	-	-	-	-	-	1.6	Up
NM_013692	Kruppel-like factor 10	Klf10	-	-	-	-	-	-	1.6	Down
XM_111014	predicted gene, OTTMUSG00000003135	-	-	-	-	-	-	-	1.6	Down
NM_145384	PQ loop repeat containing 2	Pqlc2	-	-	-	-	-	-	1.6	Up
XM_136343	gene model 205, (NCBI)	-	-	-	-	-	-	-	1.6	Up
NM_029610	LYR motif containing 1	Lym1	-	-	-	-	-	-	1.6	Down
XM_110248	F-box protein 11	-	-	-	-	-	-	-	1.6	Down
NM_172829	Beta galactoside alpha 2,6 sialyltransferase 2	St6gal2	-	-	-	-	-	-	1.6	Down
M400006633	M400006633	-	-	-	-	-	-	-	1.6	Down
NM_021420	Serine/threonine kinase 4	Stk4	-	-	-	-	-	-	1.7	Down
NM_007892	E2F transcription factor 5	E2f5	-	-	-	-	-	-	1.7	Down
M400013835	M400013835	-	-	-	-	-	-	-	1.7	Down
M400005359	M400005359	-	-	-	-	-	-	-	1.7	Up
NM_011192	Proteasome (prosome, macropain) 28 subunit, 3	Psme3	-	-	-	-	-	-	1.7	Up
M200014124	M200014124	-	-	-	-	-	-	-	1.7	Down
XM_124781	M400002157	-	-	-	-	-	-	-	1.7	Down
	Solute carrier family 5 (sodium iodide symporter),									
NM_053248	member 5	Slc5a5	-	-	-	-	-	-	1.7	Down
M400013647	M400013647	-	-	-	-	-	-	-	1.7	Down
NM_009417	Thyroid peroxidase	Tpo	-	-	-	-	-	-	1.7	Up
	Serine (or cysteine) peptidase inhibitor, clade A,									
NM_009252	member 3K	Serpina3k	-	-	-	-	-	-	1.7	Up
NM_207536	MAS-related GPR, member B1	Mrgprb1	-	-	-	-	1.6	Down	1.7	Down
M400013035	M400013035	-	-	-	-	-	2.0	Down	1.7	Down
M400012956	M400012956	-	-	-	-	-	-	-	1.7	Down
M400010635	M400010635	-	-	-	-	-	-	-	1.7	Down
NM_029456	SAPS domain family, member 3	Saps3	-	-	-	-	-	-	1.7	Down

NM_054054	Bromodomain, testis-specific	Brdt	-	-	-	-	-	-	-	1.7	Down	
M400014561	M400014561	-	-	-	-	-	-	-	-	1.7	Down	
NM_007482	Arginase 1, liver	Arg1	-	-	-	-	-	-	-	1.7	Up	
NM_172379	Expressed sequence AA536717	AA536717	-	-	-	-	-	-	-	1.7	Down	
NM_172685	Solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 24	Slc25a24	-	-	-	-	-	-	-	1.7	Down	
M300009833	M300009833	-	-	-	-	-	-	-	-	1.7	Down	
NM_009536	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	Ywhae	-	-	-	-	-	-	-	1.7	Down	
NM_030178	Bromodomain and PHD finger containing, 1	Brpf1	-	-	-	-	-	1.3	Down	1.7	Down	
M400013514	M400013514	-	-	1.6	Down	-	-	-	-	1.7	Down	
M400004435	M400004435	-	-	-	-	-	-	-	-	1.7	Up	
NM_007494,												
XM_483909	M400000966	-	-	-	-	-	-	-	-	1.7	Up	
M400004615	M400004615	-	-	-	-	1.9	Down	-	-	1.7	Down	
NM_011570	testis derived transcript	-	-	-	-	-	-	-	-	1.7	Down	
M400014988	M400014988	-	-	-	-	-	-	-	-	1.7	Up	
NM_011469	Small proline-rich protein 2B	Sprp2b	-	-	-	-	-	-	-	1.7	Down	
M400013168	M400013168	-	-	-	-	-	-	-	-	1.7	Down	
NM_053245	Aryl hydrocarbon receptor-interacting protein-like 1	Aipl1	-	-	-	-	-	-	-	1.7	Down	
NM_023056	Transmembrane protein 176B	Tmem176b	-	-	-	3.7	Up	-	3.8	Up	1.7	Up
NM_198610	Immunoglobulin superfamily, member 21	Igsf21	-	-	-	-	-	-	-	1.7	Down	
NM_029235	RIKEN cDNA 4930556L07 gene	-	-	-	-	-	-	-	-	1.7	Down	
M400018855	M400018855	-	-	-	-	-	-	-	-	1.7	Down	
NM_007896	Microtubule-associated protein, RP/EB family, member 1	Mapre1	-	-	-	-	-	-	-	1.7	Down	
NM_025695	Structural maintenance of chromosomes 6	Smc6	-	-	-	-	-	-	-	1.7	Down	
		1700037H04										
NM_026091	RIKEN cDNA 1700037H04 gene	Rik	-	-	-	-	-	-	-	1.7	Down	
NM_176963	Galactose mutarotase	Galm	-	-	-	-	-	-	-	1.7	Up	
NM_145369	WAP four-disulfide core domain 5	Wfdc5	-	-	-	-	-	-	-	1.7	Up	
M400013105	M400013105	-	-	-	-	-	-	-	-	1.7	Down	
M400013943	M400013943	-	-	-	-	-	-	-	-	1.7	Up	
NM_008809	Platelet derived growth factor receptor, beta polypeptide	Pdgfrb	-	-	-	-	-	-	-	1.7	Down	
NM_011932	Dual adaptor for phosphotyrosine and 3-phosphoinositides 1	Dapp1	-	-	-	-	-	-	-	1.7	Down	
NM_175125	RIKEN cDNA 1500011K16 gene	-	-	-	-	-	-	-	-	1.7	Down	
XM_129477	calmodulin regulated spectrin-associated protein 1-like 1	-	-	-	-	-	-	-	-	1.7	Up	
XM_130010	ribonuclease P/MRP 38 subunit (human)	-	-	-	-	-	-	-	-	1.7	Down	
XM_484324	M400007481	-	-	-	-	-	-	-	-	1.7	Down	
NM_146257	Solute carrier family 29 (nucleoside transporters), member 4	Slc29a4	-	-	-	-	-	-	-	1.7	Down	
NM_177460	Poly (ADP-ribose) polymerase family, member 16	Parp16	-	-	-	-	-	-	-	1.7	Down	

NM_177708	Reticulon 4 receptor-like 1	Rtn4r1	-	-	-	-	-	-	1.7	Up	
M400010148	M400010148	-	-	-	-	-	-	1.1	Down	1.7	Down
NM_001005											
846,NM_026											
656	M200008835	-	-	-	-	-	-	-	-	1.7	Down
NM_008663	Myosin VIIa	Myo7a	-	-	-	-	-	-	-	1.7	Down
M400012744	M400012744	-	-	-	-	-	-	2.0	Down	1.8	Down
M400014375	M400014375	-	-	-	-	-	-	-	-	1.8	Down
		1700080E11									
NM_028562	RIKEN cDNA 1700080E11 gene	Rik	-	-	-	-	-	1.7	Down	1.8	Down
M400000890	M400000890	-	-	-	-	-	-	-	-	1.8	Down
NM_021512	Nucleoporin 160	Nup160	-	-	-	-	-	-	-	1.8	Down
NM_007935,											
NM_027497	M300004011	-	-	-	-	-	-	-	-	1.8	Up
NM_008477	Kinectin 1	Ktn1	-	-	-	-	-	-	-	1.8	Down
NM_172051	Transmembrane and coiled coil domains 3	Tmcc3	-	-	-	-	-	-	-	1.8	Up
NM_007542	Biglycan	Bgn	-	-	-	-	-	-	-	1.8	Down
NM_010140	Eph receptor A3	Epha3	-	-	-	-	-	-	-	1.8	Down
NM_183315	Cortxin 1	Ctxn1	-	-	-	-	-	1.5	Down	1.8	Down
NM_010663	Keratin 17	Krt17	1.8	Down	-	-	-	4.3	Down	1.8	Down
NM_011237	RAD9 homolog (S. pombe)	Rad9	-	-	-	-	-	-	-	1.8	Down
M400005179	M400005179	-	-	-	-	-	-	-	-	1.8	Down
		2410022L05									
NM_025556	RIKEN cDNA 2410022L05 gene	Rik	-	-	-	-	-	-	-	1.8	Down
M400002187	M400002187	-	-	-	-	-	-	-	-	1.8	Down
	Eukaryotic elongation factor, selenocysteine-tRNA-										
NM_023060	specific	Eefsec	-	-	-	-	-	-	-	1.8	Down
M300001073	M300001073	-	-	-	-	-	-	-	-	1.8	Down
NM_011177	Kallikrein related-peptidase 6	Klk6	-	-	-	-	-	-	-	1.8	Down
	Eukaryotic translation initiation factor 4E binding										
NM_201256	protein 3	Ankhd1	-	-	-	-	-	-	-	1.8	Up
M200008390	M200008390	-	-	-	-	-	-	-	-	1.8	Down
NM_007967	Even skipped homeotic gene 2 homolog	Evx2	-	-	-	-	-	-	-	1.8	Up
NM_016902	Nephronophthisis 1 (juvenile) homolog (human)	Nphp1	-	-	-	-	-	-	-	1.8	Down
NM_134042	Aldehyde dehydrogenase family 6, subfamily A1	Aldh6a1	-	-	-	-	-	-	-	1.8	Down
M400013016	M400013016	-	-	-	-	-	-	-	-	1.8	Down
NM_172413	RAP2C, member of RAS oncogene family	Rap2c	-	-	-	-	-	-	-	1.8	Down
XM_127496	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	-	-	-	-	-	-	-	-	1.8	Up
M400004139	M400004139	-	-	-	2.0	Up	-	2.5	Up	1.8	Up
NM_026172	2,4-dienoyl CoA reductase 1, mitochondrial	Decr1	-	-	-	-	-	-	-	1.8	Down
XM_133252	predicted gene, EG232993	-	-	-	-	-	-	-	-	1.8	Down
NM_146656	Olfactory receptor 444	Olf444	-	-	-	-	-	2.3	Down	1.8	Down
M200003086	M200003086	-	-	-	-	-	-	-	-	1.8	Down
M400018212	M400018212	-	-	-	-	-	-	-	-	1.8	Down
NM_009075	Ribose 5-phosphate isomerase A	Rpia	-	-	-	-	-	-	-	1.8	Down



NM_153396	Microtubule associated monooxygenase, calponin and LIM domain containing 3	Mical3	-	-	-	-	-	-	-	1.8	Down
XM_134104	M400006392	-	-	-	-	-	-	-	-	1.8	Down
M400008278	M400008278	-	-	-	-	-	-	-	-	1.8	Down
XM_193795	zinc finger CCCH type containing 7B	-	-	-	-	-	-	1.0	Down	1.8	Down
M300003185	M300003185	-	-	-	-	-	-	-	-	1.8	Up
NM_139296	Monooxygenase, DBH-like 2	Moxd2	-	-	-	-	-	-	-	1.8	Down
XM_133542	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 17	-	-	-	-	-	-	1.4	Down	1.8	Down
NM_011857	Odd Oz/ten-m homolog 3 (Drosophila)	Odz3	-	-	-	-	-	-	-	1.8	Down
M200005039	M200005039	-	-	-	-	-	-	-	-	1.8	Down
NM_080795	Ligand of numb-protein X 2	Lnx2	-	-	-	-	-	-	-	1.8	Down
NM_172859	RIKEN cDNA 6330439K17 gene	6330439K17	-	-	-	-	-	-	-	1.8	Down
M400012930	M400012930	Rik	-	-	-	-	-	-	-	1.8	Down
M400019500	M400019500	-	-	-	-	-	-	-	-	1.8	Down
NM_016852	WW domain binding protein 2	Wbp2	1.5	Up	-	-	-	-	-	1.8	Up
NM_019551	Traf and Tnf receptor associated protein	Ttrap	1.6	Up	-	-	-	-	-	1.8	Up
NM_010448	Heterogeneous nuclear ribonucleoprotein A/B	Hnrnpab	-	-	-	-	-	-	-	1.8	Down
NM_018742	Blocked early in transport 1 homolog (S. cerevisiae)-like	Bet1l	-	-	-	-	-	-	-	1.8	Down
NM_146090	Zinc binding alcohol dehydrogenase, domain containing 2	Zadh2	-	-	-	-	-	-	-	1.8	Down
NM_146618	Olfactory receptor 297	Olf297	-	-	-	-	-	-	-	1.8	Down
M400000586	M400000586	-	-	-	2.5	Up	-	2.1	Up	1.8	Up
M400003791	M400003791	-	1.6	Up	-	-	-	-	-	1.8	Up
M400004905	M400004905	-	-	-	-	-	-	-	-	1.8	Up
M400006274	M400006274	-	-	-	-	-	-	-	-	1.8	Up
NM_019739	Forkhead box O1	Foxo1	-	-	-	-	-	-	-	1.8	Down
NM_177016	Solute carrier family 17 (sodium phosphate), member 4	Slc17a4	-	-	-	-	-	-	-	1.8	Up
XM_139743	M400007394	-	-	-	-	-	-	-	-	1.8	Down
NM_053208	EGL nine homolog 2 (C. elegans)	Egln2	-	-	-	-	-	-	-	1.8	Down
XM_488556	RIKEN cDNA 1700027J07 gene	-	-	-	-	-	-	-	-	1.8	Down
NM_026810	MutL homolog 1 (E. coli)	Mlh1	-	-	-	-	-	-	-	1.8	Down
NM_053158	Mitochondrial ribosomal protein L1	Mrpl1	-	-	-	-	-	-	-	1.8	Down
NM_021288	Thymidylate synthase	Tyms	-	-	-	-	-	1.4	Down	1.8	Down
XM_128466	protease, serine, 32	-	-	-	-	-	-	-	-	1.8	Up
NM_010602	Potassium inwardly rectifying channel, subfamily J, member 11	Kcnj11	-	-	-	-	-	-	-	1.8	Down
NM_138755	PHD finger protein 21A	Phf21a	-	-	-	-	-	-	-	1.8	Down
XM_125904	SLIT-ROBO Rho GTPase activating protein 1	-	-	-	-	-	-	-	-	1.8	Up
NM_138311	H1 histone family, member O, oocyte-specific	H1foo	-	-	-	-	-	-	-	1.8	Down
NM_174995	Microsomal glutathione S-transferase 2	Mgst2	-	-	-	-	-	-	-	1.8	Down
NM_025703	Transcription elongation factor A (SII)-like 8	Tceal8	-	-	-	-	-	-	-	1.8	Down
NM_026879	Chromatin modifying protein 2B	Chmp2b	-	-	-	-	-	-	-	1.8	Down

M400013087	M400013087	-	-	-	-	-	-	1.8	Down	
NM_021274	Chemokine (C-X-C motif) ligand 10	Cxcl10	-	-	-	-	-	1.8	Up	
NM_011580	Thrombospondin 1	Thbs1	-	-	-	-	-	1.8	Up	
NM_024189	YY1 associated factor 2	Yaf2	-	-	-	-	-	1.8	Down	
M400007044	M400007044	-	-	-	-	-	-	1.8	Down	
NM_001005	223	Zinc finger, HIT type 3	Znhit3	-	-	-	-	1.8	Down	
NM_144509	ADP-ribosylation factor-like 6 interacting protein 4	Arl6ip4	-	-	-	-	-	1.8	Down	
NM_147119	Olfactory receptor 632	Olf632	-	-	-	-	-	1.8	Down	
NM_009717	Neurogenic differentiation 6	Neurod6	-	-	-	-	-	1.9	Up	
NM_011603	TATA box binding protein-like 1	Tbpl1	-	-	-	-	-	1.9	Down	
XM_181390	collagen, type XX, alpha 1	-	-	-	-	-	-	1.9	Down	
M400000934	M400000934	-	-	-	-	-	-	1.9	Down	
NM_026856	Zinc finger protein 644	Zfp644	-	-	-	-	-	1.9	Down	
XM_204369	M400008851	-	-	-	-	-	-	1.9	Up	
NM_147077	Olfactory receptor 643	Olf643	-	-	-	-	-	1.9	Down	
NM_178060	Thyroid hormone receptor alpha	Thra	-	-	1.7	Up	1.8	Up	1.9	Down
M400010139	M400010139	-	-	-	1.6	Up	-	-	1.9	Up
NM_183257	Hepcidin antimicrobial peptide 2	Hamp2	-	-	-	-	-	-	1.9	Up
M400006264	M400006264	-	-	-	-	-	-	-	1.9	Down
NM_009355	Testicular serine protease 1	Tesp1	-	-	-	-	-	-	1.9	Down
NM_023530	Phospholipase A2, group XIIB	Pla2g12b	-	-	-	-	-	-	1.9	Down
M400005831	M400005831	-	-	-	-	-	2.2	Down	1.9	Down
NM_001002	786, XM_484	619	M400008569	-	-	-	-	-	1.9	Down
M200002400	M200002400	-	-	-	-	-	-	-	1.9	Down
M400008400	M400008400	-	-	-	-	-	-	-	1.9	Down
NM_027274	RIKEN cDNA 2810025M15 gene	-	-	-	-	-	1.9	Up	1.9	Down
NM_007606	Carbonic anhydrase 3	Car3	-	-	-	-	-	-	1.9	Down
XM_486005	M400007400	-	-	-	-	-	-	-	1.9	Down
XM_131103	adenosine monophosphate deaminase 1 (isoform M)	-	-	-	-	-	1.8	Down	1.9	Down
NM_173376	RNA binding motif protein, X-linked 2	Rbmx2	-	-	-	-	-	-	1.9	Down
M400004574	M400004574	-	-	-	-	-	1.8	Down	1.9	Down
NM_019813	Drebrin 1	Dbn1	-	-	-	-	-	-	1.9	Down
NM_011906	G protein-coupled receptor 175	Gpr175	-	-	-	-	-	-	1.9	Up
M400013361	M400013361	-	-	-	-	-	-	-	1.9	Down
XM_129811	coiled-coil domain containing 115	-	-	-	-	-	-	-	1.9	Down
M400016620	M400016620	-	-	-	-	-	-	-	1.9	Down
NM_021340	Retinal G protein coupled receptor	Rgr	-	-	-	-	-	-	1.9	Up
NM_080558	Sperm specific antigen 2	Ssfa2	-	-	-	-	1.6	Down	1.9	Down
NM_133854	SNAP-associated protein	Snapin	-	-	-	-	-	-	1.9	Down
M300021278	M300021278	-	-	-	-	-	-	-	1.9	Up
M400002447	M400002447	-	-	-	-	-	-	-	1.9	Down
NM_011797	Carbonic anhydrase 14	Car14	-	-	-	-	-	-	1.9	Down

NM_026484	Cyclin Y	Ccny	-	-	-	-	-	-	1.9	Down	
XM_356200	solute carrier family 22 (organic cation transporter), member 14	-	-	-	-	-	-	1.9	Down	1.9	Down
M200002576	M200002576	-	-	-	-	-	-	-	-	1.9	Up
NM_010129	Epithelial membrane protein 3	Emp3	-	-	-	-	-	-	-	1.9	Down
NM_011402	Solute carrier family 34 (sodium phosphate), member 2	Slc34a2	-	-	-	-	-	-	-	1.9	Down
NM_026168	ERGIC and golgi 2	Ergic2	-	-	-	-	-	-	-	1.9	Down
M400009849	M400009849	-	-	-	-	-	-	-	-	1.9	Down
M400013308	M400013308	-	-	-	-	-	-	2.3	Down	1.9	Down
M400018824	M400018824	-	-	-	-	-	-	-	-	1.9	Down
NM_010846	Myxovirus (influenza virus) resistance 1	Mx1	-	-	-	-	-	-	-	1.9	Up
NM_153173,											
NM_175656,											
NM_175657,											
NM_178192,											
NM_178193,	M400012321	-	-	-	-	-	-	-	-	1.9	Down
XM_129042	RIKEN cDNA 8030462N17 gene	Rnf165	-	-	-	-	-	-	-	1.9	Down
NM_021536	Ras homolog gene family, member T1	Rhot1	-	-	-	-	-	-	-	1.9	Down
XM_284281	Yip1 interacting factor homolog B (S. cerevisiae)	-	-	-	-	-	-	-	-	1.9	Down
M300019285	M300019285	-	-	-	-	-	-	-	-	2.0	Down
		C330023M0									
NM_172722	RIKEN cDNA C330023M02 gene	2Rik	-	-	-	-	-	-	-	2.0	Down
NM_009416	Tropomyosin 2, beta	Tpm2	-	-	-	-	-	1.9	Down	2.0	Down
NM_021890	Fatty acid desaturase 3	Fads3	-	-	2.1	Down	-	2.2	Down	2.0	Down
M200012858	M200012858	-	-	-	-	-	-	-	-	2.0	Up
	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited)	-	-	-	-	-	-	-	-	2.0	Down
XM_129376											
NM_011288	Mitochondrial ribosomal protein L23	Mrpl23	-	-	-	-	-	1.5	Up	2.0	Down
M400015350	M400015350	-	-	-	-	-	-	2.1	Down	2.0	Down
M400009638	M400009638	-	-	-	-	-	-	2.1	Up	2.0	Up
M400007133	M400007133	-	-	-	-	-	-	-	-	2.0	Down
NM_009143	Stromal cell derived factor 2	Sdf2	-	-	-	-	-	-	-	2.0	Down
NM_009459	Ubiquitin-conjugating enzyme E2H	Ube2h	-	-	-	-	-	-	-	2.0	Down
NM_007957	Extraembryonic, spermatogenesis, homeobox 1	Esx1	-	-	-	-	-	-	-	2.0	Down
NM_145393	YTH domain family 2	Ythdf2	-	-	-	-	-	-	-	2.0	Down
M400013337	M400013337	-	-	-	-	-	-	1.7	Down	2.0	Down
XM_141816	predicted gene, EG236844	-	-	-	-	-	-	-	-	2.0	Down
NM_008470	Keratin 16	Krt16	-	-	-	-	-	-	-	2.0	Up
NM_011358	Splicing factor, arginine/serine-rich 2 (SC-35)	Sfrs2	-	-	-	-	-	-	-	2.0	Down
NM_016763	Hydroxysteroid (17-beta) dehydrogenase 10	Hsd17b10	-	-	-	-	-	-	-	2.0	Down
	Solute carrier family 16 (monocarboxylic acid transporters), member 11	Slc16a11	-	-	-	-	-	-	-	2.0	Down
NM_153081											
M300004656	M300004656	-	-	-	-	-	-	-	-	2.0	Down
		1500031L02									
NM_025892	RIKEN cDNA 1500031L02 gene	Rik	-	-	-	-	-	-	-	2.0	Down

NM_013762	Ribosomal protein L3	Rpl3	3.0	Up	4.3	Up	4.1	Up	2.0	Up
NM_028447	Proline-rich coiled-coil 1	Prrc1	-	-	-	-	-	-	2.0	Down
NM_177325	TSR1, 20S rRNA accumulation, homolog (yeast)	Tsr1	-	-	-	-	-	-	2.0	Down
NM_175157	RIKEN cDNA 2610204G22 gene	-	-	-	-	-	-	-	2.0	Down
M400010561	M400010561	-	-	-	-	-	-	-	2.0	Down
M400018605	M400018605	-	-	-	-	-	-	-	2.0	Up
NM_025594	Zinc finger, matrin type 2	Zmat2	-	-	-	-	-	-	2.0	Down
NM_145484	Zinc finger protein 758	Zfp758	-	-	-	-	-	-	2.0	Down
M400006361	M400006361	-	-	-	-	-	-	-	2.0	Down
M400013711	M400013711	-	-	-	-	-	-	-	2.0	Down
NM_009808	Caspase 12	Casp12	-	-	-	-	-	-	2.0	Down
		1110001A07								
NM_025377	RIKEN cDNA 1110001A07 gene	Rik	-	-	-	-	-	-	2.0	Down
XM_356087	unc-13 homolog A (C. elegans)	-	-	-	-	-	-	-	2.0	Down
M400014412	M400014412	-	-	-	-	-	-	-	2.0	Down
M300019744	M300019744	-	-	-	-	-	1.6	Up	2.0	Down
NM_011313	S100 calcium binding protein A6 (calyculin)	S100a6	-	-	4.1	Up	3.9	Up	2.0	Up
M400005018	M400005018	-	1.9	Up	-	-	1.5	Up	2.0	Up
M400008034	M400008034	-	-	-	-	-	1.9	Down	2.0	Down
		9130401M01								
NM_029418	RIKEN cDNA 9130401M01 gene	Rik	-	-	-	-	-	-	2.0	Down
NM_015760	NADPH oxidase 4	Nox4	-	-	-	-	-	-	2.0	Down
NM_147089	Olfactory receptor 572	Olf572	-	-	-	-	2.1	Down	2.0	Down
NM_013495	Carnitine palmitoyltransferase 1a, liver	Cpt1a	-	-	-	-	-	-	2.0	Down
NM_018808	DnaJ (Hsp40) homolog, subfamily B, member 1	Dnajb1	-	-	-	-	-	-	2.0	Down
M400007073	M400007073	-	-	-	-	-	-	-	2.0	Down
NM_053201	Melanoma antigen, family E, 1	Magee1	-	-	-	-	-	-	2.0	Down
NM_053189	M400011769	-	-	-	-	-	-	-	2.0	Up
M400004918	M400004918	-	-	-	1.7	Down	-	-	2.0	Down
M400006616	M400006616	-	-	-	-	-	-	-	2.0	Down
M400004948	M400004948	-	-	-	-	-	-	-	2.0	Down
NM_010620	Kinesin family member 15	Kif15	-	-	-	-	-	-	2.0	Up
NM_029571	KT112 homolog, chromatin associated (S. cerevisiae)	Kti12	-	-	-	-	-	-	2.0	Down
M400001734	M400001734	-	-	-	-	-	-	-	2.0	Down
M400007750	M400007750	-	-	-	-	-	-	-	2.0	Down
		2310021H06								
NM_025990	RIKEN cDNA 2310021H06 gene	Rik	-	-	-	-	-	-	2.0	Up
M400013681	M400013681	-	-	-	-	-	-	-	2.0	Down
M200003653	M200003653	-	-	-	-	-	-	-	2.0	Down
M200007360	M200007360	-	-	-	-	-	-	-	2.0	Down
	Solute carrier family 23 (nucleobase transporters), member 2	Slc23a2	-	-	-	-	-	-	2.0	Down
NM_018824	member 2	-	-	-	-	-	-	-	2.0	Down
NM_024427	Tropomyosin 1, alpha	Tpm1	-	-	-	-	-	-	2.0	Down
XM_141574	gene model 358, (NCBI)	-	-	-	-	-	-	-	2.0	Down
NM_172678	Acyl-Coenzyme A dehydrogenase family, member 9	Acad9	-	-	-	-	-	-	2.0	Down

NM_011151	Protein phosphatase 1B, magnesium dependent, beta isoform	Ppm1b	-	-	-	-	-	-	-	2.0	Down	
NM_009390	Tolloid-like	Tll1	-	-	-	-	-	-	-	2.0	Down	
NM_010316	Guanine nucleotide binding protein (G protein), gamma 3	Gng3	-	-	-	-	-	-	-	2.0	Down	
NM_026616	Ribonuclease H2, subunit C	Rnaseh2c	-	-	-	-	-	-	-	2.0	Down	
XM_143201	poly(A) binding protein, cytoplasmic 4-like	-	-	-	-	-	-	-	-	2.0	Up	
NM_030886,												
NM_198010	M400005085	-	-	-	2.0	Down	-	-	-	2.0	Down	
M400002040	M400002040	-	-	-	-	-	-	-	-	2.0	Down	
NM_011691	Vav 1 oncogene	Vav1	-	-	-	-	-	-	-	2.0	Down	
XM_486226	RIKEN cDNA 2310007F21 gene	-	-	-	-	-	-	-	-	2.0	Down	
NM_030244	Immediate early response 5-like	ler5l	-	-	-	-	-	-	-	2.1	Down	
NM_019794	DnaJ (Hsp40) homolog, subfamily A, member 2	Dnaja2	-	-	-	-	-	-	-	2.1	Down	
NM_021313	Ring finger protein 25	Rnf25	-	-	-	-	-	1.7	Up	2.1	Up	
	Pleckstrin homology domain containing, family O member 2	Plekho2	-	-	-	1.7	Up	-	2.1	Up	2.1	Up
NM_153119	X-linked lymphocyte-regulated complex	Xlr	-	-	-	-	-	-	-	2.1	Down	
NM_011725	Deoxynucleotidyltransferase, terminal, interacting protein 1	Dnttip1	-	-	-	-	-	-	-	2.1	Down	
NM_133763												
M400001757	M400001757	-	-	-	-	-	-	-	-	2.1	Down	
M400009025	M400009025	-	-	-	-	-	-	-	-	2.1	Down	
M200005030	M200005030	-	-	-	-	-	-	-	-	2.1	Down	
NM_145209	2-5 oligoadenylate synthetase-like 1	Oasl1	-	-	-	-	-	-	-	2.1	Up	
NM_153567	SLAIN motif family, member 2	Slain2	-	-	-	-	-	-	-	2.1	Down	
M400014854	M400014854	-	-	-	-	-	-	-	-	2.1	Down	
M400016917	M400016917	-	-	-	-	-	-	1.4	Down	2.1	Down	
M400010480	M400010480	-	-	-	-	-	-	-	-	2.1	Down	
M400006200	M400006200	-	-	1.7	Down	-	-	-	-	2.1	Down	
M400002728	M400002728	-	-	-	-	-	-	-	-	2.1	Up	
M400014866	M400014866	-	-	-	-	-	-	-	-	2.1	Down	
NM_007431	Alkaline phosphatase, liver/bone/kidney	Alpl	-	-	-	-	-	-	-	2.1	Up	
NM_021550	C1GALT1-specific chaperone 1	C1galt1c1	-	-	-	-	-	-	-	2.1	Down	
M400013906	M400013906	-	-	-	-	-	-	-	-	2.1	Down	
NM_133986	T-cell leukemia translocation altered gene	Tcta	-	-	-	-	-	-	-	2.1	Down	
M400005616	M400005616	-	-	-	-	-	-	-	-	2.1	Up	
NM_080556	Transmembrane 9 superfamily member 2	Tm9sf2	-	-	-	-	-	-	-	2.1	Up	
NM_011019	Oncostatin M receptor	Osmr	-	-	-	-	-	-	-	2.1	Down	
M400005913	M400005913	-	-	-	-	-	-	-	-	2.1	Down	
M400013597	M400013597	-	-	-	-	-	-	-	-	2.1	Down	
NM_026009	Coiled-coil domain containing 47	Ccdc47	-	-	-	-	-	-	-	2.1	Down	
M200012327	M200012327	-	-	-	-	-	-	1.5	Down	2.1	Down	
XM_127421	zinc finger, DHHC domain containing 11	-	-	-	-	-	-	1.7	Down	2.1	Down	
	X-ray repair complementing defective repair in Chinese hamster cells 2	Xrcc2	-	-	-	-	-	-	-	2.1	Down	

NM_021284	V-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	Kras	-	-	-	-	-	-	2.1	Down	
M400014376	M400014376	-	-	-	-	-	-	-	2.1	Down	
M400016015	M400016015	-	-	-	-	-	-	-	2.1	Down	
XM_485555	similar to Tubulin beta-2 chain	-	-	-	3.1	Up	-	2.7	Up	2.1	Up
NM_052835	Ribosomal protein 10	Rpl10	-	-	-	-	-	-	-	2.1	Down
AF168390	RCP1 (ROOT CAP 1)	RCP1	-	-	-	-	-	2.0	Down	2.1	Down
NM_009684	Apoptotic peptidase activating factor 1	Apaf1	-	-	-	-	-	-	-	2.1	Up
NM_176979	Topoisomerase (DNA) II beta binding protein	Topbp1	-	-	-	-	-	-	-	2.1	Down
M400012898	M400012898	-	-	-	-	-	-	2.2	Down	2.1	Down
M400013432	M400013432	-	-	-	-	-	-	-	-	2.1	Up
M400015166	M400015166	-	-	-	-	-	-	-	-	2.1	Down
NM_008810	Pyruvate dehydrogenase E1 alpha 1	Pdha1	-	-	-	-	-	-	-	2.1	Down
NM_011931	Ring finger and WD repeat domain 2	Rfwd2	-	-	-	-	-	-	-	2.1	Down
NM_133999	FIG4 homolog (S. cerevisiae)	Fig4	-	-	-	-	-	-	-	2.1	Down
NM_021315	Nucleolar complex associated 3 homolog (S. cerevisiae)	Noc3l	-	-	-	-	-	-	-	2.1	Down
M400013804	M400013804	-	-	-	-	-	-	-	-	2.1	Down
NM_172402	Solute carrier family 25, member 32	Slc25a32	-	-	-	-	-	-	-	2.1	Down
NM_010830	MutS homolog 6 (E. coli)	Msh6	-	-	-	-	-	-	-	2.1	Down
NM_026254	TBC1 domain family, member 23	Tbc1d23	-	-	-	-	-	-	-	2.1	Down
NM_146532	Olfactory receptor 1170	Olf1170	-	-	-	-	-	1.7	Down	2.1	Down
NM_030695	LPS-responsive beige-like anchor	Lrba	-	-	-	-	-	-	-	2.1	Down
NM_010597	Potassium voltage-gated channel, shaker-related subfamily, beta member 1	Kcnab1	-	-	-	-	-	-	-	2.1	Down
NM_026411	RIKEN cDNA 1700021F05 gene	1700021F05	-	-	-	-	-	-	-	2.1	Down
NM_025480	Transmembrane protein 128	Rik	-	-	-	-	-	-	-	2.1	Down
NM_145604	RIKEN cDNA D230025D16 gene	Tmem128	-	-	-	-	-	-	-	2.1	Down
NM_177239	Myb-like, SWIRM and MPN domains 1	D230025D16	-	-	-	-	-	-	-	2.1	Down
M400013899	M400013899	Rik	-	-	-	-	-	1.4	Down	2.1	Down
M400009284	M400009284	Mysm1	-	-	-	-	-	-	-	2.1	Down
M400007165	M400007165	-	-	-	1.5	Up	-	-	-	2.1	Down
NM_011406	Solute carrier family 8 (sodium/calcium exchanger), member 1	-	-	-	-	-	-	-	-	2.1	Up
NM_053159	Mitochondrial ribosomal protein L3	Slc8a1	-	-	-	-	-	1.6	Down	2.1	Down
NM_198605	RIKEN cDNA F630043A04 gene	Mrpl3	-	-	-	-	-	-	-	2.1	Down
NM_016956	Hemoglobin, beta adult minor chain	F630043A04	-	-	-	-	-	-	-	2.1	Down
M400008789	M400008789	Rik	-	-	-	-	-	-	-	2.1	Up
NM_078484	Solute carrier family 35 (UDP-galactose transporter), member A2	Hbb-b1	-	-	-	-	-	-	-	2.1	Down
M400016373	M400016373	-	-	-	2.9	Up	-	-	-	2.1	Up
NM_175682	RIKEN cDNA 9930021D14 gene	Slc35a2	-	-	-	-	-	-	-	2.1	Down
		9930021D14	-	-	-	-	-	-	-	2.1	Down
		Rik	-	-	-	-	-	-	-	2.1	Down

NM_008128	Gap junction protein, beta 6	Gjb6	-	-	-	-	-	-	-	2.1	Down	
NM_001005												
525,NM_025												
438	M400009377	-	-	-	-	-	-	1.8	Down	2.1	Down	
M400013474	M400013474	-	2.3	Up	-	-	-	-	-	2.1	Up	
		5730427N09										
NM_021552	RIKEN cDNA 5730427N09 gene	Rik	-	-	-	-	-	-	-	2.2	Down	
		2010100O12										
NM_025946	RIKEN cDNA 2010100O12 gene	Rik	-	-	-	-	-	-	-	2.2	Down	
XM_485427	M400007354	-	-	-	-	-	-	-	-	2.2	Up	
M300003043	M300003043	-	-	-	-	-	-	-	-	2.2	Down	
NM_054073	Testis specific gene A13	Tsga13	2.0	Up	-	1.5	Up	-	1.2	Up	2.2	Up
NM_007644	Scavenger receptor class B, member 2	Scarb2	-	-	-	-	-	-	-	2.2	Down	
M400009141	M400009141	-	-	-	-	-	-	-	-	2.2	Up	
XM_141680	predicted gene, EG245376	-	-	-	-	-	-	1.7	Down	2.2	Down	
XM_485110	M400009213	-	-	-	-	-	-	-	-	2.2	Down	
NM_011297,												
NM_207634,												
NM_207635	M300004569	-	-	-	-	-	-	-	-	2.2	Down	
NM_030684,												
XM_485979	M400001318	-	-	-	-	-	-	-	-	2.2	Down	
M300011602	M300011602	-	-	-	-	-	-	-	-	2.2	Down	
NM_011364	SH2 domain protein 1A	Sh2d1a	1.6	Down	-	-	-	-	-	2.2	Down	
M300014326	M300014326	-	-	-	-	-	-	-	-	2.2	Down	
		1810023F06										
NM_145449	RIKEN cDNA 1810023F06 gene	Rik	-	-	-	-	-	-	-	2.2	Up	
NM_025788	BTB (POZ) domain containing 14B	Btbd14b	-	-	-	-	-	-	-	2.2	Down	
NM_011940	Interferon activated gene 202B	Ifi202b	-	-	-	-	-	-	-	2.2	Down	
M400016106	M400016106	-	2.9	Up	-	-	-	-	-	2.2	Up	
NM_013525	growth arrest specific 5	-	-	-	-	-	-	-	-	2.2	Down	
NM_011360	Sarcoglycan, epsilon	Sgce	-	-	-	-	-	-	-	2.2	Down	
NM_026378	DALR anticodon binding domain containing 3	Dalrd3	-	-	-	-	-	-	-	2.2	Down	
M200003360	M200003360	-	-	-	-	-	-	2.0	Up	2.2	Up	
NM_013747	Golgi autoantigen, golgin subfamily a, 5	Golga5	-	-	-	-	-	-	-	2.2	Down	
		3110048E14										
NM_133750	RIKEN cDNA 3110048E14 gene	Rik	-	-	-	-	-	-	-	2.2	Down	
	V-ral simian leukemia viral oncogene homolog A (ras related)											
NM_019491		Rala	-	-	-	-	-	1.7	Up	2.2	Down	
NM_172397	LIM domain containing 2	Limd2	2.3	Up	-	4.2	Up	-	-	2.2	Up	
		2900010M23										
NM_026063	RIKEN cDNA 2900010M23 gene	Rik	-	-	-	-	-	-	-	2.2	Up	
	Glycine cleavage system protein H (aminomethyl carrier)											
NM_026572		Gcsh	-	-	-	-	-	-	-	2.2	Down	
NM_181988	RAS-like, estrogen-regulated, growth-inhibitor	Rerg	-	-	-	-	-	-	-	2.2	Down	
NM_199307	Endothelin converting enzyme 1	Ece1	-	-	-	-	-	-	-	2.2	Down	

NM_021714	WW domain binding protein 11	Wbp11	1.8	Down	-	-	-	-	2.2	Down
NM_148934	Gene trap ROSA b-geo 22	Gtrgeo22	-	-	-	-	-	-	2.2	Down
M400014895	M400014895	-	-	-	-	-	-	-	2.2	Up
	Translocase of outer mitochondrial membrane 7 homolog (yeast)	Tomm7	-	-	-	-	-	-	2.2	Down
NM_025394	COMM domain containing 3	Commd3	-	-	-	-	-	-	2.2	Down
NM_147778	ER degradation enhancer, mannosidase alpha-like 3	-	-	-	-	-	-	-	2.2	Down
XM_193956	Peroxisome biogenesis factor 19	Pex19	-	-	-	-	-	-	2.2	Up
NM_023041	Ribosomal protein S3a	Rps3a	-	-	-	-	-	-	2.2	Down
NM_016959	M400010043	-	-	-	-	-	-	-	2.2	Up
M400010043	Solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member 3	Slc35a3	-	-	-	-	-	-	2.2	Down
NM_144902	M400008462	-	-	-	3.0	Up	-	-	2.2	Up
M400008462	M400000358	-	-	-	-	-	-	-	2.2	Down
M400000358	Olfactory receptor 798	Olf798	-	-	-	-	-	-	2.2	Down
NM_146556	Mal, T-cell differentiation protein 2	Mal2	-	-	-	-	-	-	2.2	Down
NM_178920	M400006253	-	-	-	-	-	-	-	2.2	Down
M400006253	WD repeat and FYVE domain containing 1	Wdfy1	1.7	Up	-	-	1.8	Up	2.2	Up
NM_027057	M400007603	-	-	-	-	-	-	-	2.2	Up
M400007603	Calcitonin receptor-like	Calcrl	2.0	Up	-	-	-	-	2.2	Up
NM_018782	ARP3 actin-related protein 3 homolog (yeast)	Actr3	-	-	-	-	-	-	2.2	Down
NM_023735	Protein kinase D3	Prkd3	-	-	-	-	1.6	Up	2.2	Down
NM_029239	M400002917	-	-	-	-	-	-	-	2.2	Down
M400002917	M400006462	-	-	-	-	-	-	-	2.2	Down
M400006462	WW domain containing E3 ubiquitin protein ligase 1	-	-	-	-	-	-	-	2.2	Down
XM_130163	Nitrilase family, member 2	Nit2	-	-	-	-	-	-	2.3	Down
NM_023175	Matrin 3	Matr3	-	-	-	-	-	-	2.3	Down
NM_010771	M400002790	-	-	-	-	-	-	-	2.3	Down
NM_011291,	Prostaglandin reductase 2	Ptgr2	-	-	-	-	-	-	2.3	Down
XM_484010,	M400007832	-	-	-	-	-	1.4	Down	2.3	Down
XM_485637	Target of EGR1, member 1 (nuclear)	Toe1	-	-	-	-	-	-	2.3	Down
NM_029880	M400005870	-	-	-	-	-	-	-	2.3	Up
M400007832	Vomeroneasal 1 receptor, E8	V1re8	-	-	-	-	-	-	2.3	Up
NM_026654	M200004221	-	-	-	-	-	-	-	2.3	Down
M400005870	D-tyrosyl-tRNA deacylase 1 homolog (S. cerevisiae)	Dtd1	-	-	-	-	-	-	2.3	Down
NM_134197	Polyadenylate-binding protein-interacting protein 2	Paip2	-	-	-	-	-	-	2.3	Down
M200004221	M400006123	-	-	-	2.4	Up	2.5	Up	2.3	Up
NM_025314	M400015238	-	-	-	-	-	-	-	2.3	Down
NM_026420	Complement component 9	C9	-	-	-	-	-	-	2.3	Down
XM_487803	carbamoyl-phosphate synthetase 1	-	-	-	-	-	-	-	2.3	Up
M400015238	M400000173	-	-	-	-	-	-	-	2.3	Down
NM_013485	Dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	Dlat	-	-	-	-	-	-	2.3	Down
XM_129769										
M400000173										
NM_145614										



NM_007630	Cyclin B2	Ccnb2	-	-	-	-	-	-	2.3	Down
M400013902	M400013902	-	-	-	-	-	-	-	2.3	Down
M300014773	M300014773	-	-	-	-	-	-	-	2.3	Down
M400000796	M400000796	-	-	-	-	-	-	-	2.3	Down
M400015855	M400015855	-	-	-	-	-	-	-	2.3	Down
NM_008245	Hematopoietically expressed homeobox	Hhex	-	-	-	-	-	-	2.3	Down
NM_018745	Antizyme inhibitor 1	Azin1	-	-	-	-	-	-	2.3	Down
NM_010555	Interleukin 1 receptor, type II	Il1r2	-	-	-	-	-	-	2.3	Up
NM_172471	Inter-alpha (globulin) inhibitor H5	Itih5	-	-	-	-	-	-	2.3	Down
NM_198647	TBC1 domain family, member 22B	Tbc1d22b	-	-	-	-	-	-	2.3	Down
NM_146761	Olfactory receptor 414	Olf414	-	-	-	-	2.4	Down	2.3	Down
NM_177163	RIKEN cDNA B330016D10 gene	-	-	-	-	-	-	-	2.3	Down
NM_028082	CCR4-NOT transcription complex, subunit 2	Cnot2	-	-	-	-	-	-	2.3	Down
XM_126785	predicted gene, OTTMUSG00000001305	-	-	-	-	-	-	-	2.3	Down
NM_011722	Dynactin 6	Dctn6	-	-	-	-	-	-	2.3	Down
		5430437P03								
NM_026636	RIKEN cDNA 5430437P03 gene	Rik	-	-	-	-	-	-	2.3	Down
M400002411	M400002411	-	-	-	-	-	-	-	2.3	Down
M400004730	M400004730	-	-	-	-	-	-	-	2.3	Up
M400013096	M400013096	-	-	-	-	-	-	-	2.3	Down
M400013304	M400013304	-	-	-	-	-	2.0	Down	2.3	Down
NM_031880	Tyrosine kinase, non-receptor, 1	Tnk1	-	-	-	-	1.9	Down	2.3	Down
M400008458	M400008458	-	-	-	-	-	-	-	2.3	Up
NM_026401	Mitochondrial ribosomal protein 63	Mrp63	-	-	-	-	-	-	2.3	Up
M200015253	M200015253	-	-	-	-	-	-	-	2.3	Down
NM_008867	Phospholipase A2 receptor 1	Pla2r1	-	-	-	-	-	-	2.3	Down
	Eukaryotic translation initiation factor 2, subunit 2 (beta)	Eif2s2	-	-	-	-	-	-	2.3	Down
NM_029696	Malate dehydrogenase 1B, NAD (soluble)	Mdh1b	-	-	-	-	-	-	2.3	Down
M400014021	M400014021	-	-	-	-	-	-	-	2.3	Down
	RMI1, RecQ mediated genome instability 1, homolog (S. cerevisiae)	Rmi1	-	-	-	-	-	-	2.3	Down
NM_028904	Axin 1	Axin1	-	-	-	-	-	-	2.3	Down
NM_181394	Anaphase promoting complex subunit 13	Anapc13	-	-	-	-	-	-	2.3	Down
NM_018764	Protocadherin 7	Pcdh7	-	-	-	-	-	-	2.3	Down
NM_026506	Small nuclear ribonucleoprotein polypeptide G	Snrpg	-	-	-	-	-	-	2.3	Down
NM_172941	Zinc finger with KRAB and SCAN domains 17	Zkscan17	-	-	-	-	-	-	2.3	Down
NM_138750,										
NM_178047	M300005608	-	-	-	-	-	-	-	2.3	Down
NM_010559,										
XM_484852,										
XM_485016	M400001046	-	-	-	-	-	-	-	2.3	Down
NM_177583	Anterior pharynx defective 1b homolog (C. elegans)	Aph1b	-	-	-	-	-	-	2.3	Down
NM_009847	CD2-associated protein	Cd2ap	-	-	-	-	-	-	2.3	Down
NM_177226	Zinc finger protein 629	Zfp629	-	-	-	-	-	-	2.3	Down

NM_007913	Early growth response 1	Egr1	-	-	-	-	-	-	2.3	Down
M400017375	M400017375	-	-	-	-	-	-	-	2.3	Down
M400014495	M400014495	-	-	-	-	-	-	-	2.3	Down
NM_026499	Splicing factor, arginine/serine-rich 6	Sfrs6	-	-	-	-	-	-	2.3	Down
M400003152	M400003152	-	-	-	-	-	-	-	2.3	Down
M400018231	M400018231	-	-	-	-	-	-	-	2.3	Down
NM_009721	ATPase, Na+/K+ transporting, beta 1 polypeptide	Atp1b1	-	-	-	-	-	-	2.3	Down
NM_022656	Nischarin	Nisch	-	-	-	-	-	-	2.3	Down
NM_144854	Open reading frame 63	ORF63	-	-	-	-	-	-	2.3	Down
M400013162	M400013162	-	-	-	-	-	-	-	2.3	Down
NM_146036	AHA1, activator of heat shock protein ATPase homolog 1 (yeast)	Ahsa1	-	-	-	-	-	-	2.3	Down
M400015129	M400015129	-	-	-	-	-	-	-	2.3	Up
NM_026058	LAG1 homolog, ceramide synthase 4	Lass4	-	-	-	-	-	-	2.3	Down
NM_025781	Transmembrane protein 170	Tmem170	-	-	-	-	2.1	Down	2.3	Down
XM_485015	zinc finger protein 804A	-	-	-	-	-	-	-	2.3	Up
M400006669	M400006669	-	-	-	-	-	-	-	2.3	Down
M400001940	M400001940	-	-	-	-	-	-	-	2.3	Up
NM_178772	Arylacetylamide deacetylase-like 1	Aadacl1	-	-	-	-	-	-	2.4	Down
M400015007	M400015007	-	-	-	-	-	-	-	2.4	Down
NM_010552	Interleukin 17A	Il17a	-	-	-	-	-	-	2.4	Down
XM_358313	CDNA sequence BC018507	BC018507	-	-	-	-	-	-	2.4	Down
M200004083	M200004083	-	-	-	-	-	-	-	2.4	Down
NM_009456	Ubiquitin-conjugating enzyme E2L 3	Ube2l3	-	-	-	-	-	-	2.4	Down
NM_011581	Thrombospondin 2	Thbs2	-	-	-	-	-	-	2.4	Down
M300002385	M300002385	-	-	-	-	-	-	-	2.4	Down
NM_011359	Surfactant associated protein C	Sftpc	2.1	Up	1.6	Up	2.2	Up	2.4	Down
NM_153055	SEC63-like (S. cerevisiae)	Sec63	-	-	-	-	-	-	2.4	Down
NM_009775	Translocator protein	Tspo	-	-	-	-	-	-	2.4	Up
NM_017372	Lysozyme 2	Lyz2	-	-	-	-	-	-	2.4	Down
M400000853	M400000853	-	-	-	-	-	-	-	2.4	Up
M400016133	M400016133	-	-	-	-	-	-	-	2.4	Down
NM_027212	Mediator complex subunit 30	Med30	-	-	-	-	-	-	2.4	Down
M400016515	M400016515	-	-	-	-	-	-	-	2.4	Down
NM_011669	Ubiquitin specific peptidase 12	Usp12	-	-	-	-	-	-	2.4	Down
NM_027504	PR domain containing 16	Prdm16	-	-	-	-	-	-	2.4	Down
M400010384	M400010384	-	-	-	2.8	Up	-	-	2.4	Up
M400010074	M400010074	-	-	-	-	-	-	-	2.4	Up
M400015208	M400015208	-	-	-	-	-	-	-	2.4	Down
NM_011757	Zinc finger and SCAN domain containing 21	Zscan21	-	-	-	-	-	-	2.4	Down
NM_024242	RIO kinase 1 (yeast)	Riok1	-	-	-	-	-	-	2.4	Down
NM_031874	RAB3D, member RAS oncogene family	Rab3d	-	-	-	-	-	-	2.4	Down
XM_109726	mediator complex subunit 13	-	-	-	-	-	-	-	2.4	Up
NM_025441										
NM_181665	M200006249	-	-	-	-	-	-	-	2.4	Down

NM_177715	Potassium channel tetramerisation domain containing 12	Kctd12	-	-	-	-	-	-	2.4	Down
NM_013504	Desmocollin 1	Dsc1	-	-	-	-	-	-	2.4	Up
NM_013787	S-phase kinase-associated protein 2 (p45)	Skp2	-	-	-	-	-	-	2.4	Down
NM_019868	Heterogeneous nuclear ribonucleoprotein H2	HnrnpH2	-	-	-	-	-	-	2.4	Down
NM_025437	Eukaryotic translation initiation factor 1A, Y-linked	Eif1ay	-	-	-	-	-	-	2.4	Down
NM_016776	MYB binding protein (P160) 1a	Mybbp1a	-	-	-	-	1.6	Up	2.4	Up
NM_011653	Tubulin, alpha 1A	Tuba1a	-	-	-	-	-	-	2.4	Down
NM_001003										
671,NM_001003672,NM_007766,NM_007767,NM_0										
	M300000897	-	-	-	-	-	-	-	2.4	Down
XM_356732	M400005944	-	-	-	-	-	-	-	2.4	Down
NM_172621	Chloride intracellular channel 5	Clic5	-	-	-	-	-	-	2.4	Down
NM_029502	Calcium activated nucleotidase 1	Cant1	-	-	-	-	2.1	Down	2.4	Up
NM_008033	Farnesyltransferase, CAAX box, alpha	Fnta	-	-	-	-	-	-	2.4	Down
NM_016796	Vesicle-associated membrane protein 4	Vamp4	-	-	-	-	-	-	2.4	Down
NM_029780	V-raf-leukemia viral oncogene 1	Raf1	-	-	-	-	-	-	2.4	Down
NM_152810	Cell division cycle 5-like (S. pombe)	Cdc5l	-	-	-	-	-	-	2.4	Down
M400014830	M400014830	-	2.2	Up	3.5	Up	3.0	Up	2.4	Up
NM_026880	PTEN induced putative kinase 1	Pink1	-	-	-	-	-	-	2.4	Down
NM_030109	Splicing factor 3b, subunit 2	Sf3b2	-	-	-	-	-	-	2.4	Down
XM_129927	TNF receptor-associated factor 3 interacting protein 1	-	-	-	-	-	-	-	2.4	Down
M400017374	M400017374	-	-	-	-	-	2.1	Down	2.4	Down
M2NC000011										
	M2NC000011	-	2.0	Down	-	-	-	-	2.4	Down
M400009664	M400009664	-	-	-	-	-	-	-	2.4	Up
NM_019437	Riboflavin kinase	Rfk	-	-	-	-	-	-	2.4	Down
NM_134114	SFT2 domain containing 1	Sft2d1	-	-	-	-	-	-	2.4	Down
XM_138063	A kinase (PRKA) anchor protein 5	-	-	-	-	-	-	-	2.4	Down
M400006289	M400006289	-	-	-	-	-	-	-	2.4	Down
NM_172479	Solute carrier family 38, member 5	Slc38a5	2.2	Up	-	-	-	-	2.4	Down
NM_008300	Heat shock protein 4	Hspa4	-	-	-	-	-	-	2.4	Down
NM_144844	Propionyl-Coenzyme A carboxylase, alpha polypeptide	Pcca	-	-	-	-	-	-	2.4	Down
NM_152812	OTU domain containing 6B	Otud6b	-	-	-	-	-	-	2.4	Down
M400001067	M400001067	-	-	-	-	-	-	-	2.4	Down
		1110004F10								
NM_019772	RIKEN cDNA 1110004F10 gene	Rik	-	-	-	-	-	-	2.4	Down
NM_133947	Nuclear mitotic apparatus protein 1	Numa1	-	-	-	-	-	-	2.4	Down
M400013066	M400013066	-	1.7	Up	-	-	-	-	2.4	Up
NM_016710	Nucleosome binding protein 1	Nsbp1	-	-	-	-	-	-	2.4	Down
M400018094	M400018094	-	-	-	-	-	-	-	2.4	Up
NM_182650	Heterogeneous nuclear ribonucleoprotein A2/B1	Hnrnpa2b1	1.8	Down	-	-	-	-	2.4	Down

NM_008966	Prostaglandin F receptor	Ptgr	-	-	-	-	-	-	2.4	Down	
M400006755	M400006755	-	-	-	-	-	-	-	2.4	Up	
M400002496	M400002496	-	-	-	1.7	Up	-	1.5	Up	2.4	Down
M400013575	M400013575	-	-	-	-	-	-	-	-	2.4	Down
NM_025301	Mitochondrial ribosomal protein L17	Mrpl17	-	-	-	-	-	-	-	2.4	Down
NM_009930	Collagen, type III, alpha 1	Col3a1	-	-	-	-	-	-	-	2.4	Down
NM_134068	Dual specificity phosphatase 22	Dusp22	-	-	-	-	-	-	-	2.4	Down
XM_140020	RIKEN cDNA 3110082D06 gene	-	-	-	-	-	-	-	-	2.4	Down
NM_029568	Microfibrillar-associated protein 4	Mfap4	-	-	-	-	-	1.7	Up	2.4	Down
NM_011277	Ring finger protein 2	Rnf2	-	-	-	-	-	-	-	2.4	Down
M400014672	M400014672	-	-	-	-	-	-	1.3	Down	2.4	Down
M400009263	M400009263	-	-	-	1.7	Down	-	2.8	Down	2.4	Down
NM_019537	Proteasome (prosome, macropain) assembly chaperone 1	Psmg1	-	-	-	-	-	-	-	2.4	Down
NM_025419	RIKEN cDNA 1110059G10 gene	1110059G10	-	-	-	-	-	-	-	2.4	Down
NM_025831	RIKEN cDNA 1300014I06 gene	Rik	-	-	-	-	-	-	-	2.4	Down
NM_130447	Dual specificity phosphatase 16	1300014I06	-	-	-	-	-	-	-	2.4	Down
NM_144545	Eukaryotic translation initiation factor 3, subunit J	Rik	-	-	-	-	-	-	-	2.4	Down
XM_488522	poly (ADP-ribose) polymerase family, member 14	Dusp16	-	-	-	-	-	-	-	2.4	Down
M300002779	M300002779	Eif3j	-	-	-	-	-	-	-	2.5	Down
M400019498	M400019498	-	-	-	-	-	-	-	-	2.5	Down
NM_177755	RIKEN cDNA 8230402K04 gene	8230402K04	-	-	-	-	-	-	-	2.5	Down
NM_008537	Alpha-methylacyl-CoA racemase	Rik	-	-	-	-	-	-	-	2.5	Down
XM_283610	RIKEN cDNA 1110034B05 gene	Amacr	-	-	-	-	-	-	-	2.5	Down
NM_146817	Olfactory receptor 1156	-	1.6	Down	-	-	-	-	-	2.5	Down
M400004431	M400004431	Olfr1156	-	-	-	-	-	2.4	Down	2.5	Down
M400013324	M400013324	-	-	-	-	-	-	-	-	2.5	Down
M400019045	M400019045	-	-	-	-	-	-	-	-	2.5	Down
NM_011240	RAN binding protein 2	-	-	-	-	-	-	-	-	2.5	Up
NM_028108	N-acetyltransferase 13	Ranbp2	-	-	-	-	-	-	-	2.5	Down
NM_178390	RIKEN cDNA 2410018C17 gene	Nat13	1.5	Down	-	-	-	-	-	2.5	Down
M200000800	M200000800	2410018C17	-	-	-	-	-	-	-	2.5	Down
NM_133885,	M200005519	Rik	-	-	-	-	-	-	-	2.5	Down
NM_173350	Mitofusin 2	-	1.5	Down	-	-	-	-	-	2.5	Down
NM_133201	M400015475	Mfn2	-	-	-	-	-	-	-	2.5	Down
M400015475	M400015475	-	-	-	-	-	-	2.4	Down	2.5	Down
NM_026382	RIKEN cDNA 6530403A03 gene	6530403A03	-	-	-	-	-	-	-	2.5	Down
NM_053145	Protocadherin beta 20	Rik	-	-	-	-	-	-	-	2.5	Down
NM_026448	Kelch-like 7 (Drosophila)	Pcdhb20	-	-	-	-	-	-	-	2.5	Down
NM_009245	Serine (or cysteine) peptidase inhibitor, clade A,	Klhl7	-	-	-	-	-	-	-	2.5	Down
		Serpina1c	-	-	-	-	-	-	-	2.5	Down

	member 1c									
NM_020048	Mediator complex subunit 20	Med20	-	-	-	-	-	-	-	2.5 Down
M300013498	M300013498	-	-	-	-	-	-	-	-	2.5 Down
M300021883	M300021883	-	-	-	-	-	-	-	-	2.5 Down
M400015680	M400015680	-	-	-	-	-	-	-	-	2.5 Down
NM_010336	Lysophosphatidic acid receptor 1	Lpar1	-	-	-	-	-	-	-	2.5 Down
	Potassium channel tetramerisation domain containing									
NM_134073	9	Kctd9	-	-	-	-	-	-	-	2.5 Down
XM_131241	fucose-1-phosphate guanylyltransferase	-	-	-	-	-	-	-	-	2.5 Down
		1110007L15								
NM_026269	RIKEN cDNA 1110007L15 gene	Rik	-	-	-	-	-	-	-	2.5 Down
M300005734	M300005734	-	-	-	-	-	-	-	-	2.5 Down
M400002700	M400002700	-	3.4	Up	-	-	-	-	-	2.5 Up
NM_145851	Cdk5 and Abl enzyme substrate 2	Cables2	-	-	-	-	-	-	-	2.5 Down
NM_027030	Decapping enzyme, scavenger	Dcps	-	-	-	-	-	-	-	2.5 Down
M200004621	M200004621	-	-	-	-	-	-	-	-	2.5 Down
NM_172477	DENN/MADD domain containing 2A	Dennd2a	-	-	-	-	-	-	-	2.5 Down
	PRP38 pre-mRNA processing factor 38 (yeast) domain									
NM_025845	containing B	Prpf38b	-	-	-	-	-	-	-	2.5 Down
NM_199476	Ribonucleotide reductase M2 B (TP53 inducible)	Rrm2b	-	-	-	-	-	-	-	2.5 Down
NM_146495	Olfactory receptor 474	Olfra474	-	1.7	Up	-	-	-	-	2.5 Up
M400018310	M400018310	-	-	-	-	-	-	-	-	2.5 Down
NM_021465	Stromal antigen 2	Stag2	-	-	-	-	-	-	-	2.5 Down
XM_357108	mitochondrial ribosomal protein L44	-	-	-	-	-	-	-	-	2.5 Down
M400014924	M400014924	-	-	-	-	-	-	-	-	2.5 Down
M400018188	M400018188	-	-	-	-	-	-	-	-	2.5 Down
NM_020588	Transmembrane protein 183A	Tmem183a	-	-	-	-	-	-	-	2.5 Down
NM_033270	E2F transcription factor 6	E2f6	-	-	-	-	-	-	-	2.5 Down
M300008022	M300008022	-	-	-	-	-	-	-	-	2.5 Down
NM_198322	Zinc finger protein 273	Zfp273	-	-	-	-	-	-	-	2.5 Down
NM_009242	Secreted acidic cysteine rich glycoprotein	Sparc	-	-	-	-	-	-	-	2.5 Down
	TAF6 RNA polymerase II, TATA box binding protein									
NM_009315	(TBP)-associated factor	Taf6	-	-	-	-	-	-	-	2.5 Up
	TAF9 RNA polymerase II, TATA box binding protein									
NM_027139	(TBP)-associated factor	Taf9	-	2.0	Down	-	-	-	-	2.5 Down
M400004545	M400004545	-	-	-	-	-	-	-	-	2.5 Down
NM_133826	ATPase, H <sup>+</sup> transporting, lysosomal V1 subunit H	Atp6v1h	-	-	-	-	-	-	-	2.5 Down
NM_172407	CDKN2A interacting protein	Cdkn2aip	-	-	-	-	-	-	-	2.5 Down
NM_007522	Bcl-associated death promoter	Bad	-	-	-	-	-	-	-	2.6 Down
M400017707	M400017707	-	-	2.2	Up	-	-	-	-	2.6 Up
M300009122	M300009122	-	-	-	-	-	-	-	-	2.6 Down
M300015383	M300015383	-	-	-	-	-	-	-	-	2.6 Down
NM_026660	Major facilitator superfamily domain containing 10	Mfsd10	-	-	-	-	-	-	-	2.6 Down
NM_199196	Suppressor of zeste 12 homolog (Drosophila)	Suz12	-	-	-	-	-	-	-	2.6 Down
XM_194043	gene model 1855, (NCBI)	-	-	-	-	-	-	-	-	2.6 Down

M400019274	M400019274	-	-	-	-	-	-	1.4	Down	2.6	Down
M400006878	M400006878	-	-	-	-	-	-	2.3	Down	2.6	Down
NM_019642	Ribophorin II	Rpn2	-	-	-	-	-	-	-	2.6	Down
NM_144911	RNA polymerase II associated protein 2	Rpap2	-	-	-	-	-	-	-	2.6	Down
NM_008048	Insulin-like growth factor binding protein 7	Igfbp7	-	-	-	-	-	-	-	2.6	Down
NM_198093	Engulfment and cell motility 1, ced-12 homolog (C. elegans)	Elmo1	-	-	-	-	-	-	-	2.6	Down
NM_011791	Ash2 (absent, small, or homeotic)-like (Drosophila)	Ash2l	-	-	-	-	-	-	-	2.6	Down
NM_015755	Hormonally upregulated Neu-associated kinase	Hunk	-	-	-	-	-	-	-	2.6	Down
M400013765	M400013765	-	-	-	-	-	-	-	-	2.6	Down
NM_013534	Leprecan-like 2	Leprel2	-	-	-	-	-	-	-	2.6	Up
NM_025369	Mitochondrial ribosomal protein S36	Mrps36	-	-	-	-	-	-	-	2.6	Down
NM_145137	Macrophage galactose N-acetyl-galactosamine specific lectin 2	Mgl2	-	-	-	-	-	-	-	2.6	Down
NM_010067	TRNA aspartic acid methyltransferase 1	Trdmt1	-	-	-	-	-	-	-	2.6	Down
NM_010217	Connective tissue growth factor	Ctgf	-	-	-	-	-	-	-	2.6	Down
M300007329	M300007329	-	-	-	-	-	-	-	-	2.6	Up
NM_022026	Aquaporin 9	Aqp9	-	-	-	-	-	-	-	2.6	Down
NM_026472	Mki67 (FHA domain) interacting nucleolar phosphoprotein	Mki67ip	-	-	-	-	-	-	-	2.6	Down
M300004871	M300004871	-	-	-	-	-	-	-	-	2.6	Down
M400013963	M400013963	-	-	-	-	-	-	-	-	2.6	Down
NM_023162	Zinc ribbon domain containing, 1	Znrd1	-	-	-	-	-	-	-	2.6	Down
NM_146654	Olfactory receptor 438	Olf438	-	-	-	-	-	-	-	2.6	Down
M200006426	M200006426	-	-	-	-	-	-	-	-	2.6	Down
NM_026395	RER1 retention in endoplasmic reticulum 1 homolog (S. cerevisiae)	Rer1	-	-	-	-	-	-	-	2.6	Down
XM_132015	cDNA sequence BC037112	-	-	-	-	-	-	2.1	Down	2.6	Down
NM_008761	FXYD domain-containing ion transport regulator 5	Fxyd5	-	-	2.8	Up	-	3.2	Up	2.6	Up
NM_020329	Dolichyl pyrophosphate phosphatase 1	Dolpp1	-	-	-	-	-	-	-	2.6	Down
M200005306	M200005306	-	-	-	-	-	-	-	-	2.6	Down
NM_009433	Testis-specific protein, Y-encoded-like 1	Tsyp11	-	-	-	-	-	-	-	2.6	Down
NM_145974	RIKEN cDNA C330016O10 gene	C330016O10	-	-	-	-	-	-	-	2.6	Down
XM_486780	predicted gene, EG434858	Rik	-	-	-	-	-	-	-	2.6	Down
M400013458	M400013458	-	-	-	1.7	Down	-	-	-	2.6	Down
NM_026752	Zinc finger, FYVE domain containing 21	Zfyve21	-	-	-	-	-	-	-	2.6	Down
NM_199448	Fasciculation and elongation protein zeta 2 (zygin II)	Fez2	-	-	-	-	-	-	-	2.6	Down
M400002432	M400002432	-	-	-	-	-	-	-	-	2.6	Up
M300003585	M300003585	-	-	-	-	-	-	-	-	2.6	Down
M400006914	M400006914	-	-	-	-	-	-	-	-	2.6	Down
XM_488078	RIKEN cDNA E130201H02 gene	-	-	-	-	-	-	-	-	2.6	Down
M300004251	M300004251	-	-	-	-	-	-	2.2	Up	2.6	Down
NM_019393	Exosome component 9	Exosc9	-	-	-	-	-	-	-	2.6	Down
NM_026832	Cell growth regulator with ring finger domain 1	Cgrrf1	-	-	-	-	-	-	-	2.6	Down

NM_199056	Inositol 1,3,4,5,6-pentakisphosphate 2-kinase	Ippk	-	-	-	-	-	-	2.6	Down
M400005236	M400005236	-	-	-	-	-	-	-	2.6	Down
M400015198	M400015198	-	-	-	-	-	-	-	2.6	Down
M400017540	M400017540	-	-	-	-	-	-	-	2.6	Down
NM_025286	Solute carrier family 31, member 2	Slc31a2	-	-	-	-	-	-	2.6	Down
NM_025531	Slowmo homolog 2 (Drosophila)	Slmo2	-	-	-	-	-	-	2.6	Down
XM_128124	WD repeat domain 67	-	1.7	Down	-	-	-	-	2.6	Down
NM_026653	Replication protein A1	Rpa1	-	-	-	-	-	-	2.6	Down
XM_358058	gene model 1499, (NCBI)	-	-	-	-	-	-	-	2.6	Up
M300000110	M300000110	-	-	-	-	-	-	-	2.6	Down
NM_198031	Tubulin, gamma complex associated protein 3	Tubgcp3	-	-	-	-	-	-	2.6	Down
NM_026070	Coiled-coil domain containing 53	Ccdc53	1.8	Down	-	-	-	-	2.6	Down
NM_181750	R3H domain 1 (binds single-stranded nucleic acids)	R3hdm1	-	-	-	-	-	-	2.6	Down
NM_172049	Transmembrane protein 18	Tmem18	-	-	-	-	-	-	2.6	Down
M400015692	M400015692	-	-	-	-	-	-	-	2.6	Down
M400016757	M400016757	-	-	-	-	-	-	-	2.6	Down
XM_357571	predicted gene, EG384325	-	1.5	Down	-	-	-	-	2.6	Down
NM_007530	B-cell receptor-associated protein 29	Bcap29	-	-	-	-	-	-	2.6	Down
NM_130448	Protocadherin 18	Pcdh18	2.3	Up	-	-	-	-	2.6	Up
M300002937	M300002937	-	-	-	-	-	-	-	2.6	Down
XM_127961	DnaJ (Hsp40) homolog, subfamily C, member 21	-	1.8	Down	-	-	-	-	2.6	Down
NM_054085	Alpha-kinase 3	Alpk3	-	-	1.6	Down	2.4	Down	2.6	Down
		1810065E05								
NM_027239	RIKEN cDNA 1810065E05 gene	Rik	-	-	-	-	-	-	2.6	Down
M400015300	M400015300	-	-	-	-	-	-	-	2.6	Down
NM_144558	Basic, immunoglobulin-like variable motif containing	Bivm	-	-	-	-	-	-	2.6	Down
NM_178194	Histone cluster 1, H2be	Hist1h2be	-	-	-	-	-	-	2.6	Down
M400014715	M400014715	-	-	-	-	-	-	-	2.6	Down
NM_008891	Pinin	Pnn	-	-	-	-	-	-	2.7	Down
M400017940	M400017940	-	-	-	-	-	1.1	Down	2.7	Down
NM_013752	Nibrin	Nbn	-	-	-	-	-	-	2.7	Down
NM_028334	Nucleoporin 37	Nup37	-	-	-	-	-	-	2.7	Down
NM_029926	Interleukin-1 receptor-associated kinase 4	Irak4	-	-	-	-	-	-	2.7	Up
M400010279	M400010279	-	-	-	-	-	1.5	Down	2.7	Down
M400006125	M400006125	-	-	-	-	-	-	-	2.7	Up
NM_015788,										
XM_484383	M200008588	-	-	-	-	-	-	-	2.7	Up
M300000378	M300000378	-	-	-	-	-	-	-	2.7	Down
M400012950	M400012950	-	-	-	-	-	-	-	2.7	Down
NM_008808	Platelet derived growth factor, alpha	Pdgfa	-	-	-	-	-	-	2.7	Down
M300002101	M300002101	-	-	-	2.3	Up	2.3	Up	2.7	Up
M400008073	M400008073	-	-	-	-	-	-	-	2.7	Up
M400013200	M400013200	-	-	-	-	-	-	-	2.7	Down
XM_356600	Predicted gene, EG382639	EG382639	-	-	-	-	-	-	2.7	Up
M400019008	M400019008	-	-	-	-	-	-	-	2.7	Down

NM_011802	Caseinolytic peptidase X (E.coli)	Clpx	-	-	-	-	-	-	2.7	Down	
M400016187	M400016187	-	-	-	-	-	-	-	2.7	Down	
NM_030703	Carboxypeptidase N, polypeptide 1	Cpn1	-	-	-	-	-	-	2.7	Up	
NM_177244	FAST kinase domains 1	Fastkd1	-	-	-	-	-	-	2.7	Up	
NM_021526	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	Psmc14	-	-	-	-	-	-	2.7	Down	
NM_010281	Gamma-glutamyl hydrolase	Ggh	-	-	-	-	-	-	2.7	Down	
M300002978	M300002978	-	-	-	-	-	-	-	2.7	Down	
M400001855	M400001855	-	-	-	-	-	-	-	2.7	Up	
M400016230	M400016230	-	-	-	-	-	-	-	2.7	Down	
NM_026018	PDZK1 interacting protein 1	Pdzk1ip1	-	-	-	-	-	-	2.7	Down	
M400004798	M400004798	-	-	-	-	-	-	-	2.7	Down	
NM_133234	Bcl-2 binding component 3	Bbc3	2.3	Up	-	-	-	-	2.7	Up	
NM_024275	mitogen-activated protein kinase kinase kinase 5	-	-	-	-	-	-	-	2.7	Down	
NM_026041	Ribosomal RNA processing 15 homolog (S. cerevisiae)	Rrp15	1.6	Down	-	-	-	-	2.7	Down	
M400000643	M400000643	-	-	-	-	-	-	-	2.7	Down	
NM_001001309	Integrin alpha 8	Itga8	-	-	-	-	-	-	2.7	Down	
NM_010700	Low density lipoprotein receptor	Ldlr	-	-	-	-	-	-	2.7	Up	
M400014359	M400014359	-	-	-	-	-	-	-	2.7	Down	
NM_175153	RIKEN cDNA 2010321M09 gene	2010321M09	-	-	-	-	-	-	2.7	Down	
XM_133956	interferon induced transmembrane protein 6	Rik	-	-	-	-	-	-	2.7	Up	
M300019653	M300019653	-	-	-	-	-	-	-	2.7	Down	
NM_019668	Ubiquitin-conjugating enzyme E2A, RAD6 homolog (S. cerevisiae)	Ube2a	-	-	-	-	-	-	2.7	Down	
NM_026437	RIKEN cDNA 1810055E12 gene	1810055E12	-	-	-	-	-	-	2.7	Down	
NM_019485	Olfactory receptor 70	Rik	-	-	-	-	-	-	2.7	Down	
NM_010741	Olfactory receptor 70	Olfr70	-	-	-	-	-	-	2.7	Down	
NM_010741	Lymphocyte antigen 6 complex, locus C1	Ly6c1	-	-	3.5	Up	-	3.1	Up	2.7	Up
NM_010184	Fc receptor, IgE, high affinity I, alpha polypeptide	Fcer1a	-	-	-	-	-	-	2.7	Up	
NM_008211	H3 histone, family 3B	H3f3b	-	-	-	-	-	-	2.7	Down	
NM_032008	Sarcolemma associated protein	Slmap	-	-	-	-	-	-	2.7	Down	
M400002804	M400002804	-	-	-	-	-	-	-	2.7	Down	
M400015111	M400015111	-	-	-	-	-	-	-	2.7	Down	
NM_207219	Expressed sequence AI314976	AI314976	-	-	-	-	-	-	2.7	Down	
NM_053158	Mitochondrial ribosomal protein L1	Mrpl1	-	-	-	-	-	-	2.7	Down	
NM_009227	Small nuclear ribonucleoprotein E	Snrpe	-	-	-	-	-	-	2.7	Down	
NM_026550	PAK1 interacting protein 1	Pak1ip1	-	-	-	-	-	-	2.7	Down	
NM_028211	RIKEN cDNA 2210016L21 gene	2210016L21	-	-	-	-	-	-	2.7	Down	
M300003442	M300003442	Rik	2.6	Up	-	-	-	1.3	Up	2.7	Up
NM_026071	Solute carrier family 25 (mitochondrial thiamine pyrophosphate carrier), member 19	Slc25a19	-	-	-	-	-	-	2.7	Down	



M300002482	M300002482	-	-	-	-	-	-	-	-	2.7	Down
		1700008O03									
XM_133454	RIKEN cDNA 1700008O03 gene	Rik	2.1	Up	-	-	-	-	-	2.7	Up
NM_023422	Histone cluster 1, H2bc	Hist1h2bc	-	-	-	-	-	-	-	2.7	Down
NM_139306	N-acylsphingosine amidohydrolase 3-like	Asah3l	-	-	-	-	-	-	-	2.7	Down
NM_175512	Dehydrogenase/reductase (SDR family) member 9	Dhrs9	-	-	-	-	-	-	-	2.7	Up
M400002482	M400002482	-	-	-	-	-	-	-	-	2.7	Down
NM_026029	Glyoxalase domain containing 4	Glod4	-	-	-	-	-	-	-	2.7	Down
	sema domain, immunoglobulin domain (Ig), short basic										
XM_138955	domain, secreted, (semaphorin) 3G	-	-	-	-	-	-	-	-	2.7	Down
NM_008190	Guanylate cyclase activator 2a (guanylin)	Guca2a	-	-	-	-	-	-	-	2.7	Down
M400000359	M400000359	-	-	-	-	-	-	-	-	2.7	Down
M400013192	M400013192	-	-	-	-	-	-	-	-	2.7	Down
XM_131470,											
XM_485546	M200011046	-	-	-	-	-	-	-	-	2.7	Up
NM_146970	Olfactory receptor 1239	Olfr1239	-	-	-	-	-	-	-	2.8	Down
M400010311	M400010311	-	-	-	-	-	-	-	-	2.8	Up
NM_011051	Programmed cell death 6	Pdcd6	-	-	-	-	-	-	-	2.8	Down
NM_139061	Vacuolar protein sorting 54 (yeast)	Vps54	1.5	Down	-	-	-	-	-	2.8	Down
XM_128550	RIKEN cDNA 1700065O13 gene	-	-	-	-	-	-	-	-	2.8	Down
XM_485607	M400004062	-	-	-	-	-	-	-	-	2.8	Up
NM_009079	Ribosomal protein L22	Rpl22	-	-	-	-	-	2.5	Up	2.8	Down
NM_146190	Tubulin, gamma complex associated protein 5	Tubgcp5	-	-	-	-	-	-	-	2.8	Down
NM_019702	Hbs1-like (S. cerevisiae)	Hbs1l	-	-	-	-	-	-	-	2.8	Down
M400014860	M400014860	-	-	-	-	-	-	-	-	2.8	Down
NM_019786	TANK-binding kinase 1	Tbk1	-	-	-	-	-	-	-	2.8	Down
		2310005N03									
NM_025511	RIKEN cDNA 2310005N03 gene	Rik	-	-	-	-	-	-	-	2.8	Down
M400003500	M400003500	-	-	-	-	-	-	-	-	2.8	Down
M400004591	M400004591	-	-	-	-	-	-	-	-	2.8	Down
NM_009441	Tetratricopeptide repeat domain 3	Ttc3	-	-	-	-	-	-	-	2.8	Down
		4833439L19									
NM_133797	RIKEN cDNA 4833439L19 gene	Rik	-	-	-	-	-	-	-	2.8	Down
NM_178392	Small nuclear RNA activating complex, polypeptide 1	Snopc1	-	-	-	-	-	-	-	2.8	Down
M300002502	M300002502	-	-	-	-	-	-	-	-	2.8	Down
NM_007597	Calnexin	Canx	-	-	-	-	-	-	-	2.8	Down
M400015625	M400015625	-	-	-	-	-	-	1.8	Down	2.8	Down
	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-										
NM_015737	acetylgalactosaminyltransferase 4	Galnt4	-	-	-	-	-	1.8	Down	2.8	Down
NM_031403	Debranching enzyme homolog 1 (S. cerevisiae)	Dbr1	-	-	-	-	-	-	-	2.8	Down
NM_134136	F-box protein 38	Fbxo38	-	-	-	-	-	-	-	2.8	Down
M300008571	M300008571	-	-	-	-	-	-	-	-	2.8	Up
M400013275	M400013275	-	-	-	-	-	-	-	-	2.8	Down
M400013710	M400013710	-	-	-	-	-	-	-	-	2.8	Down
NM_199151	general transcription factor II A, 2	-	-	-	-	-	-	-	-	2.8	Down

NM_177681	Zinc finger protein 12 IMP1 inner mitochondrial membrane peptidase-like (S. cerevisiae)	Zfp12	-	-	-	-	1.6	Down	2.8	Down
NM_028260	M400013849	Immp11	-	-	-	-	-	-	2.8	Down
M400013849	M400017144	-	-	-	-	-	-	-	2.8	Down
M400017144	M400017144	-	-	-	-	-	-	-	2.8	Up
NM_172964	Rho GTPase activating protein 28	Arhgap28	-	-	-	-	-	-	2.8	Down
NM_138605	Protein phosphatase 1, regulatory (inhibitor) subunit 3F	Ppp1r3f	-	-	2.8	Down	-	-	2.8	Down
NM_008451	Kinesin light chain 2	Klc2	-	-	-	-	-	-	2.8	Up
NM_011692	Von Hippel-Lindau binding protein 1	Vbp1	-	-	-	-	-	-	2.8	Down
M400003321	M400003321	-	-	-	-	-	-	-	2.8	Down
M400002899	M400002899	-	-	-	-	-	-	-	2.8	Down
M400019279	M400019279	-	-	-	-	-	-	-	2.8	Down
XM_488528	M400004648	-	-	-	-	-	-	-	2.8	Down
M400004816	M400004816	-	-	-	-	-	-	-	2.8	Down
M400013063	M400013063	-	1.5	Down	-	-	-	-	2.8	Down
NM_134027	Mediator complex subunit 1	Med1	-	-	-	-	-	-	2.8	Down
NM_013902	FK506 binding protein 3	Fkbp3	-	-	-	-	-	-	2.8	Down
NM_021367	Thymic stromal lymphopoietin	Tslp	-	-	-	-	-	-	2.8	Down
NM_133948	PC4 and SFRS1 interacting protein 1	Psip1	-	-	-	-	-	-	2.8	Down
NM_145960	Mitochondrial translational release factor 1	Mtrf1	-	-	-	-	-	-	2.8	Down
NM_025475	Centrosomal protein 27	Cep27	-	1.8	Down	-	-	-	2.8	Down
NM_134064	Ring finger protein 44	Rnf44	-	-	-	-	-	-	2.8	Down
NM_181414	Phosphoinositide-3-kinase, class 3	Pik3c3	-	-	-	-	-	-	2.8	Down
M400005868	M400005868	-	-	-	3.2	Up	3.7	Up	2.8	Up
NM_177765	Tubulin tyrosine ligase-like family, member 13 PH domain and leucine rich repeat protein	Ttl13	-	-	-	-	-	-	2.8	Down
XM_129968	phosphatase	Phlpp	-	-	-	-	-	-	2.8	Down
M400009824	M400009824	-	-	-	-	-	-	-	2.8	Down
NM_194344	SH3 domain and tetratricopeptide repeats 1	Sh3tc1	-	-	-	-	-	-	2.8	Up
M400012969	M400012969	-	-	-	-	-	-	-	2.8	Down
NM_013493	Cellular nucleic acid binding protein	Cnbp	-	-	-	-	-	-	2.8	Down
XM_283466	RIKEN cDNA 4930560E09 gene	-	-	-	-	-	-	-	2.8	Up
NM_025440	Mitochondrial ribosomal protein S16	Mrps16	-	-	-	-	-	-	2.9	Down
M400003518	M400003518	-	-	-	-	-	-	-	2.9	Down
M400014075	M400014075	-	-	-	-	-	-	-	2.9	Down
M400000543	M400000543	-	-	-	-	-	-	-	2.9	Down
NM_146142	Tudor domain containing 7	Tdrd7	-	-	-	-	-	-	2.9	Down
NM_023429	OClA domain containing 1	Ociad1	-	-	-	-	-	-	2.9	Down
M400006739	M400006739	-	-	-	-	-	-	-	2.9	Down
NM_025435	THO complex 7 homolog (Drosophila)	Thoc7	-	1.6	Down	-	-	-	2.9	Down
NM_016721	IQ motif containing GTPase activating protein 1	Iqgap1	-	-	-	-	-	-	2.9	Down
NM_008697	Ninein	Nin	-	-	-	-	-	-	2.9	Down
M400017576	M400017576	-	1.7	Down	-	-	-	-	2.9	Down
NM_133231	Regulatory factor X-associated protein	Rfxap	-	-	-	-	-	-	2.9	Down
NM_001005	Adhesion molecule, interacts with CXADR antigen 1	Amica1	-	-	-	-	-	-	2.9	Up

421												
NM_007597	Calnexin	Canx	-	-	-	-	-	-	-	-	-	2.9 Down
XM_485628	M200008119	-	-	-	-	-	-	-	-	-	-	2.9 Down
M300003096	M300003096	-	-	-	-	-	-	-	-	-	-	2.9 Down
NM_019788	Pallidin	Pldn	-	-	-	-	-	-	-	-	-	2.9 Down
NM_013685	Transcription factor 4	Tcf4	-	-	-	-	-	-	-	-	-	2.9 Down
M400012984	M400012984	-	-	-	-	-	-	-	-	-	-	2.9 Down
NM_013923	Ring finger protein 19A	Rnf19a	-	-	-	-	-	-	-	-	-	2.9 Down
NM_144826	UTP6, small subunit (SSU) processome component, homolog (yeast)	Utp6	-	-	-	-	-	-	1.6	Down	-	2.9 Down
NM_207544	Vomer nasal 1 receptor, D11	V1rd11	-	-	-	-	-	-	2.1	Down	-	2.9 Down
M400013284	M400013284	-	-	-	-	-	-	-	-	-	-	2.9 Down
		1810020D17										
NM_183251	RIKEN cDNA 1810020D17 gene	Rik	-	-	-	-	-	-	-	-	-	2.9 Down
NM_012008	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked	Ddx3y	1.8	Down	2.8	Down	-	-	-	-	-	2.9 Down
NM_010481	Heat shock protein 9	Hspa9	2.1	Down	-	-	-	-	-	-	-	2.9 Down
NM_019718	ADP-ribosylation factor-like 3	Arl3	-	-	-	-	-	-	-	-	-	2.9 Down
NM_172282	Transmembrane and coiled-coil domains 3	Tmco3	-	-	-	-	-	-	-	-	-	2.9 Down
NM_007381	Acyl-Coenzyme A dehydrogenase, long-chain	Acadl	2.3	Down	-	-	-	-	-	-	-	2.9 Down
NM_025950	Cell division cycle 37 homolog (S. cerevisiae)-like 1	Cdc37l1	-	-	-	-	-	-	-	-	-	2.9 Down
NM_028311	M400011641	-	-	-	-	-	-	-	-	-	-	2.9 Up
M400005500	M400005500	-	-	-	-	-	-	-	-	-	-	2.9 Down
NM_008774	Poly A binding protein, cytoplasmic 1	Pabpc1	-	-	-	-	-	-	-	-	-	2.9 Down
M400012978	M400012978	-	-	-	-	-	-	-	-	-	-	2.9 Down
M400006752	M400006752	-	-	-	-	-	-	-	-	-	-	2.9 Down
NM_008633	Microtubule-associated protein 4	Mtap4	-	-	-	-	-	-	-	-	-	2.9 Down
M400013173	M400013173	-	2.0	Down	-	-	-	-	-	-	-	2.9 Down
NM_009984	Cathepsin L	Ctsl	-	-	-	-	-	-	-	-	-	2.9 Down
NM_010942	Neuron specific gene family member 1	Nsg1	1.8	Down	-	-	-	-	-	-	-	2.9 Down
M300020278	M300020278	-	-	-	-	-	-	-	-	-	-	2.9 Down
M400013207	M400013207	-	-	-	-	-	-	-	-	-	-	2.9 Down
NM_013890	F-box and WD-40 domain protein 2	Fbxw2	-	-	-	-	-	-	-	-	-	2.9 Down
NM_028756	Solute carrier family 35, member A5	Slc35a5	-	-	-	-	-	-	-	-	-	2.9 Down
NM_148925	FYVE and coiled-coil domain containing 1	Fyco1	-	-	-	-	-	-	-	-	-	2.9 Down
NM_016912,												
NM_177270	M200003581	-	-	-	-	-	-	-	-	-	-	2.9 Down
XM_283409	Fanconi anemia, complementation group E	-	-	-	-	-	-	-	-	-	-	2.9 Down
NM_016764	Peroxiredoxin 4	Prdx4	-	-	-	-	-	-	-	-	-	2.9 Down
	Guanine nucleotide binding protein (G protein), gamma 11	Gng11	-	-	-	-	-	-	-	-	-	2.9 Down
NM_025331	Transmembrane protein 70	Tmem70	-	-	-	-	-	-	-	-	-	2.9 Down
NM_027415	PHD finger protein 5A	Phf5a	-	-	-	-	-	-	-	-	-	2.9 Down
NM_026737	PHD finger protein 5A	Phf5a	-	-	-	-	-	-	-	-	-	2.9 Down
XM_125109	predicted gene, EG214738	-	-	-	-	-	-	-	-	-	-	2.9 Down
M400001758	M400001758	-	-	-	-	-	-	-	-	-	-	2.9 Down
M400005963	M400005963	-	-	-	-	-	-	-	-	-	-	2.9 Down

NM_013624	Otogelin	Otog	-	-	-	-	-	-	2.9	Down
NM_199062	CDNA sequence BC062127	BC062127	1.9	Up	-	-	-	-	2.9	Up
M200009523	M200009523	-	-	-	-	-	-	-	2.9	Up
NM_011654	Tubulin, alpha 1B	Tuba1b	-	-	-	-	-	-	2.9	Down
NM_177618	WSC domain containing 1	Wscd1	-	-	-	-	-	-	2.9	Down
NM_026456	Transcription elongation factor B (SIII), polypeptide 1 v-abl Abelson murine leukemia viral oncogene homolog 2 (arg, Abelson-related gene)	Tceb1	-	-	-	-	-	-	2.9	Down
XM_136360	Sphingosine phosphate lyase 1	-	-	-	-	-	-	-	2.9	Up
NM_009163	RAS-related C3 botulinum substrate 1	Sgpl1	-	-	-	-	-	-	2.9	Down
NM_009007	CD164 antigen	Rac1	-	-	-	-	-	-	2.9	Down
NM_016898	Epidermal growth factor-containing fibulin-like extracellular matrix protein 1	Cd164	-	-	-	-	-	-	2.9	Down
NM_146015	Serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 3D	Efemp1	-	-	-	-	-	-	2.9	Down
NM_201376	Ly6/Plaur domain containing 2	Serpnb3d	-	-	-	-	-	-	2.9	Up
XM_128291	M400014417	-	-	-	-	-	-	-	2.9	Down
M400014417	M400014417	-	-	-	-	-	2.5	Down	3.0	Down
NM_033074	Threonyl-tRNA synthetase	Tars	-	-	-	-	-	-	3.0	Down
NM_008378	Imprinted and ancient	Impact	1.7	Down	-	-	-	-	3.0	Down
M400013187	M400013187	-	-	-	-	-	-	-	3.0	Up
M200003773	M200003773	-	1.7	Down	-	-	-	-	3.0	Down
NM_145568	Lysine-rich coiled-coil 1	Krcc1	-	-	-	-	-	-	3.0	Down
M400009224	M400009224	-	-	-	-	-	-	-	3.0	Down
NM_024437,	M300007886	-	-	-	-	-	-	-	3.0	Down
NM_024446	Cytidine monophosphate (UMP-CMP) kinase 1	Cmpk1	1.8	Down	-	-	-	-	3.0	Down
NM_025647	Protein tyrosine phosphatase, non-receptor type 20	Ptpn20	-	-	-	-	-	-	3.0	Up
NM_008978	Ubiquitin-conjugating enzyme E2E 1, UBC4/5 homolog (yeast)	Ube2e1	-	-	-	-	-	-	3.0	Down
NM_009455	Phosphatidylinositol-5-phosphate 4-kinase, type II, gamma	Pip4k2c	-	-	-	-	-	-	3.0	Down
NM_054097	M300019019	-	-	-	-	-	-	-	3.0	Down
XM_486022	M400006579	-	-	-	-	-	2.4	Down	3.0	Down
M400006579	M400006579	-	-	-	-	-	-	-	3.0	Down
NM_012019	Apoptosis-inducing factor, mitochondrion-associated 1	Aifm1	1.8	Down	-	-	-	-	3.0	Down
NM_178028	Galanin-like peptide	Galp	-	-	-	-	-	-	3.0	Up
M400013672	M400013672	-	1.5	Down	1.9	Down	-	-	3.0	Down
M400001147	M400001147	-	-	-	-	-	-	-	3.0	Down
M400013212	M400013212	-	-	-	-	-	-	-	3.0	Down
NM_011342	SEC22 vesicle trafficking protein homolog B (S. cerevisiae)	Sec22b	-	-	-	-	-	-	3.0	Down
NM_008235	Hairy and enhancer of split 1 (Drosophila)	Hes1	-	-	-	-	-	-	3.0	Down
NM_013827	Metal response element binding transcription factor 2	Mtf2	-	-	-	-	-	-	3.0	Down
NM_178926	Expressed sequence AI662250	AI662250	-	-	-	-	-	-	3.0	Down
NM_007404	A disintegrin and metallopeptidase domain 9 (meltrin gamma)	Adam9	-	-	-	-	-	-	3.0	Down

NM_027722	Nudix (nucleoside diphosphate linked moiety X)-type motif 4	Nudt4	-	-	-	-	-	-	-	3.0	Down
NM_133869	Choline/ethanolaminephosphotransferase 1	Cept1	-	-	-	-	-	-	-	3.0	Down
NM_146079	Guanylate cyclase activator 1B	Guca1b	-	-	-	-	-	-	-	3.0	Up
NM_008076	Gamma-aminobutyric acid (GABA-C) receptor, subunit rho 2	Gabbr2	-	-	-	-	-	-	-	3.0	Down
NM_024226, NM_194051, NM_194052, NM_194053, NM_194054	M300002207	-	-	-	-	-	-	-	-	3.0	Down
NM_028108	N-acetyltransferase 13	Nat13	1.8	Down	-	-	-	-	-	3.0	Down
M400006401	M400006401	-	-	-	-	-	-	-	-	3.0	Down
NM_010121	Eukaryotic translation initiation factor 2 alpha kinase 3	Eif2ak3	-	-	-	-	-	-	-	3.0	Down
NM_025432	Trafficking protein particle complex 2	Trappc2	-	-	-	-	-	-	-	3.0	Down
NM_019773	RAB9, member RAS oncogene family	Rab9	-	-	-	-	-	-	-	3.0	Down
NM_023191	WD repeat domain 61	Wdr61	-	-	-	-	-	-	-	3.0	Down
NM_011668, NM_173010	M400000820	-	-	-	-	-	-	-	-	3.0	Down
NM_021273	Creatine kinase, brain	Ckb	-	-	-	-	-	-	-	3.0	Down
M400019132	M400019132	-	-	-	-	-	-	-	-	3.0	Down
M400009216	M400009216	-	-	-	-	-	-	-	-	3.0	Down
M400017529	M400017529	-	-	-	-	-	-	-	-	3.0	Down
NM_007597	Calnexin	Canx	-	-	-	-	-	-	-	3.0	Down
NM_026369	Actin related protein 2/3 complex, subunit 5	Arpc5	1.8	Down	-	-	-	-	-	3.0	Down
NM_172947	LSM12 homolog (S. cerevisiae)	Lsm12	-	-	-	-	-	-	-	3.0	Down
NM_012052	Ribosomal protein S3	Rps3	-	-	-	-	-	-	-	3.0	Down
NM_019951	SEC11 homolog A (S. cerevisiae)	Sec11a	1.5	Down	-	-	-	-	-	3.0	Down
NM_175684	FCH and double SH3 domains 1	Fchsd1	1.7	Up	-	-	-	-	-	3.0	Up
NM_078478	Growth hormone inducible transmembrane protein	Ghitm	-	-	-	-	-	-	-	3.0	Down
M200012032	M200012032	-	-	-	-	-	-	-	-	3.0	Down
NM_011840	Mitogen-activated protein kinase kinase 5	Map2k5	-	-	-	-	-	-	-	3.0	Down
NM_009366	TSC22 domain family, member 1	Tsc22d1	-	-	-	-	1.6	Up	-	3.0	Down
NM_019999	Paroxysmal nonkinesigenic dyskinesia	Pnkd	-	-	-	-	-	-	-	3.0	Down
M300007519	M300007519	-	2.0	Down	-	-	-	-	-	3.0	Down
M300005153	M300005153	-	-	-	-	-	-	-	-	3.0	Down
M400015967	M400015967	-	-	-	-	-	-	-	-	3.0	Down
NM_010213	Four and a half LIM domains 3	Fhl3	-	-	-	-	-	-	-	3.0	Up
NM_010874	N-acetyltransferase 2 (arylamine N-acetyltransferase)	Nat2	1.7	Down	-	-	-	-	-	3.0	Down
NM_024289	Oxysterol binding protein-like 5	Osbp15	-	-	-	-	-	-	-	3.0	Down
NM_172525	Rho GTPase activating protein 29	Arhgap29	-	-	-	-	-	-	-	3.0	Down
XM_285913	M400006808	-	1.6	Down	-	-	-	-	-	3.1	Down
XM_123229	predicted gene, EG225228	-	-	-	-	-	-	-	-	3.1	Down
M400015070	M400015070	-	-	-	-	-	-	-	-	3.1	Down
NM_001001	Coiled-coil domain containing 111	Ccdc111	-	-	-	-	-	-	-	3.1	Down

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NM_029979	Tripartite motif-containing 35	Trim35	-	-	-	-	-	1.8	Up	3.1	Up	
NM_146544	Olfactory receptor 777	Olf777	-	-	-	-	-	-	-	3.1	Up	
M400013179	M400013179	-	2.0	Down	-	-	-	-	-	3.1	Down	
	serine (or cysteine) peptidase inhibitor, clade A, member 3F	-	-	-	-	-	-	-	-	3.1	Up	
XM_138237		-	-	-	-	-	-	-	-	3.1	Up	
NM_025537	Ts translation elongation factor, mitochondrial	Tsfm	1.6	Down	-	-	-	-	-	3.1	Down	
XM_131302	RIKEN cDNA 2610029I01 gene	-	1.8	Down	-	-	-	-	-	3.1	Down	
	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	Atp5c1	2.4	Down	-	-	-	-	-	3.1	Down	
NM_020615	M400018845	-	-	-	-	-	-	-	-	3.1	Down	
M400018845	M400018845	-	-	-	-	-	-	-	-	3.1	Down	
NM_007688	Cofilin 2, muscle	Cfl2	-	-	-	-	-	-	-	3.1	Down	
NM_009546	Tripartite motif-containing 25	Trim25	-	-	-	-	-	-	-	3.1	Down	
XM_486154	Brain expressed, associated with Nedd4	mCG_21548	-	-	-	-	-	-	-	3.1	Up	
M400012689	M400012689	-	-	-	-	-	-	-	-	3.1	Down	
M400018704	M400018704	-	-	-	-	-	-	-	-	3.1	Down	
	Cell division cycle 73, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	Cdc73	2.7	Down	-	-	-	-	-	3.1	Down	
NM_145991	gene model 967, (NCBI)	-	-	-	-	-	-	-	-	3.1	Down	
XM_355152		-	-	-	-	-	-	-	-	3.1	Down	
NM_011633	Tnf receptor-associated factor 5	Traf5	-	-	-	-	-	-	-	3.1	Down	
NM_007597	Calnexin	Canx	-	-	-	-	-	-	-	3.1	Down	
NM_021393	Cofactor of BRCA1	Cobra1	-	-	-	-	-	-	-	3.1	Down	
M400003566	M400003566	-	-	-	-	-	-	-	-	3.1	Down	
M400017747	M400017747	-	-	-	-	-	-	-	-	3.1	Down	
NM_026406	Ring finger protein 115	Rnf115	-	-	-	-	-	-	-	3.1	Down	
	DNA segment, Chr 1, Brigham & Womens Genetics 0212 expressed	D1Bwg0212e	1.6	Down	-	-	-	-	-	3.1	Down	
NM_028043		-	-	-	-	-	-	-	-	3.1	Down	
XM_130127	complement component 8, gamma subunit	-	-	-	-	-	-	-	-	3.1	Up	
NM_181390	Musculoskeletal, embryonic nuclear protein 1	Mustn1	-	-	-	-	-	-	-	3.1	Down	
M400014876	M400014876	-	-	-	-	-	-	-	-	3.1	Down	
NM_016805	Heterogeneous nuclear ribonucleoprotein U	Hnrnpu	-	-	-	-	-	-	-	3.1	Down	
M400012972	M400012972	-	-	-	-	-	-	-	-	3.1	Down	
NM_007950	Epiregulin	Ereg	-	-	-	-	-	-	-	3.1	Up	
NM_030215	Werner helicase interacting protein 1	Wrnip1	-	-	-	-	-	-	-	3.1	Down	
NM_008650	Methylmalonyl-Coenzyme A mutase	Mut	-	-	-	-	-	-	-	3.1	Down	
NM_001003930,NM_003933,NM_001003934,												
NM_053076	M200004172	-	-	-	-	-	-	-	-	3.1	Down	
XM_128722	arrestin domain containing 5	-	-	-	-	-	-	-	-	3.1	Up	
	Succinate dehydrogenase complex, subunit C, integral membrane protein	Pcp411	-	-	-	-	-	-	-	3.1	Down	
NM_025321		-	-	-	-	-	-	-	-	3.1	Down	
	Solute carrier family 16 (monocarboxylic acid transporters), member 9	Slc16a9	-	-	-	-	-	-	-	3.1	Down	
NM_025807		-	-	-	-	-	-	-	-	3.1	Down	

NM_028636	Mannosidase, alpha, class 2C, member 1	Man2c1	-	-	-	-	-	-	3.1	Up
NM_011933	2-4-dienoyl-Coenzyme A reductase 2, peroxisomal	Decr2	-	-	-	-	-	-	3.1	Up
NM_011650	Translin	Tsn	-	-	-	-	-	-	3.1	Down
NM_009371	Transforming growth factor, beta receptor II	Tgfbr2	-	-	-	-	-	-	3.1	Down
NM_020567	Geminin	Gmnn	1.6	Down	-	-	-	-	3.1	Down
M400002231	M400002231	-	-	-	-	-	-	-	3.2	Down
M400016632	M400016632	-	-	-	-	-	-	-	3.2	Down
NM_013556	Hypoxanthine guanine phosphoribosyl transferase 1 KRR1, small subunit (SSU) processome component, homolog (yeast)	Hprt1	-	-	-	-	-	-	3.2	Down
NM_178610	homolog (yeast)	Krr1	-	-	-	-	-	-	3.2	Down
NM_146121	RAB GTPase activating protein 1	Rabgap1	-	-	-	-	-	-	3.2	Down
NM_177106	RIKEN cDNA F830004M19 gene	-	2.3	Up	-	-	-	-	3.2	Up
M400015799	M400015799	-	-	-	-	-	-	-	3.2	Down
M400013028	M400013028	-	-	-	-	-	-	-	3.2	Down
NM_176848	F-box protein 2	Fbxo2	3.2	Up	-	-	-	-	3.2	Up
M400005810	M400005810	-	-	-	-	-	-	-	3.2	Down
M400016325	M400016325	-	-	-	-	-	-	-	3.2	Down
M400014160	M400014160	-	-	-	-	-	-	-	3.2	Down
M200007229	M200007229	-	-	-	-	-	-	-	3.2	Down
M400003188	M400003188	-	-	-	-	-	-	-	3.2	Down
M400005541	M400005541	-	-	-	-	-	-	-	3.2	Down
M400015872	M400015872	-	-	-	-	-	-	-	3.2	Down
M400016100	M400016100	-	-	-	-	-	-	-	3.2	Up
NM_023173	Dual specificity phosphatase 12	Dusp12	-	-	-	-	-	-	3.2	Down
M400005514	M400005514	-	-	-	-	-	-	-	3.2	Up
NM_177615	solute carrier family 26, member 10	-	-	-	-	-	3.2	Down	3.2	Down
NM_028339	Thioredoxin domain containing 1	Txndc1	-	-	-	-	-	-	3.2	Down
M400000530	M400000530	-	-	-	-	-	-	-	3.2	Down
NM_011992	Reticulocalbin 2	Rcn2	-	-	-	-	-	-	3.2	Down
NM_026850	Phosducin-like 3 ELOVL family member 5, elongation of long chain fatty acids (yeast)	Pdcl3	-	-	-	-	-	-	3.2	Down
NM_134255	splicing factor, arginine/serine-rich 2, interacting protein	Elovl5	-	-	-	-	-	-	3.2	Down
XM_128178	M400004302	-	-	-	-	-	-	-	3.2	Down
M400004302	immunoglobulin-like and fibronectin type III domain containing 1	-	-	-	-	-	3.2	Down	3.2	Down
NM_177642	M300006528	-	-	-	-	-	-	-	3.2	Down
M300006528	M300006528	-	-	-	-	-	-	-	3.2	Down
NM_011758	Zinc finger protein 39	Zfp39	-	-	-	-	-	-	3.2	Up
M400019364	M400019364	-	-	-	-	-	3.2	Down	3.2	Down
M400007808	M400007808	-	-	-	-	-	-	-	3.2	Down
M400007598	M400007598	-	-	-	-	-	3.3	Down	3.2	Down
NM_001005	847 Aspartylglucosaminidase	Aga	-	-	-	-	-	-	3.2	Down
NM_021355	Fibromodulin	Fmod	-	-	-	-	-	-	3.2	Up
NM_009950	CASP2 and RIPK1 domain containing adaptor with	Cradd	-	-	-	-	-	-	3.2	Down

NM_024237	death domain Fibulin 7	Fbln7	-	-	-	-	-	-	-	3.2	Down
NM_009186	Splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)	Sfrs10	1.7	Down	-	-	-	-	-	3.2	Down
NM_025937	NFKB activating protein	Nkap	2.0	Down	-	-	-	-	-	3.2	Down
NM_013755	Glycogenin	Gyg	-	-	-	-	-	-	-	3.2	Down
NM_025939	Phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoribosylaminoimidazole, succinocarboxamide synthetase	Paics	-	-	-	-	-	-	-	3.2	Down
NM_025980	Notch-regulated ankyrin repeat protein	Nrarp	-	-	-	-	-	-	-	3.2	Down
M400019499	M400019499	-	-	-	-	-	-	-	-	3.2	Down
M400008067	M400008067	-	2.8	Down	2.6	Down	-	-	-	3.2	Down
NM_001001	978	-	-	-	-	-	-	-	-	3.2	Up
NM_133766	predicted gene, 380687	Efr3a	-	-	-	-	-	-	-	3.2	Down
NM_028705	EFR3 homolog A (S. cerevisiae)	Herc3	-	-	-	-	-	-	-	3.3	Up
M300007897	Hect domain and RLD 3	-	-	-	-	-	-	-	-	3.3	Down
NM_021511	RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)	Rrs1	-	-	-	-	-	-	-	3.3	Down
NM_019432	Transmembrane protein 37	Tmem37	-	-	-	-	-	-	-	3.3	Down
XM_136041	armadillo repeat containing, X-linked 4	-	-	-	-	-	-	-	-	3.3	Down
NM_175406	ATPase, H+ transporting, lysosomal V0 subunit D2	Atp6v0d2	-	-	-	-	-	-	-	3.3	Down
NM_009835	Chemokine (C-C motif) receptor 6	Ccr6	-	-	-	-	-	-	-	3.3	Down
XM_141567,											
XM_485172	M400008303	-	-	-	-	-	-	-	-	3.3	Up
M400008142	M400008142	-	-	-	-	-	-	-	-	3.3	Up
XM_290030,											
XM_359409	M400003336	-	-	-	-	-	-	-	-	3.3	Down
NM_138956	Ras association (RalGDS/AF-6) domain family member 3	Rassf3	-	-	-	-	-	2.1	Up	3.3	Down
NM_012058	Signal recognition particle 9	Srp9	1.9	Down	-	-	-	-	-	3.3	Down
M400007798	M400007798	-	-	-	-	-	-	-	-	3.3	Down
XM_485613	M400003779	-	-	-	-	-	-	-	-	3.3	Down
M200008192	M200008192	-	-	-	-	-	-	-	-	3.3	Down
NM_029814	Chromatin modifying protein 5	Chmp5	-	-	-	-	-	-	-	3.3	Down
M300013837	M300013837	-	-	-	-	-	-	-	-	3.3	Up
M400003786	M400003786	-	-	-	-	-	-	-	-	3.3	Up
NM_008540	MAD homolog 4 (Drosophila)	Smad4	-	-	-	-	-	-	-	3.3	Down
NM_018748	Golgi autoantigen, golgin subfamily a, 4	Golga4	-	-	-	-	-	-	-	3.3	Down
M400013081	M400013081	-	2.1	Down	-	-	-	-	-	3.3	Down
NM_027338	Vacuolar protein sorting 36 (yeast)	Vps36	-	-	-	-	-	-	-	3.3	Down
NM_019443	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1	Ndufa1	-	-	-	-	-	-	-	3.3	Down
NM_198606	WD repeats and SOF domain containing 1	Wdsf1	-	-	-	-	-	-	-	3.3	Down
NM_008298	DnaJ (Hsp40) homolog, subfamily A, member 1	Dnaja1	-	-	-	-	-	-	-	3.3	Down



NM_181410	General transcription factor IIH, polypeptide 3	Gtf2h3	-	-	-	-	-	-	-	3.3	Down
NM_133681	Tetraspanin 1	Tspan1	-	-	-	-	-	-	-	3.3	Down
M400004888	M400004888	-	-	-	-	-	-	-	-	3.3	Down
NM_009145	Neuroplastin	Nptn	-	-	-	-	-	-	-	3.3	Down
	cysteine rich transmembrane BMP regulator 1 (chordin like)	-	-	-	-	-	-	-	-	3.4	Down
XM_128751	Multimerin 1	Mmnr1	-	-	-	-	-	-	-	3.4	Down
M400005050	M400005050	-	-	-	-	-	-	-	-	3.4	Down
NM_023450	RIKEN cDNA 2010204K13 gene	-	-	-	-	-	-	-	-	3.4	Down
NM_019549	Pleckstrin	Plek	-	-	-	-	-	-	-	3.4	Down
NM_028242	HIV TAT specific factor 1	Htatsf1	-	-	-	-	-	-	-	3.4	Down
M400018223	M400018223	-	-	-	-	-	-	-	-	3.4	Down
M400011585	M400011585	-	-	-	-	-	-	-	-	3.4	Down
NM_145615	Electron transferring flavoprotein, alpha polypeptide	Etfa	-	-	-	-	-	-	-	3.4	Down
M400019219	M400019219	-	-	-	-	-	-	-	-	3.4	Down
NM_177345	Mitogen-activated protein kinase associated protein 1	Mapkap1	-	-	-	-	-	-	-	3.4	Down
M400006383	M400006383	-	-	-	-	-	-	-	-	3.4	Down
M400005476	M400005476	-	-	-	-	-	-	-	-	3.4	Down
M200012364	M200012364	-	-	-	-	-	-	-	-	3.4	Down
M400007265	M400007265	-	-	-	-	-	-	-	-	3.4	Down
NM_011847	DnaJ (Hsp40) homolog, subfamily B, member 6	Dnajb6	-	-	-	-	-	-	-	3.4	Down
NM_010847	Max interacting protein 1	Mxi1	-	-	-	-	-	-	-	3.4	Down
	Budding uninhibited by benzimidazoles 3 homolog (S. cerevisiae)	Bub3	-	-	-	-	2.2	Down	-	3.4	Down
NM_009460	SMT3 suppressor of mif two 3 homolog 1 (yeast)	Sumo1	2.0	Down	-	-	-	-	-	3.4	Down
M300011672	M300011672	-	2.4	Down	-	-	-	-	-	3.4	Down
XM_129145	tetratricopeptide repeat domain 9C	-	2.2	Down	1.8	Down	-	-	-	3.4	Down
M400017753	M400017753	-	-	-	-	-	-	-	-	3.4	Down
NM_021510	Heterogeneous nuclear ribonucleoprotein H1	Hnrnp1	-	-	-	-	-	-	-	3.4	Down
NM_010423	Hairy/enhancer-of-split related with YRPW motif 1	Hey1	-	-	-	-	-	-	-	3.4	Down
M400013859	M400013859	-	-	-	-	-	-	-	-	3.4	Down
M400015854	M400015854	-	-	-	-	-	1.5	Down	-	3.4	Down
NM_011666	Ubiquitin-like modifier activating enzyme 3	Uba3	-	-	-	-	-	-	-	3.4	Down
M400015024	M400015024	-	-	-	1.6	Down	2.1	Down	-	3.4	Down
NM_022023	Glia maturation factor, beta	Gmfb	-	-	-	-	-	-	-	3.4	Down
NM_011845	Midline 2	Mid2	-	-	-	-	-	-	-	3.4	Down
	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 3	Ndufb3	-	-	-	-	-	-	-	3.4	Down
NM_028095	Methyltransferase like 10	Mettl10	-	-	1.7	Down	-	-	-	3.4	Down
NM_205536	ELK3, member of ETS oncogene family	-	1.6	Down	-	-	-	-	-	3.4	Down
NM_146087	Casein kinase 1, alpha 1	Csnk1a1	-	-	-	-	-	-	-	3.4	Up
M400017011	M400017011	-	3.5	Down	-	-	-	-	-	3.4	Down
NM_173007	Tetraspanin 12	Tspan12	-	-	-	-	-	-	-	3.4	Down
NM_175036	Leptin receptor overlapping transcript	Leprot	-	-	-	-	-	-	-	3.5	Down
XM_487295	M400003777	-	-	-	-	-	-	-	-	3.5	Down

M400006333	M400006333	-	-	-	-	-	-	-	-	3.5	Up
NM_025914	ARP6 actin-related protein 6 homolog (yeast)	Actr6	1.6	Down	-	-	-	-	-	3.5	Down
NM_009726	ATPase, Cu++ transporting, alpha polypeptide	Atp7a	-	-	-	-	-	-	-	3.5	Down
		B230219D22									
NM_181278	RIKEN cDNA B230219D22 gene	Rik	-	-	-	-	-	-	-	3.5	Down
NM_024480	SH3 binding domain protein 5 like	Sh3bp5l	-	-	-	-	-	-	-	3.5	Down
	CKLF-like MARVEL transmembrane domain containing 5	Cmtm5	-	-	-	-	-	-	-	3.5	Down
NM_026066											
M400017331	M400017331	-	-	-	-	-	-	4.2	Down	3.5	Down
NM_146369	Olfactory receptor 434	Olfr434	1.6	Down	-	-	-	-	-	3.5	Down
NM_008880	Phospholipid scramblase 2	Plscr2	-	-	-	-	-	-	-	3.5	Down
NM_018810	Makorin, ring finger protein, 1	Mkrn1	-	-	-	-	-	-	-	3.5	Down
NM_011584	Nuclear receptor subfamily 1, group D, member 2	Nr1d2	-	-	-	-	-	-	-	3.5	Down
XM_357928	M400010560	-	2.9	Down	-	-	-	-	-	3.5	Down
M400005488	M400005488	-	1.6	Down	-	-	-	-	-	3.5	Down
M400001435	M400001435	-	-	-	-	-	-	-	-	3.5	Down
NM_010211	Four and a half LIM domains 1	Fhl1	-	-	-	-	-	-	-	3.5	Down
NM_023043	Prion protein dublet	Prnd	-	-	-	-	-	-	-	3.5	Down
M300002054	M300002054	-	-	-	-	-	-	-	-	3.5	Down
M300002674	M300002674	-	-	-	-	-	-	-	-	3.5	Down
NM_008722,											
XM_486188	M300012771	-	-	-	-	-	-	-	-	3.5	Down
NM_145556	TAR DNA binding protein	Tardbp	-	-	-	-	-	-	-	3.5	Down
NM_146644	Olfactory receptor 1163	Olfr1163	-	-	-	-	-	-	-	3.5	Down
NM_007792	Cysteine and glycine-rich protein 2	Csrp2	-	-	-	-	-	-	-	3.5	Down
NM_013843	Zinc finger protein 53	Zfp53	-	-	-	-	-	-	-	3.5	Up
NM_178651	Solute carrier family 30 (zinc transporter), member 9	Slc30a9	2.0	Down	-	-	-	-	-	3.5	Down
NM_025809	C-type lectin domain family 14, member a	Clec14a	-	-	-	-	-	-	-	3.5	Down
NM_023243	Cyclin H	Ccnh	-	-	-	-	-	-	-	3.5	Down
		3110001A13									
NM_025626	RIKEN cDNA 3110001A13 gene	Rik	-	-	-	-	-	-	-	3.5	Down
XM_484355	RIKEN cDNA 2310047A01 gene	-	-	-	-	-	-	-	-	3.5	Down
NM_178680	Unc-45 homolog B (C. elegans)	Unc45b	-	-	-	-	-	-	-	3.5	Down
NM_010474	Heparan sulfate (glucosamine) 3-O-sulfotransferase 1	Hs3st1	-	-	-	-	-	-	-	3.5	Down
NM_001003											
971,NM_025											
483	M400013871	-	1.6	Down	-	-	-	-	-	3.5	Down
NM_080557	Sorting nexin 4	Snx4	-	-	-	-	-	-	-	3.5	Down
M400007030	M400007030	-	-	-	-	-	-	-	-	3.5	Down
NM_013546	Heme binding protein 1	Hebp1	-	-	-	-	-	-	-	3.5	Down
NM_023595	Deoxyuridine triphosphatase	Dut	2.3	Down	-	-	-	-	-	3.5	Down
	EGF, latrophilin seven transmembrane domain containing 1	Eltid1	-	-	-	-	-	-	-	3.5	Down
NM_133222											
		2610204K14									
NM_025997	RIKEN cDNA 2610204K14 gene	Rik	-	-	-	-	-	-	-	3.5	Down

M400013293	M400013293	-	-	-	-	-	-	-	-	3.5	Down
NM_022309	Core binding factor beta	Cbfb	-	-	-	-	-	-	-	3.5	Down
	GTPase activating protein (SH3 domain) binding protein 2	G3bp2	-	-	-	-	-	-	-	3.5	Down
NM_011816	Beta galactoside alpha 2,6 sialyltransferase 1	St6gal1	-	-	-	-	-	-	-	3.5	Down
NM_145933	M400013621	-	-	-	-	-	-	-	-	3.5	Down
M400013621	M400013621	-	-	-	-	-	-	-	-	3.5	Down
M300013133	M300013133	-	1.5	Down	-	-	-	-	-	3.6	Down
NM_174857	MAM domain containing 2	Mamdc2	-	-	-	-	-	-	-	3.6	Down
NM_010245	Friend virus susceptibility 4	-	1.7	Up	3.0	Up	3.1	Up	-	3.6	Up
M400013195	M400013195	-	-	-	-	-	-	-	-	3.6	Down
NM_019989	SH3-binding domain glutamic acid-rich protein like	Sh3bgrl	-	-	-	-	-	-	-	3.6	Down
NM_009761	BCL2/adenovirus E1B interacting protein 3-like	Bnip3l	-	-	-	-	-	-	-	3.6	Down
NM_025566	Tumor necrosis factor, alpha-induced protein 8-like 1	Tnfaip8l1	-	-	-	-	-	-	-	3.6	Up
M400001441	M400001441	-	-	-	-	-	-	-	-	3.6	Down
M300009088	M300009088	-	-	-	-	-	-	-	-	3.6	Down
NM_026182	Mitochondrial fission regulator 1	Mtfr1	-	-	-	-	-	-	-	3.6	Down
NM_007706	Suppressor of cytokine signaling 2	Socs2	-	-	-	-	-	-	-	3.6	Down
M400014702	M400014702	-	-	-	-	-	-	-	-	3.6	Down
NM_026106	Down-regulator of transcription 1	Dr1	-	-	-	-	-	-	-	3.6	Down
M400008242	M400008242	-	-	-	-	-	-	-	-	3.6	Down
NM_178734	Zinc finger protein 473	Zfp473	-	-	-	-	-	-	-	3.6	Down
NM_009222	Synaptosomal-associated protein 23	Snap23	2.0	Down	-	-	-	-	-	3.6	Down
M200005379	M200005379	-	2.2	Down	-	-	-	-	-	3.6	Down
NM_028173	Translocating chain-associating membrane protein 1	Tram1	-	-	-	-	-	-	-	3.6	Down
NM_009226	Small nuclear ribonucleoprotein D1	Snrpd1	1.9	Down	2.3	Down	-	-	-	3.6	Down
M400013325	M400013325	-	1.7	Down	-	-	-	-	-	3.6	Down
XM_355498	predicted gene, OTTMUSG00000000231	-	-	-	-	-	-	-	-	3.6	Down
NM_009041	Radixin	Rdx	-	-	-	-	-	-	-	3.6	Down
NM_029505	Adaptor-related protein complex 3, mu 2 subunit	Ap3m2	-	-	-	-	-	-	-	3.6	Down
NM_173756	Lin-52 homolog (C. elegans)	Lin52	-	-	-	-	-	-	-	3.6	Down
M400001198	M400001198	-	-	-	-	-	-	-	-	3.6	Down
M400019245	M400019245	-	-	-	-	-	-	-	-	3.6	Down
NM_133238	CD209a antigen	Cd209a	-	-	-	-	-	-	-	3.7	Down
NM_026416	S100 calcium binding protein A16	S100a16	-	-	-	-	-	-	-	3.7	Down
NM_011333	Chemokine (C-C motif) ligand 2	Ccl2	-	-	-	-	-	-	-	3.7	Up
NM_025835	Propionyl Coenzyme A carboxylase, beta polypeptide	Pccb	-	-	-	-	-	-	-	3.7	Down
NM_018796	Eukaryotic translation elongation factor 1 beta 2	Eef1b2	-	-	-	-	-	-	-	3.7	Down
M400018270	M400018270	-	2.9	Up	-	-	-	-	-	3.7	Up
NM_010284	Growth hormone receptor	Ghr	-	-	-	-	-	-	-	3.7	Down
M400012933	M400012933	-	-	-	-	-	-	-	-	3.7	Down
M400008548	M400008548	-	-	-	-	-	-	-	-	3.7	Up
NM_053170	Tripartite motif-containing 33	Trim33	1.7	Down	-	-	-	-	-	3.7	Down
NM_026141	Peptidylprolyl isomerase (cyclophilin)-like 4	Ppil4	2.1	Down	-	-	-	-	-	3.7	Down
M400002949	M400002949	-	-	-	-	-	-	-	-	3.7	Down
NM_016978	Ornithine aminotransferase	Oat	-	-	-	-	-	-	-	3.7	Down

M200007993	M200007993	-	-	-	-	-	-	-	-	3.7	Down
NM_011873	DAZ associated protein 2	Dazap2	-	-	-	-	-	-	-	3.8	Down
NM_019770, XM_486207	M400001162	-	1.7	Down	-	-	-	-	-	3.8	Down
M400019412	M400019412	-	-	-	-	-	-	-	-	3.8	Down
M400014531	M400014531	-	-	-	-	-	-	-	-	3.8	Down
M400012996	M400012996	-	-	-	-	-	-	-	-	3.8	Down
NM_009173	Seven in absentia 1B V-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	Siah1b Mycn	-	-	-	-	-	-	-	3.8	Down
NM_008709	Zinc finger, BED domain containing 3	Zbed3	-	-	-	-	-	-	-	3.8	Up
NM_028106	M400014750	-	1.9	Down	-	-	-	-	-	3.8	Down
M400014750	PRP39 pre-mRNA processing factor 39 homolog (yeast)	Prpf39	-	-	2.7	Down	-	-	-	3.8	Down
NM_177806	FERM domain containing 6	Frmd6	-	-	-	-	-	-	-	3.8	Down
NM_028127	inositol polyphosphate-4-phosphatase, type II	-	-	-	-	-	-	-	-	3.8	Down
XM_134427	protein phosphatase 1, regulatory subunit 3D	-	-	-	-	-	-	-	-	3.8	Down
XM_141580	Ubiquitin-conjugating enzyme E2B, RAD6 homology (S. cerevisiae)	Ube2b	-	-	-	-	-	-	-	3.8	Down
NM_009458	M200015455	-	1.9	Down	-	-	-	-	-	3.8	Down
NM_023719, XM_485282	Serpine1 mRNA binding protein 1	Serbp1	-	-	-	-	-	-	-	3.8	Down
NM_025814	Solute carrier family 43, member 3	Slc43a3	-	-	-	-	-	-	-	3.8	Down
NM_021398	Poly(rC) binding protein 1	Pcbp1	-	-	-	-	-	-	-	3.8	Down
NM_011865	trafficking protein particle complex 6B	-	-	-	-	-	-	-	-	3.8	Down
XM_127025	Superkiller viralicidic activity 2-like 2 (S. cerevisiae)	Skiv2l2	2.1	Down	-	-	-	-	-	3.9	Down
NM_028151	FUN14 domain containing 1	Fundc1	2.1	Down	-	-	-	-	-	3.9	Down
NM_028058	RIKEN cDNA E130309F12 gene	E130309F12 Rik	-	-	-	-	-	-	-	3.9	Up
NM_178756	M400008405	-	-	-	-	-	-	-	-	3.9	Up
M400008405	Tripartite motif-containing 2	Trim2	-	-	-	-	-	-	-	3.9	Down
NM_030706	Fatty acid binding protein 5, epidermal	Fabp5	-	-	-	-	-	-	-	3.9	Down
NM_010634	G kinase anchoring protein 1	Gkap1	1.8	Down	-	-	-	-	-	3.9	Down
NM_019832	Monocyte to macrophage differentiation-associated	Mmd	-	-	-	-	-	-	-	3.9	Down
NM_026178	FERM domain containing 4A	Frmd4a	-	-	-	-	-	-	-	3.9	Down
NM_172475	M200015235	-	-	-	-	-	-	-	-	3.9	Down
NM_027870, XM_486012	Reticulocalbin 1	Rcn1	-	-	-	-	-	-	-	3.9	Up
NM_009037	limb region 1	-	-	-	-	-	-	-	-	3.9	Up
NM_020295	Acyl-Coenzyme A binding domain containing 3	Acbd3	-	-	-	-	-	-	-	3.9	Down
NM_133225	CD4 antigen	Cd4	-	-	-	-	-	-	-	3.9	Up
NM_013488	Coiled-coil domain containing 117	Ccdc117	1.6	Down	-	-	-	-	-	3.9	Down
NM_134033	Vasoactive intestinal polypeptide	Vip	-	-	-	-	-	-	-	3.9	Up
NM_011702	M400013430	-	-	-	-	-	-	-	-	4.0	Down
M400013430	Osteoglycin	Ogn	-	-	-	-	-	-	-	4.0	Down
NM_008760											

NM_172741	RIKEN cDNA 4931406P16 gene	4931406P16									
XM_140436	mex3 homolog C (C. elegans)	Rik	1.6	Down	-	-	-	-	4.0	Down	
NM_144910,		-	2.2	Down	-	-	-	-	4.0	Down	
NM_178854	M200005971	-	-	-	-	-	-	-	4.0	Down	
XM_484500	M400001999	-	-	-	-	-	-	-	4.0	Up	
NM_201362	Coiled-coil domain containing 68	Ccdc68	1.9	Down	-	-	-	-	4.0	Down	
M400015913	M400015913	-	-	-	-	-	-	-	4.0	Down	
M400014810	M400014810	-	-	-	2.3	Down	2.8	Down	4.1	Down	
		B230380D07									
NM_172772	RIKEN cDNA B230380D07 gene	Rik	-	-	-	-	-	-	4.1	Down	
XM_485480,											
XM_485484,											
XM_485490,											
XM_485496,											
XM_486109	M400012694	-	3.1	Down	2.2	Down	-	-	4.1	Down	
M400013861	M400013861	-	-	-	-	-	-	-	4.1	Down	
	StAR-related lipid transfer (START) domain containing 13	Stard13	1.8	Down	-	-	-	-	4.1	Down	
NM_146258	M200013058	-	2.1	Down	-	-	-	-	4.1	Down	
		1110018M03									
NM_026271	RIKEN cDNA 1110018M03 gene	Rik	-	-	-	-	-	-	4.2	Down	
	cysteine rich transmembrane BMP regulator 1 (chordin like)	-	-	-	-	-	-	-	4.2	Down	
XM_128751		-	-	-	-	-	-	-	4.2	Down	
NM_016719	Growth factor receptor bound protein 14	Grb14	-	-	-	-	-	-	4.2	Down	
NM_008317	Hyaluronoglucosaminidase 1	Hyal1	3.5	Up	-	-	-	-	4.2	Up	
M200009912	M200009912	-	-	-	-	-	-	-	4.2	Down	
XM_130221	tubulin tyrosine ligase-like family, member 11	-	-	-	-	-	-	-	4.2	Up	
NM_022028	Salvador homolog 1 (Drosophila)	Sav1	-	-	-	-	-	-	4.2	Down	
NM_020007	Muscleblind-like 1 (Drosophila)	Mbnl1	-	-	-	-	-	-	4.2	Down	
M400008452	M400008452	-	-	-	-	-	-	-	4.2	Up	
M400018644	M400018644	-	-	-	-	-	-	-	4.2	Down	
NM_133354	SMT3 suppressor of mif two 3 homolog 2 (yeast)	Sumo2	-	-	-	-	-	-	4.2	Down	
M400014371	M400014371	-	2.2	Down	-	-	-	-	4.2	Down	
M200007425	M200007425	-	-	-	-	-	-	-	4.2	Down	
M400014847	M400014847	-	-	-	-	-	-	-	4.2	Down	
NM_025359	Tetraspanin 13	Tspan13	-	-	-	-	-	-	4.2	Down	
NM_212445	KDEL (Lys-Asp-Glu-Leu) containing 2	Kdelc2	-	-	-	-	-	-	4.2	Down	
M400014823	M400014823	-	-	-	-	-	-	-	4.2	Down	
NM_016787	BCL2/adenovirus E1B interacting protein 1, NIP2	Bnip2	2.2	Down	-	-	-	-	4.2	Down	
M400015284	M400015284	-	-	-	-	-	-	-	4.3	Down	
M400013056	M400013056	-	-	-	-	-	-	-	4.3	Down	
NM_028487	GC-rich promoter binding protein 1	Gpbp1	2.0	Down	-	-	-	-	4.3	Down	
NM_008056	Frizzled homolog 6 (Drosophila)	Fzd6	-	-	-	-	-	-	4.3	Down	
NM_013464	Aryl-hydrocarbon receptor	Ahr	-	-	-	-	-	-	4.3	Down	

M400007130	M400007130	-	-	-	-	-	-	-	-	4.3	Down
NM_026784	Phosphomevalonate kinase	Pmvk	-	-	1.6	Up	-	1.1	Up	-	-
XM_203393	Proline-rich polypeptide 6	Prr6	-	-	1.5	Up	-	1.1	Up	-	-
M200004573	M200004573	-	-	-	1.5	Up	-	1.2	Up	-	-
M400014534	M400014534	-	-	-	1.8	Up	-	1.2	Up	-	-
M400014595	M400014595	-	-	-	2.0	Up	-	1.2	Up	-	-
NM_177296	Transportin 3	Tnpo3	1.7	Up	-	-	-	1.2	Down	-	-
NM_175465	SEC14 and spectrin domains 1	Sestd1	2.4	Up	-	-	-	1.3	Up	-	-
M400006229	M400006229	-	-	-	2.0	Up	-	1.3	Up	-	-
	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11	Ndufb11	-	-	1.5	Up	-	1.3	Up	-	-
M400009087	M400009087	-	-	-	1.7	Up	-	1.3	Up	-	-
NM_009057	Recombination activating gene 1 activating protein 1	Rag1ap1	2.4	Up	-	-	-	1.3	Up	-	-
NM_019711	RNA binding motif, single stranded interacting protein 2	Rbms2	-	-	1.7	Up	-	1.3	Up	-	-
NM_008528	B-cell linker	Blnk	-	-	1.9	Up	-	1.3	Up	-	-
NM_144793	Solute carrier family 25, member 38	Slc25a38	2.4	Up	1.6	Up	-	1.3	Up	-	-
M400004411	M400004411	-	2.1	Up	2.2	Up	-	1.3	Up	-	-
NM_016899	RAB25, member RAS oncogene family	Rab25	-	-	1.8	Down	-	1.3	Down	-	-
NM_207669	GA repeat binding protein, beta 1	Gabpb1	-	-	1.7	Up	-	1.3	Up	-	-
	GTP binding protein (gene overexpressed in skeletal muscle)	Gem	-	-	1.8	Up	-	1.3	Up	-	-
M400003522	M400003522	-	-	-	2.1	Up	-	1.3	Up	-	-
M200011948	M200011948	-	1.6	Up	1.8	Up	-	1.3	Up	-	-
NM_025774	Prkr interacting protein 1 (IL11 inducible)	Prkrip1	-	-	1.6	Up	-	1.4	Up	-	-
NM_133182	Protein arginine N-methyltransferase 2	Prmt2	-	-	1.5	Up	-	1.4	Up	-	-
NM_011526	Transgelin	Tagln	-	-	1.6	Up	-	1.4	Up	-	-
M400014539	M400014539	-	-	-	1.7	Up	-	1.4	Up	-	-
NM_011550	MAX-like protein X	Mlx	-	-	1.5	Up	-	1.5	Up	-	-
NM_133837	Cell division cycle 123 homolog (S. cerevisiae)	Cdc123	-	-	2.2	Up	-	1.5	Up	-	-
XM_284543	exosome component 7	-	-	-	2.2	Up	-	1.5	Up	-	-
NM_009745	B-cell CLL/lymphoma 7B	Bcl7b	-	-	2.0	Up	-	1.5	Up	-	-
NM_153536	ecotropic viral integration site 5 like	-	1.8	Up	-	-	-	1.5	Up	-	-
NM_145927	Farnesyltransferase, CAAX box, beta DNA segment, Chr 4, Wayne State University 114, expressed	Fntb	-	-	-	-	-	1.5	Down	-	-
NM_133873	Acyl-CoA thioesterase 7	Acot7	-	-	1.9	Up	-	1.5	Up	-	-
NM_133348	M400017690	-	-	-	-	-	-	1.5	Down	-	-
M400017690	M400017690	-	-	-	-	-	-	1.5	Down	-	-
M400015865	M400015865	-	-	-	-	-	-	1.5	Down	-	-
NM_025282	Myocyte enhancer factor 2C	Mef2c	-	-	-	-	-	1.5	Up	-	-
M400005844	M400005844	-	-	-	-	-	-	1.5	Up	-	-
	Solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	Slc1a4	-	-	-	-	-	1.5	Down	-	-
NM_018861	M400013418	-	-	-	-	-	-	1.5	Down	-	-
M400013418	M400013418	-	-	-	-	-	-	1.5	Down	-	-
M400017359	M400017359	-	-	-	-	-	-	1.5	Down	-	-
NM_027189	Gem (nuclear organelle) associated protein 7	Gemin7	-	-	-	-	-	1.5	Up	-	-

NM_133203	Killer cell lectin-like receptor, subfamily A, member 17	Klra17	-	-	-	-	1.5	Down	-	-
M300008291	M300008291	-	-	-	-	-	1.5	Down	-	-
M400018568	M400018568	-	-	-	-	-	1.5	Down	-	-
NM_013770	Solute carrier family 25 (mitochondrial carrier, dicarboxylate transporter), member 10	Slc25a10	-	-	-	-	1.5	Up	-	-
M400014697	M400014697	-	-	-	-	-	1.5	Down	-	-
M400018857	M400018857	-	-	-	-	-	1.5	Down	-	-
NM_019586	Ubiquitin-conjugating enzyme E2, J1	Ube2j1	-	-	-	-	1.5	Up	-	-
M400002686	M400002686	-	-	-	-	-	1.5	Down	-	-
M400016368	M400016368	-	-	-	-	-	1.5	Up	-	-
M400015374	M400015374	-	-	-	-	-	1.5	Down	-	-
NM_013718	Trafficking protein particle complex 3	Trappc3	-	-	-	-	1.5	Up	-	-
NM_007421	Adenylosuccinate synthetase like 1	Adssl1	-	-	-	-	1.5	Up	-	-
XM_355643	RIKEN cDNA 0610007L01 gene	-	-	-	1.7	Up	1.5	Up	-	-
NM_007748	Cytochrome c oxidase, subunit VI a, polypeptide 1	Cox6a1	-	-	-	-	1.5	Up	-	-
M400018776	M400018776	-	-	-	-	-	1.5	Down	-	-
NM_025645	WD repeat domain 57 (U5 snRNP specific)	Wdr57	-	-	-	1.5	Up	1.5	Up	-
NM_212468	Single-stranded DNA binding protein 1	Ssbp1	-	-	-	-	1.5	Down	-	-
M400016882	M400016882	-	-	-	-	-	1.5	Down	-	-
NM_011920	ATP-binding cassette, sub-family G (WHITE), member 2	Abcg2	-	-	-	1.8	Up	1.5	Up	-
M400008118	M400008118	-	-	-	-	-	1.5	Down	-	-
NM_198415	Creatine kinase, mitochondrial 2	Ckmt2	-	-	-	-	1.5	Down	-	-
NM_011012	Opioid receptor-like 1	Oprl1	-	-	-	-	1.5	Down	-	-
M400006285	M400006285	-	-	-	-	-	1.6	Down	-	-
NM_029522	G-protein signalling modulator 2 (AGS3-like, C. elegans)	Gpsm2	-	-	-	-	1.6	Up	-	-
NM_016742	Cell division cycle 37 homolog (S. cerevisiae)	Cdc37	-	-	-	-	1.6	Up	-	-
NM_152808	Solute carrier family 44, member 2	Slc44a2	-	-	-	-	1.6	Up	-	-
XM_133399	M400002228	-	-	-	-	-	1.6	Down	-	-
XM_483932	predicted gene, EG432482	-	-	-	-	-	1.6	Up	-	-
NM_021514	Phosphofructokinase, muscle	Pfkm	-	-	-	-	1.6	Up	-	-
M400012803	M400012803	-	-	-	-	-	1.6	Up	-	-
NM_019726	G protein pathway suppressor 2	Gps2	-	-	-	-	1.6	Up	-	-
XM_134498	neuropilin (NRP) and tolloid (TLL)-like 2	-	-	-	-	-	1.6	Down	-	-
NM_021300	Reproductive homeobox 4B	Rhox4b	-	-	-	-	1.6	Down	-	-
NM_134094	Neurocalcin delta	Ncald	-	-	-	-	1.6	Up	-	-
NM_201645	UDP glucuronosyltransferase 1 family, polypeptide A6B	Ugt1a6a	-	-	-	-	1.6	Down	-	-
XM_488999	hypothetical protein A530017F20	-	-	-	-	-	1.6	Down	-	-
NM_010347	Amino-terminal enhancer of split	Aes	-	-	-	1.8	Up	1.6	Up	-
M400015088	M400015088	-	-	-	-	-	1.6	Down	-	-
NM_028672	RIKEN cDNA 4930430E16 gene	-	-	-	-	-	1.6	Down	-	-
M400006510	M400006510	-	-	-	-	-	1.6	Down	-	-
M400016889	M400016889	-	-	-	-	-	1.6	Down	-	-

NM_198113	Slingshot homolog 3 (Drosophila)	Ssh3	-	-	-	-	1.6	Down	-	-
NM_008052	Deltex 1 homolog (Drosophila)	Dtx1	-	-	-	-	1.6	Up	-	-
M40000696	M40000696	-	-	-	-	-	1.6	Down	-	-
M400009781	M400009781	-	-	-	-	-	1.6	Down	-	-
NM_022325	Cathepsin Z	Ctsz	-	-	1.5	Up	1.6	Up	-	-
M400002426	M400002426	-	-	-	-	-	1.6	Down	-	-
M400009840	M400009840	-	-	-	-	-	1.6	Down	-	-
NM_133659	Avian erythroblastosis virus E-26 (v-ets) oncogene related	Erg	-	-	-	-	1.6	Down	-	-
XM_126982	churchill domain containing 1	-	-	-	-	-	1.6	Up	-	-
M400019078	M400019078	-	-	-	-	-	1.6	Down	-	-
NM_026732	Mitochondrial ribosomal protein L14	Mrpl14	-	-	-	-	1.6	Up	-	-
NM_172714	Lin-54 homolog (C. elegans)	Lin54	-	-	-	-	1.6	Up	-	-
NM_011509	Suppressor of Ty 4 homolog 1 (S. cerevisiae)	Supt4h1	-	-	1.6	Up	1.6	Up	-	-
NM_172746,										
NM_172746	M300013785	-	-	-	1.7	Up	1.6	Up	-	-
M400008517	M400008517	-	-	-	-	-	1.6	Down	-	-
M400013974	M400013974	-	-	-	-	-	1.6	Down	-	-
M400015702	M400015702	-	-	-	-	-	1.6	Down	-	-
NM_025311	DNA segment, Chr 14, ERATO Doi 449, expressed	D14Ert449e	-	-	-	-	1.6	Up	-	-
NM_198649	Actin binding LIM protein family, member 3	Ablim3	-	-	-	-	1.6	Up	-	-
XM_133021	carboxypeptidase A2, pancreatic	-	-	-	-	-	1.6	Down	-	-
AK017169	Platelet derived growth factor, alpha	Pdgfa	-	-	-	-	1.6	Up	-	-
NM_019805	Anaphase promoting complex subunit 7	Anapc7	-	-	2.0	Up	1.6	Up	-	-
M300002605	M300002605	-	-	-	-	-	1.6	Up	-	-
M400018966	M400018966	-	-	-	-	-	1.6	Down	-	-
M400017047	M400017047	-	-	-	-	-	1.6	Down	-	-
NM_029313	chemokine-like factor	-	-	-	-	-	1.6	Down	-	-
NM_021437	RIKEN cDNA 1700123O20 gene	1700123O20	-	-	-	-	1.6	Up	-	-
NM_025628	Cytochrome c oxidase, subunit VIb polypeptide 1	Rik	-	-	-	-	1.6	Up	-	-
XM_355323	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 31	Cox6b1	-	-	-	-	1.6	Up	-	-
XM_488239	M400005993	-	-	-	-	-	1.6	Down	-	-
NM_028816	Exportin 6	Xpo6	-	-	-	-	1.6	Down	-	-
NM_026551	Dephospho-CoA kinase domain containing	Dcakd	-	-	1.5	Up	1.6	Up	-	-
M400009068	M400009068	-	-	-	-	-	1.6	Down	-	-
M400017150	M400017150	-	-	-	-	-	1.6	Down	-	-
NM_030887	Jun dimerization protein 2	Jdp2	-	-	-	-	1.6	Up	-	-
NM_008851	Phosphatidylinositol membrane-associated 1	Pitpm1	-	-	1.6	Up	1.6	Up	-	-
NM_145220	Adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 2	Appl2	-	-	1.9	Up	1.6	Up	-	-
NM_011354	Small EDRK-rich factor 2	Serf2	-	-	-	-	1.6	Up	-	-
M400000794	M400000794	-	-	-	-	-	1.6	Up	-	-
NM_027300,										
NM_028647	M300004994	-	-	-	-	-	1.6	Down	-	-



NM_033585	Protocadherin gamma subfamily A, 2	Pcdhga2	-	-	-	-	1.6	Down	-	-
NM_024240	GINS complex subunit 4 (Sid5 homolog)	Gins4	-	-	1.7	Up	1.6	Up	-	-
M200016354	M200016354	-	-	-	-	-	1.6	Up	-	-
NM_011266	Regulatory factor X-associated ankyrin-containing protein	Rfxank	-	-	-	-	1.6	Up	-	-
NM_027022	CKLF-like MARVEL transmembrane domain containing 2A	Cmtm2a	-	-	-	-	1.6	Down	-	-
NM_207547,										
XM_485887	M400009478	-	-	-	-	-	1.6	Down	-	-
M400014400	M400014400	-	-	-	-	-	1.6	Down	-	-
M400017146	M400017146	-	-	-	-	-	1.6	Down	-	-
NM_009698	Adenine phosphoribosyl transferase NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4	Aprt	-	-	-	-	1.6	Up	-	-
NM_010886	DnaJ (Hsp40) homolog, subfamily C, member 14	Ndufa4	-	-	-	-	1.6	Up	-	-
NM_028873	M400016313	Dnajc14	-	-	-	-	1.6	Up	-	-
M400016313	M400016313	-	-	-	-	-	1.6	Down	-	-
NM_029357	Protocadherin 1	Pcdh1	-	-	-	-	1.6	Up	-	-
NM_198650	Solute carrier family 22 (organic anion transporter), member 20	Slc22a20	-	-	-	-	1.6	Down	-	-
XM_486159	RIKEN cDNA 2310066E14 gene	-	-	-	-	-	1.6	Up	-	-
M200000688	M200000688	-	-	-	-	-	1.6	Up	-	-
NM_172524	RIKEN cDNA 9530066K23 gene	9530066K23								
NM_007713	CDC-like kinase 3	Rik	-	-	-	-	1.6	Down	-	-
NM_018879	Tumor suppressor candidate 4	Clk3	-	-	1.9	Up	1.6	Up	-	-
NM_053136	Protocadherin beta 11	Tusc4	-	-	-	-	1.6	Up	-	-
NM_025412	Pyrroline-5-carboxylate reductase-like	Pcdhb11	-	-	-	-	1.6	Down	-	-
NM_173453	Transmembrane protein 11	Pycl1	-	-	-	-	1.6	Up	-	-
NM_175249	Prosaposin-like 1	Tmem11	-	-	-	-	1.6	Up	-	-
XM_134573	dynein, cytoplasmic 1 light intermediate chain 2	Psap1	-	-	-	-	1.6	Down	-	-
NM_020012	Ring finger protein 14	-	-	-	-	-	1.6	Down	-	-
M400003298	M400003298	Rnf14	-	-	2.1	Up	1.6	Up	-	-
NM_153513	CDNA sequence BC028528	-	-	-	-	-	1.6	Down	-	-
NM_146075	LEM domain containing 2	BC028528	-	-	-	-	1.6	Up	-	-
M200012069	M200012069	Lemd2	-	-	-	-	1.6	Down	-	-
NM_001001		-	-	-	-	-	1.6	Up	-	-
999,NM_010327	M200003876	-	-	-	-	-	1.6	Up	-	-
M400007245	M400007245	-	-	-	-	-	1.7	Down	-	-
NM_145940	WD repeat domain, phosphoinositide interacting 1	Wipi1	-	-	1.7	Up	1.7	Up	-	-
NM_145458	PX domain containing serine/threonine kinase	Pxk	-	-	-	-	1.7	Up	-	-
NM_145380	Eukaryotic translation initiation factor 3, subunit M	Eif3m	-	-	1.7	Up	1.7	Up	-	-
M400009855	M400009855	-	-	-	-	-	1.7	Up	-	-
M400014176	M400014176	-	-	-	-	-	1.7	Up	-	-
NM_153458	Olfactomedin 3	Olfm3	-	-	-	-	1.7	Down	-	-

M200000888	M200000888	-	-	-	-	-	1.7	Up	-	-
M300017147	M300017147	-	-	-	-	-	1.7	Up	-	-
M400015445	M400015445	-	-	-	-	-	1.7	Down	-	-
NM_026246	Mitochondrial ribosomal protein L49	Mrpl49	-	-	-	-	1.7	Up	-	-
XM_285682,										
XM_487255	M400006493	-	-	-	-	-	1.7	Up	-	-
NM_146081	Protein phosphatase 4, regulatory subunit 1	Ppp4r1	-	-	1.6	Up	1.7	Up	-	-
		3930401K13								
NM_028720	RIKEN cDNA 3930401K13 gene	Rik	-	-	1.7	Up	1.7	Up	-	-
M400016199	M400016199	-	-	-	-	-	1.7	Down	-	-
NM_009012	RAD50 homolog (S. cerevisiae)	Rad50	-	-	-	-	1.7	Up	-	-
NM_025911	Coiled-coil domain containing 91	Ccdc91	-	-	1.8	Up	1.7	Up	-	-
NM_007805	Cytochrome b-561	Cyb561	-	-	1.9	Up	1.7	Up	-	-
NM_020509	Resistin like alpha	Retnla	-	-	-	-	1.7	Down	-	-
M400015101	M400015101	-	-	-	-	-	1.7	Down	-	-
NM_009085	RNA polymerase 1-1	Rpo1-1	-	-	-	-	1.7	Up	-	-
NM_011548	Transcription factor E2a	Tcfe2a	-	-	-	-	1.7	Down	-	-
NM_009541	Zinc finger and BTB domain containing 17	Zbtb17	-	-	-	-	1.7	Up	-	-
M400001836	M400001836	-	-	-	-	-	1.7	Down	-	-
M300005501	M300005501	-	-	-	-	-	1.7	Up	-	-
NM_008557	FXYD domain-containing ion transport regulator 3	Fxyd3	-	-	1.6	Up	1.7	Up	-	-
M400005589	M400005589	-	-	-	-	-	1.7	Down	-	-
M400006402	M400006402	-	-	-	-	-	1.7	Down	-	-
NM_010370	Granzyme A	Gzma	-	-	-	-	1.7	Up	-	-
	guanine nucleotide binding protein (G protein), alpha									
XM_355574	inhibiting 1	-	-	-	-	-	1.7	Down	-	-
M400003854	M400003854	-	-	-	-	-	1.7	Up	-	-
M400018959	M400018959	-	-	-	-	-	1.7	Down	-	-
NM_010920	NK2 transcription factor related, locus 6 (Drosophila)	Nkx2-6	-	-	-	-	1.7	Down	-	-
NM_177848	predicted gene, OTTMUSG00000015529	-	-	-	-	-	1.7	Down	-	-
NM_028119	Damage specific DNA binding protein 2	Ddb2	-	-	-	-	1.7	Down	-	-
M400015783	M400015783	-	-	-	-	-	1.7	Down	-	-
M400018972	M400018972	-	-	-	-	-	1.7	Down	-	-
NM_011318	Serum amyloid P-component	Apcs	-	-	-	-	1.7	Down	-	-
NM_021366	Kruppel-like factor 13	Klf13	-	-	-	-	1.7	Up	-	-
NM_025840	Basic leucine zipper and W2 domains 2	Bzw2	-	-	1.7	Up	1.7	Up	-	-
M400004479	M400004479	-	-	-	-	-	1.7	Down	-	-
NM_009515	Wiskott-Aldrich syndrome homolog (human)	Was	-	-	-	-	1.7	Up	-	-
NM_197985	Adiponectin receptor 2	Adipor2	-	-	2.0	Up	1.7	Up	-	-
NM_021522	Ubiquitin specific peptidase 14	Usp14	1.5	Up	2.4	Up	1.7	Up	-	-
M400008557	M400008557	-	-	-	-	-	1.7	Down	-	-
NM_146739	Olfactory receptor 502	Olfr502	-	-	-	-	1.7	Down	-	-
M400006293	M400006293	-	-	-	-	-	1.7	Up	-	-
NM_009054	Tripartite motif-containing 27	Trim27	-	-	1.6	Up	1.7	Up	-	-
NM_010097	SPARC-like 1 (mast9, hevin)	Sparcl1	2.3	Up	2.4	Up	1.7	Up	-	-

XM_137876	gene model 252, (NCBI)	-	-	-	-	-	1.7	Down	-	-
NM_013565	Integrin alpha 3	Itga3	-	-	-	-	1.7	Down	-	-
XM_130172	UDP-N-acetylglucosamine pyrophosphorylase 1-like 1	-	-	-	-	-	1.7	Up	-	-
M200013778	M200013778	-	-	-	-	-	1.7	Up	-	-
NM_018783	Tuftelin interacting protein 11	Tfip11	-	-	-	1.8	Up	1.7	Up	-
NM_020583	Interferon-stimulated protein	Isg20	-	-	-	1.9	Up	1.7	Up	-
NM_030597	LSM2 homolog, U6 small nuclear RNA associated (S. cerevisiae)	Lsm2	-	-	-	-	1.7	Up	-	-
M400013236	M400013236	-	-	-	-	-	1.7	Down	-	-
NM_008134	Glycosylation dependent cell adhesion molecule 1	Glycam1	-	-	-	-	1.7	Up	-	-
M400000465	M400000465	-	-	-	-	-	1.7	Down	-	-
XM_130322	M300013611	-	-	-	-	-	1.7	Down	-	-
M400009192	M400009192	-	-	-	-	-	1.7	Down	-	-
M400010215	M400010215	-	-	-	-	-	1.7	Down	-	-
NM_026000	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	Psmc9	-	-	-	-	1.7	Up	-	-
NM_011150	Lectin, galactoside-binding, soluble, 3 binding protein	Lgals3bp	-	-	-	-	1.7	Up	-	-
NM_021500	Macrophage erythroblast attacher	Maea	-	-	-	2.4	Up	1.7	Up	-
XM_194241	M-phase phosphoprotein 9	-	-	-	-	-	1.7	Up	-	-
NM_138302	Thymidine phosphorylase	Tymp	-	2.4	Up	-	-	1.7	Up	-
NM_008497	Luteinizing hormone beta	Lhb	-	-	-	-	-	1.7	Down	-
M400018442	M400018442	-	-	-	-	-	1.7	Down	-	-
NM_008713	Nitric oxide synthase 3, endothelial cell	Nos3	-	-	-	-	-	1.7	Up	-
NM_053162	Mitochondrial ribosomal protein L34	Mrpl34	-	-	-	-	-	1.7	Up	-
NM_138675	Mediator of RNA polymerase II transcription, subunit 9 homolog (yeast)	Med9	-	-	-	-	-	1.7	Up	-
XM_128634	solute carrier family 35, member B2	-	-	-	-	-	-	1.7	Up	-
NM_134125	Thyroid hormone receptor interactor 10	Trip10	-	-	-	1.6	Up	1.7	Up	-
M400018324	M400018324	-	-	-	-	2.4	Up	1.7	Up	-
NM_026242,										
XM_484640	M300021114	-	-	-	-	2.6	Up	1.7	Up	-
NM_147201	Nuclear receptor binding protein 1	Nrbp1	-	-	-	-	-	1.7	Up	-
NM_019870	N-acetyltransferase ARD1 homolog (S. cerevisiae)	Ard1	-	-	-	-	-	1.7	Up	-
NM_139272	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2	Galnt2	-	-	-	-	-	1.7	Up	-
NM_080850	PAS domain containing serine/threonine kinase	Pask	-	-	-	-	-	1.7	Down	-
NM_177624	RIKEN cDNA A430083B19 gene	A430083B19	-	-	-	-	-	1.7	Down	-
NM_008865	Rik	Rik	-	-	-	-	-	1.7	Down	-
NM_009876	Prolactin family 3, subfamily b, member 1	Pr13b1	-	-	-	-	-	1.7	Down	-
NM_198101	Cyclin-dependent kinase inhibitor 1C (P57)	Cdkn1c	-	-	-	-	-	1.7	Up	-
NM_011844	Gem-interacting protein	Gmip	-	-	-	-	-	1.7	Up	-
M300015333	Monoglyceride lipase	Mgll	-	-	-	1.9	Up	1.7	Up	-
NM_017374	M300015333	-	-	-	-	-	-	1.7	Down	-
	Protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	Ppp2cb	-	-	-	-	-	1.7	Up	-

		B430203M17											
NM_177096	RIKEN cDNA B430203M17 gene	Rik	-	-	-	-	-	1.7	Down	-	-	-	-
M200008549	M200008549	-	-	-	-	1.9	Up	-	-	1.8	Up	-	-
NM_010845	major urinary protein 3	-	-	-	-	-	-	-	-	1.8	Down	-	-
NM_181594	Enhancer of mRNA decapping 4	Edc4	-	-	-	-	-	-	-	1.8	Up	-	-
NM_053197	Sideroflexin 3	Sfxn3	-	-	-	-	-	-	-	1.8	Up	-	-
NM_007668	Cyclin-dependent kinase 5	Cdk5	-	1.7	Up	-	-	-	-	1.8	Up	-	-
M400006016	M400006016	-	-	-	-	-	-	-	-	1.8	Down	-	-
NM_026971,													
NM_198831	M400001307	-	-	-	-	-	-	-	-	1.8	Up	-	-
NM_008511	Lymphoid-restricted membrane protein	Lrmp	-	-	-	-	-	-	-	1.8	Up	-	-
		1700019E19											
NM_029601	RIKEN cDNA 1700019E19 gene	Rik	-	-	-	-	-	-	-	1.8	Up	-	-
M400009117	M400009117	-	-	-	-	-	-	-	-	1.8	Down	-	-
NM_024249	Solute carrier family 38, member 10	Slc38a10	-	-	-	-	-	-	-	1.8	Up	-	-
		6330417G02											
XM_355952	RIKEN cDNA 6330417G02 gene	Rik	-	-	-	-	-	-	-	1.8	Down	-	-
M400017065	M400017065	-	-	-	-	-	-	-	-	1.8	Down	-	-
NM_146962	Olfactory receptor 541	Olf541	-	-	-	-	-	-	-	1.8	Down	-	-
NM_172149	BCL2/adenovirus E1B interacting protein 1, NIP1	Bnip1	-	-	-	1.6	Up	-	-	1.8	Up	-	-
NM_008695	Nidogen 2	Nid2	-	-	-	-	-	-	-	1.8	Down	-	-
NM_173867	Regulator of chromosome condensation 2	Rcc2	-	-	-	-	-	-	-	1.8	Up	-	-
		2900092E17											
NM_030240	RIKEN cDNA 2900092E17 gene	Rik	-	-	-	1.7	Up	-	-	1.8	Up	-	-
NM_016777	Nuclear autoantigenic sperm protein (histone-binding)	Nasp	-	1.5	Down	-	2.3	Down	-	1.8	Down	-	-
NM_013520	FMS-like tyrosine kinase 3 ligand	Flt3l	-	-	-	-	-	-	-	1.8	Up	-	-
		Paf1, RNA polymerase II associated factor, homolog (S. cerevisiae)											
NM_019458		Paf1	-	-	-	-	-	-	-	1.8	Up	-	-
NM_130873	Keratin associated protein 16-4	Krtap16-4	-	-	-	-	-	-	-	1.8	Down	-	-
M300017046	M300017046	-	-	-	-	-	-	-	-	1.8	Down	-	-
M400018616	M400018616	-	-	-	-	-	-	-	-	1.8	Down	-	-
NM_011986	Neurochondrin	Ncdn	-	-	-	-	-	-	-	1.8	Down	-	-
NM_028188	RUN and SH3 domain containing 1	Rusc1	-	-	-	-	-	-	-	1.8	Down	-	-
NM_145993	L(3)mbt-like 2 (Drosophila)	L3mbtl2	-	-	-	-	-	-	-	1.8	Up	-	-
NM_174866	Kallikrein related-peptidase 14	Kik14	-	-	-	-	-	-	-	1.8	Down	-	-
NM_022009	Flightless I homolog (Drosophila)	Flii	-	-	-	-	-	-	-	1.8	Up	-	-
NM_025533	Nitric oxide synthase interacting protein	Nosip	-	-	-	-	-	-	-	1.8	Up	-	-
NM_026518	Ring finger protein 146	Rnf146	-	-	-	1.7	Up	-	-	1.8	Up	-	-
NM_153744,													
NM_153745	M400000133	-	-	-	-	-	-	-	-	1.8	Down	-	-
NM_016736	Negative regulator of ubiquitin-like proteins 1	Nub1	-	-	-	-	-	-	-	1.8	Up	-	-
NM_029789	LAG1 homolog, ceramide synthase 2	Lass2	-	-	-	1.9	Up	-	-	1.8	Up	-	-
NM_010693	Lymphocyte protein tyrosine kinase	Lck	-	-	-	2.3	Up	-	-	1.8	Up	-	-
NM_026765	Uridine-cytidine kinase 1-like 1	Uck1l	-	-	-	-	-	-	-	1.8	Up	-	-
XM_132434	RIKEN cDNA 0910001L09 gene	-	-	-	-	-	-	-	-	1.8	Up	-	-

NM_013853	ATP-binding cassette, sub-family F (GCN20), member 2	Abcf2	-	-	1.9	Up	1.8	Up	-	-
M400002859	M400002859	-	-	-	-	-	1.8	Down	-	-
M400018170	M400018170	-	-	-	-	-	1.8	Down	-	-
NM_008894	Polymerase (DNA directed), delta 2, regulatory subunit	Pold2	-	-	1.7	Up	1.8	Up	-	-
M400007709	M400007709	-	-	-	-	-	1.8	Down	-	-
NM_011662	TYRO protein tyrosine kinase binding protein	Tyrobp	-	-	-	-	1.8	Up	-	-
NM_134229	Vomer nasal 1 receptor, E10	V1re10	-	-	-	-	1.8	Down	-	-
NM_145492,										
NM_181326	M200008272	-	-	-	-	-	1.8	Up	-	-
		2200001115								
NM_183278	RIKEN cDNA 2200001115 gene	Rik	-	-	-	-	1.8	Down	-	-
M400004379	M400004379	-	-	-	-	-	1.8	Down	-	-
M400018266	M400018266	-	-	-	-	-	1.8	Down	-	-
NM_026639	ADP-ribosyltransferase 4	Art4	-	-	-	-	1.8	Up	-	-
		RP23-								
NM_008916	Putative phosphatase	136K12.4	-	-	1.6	Up	1.8	Up	-	-
M400016680	M400016680	-	-	-	-	-	1.8	Down	-	-
		2010001M09								
NM_027222	RIKEN cDNA 2010001M09 gene	Rik	-	-	-	-	1.8	Up	-	-
NM_175198	Prospero homeobox 2	Prox2	-	-	-	-	1.8	Down	-	-
NM_001004		5730494M16								
361	RIKEN cDNA 5730494M16 gene	Rik	-	-	1.6	Up	1.8	Up	-	-
NM_007791	Cysteine and glycine-rich protein 1	Csrp1	-	-	-	-	1.8	Up	-	-
NM_008909,										
XM_489504	M200002901	-	-	-	1.8	Up	1.8	Up	-	-
NM_011907	Three prime repair exonuclease 2	Trex2	-	-	1.5	Down	1.8	Down	-	-
NM_026960	Gasdermin D	Gsdmd	-	-	1.6	Up	1.8	Up	-	-
NM_007563	2,3-bisphosphoglycerate mutase	Bpgm	-	-	1.6	Up	1.8	Up	-	-
M300000830	M300000830	-	-	-	-	-	1.8	Up	-	-
	Hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 6	Hsd3b6	-	-	-	-	1.8	Down	-	-
NM_013821	Anaphase-promoting complex subunit 5	Anapc5	-	-	-	-	1.8	Up	-	-
NM_021505	RIKEN cDNA 2310022M17 gene	-	-	-	-	-	1.8	Up	-	-
XM_126071	Nudix (nucleoside diphosphate linked moiety X)-type motif 18	Nudt18	-	-	1.5	Up	1.8	Up	-	-
NM_153136	M400012849	-	-	-	-	-	1.8	Down	-	-
M400012849										
NM_178186,										
NM_178187,										
NM_178188,										
NM_178189	M400012458	-	-	-	-	-	1.8	Up	-	-
NM_207175	Olfactory receptor 239	Olf239	-	-	-	-	1.9	Down	-	-
NM_010249	GA repeat binding protein, beta 1	Gabpb1	-	-	-	-	1.9	Down	-	-
NM_183130	RIKEN cDNA 4930451E10 gene	-	-	-	-	-	1.9	Down	-	-
NM_009139	Chemokine (C-C motif) ligand 6	Ccl6	-	-	-	-	1.9	Up	-	-

NM_010453	Homeo box A5	Hoxa5	-	-	-	-	1.9	Up	-	-
NM_011595	Tissue inhibitor of metalloproteinase 3	Timp3	-	-	2.2	Up	1.9	Up	-	-
NM_012021	Peroxiredoxin 5	Prdx5	-	-	1.8	Up	1.9	Up	-	-
M300001777	M300001777	-	-	-	-	-	1.9	Up	-	-
NM_013638	Protamine 3	Prm3	-	-	-	-	1.9	Down	-	-
NM_020011,										
NM_203280	M200004833	-	-	-	-	-	1.9	Up	-	-
M400016716	M400016716	-	-	-	-	-	1.9	Down	-	-
		1110012M11								
NM_028617	RIKEN cDNA 1110012M11 gene	Rik	-	-	-	-	1.9	Up	-	-
NM_016753	Latexin	Lxn	-	-	-	-	1.9	Up	-	-
XM_488860	M400013873	-	-	-	-	-	1.9	Down	-	-
M400015707	M400015707	-	-	-	-	-	1.9	Down	-	-
NM_028041	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54	Ddx54	-	-	-	-	1.9	Up	-	-
	Caseinolytic peptidase, ATP-dependent, proteolytic subunit homolog (E. coli)									
NM_017393		Clpp	-	-	1.7	Up	1.9	Up	-	-
NM_030024	Proline rich 15	Prr15	-	-	1.6	Down	1.9	Down	-	-
M400017641	M400017641	-	-	-	-	-	1.9	Down	-	-
NM_009792	Calcium/calmodulin-dependent protein kinase II alpha	Camk2a	-	-	-	-	1.9	Down	-	-
XM_122081	Predicted gene, EG216185	EG216185	-	-	-	-	1.9	Up	-	-
NM_016698	Ring finger protein 10	Rnf10	-	-	1.9	Up	1.9	Up	-	-
M300016996	M300016996	-	-	-	-	-	1.9	Down	-	-
M400017190	M400017190	-	-	-	-	-	1.9	Down	-	-
NM_133662	Immediate early response 3	Ier3	-	-	2.1	Up	1.9	Up	-	-
NM_020603	WD repeat domain 46	Wdr46	-	-	-	-	1.9	Up	-	-
NM_146374	Olfactory receptor 368	Olfr368	-	-	-	-	1.9	Down	-	-
NM_026896	Mediator complex subunit 27	Med27	-	-	1.7	Up	1.9	Up	-	-
M300001561	M300001561	-	-	-	2.1	Up	1.9	Up	-	-
M200006146	M200006146	-	-	-	-	-	1.9	Up	-	-
M400013175	M400013175	-	-	-	-	-	1.9	Down	-	-
NM_008394	Interferon regulatory factor 9	Irf9	-	-	-	-	1.9	Up	-	-
	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2									
NM_146012		Ctdsp2	-	-	-	-	1.9	Up	-	-
XM_127742	oxidase assembly 1-like	-	-	-	-	-	1.9	Up	-	-
NM_011309	S100 calcium binding protein A1	S100a1	-	-	-	-	1.9	Up	-	-
	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 2, p49/p100									
NM_019408		Nfkb2	-	-	-	-	1.9	Up	-	-
XM_133543	A kinase (PRKA) anchor protein 13	-	-	-	-	-	1.9	Down	-	-
M400019334	M400019334	-	-	-	-	-	1.9	Down	-	-
		0610007C21								
NM_212470	RIKEN cDNA 0610007C21 gene	Rik	-	-	1.5	Up	1.9	Up	-	-
NM_017376,										
NM_153484	M200003750	-	-	-	2.7	Up	1.9	Up	-	-
NM_033077	DNA segment, Chr 1, Pasteur Institute 1	D1Pas1	-	-	-	-	1.9	Down	-	-
M400014708	M400014708	-	-	-	-	-	1.9	Down	-	-

NM_011895	Solute carrier family 35 (CMP-sialic acid transporter), member 1	Slc35a1	-	-	-	-	1.9	Down	-	-
M300013212	M300013212	-	-	-	-	-	1.9	Down	-	-
M400013532	M400013532	-	-	-	-	-	1.9	Down	-	-
M400013820	M400013820	-	-	-	-	-	1.9	Down	-	-
NM_013919	Ubiquitin specific peptidase 21	Usp21	-	-	2.2	Up	1.9	Up	-	-
NM_146362	Olfactory receptor 1312	Olfr1312	-	-	-	-	1.9	Down	-	-
NM_024250	PHD finger protein 10	Phf10	-	-	-	-	1.9	Up	-	-
XM_136911	pleckstrin homology domain containing, family G (with RhoGef domain) member 1	-	-	-	-	-	1.9	Down	-	-
M400003221	M400003221	-	-	-	-	-	1.9	Down	-	-
M400019250	M400019250	-	-	-	-	-	1.9	Down	-	-
NM_013613	Nuclear receptor subfamily 4, group A, member 2	Nr4a2	-	-	-	-	1.9	Up	-	-
NM_001003	405	1810049H19	-	-	-	-	1.9	Down	-	-
NM_028250	RIKEN cDNA 1810049H19 gene	Rik	-	-	-	-	1.9	Down	-	-
NM_198105	Acyl-Coenzyme A binding domain containing 6	Acbd6	-	-	-	-	1.9	Up	-	-
NM_018771	RIKEN cDNA A230072E10 gene	ORF34	-	-	-	-	1.9	Down	-	-
M200007631	GIPC PDZ domain containing family, member 1	Gipc1	-	-	1.5	Up	1.9	Up	-	-
NM_175209	M200007631	-	-	-	-	-	1.9	Up	-	-
NM_030693	RIKEN cDNA A730049H05 gene	-	-	-	-	-	1.9	Down	-	-
NM_011526	Activating transcription factor 5	Atf5	-	-	-	-	1.9	Up	-	-
M400014714	Transgelin	Tagln	-	-	2.0	Up	1.9	Up	-	-
M200006797	M400014714	-	-	-	-	-	1.9	Down	-	-
NM_009066	M200006797	-	-	-	1.7	Up	1.9	Up	-	-
M400005453	Ring finger protein 1	Ring1	-	-	1.8	Up	1.9	Up	-	-
M400017242	M400005453	-	-	-	-	-	1.9	Down	-	-
NM_133699	M400017242	-	-	-	-	-	1.9	Down	-	-
NM_010443	ATPase, H+ transporting, lysosomal V1 subunit C2	Atp6v1c2	-	-	-	-	1.9	Down	-	-
	Heme oxygenase (decycling) 2	Hmox2	-	-	1.7	Up	1.9	Up	-	-
NM_023363	RIKEN cDNA 2810426N06 gene	2810426N06	-	-	-	-	1.9	Down	-	-
NM_178112	Integrator complex subunit 8	Rik	-	-	-	-	1.9	Down	-	-
NM_026811	Late cornified envelope 1E	Ints8	-	-	-	-	1.9	Down	-	-
NM_207568	Olfr1252	Lce1e	-	-	-	-	1.9	Down	-	-
NM_024177	Mitochondrial ribosomal protein L38	Olfr1252	-	-	-	-	1.9	Down	-	-
		Mrpl38	-	-	1.9	Up	2.0	Up	-	-
NM_028018	RIKEN cDNA 2400003C14 gene	2400003C14	-	-	2.3	Up	2.0	Up	-	-
NM_001003	Amyotrophic lateral sclerosis 2 (juvenile) chromosome 946 region, candidate 13 (human)	Rik	-	-	-	-	2.0	Down	-	-
M400006973	M400006973	Als2cr13	-	-	-	-	2.0	Down	-	-
M400016663	M400016663	-	-	-	-	-	2.0	Down	-	-
NM_207262	Androgen binding protein epsilon	Abpe	-	-	-	-	2.0	Down	-	-
M400009852	M400009852	-	-	-	-	-	2.0	Down	-	-
M400010672	M400010672	-	-	-	-	-	2.0	Down	-	-
NM_007434	Thymoma viral proto-oncogene 2	Akt2	-	-	-	-	2.0	Up	-	-

XM_486652	M400009713	-	-	-	-	-	2.0	Down	-	-
NM_021354	Developmentally regulated GTP binding protein 2	Drg2	-	-	-	1.9	Up	2.0	Up	-
M400006271	M400006271	-	-	-	-	-	-	2.0	Down	-
M300009610	M300009610	-	-	-	-	1.9	Up	2.0	Up	-
XM_488375	M400002717	-	-	-	-	1.9	Up	2.0	Up	-
M400012785	M400012785	-	-	-	-	-	-	2.0	Down	-
NM_175196	RIKEN cDNA 1700041G16 gene	-	-	-	-	-	-	2.0	Down	-
	TRM1 tRNA methyltransferase 1 homolog (S. cerevisiae)	Trmt1	-	-	-	1.7	Up	2.0	Up	-
NM_020006	CDC42 effector protein (Rho GTPase binding) 4	Cdc42ep4	-	-	-	1.8	Up	2.0	Up	-
NM_016974	D site albumin promoter binding protein	Dbp	-	-	-	1.8	Up	2.0	Up	-
NM_019798	Phosphodiesterase 4A, cAMP specific	Pde4a	-	-	-	-	-	2.0	Down	-
M400017530	M400017530	-	-	-	-	-	-	2.0	Down	-
NM_029804	Heterogeneous nuclear ribonucleoprotein M	Hnrnmpm	-	-	-	2.4	Up	2.0	Up	-
M400016674	M400016674	-	-	-	-	-	-	2.0	Down	-
NM_009713	Arylsulfatase A	Arsa	-	-	-	-	-	2.0	Up	-
	Bernardinelli-Seip congenital lipodystrophy 2 homolog (human)	Bscl2	-	-	-	2.0	Up	2.0	Up	-
NM_008144	Interleukin-1 receptor-associated kinase 3	Irak3	-	-	-	-	-	2.0	Down	-
NM_028679	M400007471	-	-	-	-	-	-	2.0	Down	-
M400007471	M400007471	-	-	-	-	-	-	2.0	Down	-
M400012774	M400012774	-	-	-	-	-	-	2.0	Down	-
NM_011363	SH2B adaptor protein 1	Sh2b1	-	-	-	-	-	2.0	Up	-
NM_015735	Damage specific DNA binding protein 1	Ddb1	-	-	-	-	-	2.0	Up	-
NM_024191	ADP-ribosylation factor-like 2 binding protein	Arl2bp	-	-	-	1.8	Up	2.0	Up	-
M400015498	M400015498	-	-	-	-	-	-	2.0	Down	-
M400014619	M400014619	-	-	-	-	-	-	2.0	Down	-
NM_009135	Sodium channel, voltage-gated, type VII, alpha	Scn7a	-	-	-	-	-	2.0	Down	-
M400018978	M400018978	-	-	-	-	-	-	2.0	Down	-
NM_173047	Carbonyl reductase 3	Cbr3	-	-	-	-	-	2.0	Down	-
XM_139711	AT rich interactive domain 1B (Swi1 like)	-	-	-	-	-	-	2.0	Down	-
XM_150405	RIKEN cDNA 1600025M17 gene	-	-	-	-	-	-	2.0	Down	-
M300007351	M300007351	-	-	-	-	-	-	2.0	Down	-
M300008602	M300008602	-	-	-	-	-	-	2.0	Up	-
NM_146558	Olfactory receptor 866	Olf866	-	-	-	-	-	2.0	Down	-
NM_028777	SEC14-like 1 (S. cerevisiae)	Sec14l1	-	-	-	1.9	Up	2.0	Up	-
M400013854	M400013854	-	-	-	-	-	-	2.0	Down	-
NM_138309	Cd99 antigen-like 2	Cd99l2	-	-	-	-	-	2.0	Up	-
M400010484	M400010484	-	-	-	-	-	-	2.0	Down	-
M400009353	M400009353	-	-	-	-	-	-	2.0	Down	-
	Protein phosphatase 1A, magnesium dependent, alpha isoform	Ppm1a	-	-	-	-	-	2.0	Up	-
NM_008910	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 4	Psm4	-	-	-	-	-	2.0	Up	-
NM_008951	F-box protein 6	Fbxo6	-	-	-	-	-	2.0	Up	-
NM_015797	Isocitrate dehydrogenase 3 (NAD+) beta	Idh3b	-	-	-	-	-	2.0	Up	-



M200003437	M200003437	-	-	-	2.0	Up	2.0	Up	-	-
M400000438	M400000438	-	-	-	-	-	2.0	Up	-	-
NM_024459	Protein phosphatase 3, regulatory subunit B, alpha isoform (calcineurin B, type I)	Ppp3r1	-	-	-	-	2.0	Down	-	-
NM_001002011,NM_019390	M300005919	-	-	-	-	-	2.0	Up	-	-
M400009069	M400009069	-	-	-	-	-	2.0	Up	-	-
NM_146502	Olfactory receptor 328	Olf328	-	-	-	-	2.0	Down	-	-
NM_172307	Membrane-bound transcription factor peptidase, site 2	Mbtps2	-	-	-	-	2.0	Down	-	-
NM_026768	Mitochondrial ribosomal protein S18A	Mrps18a	-	-	-	-	2.0	Up	-	-
NM_013581	Component of oligomeric golgi complex 1	Cog1	-	-	-	-	2.0	Up	-	-
XM_128129	DENN/MADD domain containing 3	-	-	-	-	-	2.0	Up	-	-
NM_009137	Chemokine (C-C motif) ligand 22	Ccl22	-	-	1.9	Up	2.0	Up	-	-
M400000085	M400000085	-	-	-	-	-	2.0	Down	-	-
NM_001005511	Lemur tyrosine kinase 3	Lmtk3	-	-	-	-	2.0	Down	-	-
NM_022428	Iroquois related homeobox 6 (Drosophila)	Irx6	-	-	-	-	2.0	Down	-	-
M400018401	M400018401	-	-	-	-	-	2.0	Down	-	-
NM_198864	SLIT and NTRK-like family, member 3	Slitrk3	-	-	-	-	2.0	Down	-	-
M400017404	M400017404	-	-	-	-	-	2.0	Down	-	-
NM_172928	Doublecortin-like kinase 3	Dclk3	-	-	-	-	2.0	Up	-	-
M400006083	M400006083	-	-	-	-	-	2.1	Down	-	-
M400015183	M400015183	-	-	-	-	-	2.1	Down	-	-
M400018912	M400018912	-	-	-	-	-	2.1	Down	-	-
NM_011366	Sorbin and SH3 domain containing 3	Sorbs3	1.7	Up	-	-	2.1	Up	-	-
NM_019584	Beclin 1, autophagy related	Becn1	-	-	2.4	Up	2.1	Up	-	-
M300006331	M300006331	-	-	-	-	-	2.1	Up	-	-
M400012696	M400012696	-	-	-	-	-	2.1	Down	-	-
NM_027498	CDNA sequence BC033915	BC033915	-	-	-	-	2.1	Down	-	-
NM_026787	RIKEN cDNA 1110012L19 gene	Rik	-	-	1.7	Up	2.1	Up	-	-
NM_009980	C-terminal binding protein 2	Ctbp2	-	-	2.1	Up	2.1	Up	-	-
NM_011829	Inosine 5-phosphate dehydrogenase 1	Impdh1	1.7	Up	2.3	Up	2.1	Up	-	-
M400017268	M400017268	-	-	-	-	-	2.1	Down	-	-
NM_007834	Down syndrome critical region gene 3	Dscr3	-	-	-	-	2.1	Up	-	-
NM_026739	RIKEN cDNA 9530077C05 gene	9530077C05	-	-	-	-	2.1	Down	-	-
AF247559	TIM (TRIOSEPHOSPHATE ISOMERASE)	TIM	-	-	-	-	2.1	Down	-	-
NM_176910	RIKEN cDNA D930031A20 gene	-	-	-	-	-	2.1	Down	-	-
NM_011488	Signal transducer and activator of transcription 5A	Stat5a	-	-	-	-	2.1	Down	-	-
NM_148928	General transcription factor IIIC, polypeptide 5	Gtf3c5	-	-	-	-	2.1	Up	-	-
NM_030611	Aldo-keto reductase family 1, member C6	Akr1c6	-	-	-	-	2.1	Down	-	-
NM_172145	RIKEN cDNA 2610027C15 gene	2610027C15	-	-	-	-	2.1	Up	-	-

NM_019705	RanBP-type and C3HC4-type zinc finger containing 1	Rbck1	-	-	1.5	Up	2.1	Up	-	-
M300006974	M300006974	-	-	-	2.5	Up	2.1	Up	-	-
NM_026877,										
NM_198223	M200009391	-	-	-	-	-	2.1	Up	-	-
M400003397	M400003397	-	-	-	-	-	2.1	Up	-	-
NM_145376	Lysophosphatidylcholine acyltransferase 1	Lpcat1	-	-	2.3	Up	2.1	Up	-	-
NM_013674	Interferon regulatory factor 4	Irf4	-	-	-	-	2.1	Up	-	-
	Translocase of inner mitochondrial membrane 50									
NM_025616	homolog (yeast)	Timm50	-	-	-	-	2.1	Up	-	-
M400008524	M400008524	-	-	-	-	-	2.1	Up	-	-
M400018332	M400018332	-	-	-	-	-	2.1	Down	-	-
NM_172945	Ankyrin repeat domain 13b	Ankrd13b	-	-	-	-	2.1	Down	-	-
M300000151	M300000151	-	-	-	1.7	Up	2.1	Up	-	-
NM_024227	Mitochondrial ribosomal protein L28	Mrpl28	-	-	2.1	Up	2.1	Up	-	-
NM_031184	GLIS family zinc finger 2	Glis2	-	-	1.8	Up	2.1	Up	-	-
	DNA cross-link repair 1C, PSO2 homolog (S. cerevisiae)	-	-	-	-	-	2.1	Down	-	-
NM_146114										
NM_026436	Transmembrane protein 86A	Tmem86a	-	-	-	-	2.1	Up	-	-
NM_019877	Coatomer protein complex, subunit zeta 2	Copz2	-	-	-	-	2.1	Up	-	-
M400016336	M400016336	-	-	-	-	-	2.1	Down	-	-
M400018829	M400018829	-	-	-	-	-	2.1	Down	-	-
NM_013839	Nuclear receptor subfamily 1, group H, member 3	Nr1h3	-	-	-	-	2.1	Up	-	-
NM_024263	Matrix-remodelling associated 8	Mxra8	-	-	-	-	2.1	Up	-	-
NM_019704	Transmembrane protein 115	Tmem115	-	-	-	-	2.1	Up	-	-
NM_025644	Exosome component 1	Exosc1	-	-	2.1	Up	2.1	Up	-	-
M400019376	M400019376	-	-	-	-	-	2.1	Down	-	-
NM_021882	Silver	Si	-	-	-	-	2.1	Down	-	-
NM_012053	Ribosomal protein L8	Rpl8	-	-	-	-	2.1	Up	-	-
NM_007636	Chaperonin subunit 2 (beta)	Cct2	-	-	-	-	2.1	Up	-	-
NM_134209	Vomer nasal 1 receptor, G8	V1rg8	-	-	-	-	2.1	Down	-	-
NM_011293	Polymerase (RNA) II (DNA directed) polypeptide J	Polr2j	-	-	-	-	2.1	Up	-	-
NM_021423	SH3/ankyrin domain gene 3	Shank3	-	-	-	-	2.1	Up	-	-
M400009262	M400009262	-	-	-	2.3	Up	2.1	Up	-	-
NM_153057	Nodal modulator 1	Nomo1	-	-	-	-	2.1	Up	-	-
M400016104	M400016104	-	-	-	-	-	2.1	Down	-	-
NM_011588	Tripartite motif-containing 28	Trim28	-	-	1.8	Up	2.1	Up	-	-
XM_486686	predicted gene, EG434782	-	-	-	2.2	Up	2.1	Up	-	-
NM_024465	Abhydrolase domain containing 12	Abhd12	-	-	-	-	2.1	Up	-	-
		2610028A01								
NM_028228	RIKEN cDNA 2610028A01 gene	Rik	-	-	-	-	2.1	Up	-	-
M400015089	M400015089	-	-	-	-	-	2.1	Down	-	-
NM_001005										
523,NM_001										
005525,NM_										
025438	M400001164	-	-	-	-	-	2.2	Down	-	-

NM_146391	Olfactory receptor 1058	Olfr1058	-	-	-	-	2.2	Down	-	-
M400016288	M400016288	-	-	-	-	-	2.2	Down	-	-
M400005428	M400005428	-	-	-	1.6	Down	2.2	Down	-	-
		6030498E09								
NM_183126	RIKEN cDNA 6030498E09 gene	Rik	-	-	-	-	2.2	Down	-	-
XM_146963	RIKEN cDNA C530008M07 gene	-	-	-	-	-	2.2	Down	-	-
NM_008546	Microfibrillar-associated protein 2	Mfap2	1.7	Up	-	-	2.2	Up	-	-
NM_011325	Sodium channel, nonvoltage-gated 1 beta	Scnn1b	-	-	-	-	2.2	Up	-	-
NM_010387,										
NM_010388	M300010992	-	-	-	-	-	2.2	Up	-	-
NM_011777	Zyxin	Zyx	-	-	-	-	2.2	Up	-	-
NM_153792	Tnf receptor-associated factor 7	Traf7	-	-	-	-	2.2	Up	-	-
NM_007457	Adaptor protein complex AP-1, sigma 1	Ap1s1	-	-	1.8	Up	2.2	Up	-	-
M400008541	M400008541	-	-	-	-	-	2.2	Up	-	-
M400013780	M400013780	-	1.6	Up	2.3	Up	2.2	Up	-	-
M400009846	M400009846	-	-	-	-	-	2.2	Down	-	-
NM_008749	Nucleobindin 1	Nucb1	-	-	2.0	Up	2.2	Up	-	-
M400000739	M400000739	-	-	-	-	-	2.2	Down	-	-
NM_175012	Gastrin releasing peptide	Grp	-	-	-	-	2.2	Up	-	-
M300011306	M300011306	-	-	-	-	-	2.2	Down	-	-
M400014056	M400014056	-	-	-	-	-	2.2	Down	-	-
NM_011870	Calcium and integrin binding 1 (calmyrin)	Cib1	-	-	-	-	2.2	Up	-	-
M400013901	M400013901	-	-	-	-	-	2.2	Down	-	-
NM_009798	Capping protein (actin filament) muscle Z-line, beta	Capzb	-	-	-	-	2.2	Up	-	-
M400005976	M400005976	-	-	-	2.5	Up	2.2	Up	-	-
M400012714	M400012714	-	-	-	-	-	2.2	Down	-	-
NM_024206	SEC13 homolog (S. cerevisiae)	Sec13	-	-	-	-	2.2	Up	-	-
NM_009478	Uroporphyrinogen decarboxylase	Urod	-	-	1.8	Up	2.2	Up	-	-
M400018689	M400018689	-	-	-	-	-	2.2	Down	-	-
	G-protein signalling modulator 3 (AGS3-like, C. elegans)	Gpsm3	-	-	-	-	2.2	Up	-	-
NM_134116										
NM_139229	Component of oligomeric golgi complex 8	Cog8	-	-	-	-	2.2	Up	-	-
M400016692	M400016692	-	-	-	-	-	2.2	Down	-	-
M400017814	M400017814	-	-	-	-	-	2.2	Down	-	-
M400019038	M400019038	-	-	-	-	-	2.2	Down	-	-
NM_026542	Solute carrier family 25, member 39	Slc25a39	-	-	-	-	2.2	Up	-	-
NM_147016	Olfactory receptor 1049	Olfr1049	-	-	-	-	2.2	Down	-	-
		2410018G20								
NM_029354	RIKEN cDNA 2410018G20 gene	Rik	-	-	1.8	Up	2.2	Up	-	-
NM_019475	Olfactory receptor 157	Olfr157	-	-	-	-	2.2	Down	-	-
XM_484610	M300013117	-	-	-	-	-	2.2	Up	-	-
NM_019722	ADP-ribosylation factor-like 2	Arl2	-	-	2.1	Up	2.2	Up	-	-
NM_022813	Secretory carrier membrane protein 2	Scamp2	-	-	2.6	Up	2.2	Up	-	-
NM_013753	CDNA sequence X99384	X99384	-	-	-	-	2.2	Down	-	-
NM_178743	Solute carrier family 26, member 11	Slc26a11	-	-	-	-	2.2	Down	-	-

NM_023372	Ribosomal protein L38	Rpl38	-	-	-	-	2.2	Up	-	-
NM_177845	Phospholipase A2, group IVE	Pla2g4e	-	-	-	-	2.2	Down	-	-
NM_177201	PHD finger protein 8	Phf8	-	-	-	-	2.2	Down	-	-
M400016888	M400016888	-	-	-	-	-	2.2	Down	-	-
NM_033592	Protocadherin gamma subfamily A, 10	Pcdhga12	-	-	-	-	2.2	Down	-	-
NM_013648	Reticulon 2 (Z-band associated protein)	Rtn2	-	-	1.8	Up	2.2	Up	-	-
NM_010009	Cytochrome P450, family 27, subfamily b, polypeptide 1	Cyp27b1	-	-	-	-	2.2	Down	-	-
NM_009685	Amyloid beta (A4) precursor protein-binding, family B, member 1	Apbb1	-	-	2.4	Up	2.2	Up	-	-
M400016644	M400016644	-	-	-	-	-	2.2	Down	-	-
M400012344	M400012344	-	-	-	1.5	Down	2.2	Down	-	-
NM_019489	Peptidylprolyl isomerase E (cyclophilin E)	Ppie	-	-	1.6	Up	2.2	Up	-	-
NM_020595	Otoraplin	Otor	-	-	-	-	2.2	Down	-	-
NM_023912	SCY1-like 1 (S. cerevisiae)	Scyl1	-	-	-	-	2.2	Up	-	-
M300009505	M300009505	-	-	-	2.2	Up	2.2	Up	-	-
M300011420	M300011420	-	-	-	-	-	2.2	Down	-	-
NM_013746	Pleckstrin homology domain containing, family B (evectins) member 1	Plekhhb1	-	-	-	-	2.2	Up	-	-
NM_019755	Proteolipid protein 2	Plp2	-	-	-	-	2.2	Up	-	-
XM_484886	predicted gene, EG433328	-	-	-	2.5	Up	2.2	Up	-	-
NM_177005	Glycosyltransferase 1 domain containing 1	Glt1d1	-	-	-	-	2.2	Down	-	-
NM_026027	Prefoldin 1	Pfdn1	-	-	2.3	Up	2.2	Up	-	-
NM_011032	Prolyl 4-hydroxylase, beta polypeptide	P4hb	-	-	-	-	2.2	Up	-	-
NM_011727	X-linked lymphocyte-regulated 3C	Xlr3c	-	-	-	-	2.2	Down	-	-
NM_009336	Vacuolar protein sorting 72 (yeast)	Vps72	-	-	1.5	Up	2.2	Up	-	-
NM_026275	Ubiquitin-conjugating enzyme E2R 2	Ube2r2	-	-	2.0	Up	2.2	Up	-	-
NM_028021	Myosin, heavy polypeptide 14	Myh14	-	-	-	-	2.2	Down	-	-
NM_011546	Zinc finger E-box binding homeobox 1	Zeb1	-	-	2.9	Up	2.3	Up	-	-
NM_007743	Collagen, type I, alpha 2	Col1a2	-	-	-	-	2.3	Up	-	-
XM_112440	heparan sulfate (glucosamine) 3-O-sulfotransferase 2	-	-	-	-	-	2.3	Down	-	-
NM_008062	Glucose-6-phosphate dehydrogenase X-linked	G6pdx	-	-	2.1	Up	2.3	Up	-	-
M400015348	M400015348	-	-	-	-	-	2.3	Down	-	-
NM_178637	HIV-1 tat interactive protein, homolog (human)	Htatip	-	-	2.4	Up	2.3	Up	-	-
NM_001005767	Presenilin associated, rhomboid-like	Parl	-	-	2.5	Up	2.3	Up	-	-
M300004135	M300004135	-	-	-	2.0	Up	2.3	Up	-	-
M400019414	M400019414	-	-	-	-	-	2.3	Down	-	-
M400019358	M400019358	-	-	-	-	-	2.3	Down	-	-
XM_484464	predicted gene, EG432950	-	-	-	2.7	Up	2.3	Up	-	-
M400010190	M400010190	-	-	-	-	-	2.3	Down	-	-
NM_030561	CDNA sequence BC004004	BC004004	-	-	-	-	2.3	Up	-	-
M200006698	M200006698	-	-	-	1.8	Up	2.3	Up	-	-
NM_011341	Stromal cell derived factor 4	Sdf4	-	-	1.6	Up	2.3	Up	-	-
M400018610	M400018610	-	-	-	-	-	2.3	Down	-	-

M300005580	M300005580	-	-	-	-	-	2.3	Down	-	-
NM_011707	Vitronectin	Vtn	-	-	-	-	2.3	Up	-	-
NM_011526	Transgelin	Tagln	-	-	2.6	Up	2.3	Up	-	-
M200008749	M200008749	-	-	-	-	-	2.3	Down	-	-
NM_008094	Glucosidase, beta, acid	Gba	-	-	2.0	Up	2.3	Up	-	-
M400010606	M400010606	-	-	-	-	-	2.3	Down	-	-
M400013604	M400013604	-	-	-	-	-	2.3	Down	-	-
XM_128698	RAN binding protein 3	-	-	-	-	-	2.3	Up	-	-
XM_207079	M200003595	-	-	-	-	-	2.3	Up	-	-
NM_011379	Signal-induced proliferation associated gene 1	Sipa1	-	-	-	-	2.3	Up	-	-
NM_008768	Orosomucoid 1	Orm1	-	-	-	-	2.3	Down	-	-
M300008208	M300008208	-	-	-	-	-	2.3	Down	-	-
NM_153555	WD repeat domain 42A	Wdr42a	-	-	-	-	2.3	Up	-	-
NM_182991	Transmembrane protein 59-like	Tmem59l	-	-	-	-	2.3	Down	-	-
NM_023314	Eukaryotic translation initiation factor 4E member 2	Eif4e2	-	-	1.5	Up	2.3	Up	-	-
NM_027817	GRB2-related adaptor protein	Grap	-	-	2.2	Up	2.3	Up	-	-
NM_018737	Cytidine 5-triphosphate synthase 2	Ctps2	-	-	2.0	Up	2.3	Up	-	-
NM_130856	Keratin associated protein 16-8	Krtap16-8	-	-	-	-	2.3	Down	-	-
NM_010575	Integrin alpha 2b	Itga2b	-	-	2.0	Up	2.3	Up	-	-
M400014987	M400014987	-	-	-	-	-	2.3	Down	-	-
NM_134227	Vomeroneasal 1 receptor, K1	V1rk1	-	-	-	-	2.3	Down	-	-
NM_026964	Coiled-coil domain containing 124	Ccdc124	-	-	-	-	2.3	Up	-	-
M400014965	M400014965	-	-	-	-	-	2.3	Down	-	-
M400013698	M400013698	-	-	-	-	-	2.3	Down	-	-
NM_028320	Adiponectin receptor 1	Adipor1	-	-	1.9	Up	2.3	Up	-	-
NM_029791	Bicaudal D homolog 2 (Drosophila)	Bicd2	-	-	-	-	2.3	Up	-	-
NM_010233	Fibronectin 1	Fn1	1.8	Up	2.6	Up	2.3	Up	-	-
M400015386	M400015386	-	-	-	-	-	2.3	Down	-	-
M400009816	M400009816	-	-	-	-	-	2.3	Down	-	-
NM_021549	Polynucleotide kinase 3- phosphatase	Pnkp	-	-	-	-	2.3	Up	-	-
NM_145524	Methyltransferase like 8	Mettl8	-	-	-	-	2.3	Up	-	-
NM_207576	Olfactory receptor 1514	Olf221	-	-	-	-	2.3	Down	-	-
	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	Atp5d	-	-	-	-	2.3	Up	-	-
NM_025313										
NM_019396	Cysteine and histidine rich 1	Cyhr1	-	-	2.2	Up	2.3	Up	-	-
M400015982	M400015982	-	-	-	-	-	2.3	Down	-	-
XM_485950	M400007895	-	-	-	-	-	2.3	Up	-	-
NM_008049	Ferritin light chain 2	Ftl2	-	-	-	-	2.3	Up	-	-
NM_026316	Aldehyde dehydrogenase 3 family, member B1	Aldh3b1	-	-	1.8	Up	2.3	Up	-	-
M400012965	M400012965	-	-	-	-	-	2.3	Down	-	-
M400016362	M400016362	-	-	-	-	-	2.3	Down	-	-
NM_207207	Mitochondrial ribosomal protein S26	Mrps26	-	-	2.1	Up	2.3	Up	-	-
NM_008185	Glutathione S-transferase, theta 1	Gstt1	-	-	-	-	2.4	Up	-	-
M400018806	M400018806	-	-	-	-	-	2.4	Down	-	-
NM_032398	Plasmalemma vesicle associated protein	Plvap	-	-	1.6	Up	2.4	Up	-	-

NM_019909	M400011342	-	-	-	-	2.4	Up	-	-
		2700038C09							
NM_025598	RIKEN cDNA 2700038C09 gene	Rik	-	-	-	2.4	Up	-	-
NM_008640	Lysosomal-associated protein transmembrane 4A	Laptm4a	1.7	Up	2.2	2.4	Up	-	-
M400014364	M400014364	-	-	-	-	2.4	Down	-	-
NM_001001									
805	Olfactory receptor 576	Olf576	-	-	-	2.4	Down	-	-
M400017845	M400017845	-	-	-	-	2.4	Down	-	-
M400019304	M400019304	-	-	-	-	2.4	Down	-	-
	SWI/SNF related, matrix associated, actin dependent								
NM_011417	regulator of chromatin, subfamily a, member 4	Smarca4	-	-	-	2.4	Up	-	-
NM_144941	Microtubule-associated protein 7 domain containing 1	Mtap7d1	-	-	-	2.4	Up	-	-
M400012913	M400012913	-	-	-	-	2.4	Up	-	-
M400014780	M400014780	-	-	-	-	2.4	Down	-	-
NM_054038	Secretoglobin, family 3A, member 2	Scgb3a2	3.0	Up	2.4	2.4	Up	-	-
NM_019913	Thioredoxin 2	Txn2	-	-	-	2.4	Up	-	-
	Thioredoxin domain containing 12 (endoplasmic								
NM_025334	reticulum)	Txndc12	-	-	1.7	2.4	Up	-	-
NM_011434	Superoxide dismutase 1, soluble	Sod1	-	-	-	2.4	Up	-	-
NM_015749	Transcobalamin 2	Tcn2	-	-	2.1	2.4	Up	-	-
M400015270	M400015270	-	-	-	-	2.4	Down	-	-
NM_007749	Cytochrome c oxidase, subunit VIc	Cox7c	-	-	-	2.4	Up	-	-
M400003897	M400003897	-	-	-	2.3	2.4	Up	-	-
XM_205477	RIKEN cDNA 6330545A04 gene	-	-	-	-	2.4	Down	-	-
M400017096	M400017096	-	-	-	-	2.4	Down	-	-
NM_008233	Hepatoma-derived growth factor, related protein 2	Hdgfrp2	-	-	2.7	2.4	Up	-	-
NM_013833	Retina and anterior neural fold homeobox	Rax	-	-	-	2.4	Down	-	-
NM_009415	Triosephosphate isomerase 1	Tpi1	-	-	-	2.4	Up	-	-
NM_009720	ATX1 (antioxidant protein 1) homolog 1 (yeast)	Atox1	-	-	-	2.4	Up	-	-
XM_282920	polymerase (RNA) II (DNA directed) polypeptide E	-	-	-	-	2.4	Up	-	-
NM_018740	Retinoic acid induced 12	Rai12	-	-	1.8	2.4	Up	-	-
M400017102	M400017102	-	-	-	-	2.4	Down	-	-
NM_177300	RIKEN cDNA B130040O20 gene	-	-	-	-	2.4	Down	-	-
NM_025347	Yippee-like 3 (Drosophila)	Ypel3	-	-	2.2	2.4	Up	-	-
M400018386	M400018386	-	-	-	-	2.4	Down	-	-
	Spermatogenesis associated glutamate (E)-rich protein								
NM_027609	4f	Speer4f	-	-	-	2.4	Down	-	-
XM_129647	glutamyl-prolyl-tRNA synthetase	-	1.7	Up	2.4	2.4	Up	-	-
M400018134	M400018134	-	-	-	-	2.4	Down	-	-
NM_011637	Three prime repair exonuclease 1	Trex1	-	-	-	2.4	Up	-	Up
	SplA/ryanodine receptor domain and SOCS box								
NM_027141	containing 3	Spsb3	-	-	1.6	2.4	Up	-	-
NM_021713	Melanocyte proliferating gene 1	Myg1	-	-	1.7	2.4	Up	-	-
NM_144927	CDNA sequence BC019943	BC019943	-	-	1.6	2.4	Up	-	-
NM_007904	Endothelin receptor type B	Ednrb	-	-	3.0	2.4	Up	-	-

NM_025804	Transcription factor 25 (basic helix-loop-helix)	Tcf25	-	-	-	-	2.4	Up	-	-
M400003361	M400003361	-	-	-	-	-	2.4	Up	-	-
NM_145070	Huntingtin interacting protein 1 related	Hip1r	-	-	2.2	Up	2.5	Up	-	-
M400009984	M400009984	-	-	-	-	-	2.5	Down	-	-
M400016877	M400016877	-	-	-	-	-	2.5	Down	-	-
M400000341	M400000341	-	-	-	-	-	2.5	Down	-	-
NM_016906	Sec61 alpha 1 subunit (S. cerevisiae)	Sec61a1	-	-	1.7	Up	2.5	Up	-	-
NM_018756	2-cell-stage, variable group, member 1	Tcstv1	-	-	-	-	2.5	Down	-	-
NM_011709	Whey acidic protein	Wap	-	-	-	-	2.5	Down	-	-
NM_144913	Methylphosphate capping enzyme	Mepce	-	-	1.9	Up	2.5	Up	-	-
NM_174996	DNA segment, Chr 4, ERATO Doi 22, expressed	D4Erttd22e	-	-	2.3	Up	2.5	Up	-	-
M400013736	M400013736	-	-	-	-	-	2.5	Down	-	-
NM_011956	Nucleotide binding protein 2	Nubp2	-	-	1.7	Up	2.5	Up	-	-
NM_023871	SET translocation	Set	-	-	3.1	Up	2.5	Up	-	-
M400014442	M400014442	-	-	-	-	-	2.5	Down	-	-
NM_011968	Proteasome (prosome, macropain) subunit, alpha type 6	Pasma6	-	-	-	-	2.5	Up	-	-
NM_019673	Actin-like 6A	Actl6a	-	-	2.0	Up	2.5	Up	-	-
NM_021281	Cathepsin S	Ctss	-	-	2.4	Up	2.5	Up	-	-
XM_148073,										
XM_358847	M400000601	-	-	-	-	-	2.5	Down	-	-
XM_130703	zinc finger, NFX1-type containing 1	-	-	-	1.6	Up	2.5	Up	-	-
NM_153420	Acid phosphatase-like 2	Acpl2	-	-	-	-	2.5	Down	-	-
M400002193	M400002193	-	-	-	-	-	2.5	Down	-	-
NM_011526	Transgelin	Tagln	-	-	2.8	Up	2.5	Up	-	-
M400015817	M400015817	-	-	-	-	-	2.5	Down	-	-
M400009775	M400009775	-	-	-	-	-	2.5	Down	-	-
XM_126252	trafficking protein particle complex 1	-	-	-	-	-	2.5	Up	-	-
M400000745	M400000745	-	-	-	-	-	2.5	Down	-	-
NM_026304	Lethal, Chr 7, Rinchik 6	I7Rn6	-	-	2.5	Up	2.5	Up	-	-
NM_013610	Ninjurin 1	Ninj1	-	-	-	-	2.5	Up	-	-
NM_172120	Vacuolar protein sorting 41 (yeast)	Vps41	-	-	2.3	Up	2.5	Up	-	-
NM_010390	Histocompatibility 2, Q region locus 1	H2-K1	-	-	-	-	2.5	Down	-	-
NM_009100	Repetin	Rptn	-	-	-	-	2.5	Down	-	-
NM_008997	RAB11B, member RAS oncogene family	Rab11b	-	-	2.2	Up	2.5	Up	-	-
NM_021502	Trafficking protein particle complex 2-like	Trappc2l	-	-	-	-	2.5	Up	-	-
M400010410	M400010410	-	-	-	-	-	2.6	Down	-	-
M400019231	M400019231	-	-	-	-	-	2.6	Down	-	-
XM_204283	palladin, cytoskeletal associated protein	-	-	-	2.6	Up	2.6	Up	-	-
M400014002	M400014002	-	-	-	-	-	2.6	Down	-	-
M400018164	M400018164	-	-	-	-	-	2.6	Down	-	-
M400006317	M400006317	-	-	-	-	-	2.6	Down	-	-
NM_019910	Demilune cell and parotid protein 1	Dcpp1	-	-	-	-	2.6	Down	-	-
NM_008212	Hydroxyacyl-Coenzyme A dehydrogenase	Hadh	1.6	Up	2.1	Up	2.6	Up	-	-
NM_181517	Importin 7	Ipo7	-	-	-	-	2.6	Down	-	-

NM_019542	N-acetylglucosamine kinase	Nagk	-	-	2.4	Up	2.6	Up	-	-
M40000335	M40000335	-	-	-	-	-	2.6	Down	-	-
NM_008842	Proviral integration site 1	Pim1	-	-	-	-	2.6	Up	-	-
M400019420	M400019420	-	-	-	-	-	2.6	Down	-	-
	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1, p105	Nfkb1	-	-	1.8	Up	2.6	Up	-	-
NM_010119	EH-domain containing 1	Ehd1	-	-	1.9	Up	2.6	Up	-	-
M400015185	M400015185	-	-	-	-	-	2.6	Down	-	-
NM_133916	Eukaryotic translation initiation factor 3, subunit B	Eif3b	-	-	1.5	Up	2.6	Up	-	-
NM_013492	Clusterin	Clu	-	-	-	-	2.6	Up	-	-
NM_007574	Complement component 1, q subcomponent, C chain	C1qc	-	-	2.1	Up	2.6	Up	-	-
NM_026428	Dicarbonyl L-xylulose reductase	Dcxr	-	-	2.0	Up	2.6	Up	-	-
	Protein tyrosine phosphatase, receptor type, C polypeptide-associated protein	Ptprcap	-	-	-	-	2.6	Up	-	-
NM_016933	RAD52 motif 1	Rdm1	-	-	-	-	2.6	Up	-	-
NM_025654	WNT1 inducible signaling pathway protein 2	Wisp2	-	-	-	-	2.6	Up	-	-
NM_016873	Nucleolar protein 3 (apoptosis repressor with CARD domain)	Nol3	-	-	-	-	2.6	Up	-	-
NM_030152	Transmembrane protein 205	Tmem205	2.2	Up	1.7	Up	2.6	Up	-	-
NM_178577	Serine (or cysteine) peptidase inhibitor, clade F, member 1	Serpinf1	-	-	2.5	Up	2.6	Up	-	-
NM_011340	M400013670	-	-	-	-	-	2.6	Down	-	-
M400013670	M400013670	-	-	-	-	-	2.6	Down	-	-
NM_175027	Fanconi anemia, complementation group B	Fancb	-	-	-	-	2.6	Down	-	-
M400019382	M400019382	-	-	-	-	-	2.6	Down	-	-
NM_008816	Platelet/endothelial cell adhesion molecule 1	Pecam1	-	-	-	-	2.6	Up	-	-
NM_213733	Aminopeptidase-like 1	Npepl1	-	-	-	-	2.6	Down	-	-
NM_026859	MAF1 homolog (S. cerevisiae)	Maf1	-	-	2.3	Up	2.6	Up	-	-
M400006453	M400006453	-	-	-	-	-	2.6	Up	-	-
NM_009081	Ribosomal protein L28	Rpl28	-	-	-	-	2.6	Up	-	-
NM_013811	Dynein, axonemal, heavy chain 8	Dnahc8	-	-	-	-	2.7	Up	-	-
NM_177343	Calcium/calmodulin-dependent protein kinase ID	Camk1d	-	-	-	-	2.7	Down	-	-
	Protein phosphatase 1, regulatory (inhibitor) subunit 13B	Ppp1r13b	-	-	1.9	Up	2.7	Up	-	-
NM_011625	M400012862	-	-	-	-	-	2.7	Down	-	-
M400012862	M400012862	-	-	-	-	-	2.7	Down	-	-
NM_145541	RAS-related protein-1a	Rap1a	2.5	Down	-	-	2.7	Down	-	-
M400008090	M400008090	-	-	-	-	-	2.7	Down	-	-
M300003896	M300003896	-	-	-	-	-	2.7	Up	-	-
NM_011842	Metastasis-associated gene family, member 2	Mta2	-	-	-	-	2.7	Up	-	-
NM_199012	FCH and double SH3 domains 2	Fchsd2	-	-	2.1	Up	2.7	Up	-	-
NM_283480	HEAT repeat containing 5B	-	-	-	2.0	Down	2.7	Down	-	-
XM_283480	M400016993	-	-	-	-	-	2.7	Down	-	-
M400016993	M400016993	-	-	-	-	-	2.7	Down	-	-
	Glutamate receptor, ionotropic, N-methyl D-aspartate-associated protein 1 (glutamate binding)	Grina	-	-	1.9	Up	2.7	Up	-	-
NM_023168	Calponin 2	Cnn2	-	-	-	-	2.7	Up	-	-
NM_007725	M400014947	-	-	-	-	-	2.7	Down	-	-
M400014947	M400014947	-	-	-	-	-	2.7	Down	-	-



NM_177785	CDNA sequence BC049635	BC049635	-	-	-	-	2.7	Down	-	-
M400002596	M400002596	-	-	-	-	-	2.7	Down	-	-
NM_008014	Protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform	Ppm1g	-	-	2.3	Up	2.7	Up	-	-
NM_053071	Cytochrome c oxidase, subunit VIc	Cox6c	-	-	3.0	Up	2.7	Up	-	-
NM_146606	Olfactory receptor 24	Olf24	-	-	-	-	2.7	Down	-	-
XM_357498	vomeronal 2, receptor 16	-	-	-	-	-	2.7	Down	-	-
NM_194347	CDNA sequence AY358078	AY358078	-	-	-	-	2.7	Down	-	-
NM_007744	Catechol-O-methyltransferase	Comt	-	-	2.6	Up	2.7	Up	-	-
NM_147779	Surfactant associated protein B	Sftpb	3.5	Up	2.9	Up	2.7	Up	-	-
NM_010686	Lysosomal-associated protein transmembrane 5	Laptm5	-	-	-	-	2.7	Up	-	-
M400018290	M400018290	-	-	-	-	-	2.7	Down	-	-
		1110032A03								
NM_023483	RIKEN cDNA 1110032A03 gene	Rik	-	-	2.7	Up	2.7	Up	-	-
NM_010386	Histocompatibility 2, class II, locus DMA	H2-DMA	-	-	-	-	2.7	Up	-	-
M400017618	M400017618	-	-	-	-	-	2.7	Down	-	-
NM_025424	Neuron derived neurotrophic factor	Nenf	-	-	-	-	2.7	Up	-	-
NM_054077	Proline arginine-rich end leucine-rich repeat	Prelp	-	-	2.8	Up	2.7	Up	-	-
NM_027219	CDC42 effector protein (Rho GTPase binding) 1	Cdc42ep1	-	-	-	-	2.7	Up	-	-
		1110032A13								
NM_199197	RIKEN cDNA 1110032A13 gene	Rik	-	-	2.7	Up	2.7	Up	-	-
NM_013706	CD52 antigen	Cd52	-	-	-	-	2.7	Up	-	-
M400000459	M400000459	-	-	-	-	-	2.7	Down	-	-
M400016871	M400016871	-	-	-	-	-	2.7	Down	-	-
NM_175505	RIKEN cDNA gene D630044L22 gene	-	-	-	-	-	2.7	Down	-	-
NM_008525	Aminolevulinatase, delta-, dehydratase	Alad	-	-	2.1	Up	2.7	Up	-	-
NM_010489	Hyaluronoglucosaminidase 2	Hyal2	-	-	2.3	Up	2.7	Up	-	-
NM_207025	Taste receptor, type 2, member 123	Tas2r123	-	-	-	-	2.7	Down	-	-
NM_031178	Toll-like receptor 9	Tlr9	-	-	-	-	2.7	Down	-	-
M400006098	M400006098	-	-	-	2.4	Up	2.8	Up	-	-
NM_025624	Proteasome maturation protein	Pomp	-	-	-	-	2.8	Up	-	-
XM_484732	predicted gene, EG433184	-	-	-	-	-	2.8	Up	-	-
M400003019	M400003019	-	-	-	2.7	Up	2.8	Up	-	-
NM_007637	Chaperonin subunit 5 (epsilon)	Cct5	-	-	-	-	2.8	Up	-	-
XM_194000	RIKEN cDNA 9630050M13 gene	-	-	-	-	-	2.8	Down	-	-
M400018833	M400018833	-	-	-	-	-	2.8	Down	-	-
NM_024457	RAS related protein 1b	Rap1b	-	-	2.4	Up	2.8	Up	-	-
M400009817	M400009817	-	-	-	-	-	2.8	Down	-	-
M400018579	M400018579	-	-	-	-	-	2.8	Down	-	-
NM_009964	Crystallin, alpha B	Cryab	-	-	3.6	Up	2.8	Up	-	-
NM_025396	6-phosphogluconolactonase	Pgls	-	-	1.7	Up	2.8	Up	-	-
NM_134155	Breast cancer metastasis-suppressor 1	Brms1	-	-	1.8	Up	2.8	Up	-	-
M400001783	M400001783	-	-	-	-	-	2.8	Down	-	-
NM_025344	Eukaryotic translation initiation factor 3, subunit F	Eif3f	-	-	-	-	2.8	Up	-	-
NM_027196	Polymerase (DNA-directed), delta 4	Pold4	-	-	1.7	Up	2.8	Up	-	-

M400014267	M400014267	-	-	-	-	-	2.8	Down	-	-
M400018133	M400018133	-	-	-	-	-	2.8	Down	-	-
NM_175422	RIKEN cDNA 4631423B10 gene	-	-	-	-	-	2.8	Down	-	-
M300013400	M300013400	-	2.0	Up	3.1	Up	2.8	Up	-	-
NM_011874	Proteasome (prosome, macropain) 26S subunit, ATPase, 4	Psmc4	-	-	2.2	Up	2.8	Up	-	-
NM_134129	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae)	Prpf19	-	-	2.3	Up	2.8	Up	-	-
NM_011239	DiGeorge syndrome critical region gene 8	Ranbp1	-	-	-	-	2.8	Up	-	-
M400014003	M400014003	-	-	-	-	-	2.8	Down	-	-
M400017196	M400017196	-	-	-	-	-	2.8	Down	-	-
NM_007835	Dynactin 1	Dctn1	-	-	2.2	Up	2.8	Up	-	-
NM_009342	Dynein light chain Tctex-type 1	Dynlt1	-	-	2.4	Up	2.8	Up	-	-
NM_026695	Electron transferring flavoprotein, beta polypeptide	Etfb	-	-	2.6	Up	2.8	Up	-	-
NM_025637	RWD domain containing 3	Rwdd3	-	-	-	-	2.8	Up	-	-
NM_010015	defender against cell death 1	-	-	-	-	-	2.8	Up	-	-
NM_134236	Vomeronasal 1 receptor, H11	V1rh11	-	-	-	-	2.8	Down	-	-
M400016794	M400016794	-	-	-	-	-	2.8	Down	-	-
NM_007693	Chromogranin A	Chga	-	-	-	-	2.8	Down	-	-
NM_008879	Lymphocyte cytosolic protein 1	Lcp1	-	-	2.7	Up	2.8	Up	-	-
M400008580	M400008580	-	1.7	Up	2.1	Up	2.8	Up	-	-
NM_008450	Kinesin light chain 1	Klc1	-	-	3.4	Up	2.8	Up	-	-
NM_017467	Zinc finger protein 316	Zfp316	-	-	-	-	2.9	Down	-	-
NM_025289	Transforming growth factor beta regulated gene 1	Tbrg1	-	-	-	-	2.9	Up	-	-
NM_027151	Dynactin 2	Dctn2	-	-	-	-	2.9	Up	-	-
NM_207105	Histocompatibility 2, class II antigen A, beta 1	H2-Ab1	-	-	-	-	2.9	Up	-	-
NM_023247	RIKEN cDNA 4733401H18 gene	4733401H18	-	-	2.4	Up	2.9	Up	-	-
NM_013595	Methyl-CpG binding domain protein 3	Rik	-	-	2.7	Up	2.9	Up	-	-
M400016354	M400016354	Mbd3	-	-	-	-	2.9	Down	-	-
NM_011930	Chloride channel 7	-	-	-	-	-	2.9	Down	-	-
NM_010202	Fibroblast growth factor 4	Clcn7	-	-	-	-	2.9	Down	-	-
XM_356994	predicted gene, EG383341	Fgf4	-	-	-	-	2.9	Down	-	-
M400001295	M400001295	-	-	-	-	-	2.9	Up	-	-
NM_025842	Vacuolar protein sorting 28 (yeast)	-	-	-	-	-	2.9	Down	-	-
NM_133666	NADH dehydrogenase (ubiquinone) flavoprotein 1	Vps28	-	-	-	-	2.9	Up	-	-
NM_011315	Serum amyloid A 3	Ndufv1	-	-	2.2	Up	2.9	Up	-	-
NM_010742	Lymphocyte antigen 6 complex, locus D	Saa3	-	-	-	-	2.9	Up	-	-
NM_010705	Lectin, galactose binding, soluble 3	Ly6d	-	-	-	-	2.9	Up	-	-
NM_010189	Fc receptor, IgG, alpha chain transporter	Lgals3	-	-	-	-	2.9	Up	-	-
M400016735	M400016735	Fcgrt	-	-	2.6	Up	2.9	Up	-	-
NM_201353	Solute carrier family 6 (neurotransmitter transporter, L-proline), member 7	-	-	-	-	-	2.9	Down	-	-
XM_128001	GPI-anchored HDL-binding protein 1	Slc6a7	-	-	-	-	2.9	Up	-	-
M400008511	M400008511	-	-	-	-	-	2.9	Up	-	-

M400018402	M400018402	-	-	-	-	2.9	Down	-	-
NM_025326	Transmembrane protein 176A	Tmem176a	-	-	-	2.9	Up	-	-
M400000941	M400000941	-	-	2.1	Up	2.9	Up	-	-
M400019166	M400019166	-	-	-	-	2.9	Down	-	-
NM_026638,									
NM_138754	M200005892	-	-	2.4	Up	2.9	Up	-	-
M400016722	M400016722	-	-	-	-	2.9	Down	-	-
	Protein phosphatase 2, regulatory subunit B (B56), alpha isoform	Ppp2r5a	-	-	2.3	Up	2.9	Up	-
NM_144880	Fractured callus expressed transcript 1	Fxc1	-	-	2.1	Up	2.9	Up	-
NM_019502	M400004745	-	-	-	-	3.0	Down	-	-
XM_355972	Neural precursor cell expressed, developmentally down-regulated gene 8	Nedd8	-	-	-	-	3.0	Up	-
NM_008683	Heterogeneous nuclear ribonucleoprotein L	Hnrnpl	-	-	2.1	Up	3.0	Up	-
NM_177301	Eukaryotic translation initiation factor 3, subunit D	Eif3d	-	-	2.4	Up	3.0	Up	-
NM_018749	Dynactin 5	Plk1	-	-	2.5	Up	3.0	Up	-
NM_021608	RAB14, member RAS oncogene family	Rab14	-	-	-	-	3.0	Up	-
NM_026697	Proteasome (prosome, macropain) 26S subunit, non- ATPase, 8	Psmc8	-	-	2.3	Up	3.0	Up	-
NM_026545	Ras homolog gene family, member C	Rhoc	-	-	2.7	Up	3.0	Up	-
NM_007484	M400015957	-	-	-	-	3.0	Down	-	-
M400015957	CD79B antigen	Cd79b	-	-	-	-	3.0	Up	-
NM_008339	TRNA-yW synthesizing protein 1 homolog (S. cerevisiae)	Tyw1	-	-	-	-	3.0	Down	-
NM_178897	Actin related protein 2/3 complex, subunit 4	Arpc4	-	-	1.9	Up	3.0	Up	-
NM_026552	M400001273	-	-	-	-	3.0	Up	-	-
M400001273	Harvey rat sarcoma virus oncogene 1	Hras1	-	-	3.0	Up	3.0	Up	-
NM_008284	M400012900	-	-	-	-	3.0	Down	-	-
M400012900	Mitochondrial ribosomal protein L54	Mrpl54	-	-	2.3	Up	3.0	Up	-
NM_025317	M400010481	-	-	-	-	3.0	Down	-	-
M400010481	M400014203	-	-	-	-	3.0	Down	-	-
M400014203	M400014197	-	-	-	-	3.0	Down	-	-
M400014197	Chloride channel calcium activated 2	Clca2	-	-	-	-	3.0	Down	-
NM_030601	RIKEN cDNA D930014E17 gene	D930014E17 Rik	-	-	-	-	3.0	Up	-
NM_020616	Calcium binding atopy-related autoantigen 1	Cbara1	-	-	3.1	Up	3.0	Up	-
NM_144822	Splicing factor 3b, subunit 5	Sf3b5	-	-	2.4	Up	3.0	Up	-
NM_175102	Seryl-aminoacyl-tRNA synthetase	Sars	-	-	2.4	Up	3.0	Up	-
NM_011319	Protein kinase C, delta binding protein	Prkcdbp	-	-	2.7	Up	3.0	Up	-
NM_028444	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8	Ndufb8	-	-	2.2	Up	3.0	Up	-
NM_026061	N-terminal Asn amidase	Ntan1	-	-	2.1	Up	3.0	Up	-
NM_010946	Olfactory receptor 1414	Olfr1414	-	-	-	-	3.1	Down	-
NM_147039	M400005471	-	-	-	-	3.1	Down	-	-
M400005471	Coronin, actin binding protein 1A	Coro1a	-	-	-	-	3.1	Up	-
NM_009898									

NM_011778	Coronin, actin binding protein 1B	Coro1b	-	-	2.7	Up	3.1	Up	-	-
NM_011966	Proteasome (prosome, macropain) subunit, alpha type 4	Pasma4	-	-	-	-	3.1	Up	-	-
NM_012002	COP9 (constitutive photomorphogenic) homolog, subunit 6 (Arabidopsis thaliana)	Cops6	-	-	-	-	3.1	Up	-	-
M400017272	M400017272	-	-	-	-	-	3.1	Down	-	-
M400016330	M400016330	-	-	-	-	-	3.1	Down	-	-
NM_145424	CDNA sequence BC089597	BC089597	-	-	2.6	Down	3.1	Down	-	-
M200013018	M200013018	-	-	-	2.2	Up	3.1	Up	-	-
M400014217	M400014217	-	-	-	-	-	3.1	Down	-	-
NM_177039	RIKEN cDNA A530016L24 gene	A530016L24	-	-	-	-	-	-	-	-
NM_133838	EH-domain containing 4	Rik	-	-	2.2	Down	3.1	Down	-	-
M400005013	M400005013	Ehd4	-	-	2.9	Up	3.1	Up	-	-
M400015189	M400015189	-	-	-	-	-	3.1	Down	-	-
XM_485807	predicted gene, EG434067	-	-	-	-	-	3.1	Down	-	-
NM_013677	Surfeit gene 1	Surf1	-	-	2.9	Up	3.1	Up	-	-
M400013125	M400013125	-	-	-	-	-	3.1	Down	-	-
M400013671	M400013671	-	-	-	1.7	Down	3.1	Down	-	-
NM_027799	Ankyrin repeat domain 40	Ankrd40	-	-	-	-	3.1	Up	-	-
XM_357260	sperm flagellar 1	-	2.2	Up	2.3	Up	3.1	Up	-	-
XM_193559	predicted gene, EG268300	-	-	-	-	-	3.1	Up	-	-
XM_486168	predicted gene, EG434356	-	-	-	-	-	3.2	Up	-	-
M400017808	M400017808	-	-	-	-	-	3.2	Down	-	-
NM_011732	Y box protein 1	Ybx1	-	-	3.1	Up	3.2	Up	-	-
NM_172609	Translocase of outer mitochondrial membrane 22 homolog (yeast)	Tomm22	-	-	2.3	Up	3.2	Up	-	-
M200014304	M200014304	-	-	-	-	-	3.2	Down	-	-
NM_008705	Non-metastatic cells 2, protein (NM23B) expressed in	Nme2	-	-	3.0	Up	3.2	Up	-	-
NM_153790	Scavenger receptor class F, member 2	Scarf2	-	-	2.3	Up	3.2	Up	-	-
NM_007472	Aquaporin 1	Aqp1	-	-	-	-	3.2	Up	-	-
M400014620	M400014620	-	-	-	-	-	3.2	Down	-	-
M400014758	M400014758	-	-	-	-	-	3.2	Down	-	-
NM_029441	Chromodomain protein, Y chromosome-like 2	Cdyl2	-	-	3.6	Up	3.2	Up	-	-
NM_025324	Zinc finger protein 524	Zfp524	-	-	2.3	Up	3.2	Up	-	-
NM_012037	Vesicle amine transport protein 1 homolog (T californica)	Vat1	1.8	Up	3.2	Up	3.2	Up	-	-
NM_009870	Cyclin-dependent kinase 4	Cdk4	-	-	2.3	Up	3.2	Up	-	-
NM_025989	Glycoprotein 2 (zymogen granule membrane)	Gp2	-	-	-	-	3.2	Down	-	-
M400006237	M400006237	-	-	-	-	-	3.2	Down	-	-
NM_053267	Selenoprotein M	Selm	-	-	-	-	3.2	Up	-	-
NM_020494	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24	Ddx24	-	-	2.9	Up	3.2	Up	-	-
NM_019391	Lymphocyte specific 1	Lsp1	1.8	Up	-	-	3.2	Up	-	-
NM_010194	Feline sarcoma oncogene	Fes	-	-	-	-	3.2	Up	-	-
NM_013477	ATPase, H+ transporting, lysosomal V0 subunit D1	Atp6v0d1	-	-	2.8	Up	3.2	Up	-	-

NM_175510	RIKEN cDNA C030018G13 gene	-	-	-	-	-	3.2	Down	-	-
NM_146508	Olfactory receptor 959	Olfr959	-	-	-	-	3.2	Down	-	-
NM_027015	Predicted gene, ENSMUSG00000050621	Rps27	-	-	-	-	3.3	Up	-	-
M400016846	M400016846	-	-	-	-	-	3.3	Down	-	-
NM_009795	Calpain, small subunit 1	Capns1	-	-	2.0	Up	3.3	Up	-	-
	Nudix (nucleoside diphosphate linked moiety X)-type motif 16-like 1	Nudt1611	-	-	-	-	3.3	Up	-	-
NM_025839	M400008439	-	-	-	2.8	Up	3.3	Up	-	-
M400009305	M400009305	-	-	-	2.6	Up	3.3	Up	-	-
NM_013549	Histone cluster 2, H2aa1	Hist2h2aa1	-	-	2.0	Up	3.3	Up	-	-
NM_010398	Histocompatibility 2, T region locus 23	H2-D1	-	-	2.6	Up	3.3	Up	-	-
M400008287	M400008287	-	-	-	-	-	3.3	Up	-	-
NM_009923	2,3-cyclic nucleotide 3 phosphodiesterase	Cnp	-	-	-	-	3.3	Up	-	-
NM_011042	Poly(rC) binding protein 2	Pcbp2	-	-	3.1	Up	3.3	Up	-	-
NM_177683	Vestigial like 4 (Drosophila)	Vgll4	-	-	-	-	3.3	Up	-	-
	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein, alpha 1	-	-	-	2.4	Up	3.3	Down	-	-
XM_133979	M400001344	-	1.9	Up	3.4	Up	3.3	Up	-	-
M400016662	M400016662	-	-	-	-	-	3.3	Down	-	-
NM_010635	Kruppel-like factor 1 (erythroid)	Klf1	-	-	-	-	3.3	Down	-	-
NM_177882	Zinc finger protein 786	Zfp786	-	-	-	-	3.3	Down	-	-
NM_016985	Myotubularin related protein 1	Mtmr1	-	-	-	-	3.3	Down	-	-
M400017319	M400017319	-	-	-	-	-	3.3	Down	-	-
M400001124	M400001124	-	-	-	-	-	3.4	Down	-	-
XM_484142	M300002514	-	-	-	2.4	Down	3.4	Down	-	-
XM_486018	predicted gene, EG434253	-	-	-	2.7	Up	3.4	Up	-	-
XM_484271	predicted gene, EG432767	-	-	-	3.1	Up	3.4	Up	-	-
XM_489353	M300018823	-	-	-	-	-	3.4	Down	-	-
NM_145486	Membrane-associated ring finger (C3HC4) 2	3-Mar	-	-	2.9	Up	3.4	Up	-	-
NM_146307	Olfactory receptor 498	Olfr498	-	-	-	-	3.4	Down	-	-
NM_010312	Guanine nucleotide binding protein (G protein), beta 2	Gnb2	-	-	2.1	Up	3.4	Up	-	-
	Elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1	Elov1	2.2	Up	2.8	Up	3.4	Up	-	-
NM_019422		1700027D21								
NM_029661	RIKEN cDNA 1700027D21 gene	Rik	-	-	-	-	3.5	Down	-	-
M200014754	M200014754	-	-	-	2.9	Up	3.5	Up	-	-
M400016473	M400016473	-	-	-	-	-	3.5	Down	-	-
	Proteasome (prosome, macropain) subunit, beta type 10	Psmb10	-	-	-	-	3.5	Up	-	-
NM_013640										
NM_019682	Dynein light chain LC8-type 1	Dynl1	-	-	3.5	Up	3.5	Up	-	-
NM_177586	Eukaryotic translation initiation factor 5A2	Eif5a2	-	-	-	-	3.5	Down	-	-
NM_007503,										
NM_052823,										
NM_052824	M200004498	-	-	-	-	-	3.5	Up	-	-
M400016376	M400016376	-	-	-	-	-	3.5	Down	-	-

NM_009932	Collagen, type IV, alpha 2	Col4a2	-	-	3.4	Up	3.6	Up	-	-
NM_026776	Vacuolar protein sorting 25 (yeast)	Vps25	-	-	-	-	3.6	Up	-	-
NM_009187	Cytochrome c oxidase subunit VIIa polypeptide 2-like	Cox7a2l	-	-	3.6	Up	3.6	Up	-	-
NM_021480	L-threonine dehydrogenase	Tdh	-	-	-	-	3.6	Down	-	-
NM_013805	Claudin 5	Cldn5	-	-	2.6	Up	3.6	Up	-	-
NM_010925	Ribosomal RNA processing 1 homolog (S. cerevisiae)	Rrp1	-	-	2.4	Up	3.6	Up	-	-
NM_007806	Cytochrome b-245, alpha polypeptide	Cyba	-	-	2.1	Up	3.7	Up	-	-
NM_024223	Cysteine rich protein 2	Crip2	2.2	Up	3.4	Up	3.7	Up	-	-
NM_019674	Protein phosphatase 4, catalytic subunit	Ppp4c	-	-	3.0	Up	3.7	Up	-	-
NM_011952	Mitogen-activated protein kinase 3	Mapk3	-	-	3.2	Up	3.7	Up	-	-
NM_009746	B-cell CLL/lymphoma 7C	Bcl7c	-	-	2.0	Up	3.7	Up	-	-
NM_009975	Casein kinase 2, beta polypeptide	Cskn2b	-	-	2.9	Up	3.7	Up	-	-
NM_080555	Phosphatidic acid phosphatase type 2B	Ppap2b	2.0	Up	3.6	Up	3.7	Up	-	-
NM_011664,										
NM_011664	M400000325	-	-	-	2.9	Up	3.7	Up	-	-
XM_488111	M400006455	-	-	-	2.8	Up	3.7	Up	-	-
NM_025827	Lon peptidase 2, peroxisomal	Lonp2	-	-	-	-	3.8	Down	-	-
NM_177068	Olfactomedin-like 2B	Olfml2b	-	-	-	-	3.8	Down	-	-
M400015250	M400015250	-	-	-	-	-	3.8	Down	-	-
M300000821	M300000821	-	-	-	-	-	3.8	Up	-	-
NM_008788	Procollagen C-endopeptidase enhancer protein	Pcolce	1.9	Up	3.5	Up	3.8	Up	-	-
M400002436	M400002436	-	-	-	-	-	3.8	Down	-	-
NM_172464	Dishevelled associated activator of morphogenesis 1	Daam1	-	-	-	-	3.8	Down	-	-
M400006308	M400006308	-	-	-	-	-	3.9	Down	-	-
M400014763	M400014763	-	-	-	-	-	3.9	Down	-	-
NM_010494	Intercellular adhesion molecule 2	Icam2	-	-	3.7	Up	3.9	Up	-	-
NM_010027	D-dopachrome tautomerase	Ddt	-	-	-	-	3.9	Up	-	-
NM_008975	Protein tyrosine phosphatase 4a3	Ptp4a3	-	-	3.3	Up	3.9	Up	-	-
NM_007645	CD37 antigen	Cd37	-	-	2.5	Up	3.9	Up	-	-
NM_009087	RNA polymerase 1-3	Rpo1-3	-	-	-	-	3.9	Up	-	-
M400004930	M400004930	-	-	-	-	-	4.0	Down	-	-
NM_134079	Adenosine kinase	Adk	-	-	-	-	4.0	Up	-	-
NM_008675	Neuroblastoma, suppression of tumorigenicity 1	Nbl1	-	-	3.8	Up	4.0	Up	-	-
NM_024170	CAAX box 1 homolog A (human)	Cxx1a	-	-	3.1	Up	4.0	Up	-	-
M400008433	M400008433	-	-	-	3.5	Up	4.0	Up	-	-
M400006868	M400006868	-	-	-	2.8	Up	4.1	Up	-	-
XM_140042	Predicted gene, EG240110	EG240110	-	-	-	-	4.1	Down	-	-
NM_013502	C-terminal binding protein 1	Ctbp1	-	-	-	-	4.1	Up	-	-
NM_022314	Tropomyosin 3, gamma	Tpm3	-	-	4.0	Up	4.1	Up	-	-
NM_198190	Neurotrophin 5	Ntf5	-	-	-	-	4.1	Down	-	-
NM_009373	Transglutaminase 2, C polypeptide	Tgm2	2.0	Up	3.8	Up	4.1	Up	-	-
M400017455	M400017455	-	-	-	-	-	4.2	Down	-	-
NM_011912	Ventral anterior homeobox containing gene 2	Vax2	-	-	-	-	4.2	Down	-	-
NM_016738	Ribosomal protein L13	Rpl13	-	-	4.2	Up	4.2	Up	-	-
NM_027687	Calcium-binding tyrosine-(Y)-phosphorylation regulated	Cabyr	-	-	-	-	4.2	Down	-	-

	(fibrousheathin 2)												
M400016688	M400016688	-	-	-	-	-	-	4.2	Down	-	-	-	-
NM_016794	Vesicle-associated membrane protein 8	Vamp8	-	-	3.9	Up	-	4.2	Up	-	-	-	-
		1810009A15											
NM_025463	RIKEN cDNA 1810009A15 gene	Rik	-	-	-	-	-	-	-	-	-	-	-
M200015711	M200015711	-	2.1	Up	-	-	-	-	-	-	-	-	-
M400005134	M400005134	-	2.2	Up	-	-	-	-	-	-	-	-	-
M400014138	M400014138	-	1.6	Down	-	-	-	-	-	-	-	-	-
NM_013535	Gene rich cluster, C10 gene	Grccl0	1.6	Up	-	-	-	-	-	-	-	-	-
M400015121	M400015121	-	1.8	Down	1.5	Down	-	-	-	-	-	-	-
NM_019479	Hairy and enhancer of split 6 (Drosophila)	Hes6	-	-	1.5	Down	-	-	-	-	-	-	-
NM_007425	Advanced glycosylation end product-specific receptor	Ager	-	-	1.5	Up	-	-	-	-	-	-	-
NM_010638	Kruppel-like factor 9	Klf9	-	-	1.5	Up	-	-	-	-	-	-	-
NM_028048	Solute carrier family 25, member 35	Slc25a35	-	-	1.5	Up	-	-	-	-	-	-	-
NM_008688	Nuclear factor I/C	Nfic	-	-	1.5	Up	-	-	-	-	-	-	-
NM_009678	Adaptor protein complex AP-1, mu 2 subunit	Ap1m2	-	-	1.5	Up	-	-	-	-	-	-	-
NM_011767	Zinc finger RNA binding protein	Zfr	-	-	1.5	Up	-	-	-	-	-	-	-
NM_013529	Glutamine fructose-6-phosphate transaminase 2	Gfpt2	-	-	1.5	Up	-	-	-	-	-	-	-
M400005551	M400005551	-	-	-	1.5	Up	-	-	-	-	-	-	-
NM_007497,													
XM_204339	M400005232	-	-	-	1.5	Down	-	-	-	-	-	-	-
NM_008214	Histidyl-tRNA synthetase	Hars	-	-	1.5	Up	-	-	-	-	-	-	-
NM_175374	Mitochondrial translational release factor 1-like	Mtrf11	-	-	1.5	Down	-	-	-	-	-	-	-
NM_008360	Interleukin 18	Il18	-	-	1.6	Down	-	-	-	-	-	-	-
M400007350	M400007350	-	-	-	1.6	Up	-	-	-	-	-	-	-
		1810014F10											
NM_026928	RIKEN cDNA 1810014F10 gene	Rik	-	-	1.6	Up	-	-	-	-	-	-	-
NM_011818	Germ cell-less homolog 1 (Drosophila)	Gmcl1	-	-	1.6	Up	-	-	-	-	-	-	-
XM_136663	predicted gene, OTTMUSG00000013920	-	-	-	1.6	Up	-	-	-	-	-	-	-
XM_128627	RIKEN cDNA 2310061I04 gene	-	-	-	1.6	Up	-	-	-	-	-	-	-
M400004865	M400004865	-	-	-	1.6	Up	-	-	-	-	-	-	-
NM_007444	S-adenosylmethionine decarboxylase 2	Amd2	-	-	1.6	Up	-	-	-	-	-	-	-
NM_145630	Pyruvate dehydrogenase kinase, isoenzyme 3	Pdk3	-	-	1.6	Down	-	-	-	-	-	-	-
M300003149	M300003149	-	-	-	1.6	Up	-	-	-	-	-	-	-
NM_026175	Splicing factor 3a, subunit 1	Sf3a1	-	-	1.6	Up	-	-	-	-	-	-	-
NM_198886	Zinc finger and BTB domain containing 12	Zbtb12	-	-	1.6	Up	-	-	-	-	-	-	-
NM_011926	CEA-related cell adhesion molecule 1	Ceacam1	-	-	1.6	Up	-	-	-	-	-	-	-
NM_173402	Regulator of G-protein signaling 12	Rgs12	-	-	1.6	Up	-	-	-	-	-	-	-
NM_153166	Copine V	Cpne5	-	-	1.6	Up	-	-	-	-	-	-	-
NM_199449	Zinc fingers and homeoboxes 2	Zhx2	-	-	1.6	Up	-	-	-	-	-	-	-
NM_145823	Phosphatidylinositol transfer protein, cytoplasmic 1	Pitpnc1	-	-	1.6	Up	-	-	-	-	-	-	-
NM_009447	Tubulin, alpha 4A	Tuba4a	1.7	Down	1.6	Down	-	-	-	-	-	-	-
		A830007P12											
NM_146115	RIKEN cDNA A830007P12 gene	Rik	-	-	1.6	Up	-	-	-	-	-	-	-
NM_009825	Serine (or cysteine) peptidase inhibitor, clade H,	Serpinh1	-	-	1.6	Up	-	-	-	-	-	-	-

	member 1									
NM_026858	XRCC6 binding protein 1	Xrcc6bp1	-	-	1.7	Down	-	-	-	-
NM_008393	Iroquois related homeobox 3 (Drosophila)	Irx3	-	-	1.7	Up	-	-	-	-
	eukaryotic translation initiation factor 1A domain									
XM_129120	containing	-	-	-	1.7	Up	-	-	-	-
NM_026114	Eukaryotic translation initiation factor 2, subunit 1 alpha	Eif2s1	-	-	1.7	Up	-	-	-	-
XM_354675	AT rich interactive domain 4A (Rbp1 like)	-	-	-	1.7	Up	-	-	-	-
NM_017370	Haptoglobin	Hp		1.7	Up					
NM_009516	Wee 1 homolog (S. pombe)	Wee1	-	-	1.7	Down	-	-	-	-
M400004994	M400004994	-	-	-	1.7	Down	-	-	-	-
NM_009742	B-cell leukemia/lymphoma 2 related protein A1a	Bcl2a1a	-	-	1.7	Up	-	-	-	-
XM_135146	DnaJ (Hsp40) homolog, subfamily C, member 13	DnaJ	-	-	1.7	Up	-	-	-	-
M400009168	M400009168	-	-	-	1.7	Down	-	-	-	-
NM_008005	Fibroblast growth factor 18	Fgf18	-	-	1.7	Up	-	-	-	-
	TIP41, TOR signalling pathway regulator-like (S. cerevisiae)	Tipr1	-	-	1.7	Up	-	-	-	-
NM_145513	COX19 cytochrome c oxidase assembly homolog (S. cerevisiae)	Cox19	-	-	1.7	Up	-	-	-	-
NM_197980	M400015826	-	-	-	1.7	Down	-	-	-	-
M400015826	M400015826	-	-	-	1.7	Down	-	-	-	-
M300005301	M300005301	-	-	-	1.7	Up	-	-	-	-
NM_012027	Myosin phosphatase Rho interacting protein	Mprp	-	-	1.7	Up	-	-	-	-
NM_019521	Growth arrest specific 6	Gas6	-	-	1.7	Up	-	-	-	-
	Transient receptor potential cation channel, subfamily M, member 7	Trpm7	-	-	1.7	Up	-	-	-	-
NM_021450	Solute carrier family 35, member B1	Slc35b1	-	-	1.7	Up	-	-	-	-
NM_016752	M400011184	-	-	-	1.7	Down	-	-	-	-
M400011184	M400011184	-	-	-	1.7	Down	-	-	-	-
M400008854	M400008854	-	-	-	1.7	Up	-	-	-	-
NM_026130	Signal recognition particle receptor (docking protein)	Srpr	-	-	1.7	Up	-	-	-	-
M400005791	M400005791	-	-	-	1.7	Up	-	-	-	-
NM_031375	Neugrin, neurite outgrowth associated	Ngrn	-	-	1.7	Up	-	-	-	-
NM_010849	Myelocytomatosis oncogene	Myc	-	-	1.7	Up	-	-	-	-
NM_009794	Calpain 2	Capn2	-	-	1.7	Up	-	-	-	-
	RIKEN cDNA D030056L22 gene	D030056L22								
NM_177640	RIKEN cDNA D030056L22 gene	Rik	-	-	1.7	Up	-	-	-	-
XM_125538	sestrin 1	-	-	-	1.7	Up	-	-	-	-
M400010474	M400010474	-	-	-	1.8	Up	-	-	-	-
NM_016711	Tropomodulin 2	Tmod2	-	-	1.8	Up	-	-	-	-
NM_025859	ADP-ribosylation factor-like 1	Arl1	-	-	1.8	Up	-	-	-	-
NM_178239	NADPH dependent diflavin oxidoreductase 1	-	-	-	1.8	Up	-	-	-	-
NM_183144	Inositol polyphosphate-5-phosphatase A	Inpp5a	-	-	1.8	Up	-	-	-	-
M400008179	M400008179	-	-	-	1.8	Up	-	-	-	-
XM_134711	angiomotin-like 1	-	-	-	1.8	Up	-	-	-	-
NM_144804	DEP domain containing 7	Depdc7	-	-	1.8	Up	-	-	-	-
NM_029673	Inner membrane protein, mitochondrial	Immt	-	-	1.8	Up	-	-	-	-
M400003009	M400003009	-	-	-	1.8	Up	-	-	-	-



NM_019827, XM_489542	M300003521	-	-	-	1.8	Up	-	-	-	-
		1700025E21								
NM_029373	RIKEN cDNA 1700025E21 gene	Rik	-	-	1.8	Up	-	-	-	-
M400001063	M400001063	-	-	-	1.8	Up	-	-	-	-
NM_008355	Interleukin 13	Il13	-	-	1.8	Up	-	-	-	-
NM_008892	Polymerase (DNA directed), alpha 1	Pola1	-	-	1.8	Down	-	-	-	-
NM_017472	Sorting nexin 3	Snx3	-	-	1.8	Up	-	-	-	-
XM_356935	Predicted gene, EG383229	EG383229	-	-	1.8	Up	-	-	-	-
XM_129951	alkaline phosphatase, intestinal	-	-	-	1.8	Up	-	-	-	-
XM_129803	ring finger protein 149	-	1.7	Down	1.8	Up	-	-	-	-
M400010338	M400010338	-	-	-	1.8	Up	-	-	-	-
NM_133954	Expressed sequence AA960436	AA960436	-	-	1.8	Up	-	-	-	-
NM_018776	Cytokine receptor-like factor 3	Crif3	-	-	1.8	Down	-	-	-	-
M400014919	M400014919	-	-	-	1.8	Down	-	-	-	-
NM_008846	Phosphatidylinositol-4-phosphate 5-kinase, type 1 beta Glycine amidinotransferase (L-arginine:glycine amidinotransferase)	Pip5k1b Gatm	-	-	1.8	Up	-	-	-	-
NM_008826	Phosphofructokinase, liver, B-type	Pfkl	-	-	1.8	Up	-	-	-	-
XM_130138	speckle-type POZ protein-like	-	-	-	1.9	Up	-	-	-	-
NM_033588	Protocadherin gamma subfamily A, 10	Pcdhga12	2.7	Up	1.9	Up	-	-	-	-
NM_145995, NM_178115	M300012454	-	-	-	1.9	Down	-	-	-	-
XM_127537	RIKEN cDNA A930021C24 gene	-	-	-	1.9	Down	-	-	-	-
M400010452	M400010452	-	-	-	1.9	Up	-	-	-	-
NM_172782	Nuclear transport factor 2-like export factor 2	Nxt2	-	-	1.9	Up	-	-	-	-
NM_025450	Mitochondrial ribosomal protein S17	Mrps17	-	-	1.9	Up	-	-	-	-
NM_177684	Zinc finger protein 637	Zfp637	-	-	1.9	Up	-	-	-	-
NM_021897	Transformation related protein 53 inducible nuclear protein 1	Trp53inp1	-	-	1.9	Up	-	-	-	-
NM_008784	Immunoglobulin (CD79A) binding protein 1 Protein kinase, AMP-activated, gamma 2 non-catalytic subunit	Igbbp1 Prkag2	-	-	1.9	Up	-	-	-	-
NM_145401 XM_357381	M400003302	-	1.9	Up	1.9	Up	-	-	-	-
NM_176849	Arginine and glutamate rich 1	Arglu1	2.5	Down	1.9	Down	-	-	-	-
NM_011636	Phospholipid scramblase 1	Plscr1	-	-	1.9	Up	-	-	-	-
M400008878	M400008878	-	-	-	1.9	Up	-	-	-	-
M400016066	M400016066	-	-	-	1.9	Up	-	-	-	-
NM_019468	Glucose-6-phosphate dehydrogenase 2	G6pd2	-	-	1.9	Up	-	-	-	-
NM_134017	Methionine adenosyltransferase II, beta	Mat2b	-	-	1.9	Up	-	-	-	-
M400003423	M400003423	-	-	-	1.9	Up	-	-	-	-
M400016507	M400016507	-	-	-	2.0	Up	-	-	-	-
NM_145470	DEP domain containing 6	Depdc6	-	-	2.0	Up	-	-	-	-
NM_009473	Nuclear receptor subfamily 1, group H, member 2	Nr1h2	-	-	2.0	Up	-	-	-	-
M400003151	M400003151	-	1.9	Up	2.0	Up	-	-	-	-

XM_355777	gene model 1067, (NCBI)	-	-	-	2.0	Up	-	-	-	-
M400012719	M400012719	-	-	-	2.0	Up	-	-	-	-
	Minichromosome maintenance deficient 3 (S. cerevisiae)	Mcm3	-	-	2.0	Up	-	-	-	-
NM_008563	Embigin	Emb	-	-	2.0	Up	-	-	-	-
M400008404	M400008404	-	-	-	2.0	Up	-	-	-	-
M400004907	M400004907	-	-	-	2.0	Down	-	-	-	-
NM_009797	Capping protein (actin filament) muscle Z-line, alpha 1	Capza1	-	-	2.0	Up	-	-	-	-
XM_485269	M400004754	-	-	-	2.0	Up	-	-	-	-
NM_017375	Osteoclast stimulating factor 1	Ostf1	-	-	2.1	Up	-	-	-	-
XM_355858	RIKEN cDNA 2310014L17 gene	-	-	1.9	Down	2.1	Down	-	-	-
M200003942	M200003942	-	-	-	2.1	Up	-	-	-	-
	Dolichyl-phosphate (UDP-N-acetylglucosamine) acetylglucosaminophosphotransferase 1 (GlcNAc-1-P transferase)	Dpagt1	-	-	2.1	Up	-	-	-	-
NM_007875	Golgi reassembly stacking protein 2	Gorasp2	-	-	2.1	Up	-	-	-	-
NM_009321	Tubulin cofactor a	Tbca	-	-	2.1	Up	-	-	-	-
M400012954	M400012954	-	-	-	2.1	Up	-	-	-	-
M400010274	M400010274	-	-	-	2.1	Up	-	-	-	-
NM_145434	Nuclear receptor subfamily 1, group D, member 1	Nr1d1	-	-	2.1	Up	-	-	-	-
XM_132633	M400010432	-	-	-	2.1	Up	-	-	-	-
	RIKEN cDNA D930005D10 gene	D930005D10 Rik	-	-	2.1	Up	-	-	-	-
NM_178702	950	Rab3ip	-	-	2.1	Up	-	-	-	-
NM_001003	RAB3A interacting protein	Rab3ip	-	-	2.1	Up	-	-	-	-
NM_011343	SEC61, gamma subunit	Sec61g	-	-	2.1	Up	-	-	-	-
NM_146378	Olfactory receptor 794	Olf794	-	-	2.1	Down	-	-	-	-
NM_025527	Signal recognition particle 19	Srp19	-	1.5	Up	2.1	Up	-	-	-
NM_025338	Aurora kinase A interacting protein 1	Aurkaip1	-	-	2.1	Up	-	-	-	-
NM_019566	Ras homolog gene family, member G	Rhog	-	1.7	Up	2.1	Up	-	-	-
NM_130860	Cyclin-dependent kinase 9 (CDC2-related kinase)	Cdk9	-	-	2.2	Up	-	-	-	-
NM_022993	Low-density lipoprotein receptor-related protein 10	Lrp10	-	-	2.2	Up	-	-	-	-
M400008768	M400008768	-	-	-	2.2	Up	-	-	-	-
NM_023134	Surfactant associated protein A1	Sftpa1	-	2.2	Up	2.2	Up	-	-	-
NM_183086	Mitochondrial ribosomal protein S10	Mrps10	-	-	2.2	Up	-	-	-	-
M300005151	M300005151	-	-	-	2.3	Up	-	-	-	-
XM_356077	M200014508	-	-	-	2.3	Up	-	-	-	-
	Methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahydrofolate cyclohydrolase,	Mthfd1	-	-	2.3	Up	-	-	-	-
NM_138745	formyltetrahydrofolate sy	Mthfd1	-	-	2.3	Up	-	-	-	-
XM_486685	M400003640	-	-	-	2.3	Up	-	-	-	-
XM_135707,										
XM_485815	M400003210	-	-	-	2.3	Down	-	-	-	-
NM_010676	Keratin associated protein 8-2	Krtap8-2	-	-	2.3	Down	-	-	-	-
M400010282	M400010282	-	-	-	2.3	Up	-	-	-	-

M400000391	M400000391	-	-	-	2.3	Up	-	-	-	-
NM_020266,										
NM_178055	M200008553	-	-	-	2.4	Up	-	-	-	-
NM_010550	Interleukin 11 receptor, alpha chain 2	Il11ra2	-	-	2.4	Up	-	-	-	-
M400008351	M400008351	-	-	-	2.4	Up	-	-	-	-
NM_029498	Zinc finger, MYM-type 2	Zmym2	-	-	2.4	Down	-	-	-	-
M400001952	M400001952	-	-	-	2.4	Up	-	-	-	-
NM_146571	Olfactory receptor 1015	Olfr1015	-	-	2.4	Down	-	-	-	-
M400013585	M400013585	-	-	-	2.4	Up	-	-	-	-
NM_010394	Histocompatibility 2, Q region locus 7	H2-Q7	-	-	2.4	Up	-	-	-	-
M400008166	M400008166	-	-	-	2.6	Up	-	-	-	-
NM_175416	RIKEN cDNA C030007109 gene	-	-	-	2.6	Up	-	-	-	-
M400005291	M400005291	-	-	-	2.6	Up	-	-	-	-
M400009196	M400009196	-	-	-	2.6	Up	-	-	-	-
M400003166	M400003166	-	-	-	2.6	Up	-	-	-	-
	Heat shock protein 90kDa alpha (cytosolic), class B member 1	Hsp90ab1	-	-	2.6	Up	-	-	-	-
NM_008302										
M400010585	M400010585	-	3.9	Up	2.7	Up	-	-	-	-
	Nudix (nucleoside diphosphate linked moiety X)-type motif 8	Nudt8	-	-	2.7	Up	-	-	-	-
NM_025529										
	Signal peptidase complex subunit 1 homolog (S. cerevisiae)	Spcs1	-	-	2.7	Up	-	-	-	-
NM_026911										
	Solute carrier family 6 (neurotransmitter transporter, taurine), member 6	Slc6a6	-	-	2.7	Up	-	-	-	-
NM_009320										
	RIKEN cDNA 2310056P07 gene	2310056P07	-	-	2.7	Up	-	-	-	-
NM_027342										
	RIKEN cDNA 1810027O10 gene	Rik	-	-	2.7	Up	-	-	-	-
XM_109683										
	H19 fetal liver mRNA	-	1.9	Up	2.8	Up	-	-	-	-
NR_001592										
	Proline synthetase co-transcribed	Prosc	-	-	2.8	Up	-	-	-	-
NM_054057										
	M400004588	-	-	-	2.9	Up	-	-	-	-
M400004588										
	M400004770	-	-	-	2.9	Up	-	-	-	-
M400004770										
	M400008608	-	-	-	3.0	Up	-	-	-	-
XM_125178										
	myosin XVI	-	-	-	3.1	Down	-	-	-	-
XM_356059										
	Ribosomal protein L7a	Rpl7a	-	-	3.2	Up	-	-	-	-
NM_013721										
	Small glutamine-rich tetratricopeptide repeat (TPR)-containing, beta	Sgtb	-	-	3.2	Up	-	-	-	-
NM_144838										
	Inhibitor of DNA binding 3	Id3	-	-	3.2	Up	-	-	-	-
NM_008321										
	CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated)	Cd74	-	-	3.5	Up	-	-	-	-
NM_010545										
	M400004366	-	-	-	3.5	Up	-	-	-	-
M400004366										
	Lectin, galactose binding, soluble 9	Lgals9	-	-	3.6	Up	-	-	-	-
NM_010708										
	Nuclear factor I/X	Nfix	-	-	3.7	Up	-	-	-	-
NM_010906										
	M400010174	-	3.1	Up	3.8	Up	-	-	-	-
M400010174										
	predicted gene, OTTMUSG00000004481	-	-	-	4.1	Up	-	-	-	-
XM_485358										
	Integral membrane protein 2C	Itm2c	-	-	4.1	Up	-	-	-	-
NM_022417										

M400009721	M400009721	-	-	-	4.2	Up	-	-	-	-
NM_009696	Apolipoprotein E	ApoE	3.1	Up	4.3	Up	-	-	-	-
M400001135	M400001135	-	-	-	-	-	-	-	-	-
M400001650	M400001650	-	1.5	Up	-	-	-	-	-	-
M400003747	M400003747	-	1.5	Up	-	-	-	-	-	-
		2700062C07								
NM_026529	RIKEN cDNA 2700062C07 gene	Rik	1.5	Up	-	-	-	-	-	-
XM_130308	low density lipoprotein receptor-related protein 2	-	1.5	Up	-	-	-	-	-	-
M400002073	M400002073	-	1.5	Up	-	-	-	-	-	-
NM_008350	Interleukin 11	Il11	1.5	Up	-	-	-	-	-	-
NM_207239	General transcription factor III C 1	Gtf3c1	1.5	Up	-	-	-	-	-	-
M400018110	M400018110	-	1.5	Up	-	-	-	-	-	-
M400014367	M400014367	-	1.5	Up	-	-	-	-	-	-
NM_172122	Ciliary rootlet coiled-coil, rootletin	Crocc	1.5	Up	-	-	-	-	-	-
M400017352	M400017352	-	1.5	Up	-	-	-	-	-	-
NM_023277	Junction adhesion molecule 3	Jam3	1.5	Up	-	-	-	-	-	-
XM_129740	RIKEN cDNA 4921511C04 gene	-	1.5	Up	-	-	-	-	-	-
M400002211	M400002211	-	1.5	Down	-	-	-	-	-	-
M400008742	M400008742	-	1.5	Up	-	-	-	-	-	-
NM_172429	Survival motor neuron domain containing 1	Smndc1	1.6	Down	-	-	-	-	-	-
M400015370	M400015370	-	1.6	Up	-	-	-	-	-	-
NM_013777,										
NM_013778	M300002624	-	1.6	Down	-	-	-	-	-	-
NM_023493	Camello-like 5	Cml5	1.6	Up	-	-	-	-	-	-
M400009910	M400009910	-	1.6	Up	-	-	-	-	-	-
	Transducin-like enhancer of split 2, homolog of									
NM_019725	Drosophila E(spl)	Tle2	1.6	Up	-	-	-	-	-	-
NM_206869	Vomerolnasal 1 receptor, D16	V1rd16	1.6	Up	-	-	-	-	-	-
NM_013616	Olfactory receptor 65	Olf65	1.6	Up	-	-	-	-	-	-
M400014366	M400014366	-	1.6	Up	-	-	-	-	-	-
M200013290	M200013290	-	1.6	Down	-	-	-	-	-	-
M400005542	M400005542	-	1.6	Down	-	-	-	-	-	-
M400015631	M400015631	-	1.6	Up	-	-	-	-	-	-
	Proteasome (prosome, macropain) subunit, alpha type									
NM_011969	7	Psm7	1.6	Down	-	-	-	-	-	-
NM_028976	Golgi reassembly stacking protein 1	Gorasp1	1.6	Down	-	-	-	-	-	-
NM_010169	Coagulation factor II (thrombin) receptor	F2r	1.6	Up	-	-	-	-	-	-
NM_026325	Transmembrane protein 179B	Tmem179b	1.6	Down	-	-	-	-	-	-
XM_354644	gene model 884, (NCBI)	-	1.6	Up	-	-	-	-	-	-
NM_007417	Adrenergic receptor, alpha 2a	Adra2a	1.6	Down	-	-	-	-	-	-
NM_027450	GLI pathogenesis-related 2	Glpr2	1.6	Down	-	-	-	-	-	-
NM_153788	Centaurin, beta 1	Centb1	1.6	Up	-	-	-	-	-	-
M400015845	M400015845	-	1.6	Up	-	-	-	-	-	-
M400019365	M400019365	-	1.6	Up	-	-	-	-	-	-
M400009552	M400009552	-	1.6	Up	-	-	-	-	-	-

XM_489349,											
XM_489372	M400015885	-	1.6	Up	-	-	-	-	-	-	-
M200008417	M200008417	-	1.6	Up	-	-	-	-	-	-	-
NM_008147	Glycoprotein 49 A	Gp49a	1.6	Down	-	-	-	-	-	-	-
M400016299	M400016299	-	1.6	Up	-	-	-	-	-	-	-
M200011262	M200011262	-	1.6	Down	-	-	-	-	-	-	-
NM_139148	Chloride channel calcium activated 4	Clca4	1.7	Up	-	-	-	-	-	-	-
NM_138748	Protein phosphatase 2A, regulatory subunit B (PR 53)	Ppp2r4	1.7	Up	-	-	-	-	-	-	-
XM_355790	Exocyst complex component 6B	Exoc6b	1.7	Up	-	-	-	-	-	-	-
XM_143622	M400003506	-	1.7	Up	-	-	-	-	-	-	-
NM_001001											
297,NM_177											
588	M300019341	-	1.7	Up	-	-	-	-	-	-	-
M300000346	M300000346	-	1.7	Up	-	-	-	-	-	-	-
NM_021528	Carbohydrate sulfotransferase 12	Chst12	1.7	Up	-	-	-	-	-	-	-
	Dapper homolog 1, antagonist of beta-catenin										
NM_021532	(xenopus)	Dact1	1.7	Up	-	-	-	-	-	-	-
NM_146832	Olfactory receptor 134	Olf134	1.7	Up	-	-	-	-	-	-	-
M400017182	M400017182	-	1.7	Up	-	-	-	-	-	-	-
NM_133199	Sodium channel, voltage-gated, type IV, alpha	Scn4a	1.7	Up	-	-	-	-	-	-	-
	Solute carrier family 2 (facilitated glucose transporter),										
	member 1	Slc2a1	1.7	Up	-	-	-	-	-	-	-
NM_011400	Amine oxidase, copper containing 2 (retina-specific)	Aoc2	1.7	Up	-	-	-	-	-	-	-
NM_178932											
NM_130883	M400007427	-	1.7	Up	-	-	-	-	-	-	-
XM_136108	M300013050	-	1.7	Up	-	-	-	-	-	-	-
M300004664	M300004664	-	1.7	Up	-	-	-	-	-	-	-
M400016857	M400016857	-	1.7	Up	-	-	-	-	-	-	-
M400019232	M400019232	-	1.7	Up	-	-	-	-	-	-	-
NM_177740	RGM domain family, member A	Rgma	1.7	Up	-	-	-	-	-	-	-
M400016147	M400016147	-	1.7	Up	-	-	-	-	-	-	-
M400015065	M400015065	-	1.7	Up	-	-	-	-	-	-	-
M400016838	M400016838	-	1.7	Up	-	-	-	-	-	-	-
NM_010678	AF4/FMR2 family, member 3	Aff3	1.7	Up	-	-	-	-	-	-	-
M300014625	M300014625	-	1.7	Up	-	-	-	-	-	-	-
M300019645	M300019645	-	1.7	Up	-	-	-	-	-	-	-
M400015360	M400015360	-	1.8	Up	-	-	-	-	-	-	-
M300007598	M300007598	-	1.8	Up	-	-	-	-	-	-	-
M400016886	M400016886	-	1.8	Up	-	-	-	-	-	-	-
NM_199032	Centrosomal protein 135	Cep135	1.8	Up	-	-	-	-	-	-	-
NM_025933	HIG1 domain family, member 2A	Higd2a	1.8	Up	-	-	-	-	-	-	-
NM_153798	Polymerase (RNA) II (DNA directed) polypeptide B	Polr2b	1.8	Down	-	-	-	-	-	-	-
M300001943	M300001943	-	1.8	Up	-	-	-	-	-	-	-
NM_177302	RIKEN cDNA B530045E10 gene	-	1.8	Up	-	-	-	-	-	-	-
NM_153568	Leucine rich repeat containing 66	Lrrc66	1.8	Up	-	-	-	-	-	-	-
NM_175149	RIKEN cDNA 2310022B05 gene	2310022B05	1.8	Up	-	-	-	-	-	-	-

M400019333	M400019333	Rik	-	1.8	Up	-	-	-	-	-	-
		1810029B16									
NM_025465	RIKEN cDNA 1810029B16 gene	Rik		1.8	Down	-	-	-	-	-	-
XM_128030	transmembrane 7 superfamily member 4	-		1.8	Up	-	-	-	-	-	-
		1110028C15									
NM_177645	RIKEN cDNA 1110028C15 gene	Rik		1.8	Up	-	-	-	-	-	-
NM_013467	Aldehyde dehydrogenase family 1, subfamily A1	Aldh1a1		1.8	Up	-	-	-	-	-	-
NM_172623	Triggering receptor expressed on myeloid cells-like 4	Trem14		1.8	Down	-	-	-	-	-	-
NM_145506	Erythrocyte protein band 4.1-like 5	Epb4.115		1.9	Up	-	-	-	-	-	-
M400018495	M400018495	-		1.9	Up	-	-	-	-	-	-
XM_354546,											
XM_359256	M300014543	-		1.9	Up	-	-	-	-	-	-
M400012812	M400012812	-		1.9	Up	-	-	-	-	-	-
NM_172535	IQ motif and ubiquitin domain containing	Iqub		1.9	Up	-	-	-	-	-	-
NM_016928	Toll-like receptor 5	Tlr5		1.9	Up	-	-	-	-	-	-
NM_177056	Transmembrane protein 198	Tmem198		1.9	Up	-	-	-	-	-	-
	Sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B										
NM_013662	Protein phosphatase 1, regulatory (inhibitor) subunit 14A	Sema6b		1.9	Up	-	-	-	-	-	-
NM_026731	Phospholipase A2, group III	Ppp1r14a		1.9	Up	-	-	-	-	-	-
NM_172791	M400013199	Pla2g3		1.9	Up	-	-	-	-	-	-
M400013199	M400013199	-		1.9	Up	-	-	-	-	-	-
NM_023850	Carbohydrate (keratan sulfate Gal-6) sulfotransferase 1	Chst1		1.9	Up	-	-	-	-	-	-
NM_153787	BCL2-associated transcription factor 1	Bclaf1		1.9	Up	-	-	-	-	-	-
M400002344	M400002344	-		1.9	Up	-	-	-	-	-	-
M300004372	M300004372	-		1.9	Up	-	-	-	-	-	-
NM_134012	Mbt domain containing 1	Mbtd1		2.0	Up	-	-	-	-	-	-
M400000577	M400000577	-		2.0	Up	-	-	-	-	-	-
M400005095	M400005095	-		2.0	Up	-	-	-	-	-	-
M200008055	M200008055	-		2.0	Up	-	-	-	-	-	-
M400008518	M400008518	-		2.0	Up	-	-	-	-	-	-
M400018258	M400018258	-		2.0	Up	-	-	-	-	-	-
	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide										
NM_018871	Solute carrier family 6 (neurotransmitter transporter, glycine), member 9	Ywhag		2.0	Up	-	-	-	-	-	-
NM_008135	SEBOX homeobox	Slc6a9		2.0	Up	-	-	-	-	-	-
NM_008759	M400018969	Sebox		2.0	Up	-	-	-	-	-	-
M400018969	M400018969	-		2.0	Up	-	-	-	-	-	-
NM_007392,											
NM_183274	M300010088	-		2.0	Up	-	-	-	-	-	-
M400008735	M400008735	-		2.0	Up	-	-	-	-	-	-
M400004623	M400004623	-		2.0	Up	-	-	-	-	-	-
NM_026892	Eukaryotic translation initiation factor 1B	Eif1b		2.0	Down	-	-	-	-	-	-
XM_145945	ubiquitin specific peptidase 35	-		2.0	Up	-	-	-	-	-	-

M400012787	M400012787	-	2.1	Down	-	-	-	-	-	-
M200005725	M200005725	-	2.1	Up	-	-	-	-	-	-
M400017435	M400017435	-	2.1	Up	-	-	-	-	-	-
M400015620	M400015620	-	2.1	Up	-	-	-	-	-	-
NM_008329	Interferon activated gene 204	Ifi204	2.1	Down	-	-	-	-	-	-
NM_008356	Interleukin 13 receptor, alpha 2	Il13ra2	2.1	Up	-	-	-	-	-	-
XM_142043	gene model 377, (NCBI)	-	2.1	Up	-	-	-	-	-	-
NM_026602	Breast carcinoma amplified sequence 2	Bcas2	2.1	Down	-	-	-	-	-	-
NM_133758	Ubiquitin specific peptidase 47	Usp47	2.1	Down	-	-	-	-	-	-
XM_140041	cDNA sequence BC032203	-	2.1	Up	-	-	-	-	-	-
M400002494	M400002494	-	2.2	Up	-	-	-	-	-	-
NM_134216	Vomeronasal 1 receptor, H7	V1rh7	2.2	Up	-	-	-	-	-	-
M400019145	M400019145	-	2.2	Up	-	-	-	-	-	-
M400004316	M400004316	-	2.2	Up	-	-	-	-	-	-
NM_176917	Methyltransferase like 4	Mettl4	2.2	Up	-	-	-	-	-	-
NM_010513	Insulin-like growth factor I receptor	Igf1r	2.2	Up	-	-	-	-	-	-
NM_009121	Spermidine/spermine N1-acetyl transferase 1	Sat1	2.2	Down	-	-	-	-	-	-
NM_153505	NCK associated protein 1 like	Nckap1	2.2	Down	-	-	-	-	-	-
NM_145365	CAMP responsive element binding protein 3-like 3	Creb3l3	2.2	Up	-	-	-	-	-	-
M400009372	M400009372	-	2.2	Down	-	-	-	-	-	-
M400016344	M400016344	-	2.3	Up	-	-	-	-	-	-
M400003406	M400003406	-	2.3	Up	-	-	-	-	-	-
M400014084	M400014084	-	2.3	Up	-	-	-	-	-	-
M400018943	M400018943	-	2.3	Up	-	-	-	-	-	-
NM_198710	Synaptophysin-like protein	Sypl	2.3	Down	-	-	-	-	-	-
M400015075	M400015075	-	2.3	Up	-	-	-	-	-	-
NM_175229	Serine/arginine repetitive matrix 2	Srrm2	2.3	Up	-	-	-	-	-	-
M400005812	M400005812	-	2.3	Up	-	-	-	-	-	-
M400019502	M400019502	-	2.4	Up	-	-	-	-	-	-
NM_172929	RIKEN cDNA 2210418O10 gene	-	2.4	Up	-	-	-	-	-	-
NM_019985	C-type lectin domain family 1, member b	Clec1b	2.4	Down	-	-	-	-	-	-
NM_019740	Forkhead box O3a	Foxo3a	2.4	Up	-	-	-	-	-	-
M400018255	M400018255	-	2.4	Up	-	-	-	-	-	-
M400019155	M400019155	-	2.4	Up	-	-	-	-	-	-
M400019461	M400019461	-	2.4	Up	-	-	-	-	-	-
		1700021K02								
NM_023064	RIKEN cDNA 1700021K02 gene	Rik	2.5	Up	-	-	-	-	-	-
NM_033525	Nephronectin	Npnt	2.5	Up	-	-	-	-	-	-
NM_028134,										
NM_153121	M400004580	-	2.5	Up	-	-	-	-	-	-
M400003086	M400003086	-	2.5	Up	-	-	-	-	-	-
M400005128	M400005128	-	2.5	Up	-	-	-	-	-	-
XM_484543	predicted gene, EG433016	-	2.5	Down	-	-	-	-	-	-
NM_146277	Olfactory receptor 1412	Olfr1412	2.5	Up	-	-	-	-	-	-
XM_485426	Predicted gene, OTTMUSG00000009006	OTTMUSG0	2.6	Down	-	-	-	-	-	-

		000009006										
NM_018814	Pecanex homolog (Drosophila)	Pcnx	2.6	Down	-	-	-	-	-	-	-	-
NM_019497	G protein-coupled receptor kinase 4	Grk4	2.6	Up	-	-	-	-	-	-	-	-
NM_008968	Prostaglandin I2 (prostacyclin) synthase	Ptgis	2.6	Up	-	-	-	-	-	-	-	-
NM_009067	RalA binding protein 1	Ralbp1	2.6	Down	-	-	-	-	-	-	-	-
	Engulfment and cell motility 3, ced-12 homolog (C. elegans)	Elmo3	2.6	Up	-	-	-	-	-	-	-	-
NM_172760	ring finger protein 7	-	2.6	Down	-	-	-	-	-	-	-	-
XM_135065												
NM_147153,												
NM_178851	M300005568	-	2.7	Up	-	-	-	-	-	-	-	-
NM_009442	Transcription termination factor 1	Ttf1	2.8	Down	-	-	-	-	-	-	-	-
M400001355	M400001355	-	2.8	Down	-	-	-	-	-	-	-	-
NM_172705	PHD finger protein 13	Phf13	2.8	Up	-	-	-	-	-	-	-	-
	G protein-coupled receptor, family C, group 5, member D	Gprc5d	2.8	Up	-	-	-	-	-	-	-	-
NM_053118												
M300013623	M300013623	-	2.8	Down	-	-	-	-	-	-	-	-
M400015950	M400015950	-	2.9	Up	-	-	-	-	-	-	-	-
NM_207545	Vomer nasal 1 receptor, D17	V1rd17	2.9	Up	-	-	-	-	-	-	-	-
M400015264	M400015264	-	2.9	Up	-	-	-	-	-	-	-	-
M400017869	M400017869	-	3.0	Up	-	-	-	-	-	-	-	-
NM_177639	Discs, large (Drosophila) homolog-associated protein 1	Dlgap1	3.0	Down	-	-	-	-	-	-	-	-
M400018450	M400018450	-	3.0	Up	-	-	-	-	-	-	-	-
NM_153122	5-oxoprolinase (ATP-hydrolysing)	Oplah	3.1	Up	-	-	-	-	-	-	-	-
M400007248	M400007248	-	3.2	Up	-	-	-	-	-	-	-	-
M400015752	M400015752	-	3.2	Up	-	-	-	-	-	-	-	-
M2NC00000												
1	M2NC000001	-	3.3	Up	-	-	-	-	-	-	-	-
M400000614	M400000614	-	3.5	Down	-	-	-	-	-	-	-	-
NM_008835	per-hexamer repeat gene 4	-	3.5	Up	-	-	-	-	-	-	-	-
M400019039	M400019039	-	3.6	Up	-	-	-	-	-	-	-	-
M400016839	M400016839	-	3.6	Up	-	-	-	-	-	-	-	-
M400017932	M400017932	-	3.6	Up	-	-	-	-	-	-	-	-
NM_009343	PHD finger protein 1	Phf1	3.7	Up	-	-	-	-	-	-	-	-
M400010483	M400010483	-	3.8	Down	-	-	-	-	-	-	-	-
M400018915	M400018915	-	3.8	Down	-	-	-	-	-	-	-	-
NM_146203	Zinc finger protein 764	Zfp764	3.9	Up	-	-	-	-	-	-	-	-
M2NC00000												
1	M2NC000001	-	3.9	Up	-	-	-	-	-	-	-	-
M400002142	M400002142	-	3.9	Up	-	-	-	-	-	-	-	-
NM_177362	Zinc finger protein 771	Zfp771	4.0	Down	-	-	-	-	-	-	-	-
	Gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 6	Gabra6	4.1	Up	-	-	-	-	-	-	-	-
NM_008068												
NM_011171	Protein C receptor, endothelial	Procr	4.1	Down	-	-	-	-	-	-	-	-
NM_178929	Kazal-type serine peptidase inhibitor domain 1	Kazald1	4.2	Down	-	-	-	-	-	-	-	-
M400014473	M400014473	-	4.3	Up	-	-	-	-	-	-	-	-



NM_028870	Clathrin, light polypeptide (Lcb)	Cltb	4.3	Down	-	-	-	-	-	-
<b>Other ID</b>	<b>Gene Name</b>	<b>Gene ID</b>	<b>12</b>	<b>Direction</b>	<b>24</b>	<b>Direction</b>	<b>48</b>	<b>Direction</b>	<b>120</b>	<b>Direction</b>
M400003830	M400003830	-	-	-	-	-	1.6	Up	-	-
NM_023538	Acylglycerol kinase	Agk	-	-	-	-	1.6	Up	-	-
NM_199009	RIKEN cDNA 4632419K20 gene	4632419K20	-	-	-	-	-	-	-	-
NM_026407	Transmembrane protein 39a	Rik	-	-	1.6	Down	-	-	-	-
NM_178598	Transgelin 2	Tmem39a	-	-	3.0	Down	-	-	-	-
NM_001005	Smg-7 homolog, nonsense mediated mRNA decay factor (C. elegans)	Tagln2	-	-	-	-	1.5	Down	-	-
XM_138906	NIMA (never in mitosis gene a)- related kinase 10	Smg7	-	-	1.7	Down	-	-	-	-
XM_355325	PR domain containing 12	-	-	-	1.8	Down	-	-	-	-
M400017999	M400017999	-	-	-	2.0	Down	-	-	-	-
M200012728	M200012728	-	-	-	2.4	Down	-	-	-	-
XM_284024	tRNA selenocysteine associated protein 1	-	-	-	1.6	Down	-	-	-	-
NM_027304	H1 histone family, member N, testis-specific	-	-	-	1.8	Up	-	-	-	-
NM_175538	RIKEN cDNA E130304F04 gene	H1fnt	-	-	-	-	1.7	Up	-	-
NM_153133	Retinol dehydrogenase 9	E130304F04	-	-	-	-	-	-	-	-
NM_025874	RIKEN cDNA 2310076L09 gene	Rik	-	-	1.7	Down	-	-	-	-
NM_011260	Regenerating islet-derived 3 gamma	Rdh9	-	-	1.5	Down	-	-	-	-
NM_172424	Mediator complex subunit 13-like	2310076L09	-	-	-	-	-	-	-	-
M400006071	M400006071	Rik	-	-	-	-	1.8	Up	-	-
M400004205	M400004205	Reg3g	2.1	Up	-	-	-	-	-	-
M400007608	M400007608	Med13l	-	-	-	-	1.8	Up	-	-
NM_009235	SRY-box containing gene 15	-	-	-	-	-	1.7	Up	-	-
XM_355166	Coiled-coil domain containing 147	-	-	-	-	-	2.0	Up	-	-
NM_172612	Rho family GTPase 1	-	-	-	3.4	Down	-	-	-	-
M400006461	M400006461	Sox15	-	-	-	-	-	-	1.5	Up
NM_016908	Synaptotagmin V	Ccdc147	-	-	-	-	-	-	1.5	Down
NM_010727	Ligand of numb-protein X 1	Rnd1	-	-	-	-	-	-	1.5	Down
XM_204668	growth arrest-specific 2 like 2	-	-	-	-	-	-	-	1.5	Down
NM_145559	Solute carrier family 2 (facilitated glucose transporter), member 9	Syt5	-	-	-	-	-	-	1.5	Up
NM_009244	Serine (or cysteine) preptidase inhibitor, clade A, member 1b	Lnx1	-	-	-	-	-	-	1.5	Down
NM_008579	Meiosis expressed gene 1	-	-	-	-	-	-	-	1.5	Up
NM_008584	Mesenchyme homeobox 2	Slc2a9	-	-	-	-	-	-	1.5	Down
M400000478	M400000478	Serpina1b	-	-	-	-	-	-	1.5	Down
NM_028887	SMC hinge domain containing 1	Meig1	-	-	-	-	-	-	1.5	Down
NM_010750	Mab-21-like 1 (C. elegans)	Meox2	-	-	-	-	-	-	1.5	Down
M400009301	M400009301	-	-	-	-	-	-	-	1.5	Down
		Smchd1	-	-	-	-	-	-	1.5	Up
		Mab2111	-	-	-	-	-	-	1.5	Down
		-	-	-	-	-	-	-	1.5	Down

NM_175665	Histone cluster 1, H2bk	Hist1h2bk	-	-	-	-	-	-	1.5	Down
M400009033	M400009033	-	-	-	1.9	Down	-	-	1.5	Down
NM_013739	Docking protein 3	Dok3	-	-	-	-	-	-	1.5	Up
M400013646	M400013646	-	-	-	-	-	-	-	1.5	Down
M400017464	M400017464	-	-	-	-	-	-	-	1.5	Down
NM_008662	myosin VI	-	-	-	-	-	-	-	1.5	Down
NM_010738	Lymphocyte antigen 6 complex, locus A	Ly6a	-	-	-	-	-	-	1.5	Up
		1110020A21								
XM_148821	RIKEN cDNA 1110020A21 gene	Rik	-	-	-	-	-	-	1.5	Up
NM_177591,										
NM_183336	M300007562	-	-	-	-	-	-	-	1.5	Up
NM_145147	GTP binding protein 6 (putative)	Gtpbp6	-	-	-	-	-	-	1.5	Up
NM_145355	Ring finger protein 185	Rnf185	-	-	-	-	1.6	Up	1.5	Up
	UTP20, small subunit (SSU) processome component, homolog (yeast)	Utp20	-	-	-	-	-	-	1.5	Down
XM_125867	transcription elongation regulator 1 (CA150)	-	-	-	-	-	-	-	1.5	Down
NM_019512	Villin 1	Vil1	-	-	-	-	-	-	1.6	Down
NM_009509	olfactomedin 4	-	-	-	-	-	1.5	Up	1.6	Up
XM_354831	M300001802	-	-	-	-	-	-	-	1.6	Up
M300001802	M300001802	-	-	-	-	-	-	-	1.6	Up
M400007957	M400007957	-	-	-	-	-	-	-	1.6	Down
NM_053008	Oligodendrocyte transcription factor 3	Olig3	-	-	-	-	-	-	1.6	Up
		4931428L18								
NM_027637	RIKEN cDNA 4931428L18 gene	Rik	-	-	-	-	-	-	1.6	Up
M400009113	M400009113	-	-	-	-	-	-	-	1.6	Up
XM_484254	M400002775	-	-	-	-	-	-	-	1.6	Down
XM_355364	RIKEN cDNA 1700126L10 gene	-	-	-	2.0	Down	-	-	1.6	Down
M200013616	M200013616	-	-	-	-	-	-	-	1.6	Up
M400017952	M400017952	-	-	-	-	-	-	-	1.6	Down
NM_010459	Homeo box B4	Hoxb4	-	-	-	-	-	-	1.6	Down
NM_144510	inhibitor of growth family, member 4	-	-	-	-	-	-	-	1.6	Up
NM_027373	Actin filament associated protein 1	Afap1	-	-	-	-	-	-	1.6	Up
NM_029494	RAB30, member RAS oncogene family	Rab30	-	-	-	-	-	-	1.6	Down
	Guanine nucleotide binding protein (G protein), gamma 4	Gng4	-	-	-	-	-	-	1.6	Down
NM_010317	Guanosine monophosphate reductase	Gmpr	-	-	-	-	-	-	1.6	Down
NM_025508	Excision repair cross-complementing rodent repair deficiency complementation group 6 - like	Ercc6l	-	-	-	-	-	-	1.6	Up
NM_146235	Bone morphogenetic protein 3	Bmp3	-	-	-	-	-	-	1.6	Down
NM_173404	Glucagon-like peptide 2 receptor	Glp2r	-	-	-	-	-	-	1.6	Down
NM_175681	Glycosyltransferase 8 domain containing 4	Glt8d4	-	-	-	-	-	-	1.6	Down
NM_198612	ATPase, H+ transporting, lysosomal V1 subunit A	Atp6v1a	-	-	-	-	-	-	1.6	Down
NM_007508	M400012544	-	-	-	-	-	-	-	1.6	Down
NM_183219	Dynein, axonemal, heavy chain 3	Dnahc3	-	-	-	-	-	-	1.6	Up
XM_355934	Adenosine deaminase	Ada	-	-	-	-	-	-	1.6	Up
NM_007398	Neuron navigator 2	Nav2	-	-	-	-	-	-	1.6	Up
NM_175272										

XM_134514	ankyrin repeat domain 11 Leucine rich repeat and fibronectin type III domain containing 5	-	-	-	-	-	-	-	1.6	Down
NM_178714		Lrnf5	-	-	-	-	-	-	1.6	Up
XM_132178	UDP glucuronosyltransferase 2 family, polypeptide B36	-	-	-	-	-	-	-	1.6	Up
M400017643	M400017643	-	-	-	-	-	-	-	1.6	Down
NM_026538	DEAD (Asp-Glu-Ala-Asp) box polypeptide 56	Ddx56	-	-	-	-	-	-	1.6	Down
NM_019938	Polyamine modulated factor 1 binding protein 1	Pmfbp1	-	-	-	-	-	1.6	Up	Up
M300007087	M300007087	-	-	-	-	-	-	-	1.6	Up
M400008183	M400008183	-	-	-	-	-	-	-	1.6	Down
	Origin recognition complex, subunit 3-like (S. cerevisiae)	Orc3l	-	-	-	-	-	-	1.6	Down
NM_015824		Snopc2	-	-	-	-	-	-	1.6	Down
NM_133968	Small nuclear RNA activating complex, polypeptide 2									
NM_145963,										
XM_484830	M200015241	-	-	-	-	-	-	-	1.6	Up
NM_177613	Cell division cycle 34 homolog (S. cerevisiae)	Cdc34	-	-	-	-	-	-	1.6	Down
NM_021565	Midnolin	Midn	-	-	-	-	-	-	1.6	Down
NM_001004										
190	Zinc finger protein 560	Zfp560	-	-	-	-	-	-	1.6	Down
NM_018807	Pleiomorphic adenoma gene-like 2	Plagl2	-	-	-	-	-	-	1.6	Up
	Endoplasmic reticulum chaperone SIL1 homolog (S. cerevisiae)	Sil1	-	-	-	-	-	-	1.6	Down
NM_030749										
XM_109767	clathrin interactor 1	-	-	-	-	-	-	-	1.6	Up
NM_009660	Arachidonate 15-lipoxygenase	Alox15	-	-	-	-	-	-	1.6	Up
XM_132261	phosphoglycerate mutase family member 5	-	-	-	-	-	-	-	1.6	Down
M400010303	M400010303	-	-	-	-	-	-	2.1	Up	Up
XM_134467	RIKEN cDNA 1700030J22 gene	-	-	-	-	-	-	-	1.6	Up
NM_008221	Hemoglobin Y, beta-like embryonic chain	Hbb-y 3322402L07	-	-	-	-	-	-	1.6	Up
NM_023727	RIKEN cDNA 3322402L07 gene	Rik	-	-	-	-	-	-	1.6	Down
NM_178202	Histone cluster 1, H2bp	Hist1h2bp	-	-	-	-	-	-	1.6	Down
	glutaminyl-peptide cyclotransferase (glutaminyl cyclase)	-	-	-	-	-	-	-	1.6	Down
XM_128770										
NM_133925	RNA binding motif protein 28	Rbm28	-	-	-	1.5	Down	-	1.6	Down
NM_023386	Receptor transporter protein 4	Rtp4	-	-	-	-	-	-	1.6	Up
M400006667	M400006667	-	-	-	-	-	-	-	1.6	Down
NM_011562	Teratocarcinoma-derived growth factor	Tdgf1	-	-	-	-	-	-	1.6	Down
	Protein phosphatase 2, regulatory subunit B (B56), epsilon isoform	Ppp2r5e	-	-	-	-	-	-	1.6	Down
NM_012024										
	Solute carrier family 27 (fatty acid transporter), member 1	Slc27a1	-	-	-	-	-	-	1.6	Up
NM_011977										
M400000541	M400000541	-	-	-	-	-	-	-	1.6	Down
M400000791	M400000791	-	-	-	-	-	-	-	1.6	Down
	src homology 2 domain-containing transforming protein C2	-	-	-	-	-	-	-	1.6	Up
XM_125779										
NM_020032	Polymerase (DNA directed), lambda	Poll	-	-	-	-	-	-	1.6	Down

M400007658	M400007658	-	-	-	-	-	-	-	1.7	Up
NM_001005419	2-aminoethanethiol (cysteamine) dioxygenase	Ado	-	-	-	-	-	-	1.7	Down
NM_010829	MutS homolog 3 (E. coli)	Msh3	-	-	-	-	-	-	1.7	Down
NM_011310	S100 calcium binding protein A3	S100a3	-	-	-	-	-	-	1.7	Up
NM_013679	Seminal vesicle secretory protein 6	Svs6	-	-	-	-	-	-	1.7	Up
M400005979	M400005979	-	-	-	-	-	-	-	1.7	Up
NM_013759	Selenoprotein X 1	Sepx1	-	-	-	-	-	-	1.7	Up
NM_130857	Keratin associated protein 16-5	Krtap16-5	-	-	-	-	-	-	1.7	Down
NM_033174	Small nuclear ribonucleoprotein N	Snrpn	-	-	-	-	-	-	1.7	Down
NM_172270	protein kinase C binding protein 1	-	-	-	-	-	1.5	Down	1.7	Down
M400014959	M400014959	-	-	-	-	-	-	-	1.7	Down
NM_008176	Chemokine (C-X-C motif) ligand 1	Cxcl1	-	-	-	-	-	-	1.7	Up
NM_027275	Pentatricopeptide repeat domain 3	Ptcd3	-	-	-	-	-	-	1.7	Down
M300007812	M300007812	-	-	-	-	-	-	-	1.7	Down
NM_001005232	Developing brain homeobox 1	Dbx1	-	-	-	-	-	-	1.7	Down
NM_009490	Vomerolnasal 2, receptor 30	Vmn2r30	-	-	-	-	-	-	1.7	Down
NM_146809	Olfactory receptor 1426	Olfr1426	-	-	-	-	-	-	1.7	Down
M400008629	M400008629	-	-	-	-	-	-	-	1.7	Up
M400009558	M400009558	-	-	-	-	-	-	-	1.7	Up
NM_008376, NM_175860	M300015854	-	-	-	-	-	-	-	1.7	Down
NM_010775	Mannose binding lectin (A)	Mbl1	-	-	-	-	-	-	1.7	Up
NM_026367	G patch domain containing 2	Gpatch2	-	-	-	-	-	-	1.7	Up
NM_146588	Olfactory receptor 1030	Olfr1030	-	-	-	-	-	-	1.7	Down
NM_176992	RIKEN cDNA A730020M07 gene	-	-	-	-	-	-	-	1.7	Up
XM_139761	M400001866	-	-	-	-	-	-	-	1.7	Down
NM_009776	Serine (or cysteine) peptidase inhibitor, clade G, member 1	Serping1	-	-	-	-	-	-	1.7	Up
M400009882	M400009882	-	-	-	-	-	-	-	1.7	Down
M400010594	M400010594	-	-	-	-	-	-	-	1.7	Down
NM_144885	CDNA sequence BC005624	BC005624	-	-	-	-	-	-	1.7	Up
M400017071	M400017071	-	-	-	-	-	-	-	1.7	Up
NM_025912	RIKEN cDNA 2010011I20 gene	2010011I20 Rik	-	-	-	-	-	-	1.7	Down
NM_009256	Serine (or cysteine) peptidase inhibitor, clade B, member 9	Serpib9	-	-	-	-	-	-	1.7	Up
NM_146193	BTB (POZ) domain containing 1	Btbd1	-	-	-	-	-	-	1.7	Down
NM_011632	Tnf receptor-associated factor 3	Traf3	-	-	-	-	-	-	1.7	Up
NM_018805	Heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1	Hs3st3b1	-	-	-	-	-	-	1.7	Up
NM_178384	Zinc finger protein 74	Zfp74	-	-	-	-	-	-	1.7	Up
M300020890	M300020890	-	-	-	-	-	-	-	1.7	Up
NM_147092	Olfactory receptor 561	Olfr561	-	-	-	-	-	-	1.7	Up

M400008754	M400008754	-	-	-	-	-	-	-	-	1.7	Down
NM_010739	Mucin 13, epithelial transmembrane	Muc13	-	-	-	-	-	-	-	1.7	Up
NM_181416	Rho GTPase activating protein 11A	Arhgap11a	-	-	2.0	Down	-	-	-	1.7	Down
		C920005C14									
NM_177391	RIKEN cDNA C920005C14 gene	Rik	-	-	-	-	-	-	-	1.7	Up
NM_010914	Nuclear transcription factor-Y beta	Nfyb	-	-	-	-	-	-	-	1.7	Down
XM_203344	keratin 28	-	-	-	-	-	-	-	-	1.7	Down
NM_199060	CDNA sequence AF067061	AF067061	-	-	-	-	-	-	-	1.7	Up
NM_023336	Bromodomain containing 3	Brd3	-	-	-	-	-	-	-	1.7	Down
XM_130491	bromo adjacent homology domain containing 1	-	-	-	-	-	-	-	-	1.7	Down
M400005519	M400005519	-	-	-	-	-	-	-	-	1.7	Down
		0610007P14									
NM_021446	RIKEN cDNA 0610007P14 gene	Rik	-	-	2.8	Down	2.8	Up	-	1.7	Up
M400014221	M400014221	-	-	-	-	-	-	-	-	1.7	Down
M400016058	M400016058	-	-	-	-	-	-	-	-	1.7	Down
NM_011796	Calpain 10	Capn10	-	-	-	-	-	-	-	1.7	Down
	SPC24, NDC80 kinetochore complex component,										
NM_026282	homolog (S. cerevisiae)	Spc24	-	-	-	-	-	-	-	1.7	Down
M400007958	M400007958	-	-	-	-	-	-	-	-	1.7	Down
M400004678	M400004678	-	-	-	-	-	-	-	-	1.7	Down
M400017950	M400017950	-	-	-	-	-	-	-	-	1.7	Down
NM_001005											
523,NM_001											
005525,NM_											
025438,XM_											
485682	M400009378	-	-	-	-	-	-	-	-	1.7	Down
XM_145500	M400000476	-	-	-	-	-	-	-	-	1.7	Down
M400005937	M400005937	-	-	-	-	-	-	-	-	1.7	Down
NM_146106	Lysophospholipase-like 1	Lyplal1	-	-	-	-	-	-	-	1.7	Down
	Retinoic acid receptor responder (tazarotene induced)										
NM_027852	2	Rarres2	-	-	-	-	-	-	-	1.7	Up
	Solute carrier family 2 (facilitated glucose transporter),										
NM_172659	member 6	Slc2a6	-	-	-	-	-	-	-	1.7	Up
M200001444	M200001444	-	-	-	-	-	-	-	-	1.7	Down
M300017021	M300017021	-	-	-	-	-	-	-	-	1.7	Down
NM_008039	Formyl peptide receptor 2	Fpr2	-	-	-	-	-	-	-	1.7	Up
NM_011123	Proteolipid protein (myelin) 1	Pip1	-	-	-	-	-	-	-	1.7	Up
NM_020291	Olfactory receptor 480	Olf480	-	-	-	-	-	-	-	1.7	Down
NM_009467	UDP glucuronosyltransferase 2 family, polypeptide B5	Ugt2b5	-	-	-	-	2.3	Down	-	1.8	Down
XM_484487	apolipoprotein L 6	-	-	-	-	-	-	-	-	1.8	Up
M400001914	M400001914	-	-	-	-	-	-	-	-	1.8	Down
M400003651	M400003651	-	-	-	-	-	-	-	-	1.8	Down
NM_027016	SEC62 homolog (S. cerevisiae)	Sec62	-	-	-	-	-	-	-	1.8	Up
NM_007632	Cyclin D3	Ccnd3	-	-	-	-	-	-	-	1.8	Up
M400003178	M400003178	-	-	-	-	-	-	-	-	1.8	Down

M400018621	M400018621	-	-	-	-	-	-	-	-	1.8	Up
M400015410	M400015410	-	-	-	-	-	-	-	-	1.8	Up
NM_183208	Zinc finger, MIZ-type containing 1	Zmiz1	-	-	-	-	-	1.5	Up	1.8	Up
NM_010274	Glycerol phosphate dehydrogenase 2, mitochondrial	Gpd2	-	-	-	-	-	-	-	1.8	Down
NM_198680	Serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 3B	Serpnb3b	-	-	-	-	-	-	-	1.8	Down
NM_007442	Aristaless 4	Alx4	-	-	-	-	-	-	-	1.8	Up
M400005234	M400005234	-	-	-	1.9	Down	-	-	-	1.8	Down
XM_486221	M200010836	-	-	-	-	-	-	-	-	1.8	Down
M400008409	M400008409	-	-	-	-	-	-	-	-	1.8	Down
NM_020506	Exportin 4	Xpo4	-	-	-	-	-	-	-	1.8	Up
NM_008745	Neurotrophic tyrosine kinase, receptor, type 2	Ntrk2	-	-	-	-	-	-	-	1.8	Down
NM_145939	Asparagine-linked glycosylation 3 homolog (yeast, alpha-1,3-mannosyltransferase)	Alg3	-	-	-	-	-	1.8	Up	1.8	Up
M400001920	M400001920	-	-	-	-	-	-	-	-	1.8	Down
NM_008800	Phosphodiesterase 1B, Ca2+-calmodulin dependent	Pde1b	-	-	-	-	-	-	-	1.8	Up
NM_146067	RIKEN cDNA C530044N13 gene	C530044N13	-	-	-	-	-	-	-	1.8	Down
M400014020	M400014020	Rik	-	-	-	-	-	-	-	1.8	Down
M400015106	M400015106	-	-	-	-	-	-	-	-	1.8	Up
NM_144874	COX15 homolog, cytochrome c oxidase assembly protein (yeast)	Cox15	-	-	-	-	-	-	-	1.8	Up
M400003742	M400003742	-	-	-	-	-	-	-	-	1.8	Down
XM_356346	RIKEN cDNA 1700031F05 gene	1700031F05	-	-	-	-	-	-	-	1.8	Up
M300002625	M300002625	Rik	-	-	-	2.7	Down	-	-	1.8	Down
NM_175279	Ras association (RalGDS/AF-6) domain family (N-terminal) member 10	Rassf10	-	-	-	-	-	-	-	1.8	Down
XM_126635	dysferlin interacting protein 1	-	-	-	-	-	-	-	-	1.8	Down
NM_053191	Peptidase inhibitor 15	Pi15	-	-	2.5	Down	-	-	-	1.8	Down
M400004291	M400004291	-	-	-	-	-	-	-	-	1.8	Up
XM_132325	Expressed sequence AU042671	AU042671	-	-	-	-	-	-	-	1.8	Up
M400018580	M400018580	-	-	-	-	-	-	-	-	1.8	Down
M400005969	M400005969	-	-	-	-	-	-	-	-	1.8	Down
M400010166	M400010166	-	-	-	-	-	-	-	-	1.8	Up
M400010588	M400010588	-	-	-	-	-	-	-	-	1.8	Down
M400017928	M400017928	-	-	-	-	-	-	-	-	1.8	Down
NM_178664	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase-like 1	B3gnt1	-	-	-	-	-	-	-	1.8	Up
NM_026872	Ubiquitin-associated protein 2	Ubap2	-	-	-	-	-	-	-	1.8	Down
NM_133737	LanC (bacterial lantibiotic synthetase component C)-like 2	Lancl2	-	-	-	-	-	-	-	1.8	Up
NM_173442	Glucosaminyl (N-acetyl) transferase 1, core 2	Gcnt1	-	-	-	-	-	-	-	1.8	Down
XM_128557	WD repeat domain 90	-	-	-	-	-	-	-	-	1.8	Down
M400014661	M400014661	-	-	-	-	-	-	-	-	1.8	Up

XM_131596	RIKEN cDNA 1700041C02 gene	-	-	-	-	-	-	-	1.8	Down
XM_141933	predicted gene, EG236891	-	-	-	-	-	-	-	1.8	Down
M200015095	M200015095	-	-	-	2.2	Down	-	-	1.8	Down
M400014666	M400014666	-	-	-	-	-	-	-	1.8	Up
NM_007956	Estrogen receptor 1 (alpha)	Esr1	-	-	-	-	-	-	1.8	Up
NM_009851	CD44 antigen	Cd44	-	-	-	-	-	-	1.8	Up
NM_023617	Aldehyde oxidase 3	Aox3	-	-	-	-	-	-	1.8	Down
XM_488662	M400019370	-	-	-	-	-	-	-	1.8	Down
M400012885	M400012885	-	-	-	-	-	-	-	1.8	Up
XM_487737	M400003071	-	-	-	1.8	Down	-	-	1.8	Down
M400016649	M400016649	-	-	-	-	-	-	-	1.9	Up
NM_010631	Kinesin family member C3	Kifc3	-	-	-	-	-	-	1.9	Up
NM_198304	Nucleoporin 188	Nup188	-	-	-	-	-	-	1.9	Down
XM_138671	gene model 274, (NCBI)	-	-	-	-	-	-	-	1.9	Up
NM_178871	transforming growth factor beta regulated gene 3	-	-	-	-	-	-	-	1.9	Down
M400016165	M400016165	-	-	-	-	-	-	-	1.9	Down
	8430408G22									
NM_145980	RIKEN cDNA 8430408G22 gene	Rik	-	-	-	-	-	-	1.9	Down
NM_008061	Glucose-6-phosphatase, catalytic	G6pc	-	-	-	-	-	-	1.9	Up
M400005573	M400005573	-	-	-	-	-	-	-	1.9	Up
NM_009157	Mitogen-activated protein kinase kinase 4	Map2k4	-	-	-	-	-	-	1.9	Up
NM_023138	Mitogen-activated protein kinase kinase 2	Map2k2	-	-	-	-	-	-	1.9	Down
NM_027403	Pregnancy-specific glycoprotein 21	Psg21	-	-	-	-	-	-	1.9	Up
M300003391	M300003391	-	-	-	-	-	2.3	Up	1.9	Up
NM_008241	Forkhead box G1	Foxg1	-	-	-	-	-	-	1.9	Down
	Macrophage galactose N-acetyl-galactosamine specific									
	lectin 1	Mgl1	-	-	-	-	-	-	1.9	Down
M400014744	M400014744	-	-	-	1.9	Down	-	-	1.9	Down
M400005885	M400005885	-	-	-	-	-	-	-	1.9	Down
NM_009114	S100 calcium binding protein A9 (calgranulin B)	S100a9	-	-	-	-	-	-	1.9	Up
M400003712	M400003712	-	-	-	-	-	-	-	1.9	Up
NM_133206	Zinc and ring finger 1	Znrf1	-	-	-	-	-	-	1.9	Down
M300005635	M300005635	-	-	-	-	-	-	-	1.9	Up
NM_175197	RIKEN cDNA 1700055D18 gene	-	-	-	-	-	1.6	Up	1.9	Up
M400000405	M400000405	-	-	-	-	-	-	-	1.9	Down
NM_013559	Heat shock 105kDa/110kDa protein 1	Hsph1	-	-	-	-	-	-	1.9	Up
NM_198861	CDNA sequence BC046404	BC046404	-	-	1.8	Down	-	-	1.9	Down
NM_027882	Capicua homolog (Drosophila)	Cic	-	-	-	-	-	-	1.9	Up
M400015381	M400015381	-	-	-	-	-	-	-	1.9	Down
M400019258	M400019258	-	-	-	-	-	-	-	1.9	Down
M400015926	M400015926	-	-	-	-	-	-	-	1.9	Down
M400004663	M400004663	-	-	-	-	-	-	-	1.9	Up
M400016384	M400016384	-	-	-	-	-	-	-	1.9	Down
NM_023137	Ubiquitin D	Ubd	-	-	2.5	Up	-	-	1.9	Up
M300008873	M300008873	-	-	-	-	-	-	-	1.9	Up

M400002317	M400002317	-	-	-	-	-	-	-	1.9	Down	
NM_023738	Ubiquitin-activating enzyme E1-like	Ube1l	-	-	-	-	-	-	1.9	Up	
NM_029803	Interferon, alpha-inducible protein 27	Ifi27	-	-	-	-	-	-	1.9	Up	
M400005931	M400005931	-	-	-	-	-	-	-	1.9	Down	
M300006351	M300006351	-	-	-	-	-	2.5	Up	1.9	Up	
M400013520	M400013520	-	-	-	-	-	-	-	1.9	Up	
NM_146224	Suppressor of hairy wing homolog 4 (Drosophila)	Suhw4	-	-	-	1.8	Down	-	1.9	Down	
M300019862	M300019862	-	-	-	-	-	-	-	1.9	Up	
NM_177723	V-set and immunoglobulin domain containing 8	Vsig8	-	-	-	-	-	-	1.9	Up	
M400002815	M400002815	-	-	-	-	-	-	-	2.0	Down	
NM_007971	Enhancer of zeste homolog 2 (Drosophila)	Ezh2	-	-	-	-	-	-	2.0	Up	
NM_153407	Cysteine-serine-rich nuclear protein 2	Csrnp2	-	-	-	-	-	-	2.0	Up	
M400001652	M400001652	-	-	-	-	-	-	-	2.0	Up	
M400012977	M400012977	-	-	-	-	-	-	-	2.0	Up	
M400016385	M400016385	-	-	-	-	-	-	-	2.0	Up	
M400010205	M400010205	-	-	-	-	-	-	-	2.0	Up	
NM_011888	Chemokine (C-C motif) ligand 19	Ccl19	-	-	-	-	-	-	2.0	Up	
NM_175252	RIKEN cDNA 6720457D02 gene	-	-	-	-	-	-	-	2.0	Down	
	TAF1 RNA polymerase II, TATA box binding protein										
XM_194622	(TBP)-associated factor	-	-	-	-	-	-	2.1	Up	2.0	Up
NM_008012	Aldo-keto reductase family 1, member B8	Akr1b7	-	-	-	-	-	-	2.0	Up	
XM_484154	M200010848	-	-	-	-	-	-	-	2.0	Down	
M400017062	M400017062	-	-	-	-	-	-	-	2.0	Up	
M400017548	M400017548	-	-	-	-	-	-	-	2.0	Down	
M300001934	M300001934	-	-	-	-	-	-	1.5	Up	2.0	Up
M400002431	M400002431	-	-	-	-	-	-	-	2.0	Up	
NM_029653	Death associated protein kinase 1	Dapk1	-	-	-	-	-	-	2.0	Down	
M400009287	M400009287	-	-	-	-	2.3	Up	-	2.0	Down	
M400014591	M400014591	-	-	-	-	-	-	-	2.0	Down	
M400008184	M400008184	-	-	-	-	-	-	-	2.0	Down	
M400016650	M400016650	-	-	-	-	-	-	-	2.0	Down	
NM_175354	RIKEN cDNA C030016D13 gene	-	-	-	-	-	-	-	2.0	Up	
M400008469	M400008469	-	-	-	-	-	-	-	2.0	Down	
XM_128979	PRELI domain containing 2	-	-	-	-	-	-	-	2.0	Up	
XM_356816	M400001979	-	-	-	-	-	-	-	2.0	Down	
XM_485965	M3000020322	-	-	-	-	-	-	-	2.0	Up	
M400010262	M400010262	-	-	-	-	-	-	-	2.0	Down	
NM_016892	Copper chaperone for superoxide dismutase	Ccs	-	-	-	-	-	-	2.0	Down	
M300003323	M300003323	-	-	-	-	-	-	-	2.0	Down	
NM_007567	Bassoon	Bsn	-	-	-	-	-	-	2.0	Up	
NM_207636	Fibronectin type III domain containing 3a	Fndc3a	-	-	-	-	-	2.0	Up	2.0	Up
NM_025743	RIKEN cDNA 4933400A11 gene	-	-	-	-	-	-	-	2.0	Down	
NM_011677	Uracil DNA glycosylase	Ung	-	-	-	-	-	-	2.0	Down	
XM_135033	M400005691	-	-	-	-	-	-	-	2.0	Down	
XM_133991	RIKEN cDNA 1700018L24 gene	-	-	-	-	-	-	1.8	Down	2.0	Down



NM_007665	Cadherin 3	Cdh3	-	-	-	-	2.7	Up	2.0	Up
M400008571	M400008571	-	-	-	-	-	-	-	2.0	Down
NM_011549	Transcription factor EB	Tcfef	-	-	-	-	-	-	2.1	Up
M400009928	M400009928	-	-	-	-	-	-	-	2.1	Down
M400013837	M400013837	-	-	-	-	-	-	-	2.1	Down
NM_146107	ARP1 actin-related protein 1 homolog B (yeast)	Actr1b	-	-	-	-	-	-	2.1	Up
NM_178927	M400012512	-	-	-	2.3	Down	-	-	2.1	Down
NM_023524	TCF3 (E2A) fusion partner	Tfpt	-	-	-	-	-	-	2.1	Down
XM_146438	predicted gene, EG244595	-	-	-	-	-	-	-	2.1	Down
		1300010M03								
NM_028933	RIKEN cDNA 1300010M03 gene	Rik	-	-	-	-	-	-	2.1	Up
XM_136698	M400006270	-	-	-	-	-	-	-	2.1	Down
XM_144000	predicted gene, OTTMUSG00000008519	-	-	-	-	-	-	-	2.1	Down
M400016204	M400016204	-	-	-	-	-	3.4	Up	2.1	Up
NM_172775	Plexin B1	Plxnb1	-	-	-	-	-	-	2.1	Up
NM_016759	RUN domain containing 3A	Rundc3a	-	-	-	-	-	-	2.1	Up
	Transmembrane protein 8 (five membrane-spanning domains)	Tmem8	-	-	-	-	2.5	Up	2.1	Up
NM_025860	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	Ddx18	-	-	-	-	2.0	Up	2.1	Up
M400001937	M400001937	-	-	-	1.7	Down	-	-	2.1	Down
M400006474	M400006474	-	-	-	-	-	-	-	2.1	Up
M300006166	M300006166	-	-	-	-	-	-	-	2.1	Down
NM_025271	Actin-like 7b	Actl7b	-	-	-	-	-	-	2.1	Down
NM_178669	Clarin 3	Clrn3	-	-	-	-	-	-	2.1	Up
M400016276	M400016276	-	-	-	-	-	-	-	2.1	Down
M200011755	M200011755	-	-	-	-	-	-	-	2.1	Up
M400019098	M400019098	-	-	-	-	-	-	-	2.1	Down
NM_175423	ORAI calcium release-activated calcium modulator 1	Orai1	-	-	-	-	1.8	Up	2.1	Up
M400010006	M400010006	-	-	-	-	-	-	-	2.1	Down
M400013095	M400013095	-	-	-	-	-	-	-	2.1	Down
NM_145227	2-5 oligoadenylate synthetase 2	Oas2	-	-	-	-	-	-	2.1	Up
M400017407	M400017407	-	-	-	-	-	-	-	2.1	Down
NM_015786	Histone cluster 1, H1c	Hist1h1c	-	-	-	-	-	-	2.1	Down
M400006446	M400006446	-	-	-	1.9	Down	-	-	2.1	Up
NM_007519	Bile acid-Coenzyme A: amino acid N-acyltransferase	Baat	-	-	-	-	-	-	2.1	Up
M400004672	M400004672	-	-	-	-	-	-	-	2.1	Down
NM_172378	CDNA sequence BC026439	BC026439	-	-	-	-	-	-	2.1	Up
M400019205	M400019205	-	-	-	-	-	-	-	2.1	Down
	Ribonuclease L (2, 5-oligoadenylate synthetase-dependent)	Rnasel	-	-	-	-	-	-	2.2	Down
NM_011882	M400017634	-	-	-	-	-	-	-	2.2	Down
XM_283061	M400017634	-	-	-	-	-	-	-	2.2	Down
M400001558	M400001558	-	-	-	-	-	-	-	2.2	Up
M400007946	M400007946	-	-	-	-	-	-	-	2.2	Down
M400013543	M400013543	-	-	-	-	-	-	-	2.2	Up
NM_018851	SAM domain and HD domain, 1	Samhd1	-	-	-	-	-	-	2.2	Up

NM_009743	Bcl2-like 1	Bcl21	-	-	-	-	-	-	-	2.2	Up
M400018688	M400018688	-	-	-	-	-	-	-	-	2.2	Down
NM_026272	Nuclear prelamin A recognition factor	Narf	-	-	1.8	Down	-	-	-	2.2	Down
M400008808	M400008808	-	-	-	-	-	-	-	-	2.2	Down
M400019092	M400019092	-	-	-	-	-	-	-	-	2.2	Down
M400001607	M400001607	-	-	-	1.6	Down	-	-	-	2.2	Up
NM_011261	Reelin	Reln	-	-	-	-	-	-	-	2.2	Up
	IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)	Imp4	-	-	-	-	1.5	Up	-	2.2	Up
NM_198866	DNA binding protein with his-thr domain	Dbpht2	-	-	2.0	Down	-	-	-	2.2	Down
M200012931	M200012931	-	-	-	-	-	-	-	-	2.2	Down
M400013664	M400013664	-	-	-	-	-	-	-	-	2.2	Down
M400012844	M400012844	-	-	-	-	-	-	-	-	2.2	Down
NM_199311	C-type lectin domain family 4, member a1	Clec4a1	-	-	-	-	-	-	-	2.2	Up
M300013617	M300013617	-	3.4	Up	-	-	-	-	-	2.2	Up
XM_486960	M400006830	-	-	-	-	-	-	-	-	2.2	Down
NM_201372	Coiled-coil domain containing 84	Ccdc84	-	-	-	-	-	-	-	2.2	Down
	Ctr9, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	Ctr9	-	-	-	-	-	-	-	2.3	Up
NM_009431	predicted gene, EG436008	-	-	-	-	-	1.6	Down	-	2.3	Down
XM_488079	M400012874	-	-	-	-	-	-	-	-	2.3	Down
M400012874	M400012874	-	-	-	-	-	-	-	-	2.3	Down
M400004224	M400004224	-	-	-	3.0	Down	-	-	-	2.3	Down
M400007536	M400007536	-	-	-	-	-	-	-	-	2.3	Down
	1810011H11	Rik	-	-	-	-	-	-	-	2.3	Down
XM_358452	RIKEN cDNA 1810011H11 gene	-	-	-	-	-	-	-	-	2.3	Down
M400004010	M400004010	-	-	-	-	-	2.3	Up	-	2.3	Up
NM_010734	Leukocyte specific transcript 1	Lst1	-	-	-	-	-	-	-	2.3	Up
NM_009394	Troponin C2, fast	Tnnc2	-	-	-	-	-	-	-	2.3	Down
	4933405O20	Rik	-	-	-	-	-	-	-	2.3	Down
NM_172901	RIKEN cDNA 4933405O20 gene	-	-	-	-	-	-	-	-	2.3	Down
XM_484223	predicted gene, EG432730	-	-	-	-	-	-	-	-	2.3	Down
	RP23-244H7.9	Zfp7	-	-	-	-	-	-	-	2.3	Up
NM_194357	Antimicrobial peptide RYA3	-	-	-	-	-	-	-	-	2.3	Up
NM_145916	Zinc finger protein 7	Zfp7	-	-	-	-	-	-	-	2.3	Up
M400018184	M400018184	-	-	-	-	-	-	-	-	2.3	Up
M400018439	M400018439	-	-	-	2.5	Down	-	-	-	2.3	Down
M400014785	M400014785	-	-	-	-	-	-	-	-	2.3	Down
M400019448	M400019448	-	-	-	-	-	-	-	-	2.3	Down
M400010510	M400010510	-	-	-	-	-	-	-	-	2.3	Down
NM_148953	Ankyrin repeat and SOCS box-containing 16	Asb16	-	-	-	-	-	-	-	2.3	Up
M400015582	M400015582	-	-	-	-	-	-	-	-	2.4	Down
	Hyperpolarization-activated, cyclic nucleotide-gated K+ 3	Hcn3	-	-	-	-	-	-	-	2.4	Up
NM_008227	WD repeat domain 22	Wdr22	-	-	3.4	Down	-	-	-	2.4	Down
NM_177267	RIKEN cDNA 3110001I22 gene	Bfar	-	-	-	-	-	-	-	2.4	Down
NM_025976			-	-	-	-	-	-	-	2.4	Down

NM_009048	RalBP1 associated Eps domain containing protein	Reps1	-	-	-	-	-	-	2.4	Down
XM_110852	par-3 partitioning defective 3 homolog B (C. elegans)	-	-	-	-	-	-	-	2.4	Down
M400005597	M400005597	-	-	-	-	-	1.7	Up	2.4	Up
XM_125372	predicted gene, EG236622	-	-	-	-	-	-	-	2.4	Down
M400003418	M400003418	-	-	-	-	-	-	-	2.4	Up
NM_146601	Olfactory receptor 710	Olf710	-	-	2.3	Down	-	-	2.4	Down
NM_011597	Tight junction protein 2	Tjp2	-	-	-	-	-	-	2.4	Up
NM_007928	MAP/microtubule affinity-regulating kinase 2	Mark2	-	-	-	-	-	-	2.4	Up
M400002691	M400002691	-	-	-	1.7	Down	-	-	2.4	Down
M400013569	M400013569	-	-	-	-	-	-	-	2.4	Up
NM_029377	Lin-37 homolog (C. elegans)	Lin37	-	-	-	-	-	-	2.4	Down
NM_027137	Late cornified envelope 1D	Lce1d	-	-	-	-	-	-	2.4	Up
M400013451	M400013451	-	-	-	1.7	Down	-	-	2.4	Down
NM_177146	RIKEN cDNA 9330175E14 gene	-	-	-	-	-	-	-	2.5	Up
M400003468	M400003468	-	-	-	-	-	1.5	Down	2.5	Down
NM_130887	Papilin, proteoglycan-like sulfated glycoprotein	Papln	-	-	-	-	-	-	2.5	Up
XM_148839	predicted gene, EG225609	-	-	-	-	-	-	-	2.5	Down
NM_011658	Twist gene homolog 1 (Drosophila)	Twist1	-	-	-	-	-	-	2.5	Up
NM_011973	Renal tumor antigen	Rage	-	-	-	-	-	-	2.5	Up
M400017343	M400017343	-	-	-	-	-	-	-	2.5	Up
M400008560	M400008560	-	-	-	-	-	-	-	2.5	Up
NM_178688	Actin-binding LIM protein 1	Ablim1	-	-	-	-	-	-	2.5	Up
M400013606	M400013606	-	-	-	-	-	-	-	2.5	Down
NM_011128	Pancreatic lipase-related protein 2	Pnliprp2	-	-	-	-	-	-	2.5	Up
M400005241	M400005241	-	-	-	-	-	-	-	2.5	Up
M400002335	M400002335	-	-	-	1.7	Down	1.5	Down	2.5	Down
M400012836	M400012836	-	-	-	-	-	2.8	Up	2.5	Up
		D230037D09								
NM_177140	RIKEN cDNA D230037D09 gene	Rik	-	-	-	-	-	-	2.5	Down
M200006909	M200006909	-	-	-	-	-	-	-	2.6	Up
M300006384	M300006384	-	-	-	-	-	-	-	2.6	Up
XM_484980	M300016620	-	-	-	-	-	-	-	2.6	Down
M400006276	M400006276	-	-	-	-	-	-	-	2.6	Down
NM_133974	CUB domain containing protein 1	Cdcp1	-	-	-	-	-	-	2.6	Down
XM_142259	predicted gene, EG245676	-	-	-	-	-	-	-	2.6	Down
XM_127436	bromodomain containing 9	-	-	-	-	-	-	-	2.6	Down
M400018104	M400018104	-	-	-	-	-	-	-	2.6	Up
XM_356900,										
XM_489652	M400000593	-	-	-	-	-	-	-	2.6	Up
M400013802	M400013802	-	-	-	-	-	-	-	2.6	Up
XM_144572	transmembrane protein 132B	-	-	-	1.6	Down	-	-	2.6	Down
	Ras association (RalGDS/AF-6) domain family (N-									
NM_146240	terminal) member 9	Rassf9	-	-	-	-	-	-	2.6	Down
M400015761	M400015761	-	-	-	-	-	-	-	2.6	Up
NM_008541	MAD homolog 5 (Drosophila)	Smad5	-	-	-	-	-	-	2.6	Down

NM_024287	RAB6, member RAS oncogene family	Rab6	-	-	-	-	-	-	-	2.6	Up
M400001985	M400001985	-	-	-	-	-	-	-	-	2.6	Down
NM_009609,											
NM_013798	M300012334	-	-	-	-	-	-	-	-	2.6	Down
NM_011852,											
NM_145211	M300000160	-	-	-	-	-	-	-	-	2.6	Up
NM_172287	Spire homolog 2 (Drosophila)	Spire2	-	-	3.2	Down	-	-	-	2.6	Up
NM_008659	Myosin IC	Myo1c	-	-	-	-	-	-	-	2.6	Down
AK014509	growth arrest specific 2	-	-	-	-	-	-	-	-	2.6	Down
	ganglioside-induced differentiation-associated-protein 10	-	-	-	-	-	-	-	-	2.6	Up
NM_010268	10	-	-	-	-	-	-	-	-	2.6	Up
NM_009076	Ribosomal protein L12	Rpl12	-	-	-	-	-	-	-	2.7	Down
NM_144900	ATPase, Na+/K+ transporting, alpha 1 polypeptide	Atp1a1	1.8	Down	-	-	-	-	-	2.7	Down
NM_025583	Chymotrypsinogen B1	Ctrb1	-	-	-	-	-	-	-	2.7	Up
NM_008599	Chemokine (C-X-C motif) ligand 9	Cxcl9	-	-	-	-	-	-	-	2.7	Up
M300011766	M300011766	-	-	-	-	-	-	-	-	2.7	Down
NM_033444	Chloride intracellular channel 1	Clic1	-	-	-	-	-	-	-	2.7	Up
M400013279	M400013279	-	-	-	-	-	-	1.5	Down	2.7	Down
NM_019494	Chemokine (C-X-C motif) ligand 11	Cxcl11	-	-	-	-	-	-	-	2.7	Up
NM_028030	RNA binding protein with multiple splicing 2	Rbpms2	-	-	-	-	-	1.8	Up	2.7	Up
M400015052	M400015052	-	-	-	-	-	-	-	-	2.7	Up
M400016135	M400016135	-	-	-	-	-	-	-	-	2.7	Down
NM_147027	Olfactory receptor 31	Olfr31	-	-	-	-	-	-	-	2.7	Down
NM_001001											
452	Taste receptor, type 2, member 143	Tas2r143	-	-	-	-	-	-	-	2.7	Down
NM_175365	M400004829	-	-	-	-	-	-	-	-	2.7	Down
	Eukaryotic translation initiation factor 2, subunit 3, structural gene X-linked	Eif2s3x	-	-	-	-	-	1.6	Up	2.7	Up
NM_012010											
NM_175467	Serine palmitoyltransferase, long chain base subunit 3	Sptlc3	-	-	2.0	Down	-	-	-	2.7	Up
NM_009922	Calponin 1	Cnn1	-	-	2.2	Down	-	-	-	2.7	Down
NM_013751	HRAS-like suppressor	Hrasls	-	-	-	-	-	-	-	2.7	Up
	Sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A	Sema4a	1.8	Up	-	-	-	-	-	2.8	Up
NM_013658											
M400013762	M400013762	-	-	-	-	-	-	-	-	2.8	Up
M400016853	M400016853	-	-	-	-	-	-	-	-	2.8	Down
NM_021394	Z-DNA binding protein 1	Zbp1	-	-	1.5	Down	-	-	-	2.8	Up
XM_203404	src family associated phosphoprotein 1	-	-	-	-	-	-	-	-	2.8	Down
	Serine (or cysteine) peptidase inhibitor, clade A, member 6	Serpina6	-	-	-	-	-	-	-	2.8	Up
NM_007618											
M400016433	M400016433	-	-	-	-	-	-	-	-	2.8	Down
NM_029772	Cation channel, sperm associated 3	Catsper3	-	-	-	-	-	-	-	2.9	Down
M400015789	M400015789	-	-	-	-	-	-	-	-	2.9	Up
	potassium channel tetramerisation domain containing 14	-	-	-	-	-	-	-	-	2.9	Down
XM_133614											

M400015776	M400015776	-	-	-	-	-	-	-	2.9	Up
NM_177577	Doublecortin domain containing 2a	Dcdc2a	-	-	-	-	-	-	2.9	Up
NM_133816	SH3-domain binding protein 4	Sh3bp4	-	-	-	-	-	-	2.9	Up
NM_173740	Monoamine oxidase A	Maoa	-	-	-	-	-	-	2.9	Down
NM_201644	UDP glucuronosyltransferase 1 family, polypeptide A6B	Ugt1a6a	-	-	-	-	1.6	Up	2.9	Up
M400016895	M400016895	-	-	-	-	-	-	-	2.9	Down
M400006760	M400006760	-	-	-	-	-	-	-	2.9	Down
XM_130548	ESF1, nucleolar pre-rRNA processing protein, homolog (S. cerevisiae)	-	-	-	1.8	Down	-	-	3.0	Down
NM_175526	C-type lectin domain family 1, member a	Clec1a	-	-	-	-	-	-	3.0	Down
NM_011242	RAS, guanyl releasing protein 2	Rasgrp2	-	-	-	-	-	-	3.0	Down
M400009925	M400009925	-	-	-	-	-	-	-	3.0	Down
XM_484795	high mobility group protein 1-like	-	-	-	-	-	-	-	3.0	Down
M400014765	M400014765	-	-	-	-	-	-	-	3.0	Down
NM_010173	Fatty acid amide hydrolase	Faah	-	-	-	-	-	-	3.0	Up
NM_144881	Hedgehog acyltransferase	Hhat	-	-	-	-	-	-	3.1	Up
NM_028800	Serine/threonine kinase 40	Stk40	-	-	-	-	-	-	3.1	Up
M400018670	M400018670	-	-	-	-	-	-	-	3.1	Down
NM_010917	Nidogen 1	Nid1	-	-	-	-	-	-	3.1	Up
NM_133784	WW domain containing transcription regulator 1	Wwtr1	-	-	-	-	-	-	3.1	Down
M300017518	M300017518	-	-	-	-	-	3.4	Down	3.1	Down
NM_205822	Oocyte maturation, beta	Omt2b	-	-	-	-	-	-	3.1	Down
NM_025613	EP300 interacting inhibitor of differentiation 1	Eid1	-	-	-	-	-	-	3.1	Down
NM_181591	Thioredoxin domain containing 3 (spermatzoa)	Txndc3	-	-	-	-	-	-	3.2	Up
M400005091	M400005091	-	-	-	-	-	-	-	3.2	Down
NM_027377	M200008534	-	-	-	-	-	-	-	3.2	Down
NM_011586	Myosin XVIIIa	Myo18a	-	-	-	-	-	-	3.2	Down
M400014265	M400014265	-	-	-	-	-	-	-	3.2	Down
NM_025679	RIKEN cDNA 5730470L24 gene	5730470L24 Rik	2.0	Up	-	-	1.7	Up	3.2	Up
M400018999	M400018999	-	-	-	-	-	-	-	3.3	Up
NM_008150	Glypican 4	Gpc4	-	-	-	-	-	-	3.3	Up
NM_197990	RIKEN cDNA 1700025G04 gene	1700025G04 Rik	-	-	-	-	-	-	3.3	Down
NM_007617	Caveolin 3	Cav3	-	-	3.1	Down	-	-	3.3	Down
NM_018797	Plexin C1	Plxnc1	-	-	-	-	-	-	3.3	Up
XM_484024	M400002019	-	-	-	-	-	-	-	3.3	Down
NM_025296	Cytosolic iron-sulfur protein assembly 1 homolog (S. cerevisiae)	Ciao1	-	-	-	-	-	-	3.3	Down
M400017422	M400017422	-	-	-	-	-	-	-	3.4	Up
M400010161	M400010161	-	-	-	-	-	-	-	3.4	Up
M400013907	M400013907	-	-	-	-	-	-	-	3.4	Up
NM_008390	Interferon regulatory factor 1	Irf1	-	-	-	-	-	-	3.4	Up
NM_024212	Ribosomal protein L4	Rpl4	-	-	-	-	-	-	3.4	Down

NM_021883	Tropomodulin 1	Tmod1	-	-	-	-	-	-	3.4	Up
NM_026286	Ferritin mitochondrial	Ftmt	-	-	-	-	-	-	3.4	Down
NM_147218	ATP-binding cassette, sub-family A (ABC1), member 6	Abca6	-	-	-	-	-	-	3.4	Up
NM_013886	hepatoma-derived growth factor, related protein 3	-	-	-	-	-	-	-	3.4	Up
M400008980	M400008980	-	-	-	-	-	-	-	3.4	Up
NM_134199	Vomeronasal 1 receptor, F2	V1rf2	-	-	-	-	-	-	3.5	Up
NM_010142	Eph receptor B2	Ephb2	-	-	-	-	3.2	Up	3.5	Up
M300017458	M300017458	-	-	-	-	-	-	-	3.5	Down
NM_030738	Vomeronasal 1 receptor, D6	V1rd6	-	-	-	-	-	-	3.5	Up
NM_027188	SET and MYND domain containing 3	Smyd3	-	-	-	-	-	-	3.6	Up
M400013235	M400013235	-	-	-	3.0	Up	-	-	3.6	Up
XM_127419	multiple C2 domains, transmembrane 1	-	-	-	-	-	-	-	3.6	Up
NM_153108	Defensin beta 8	Defb8	-	-	-	-	3.1	Down	3.7	Down
M400014918	M400014918	-	-	-	-	-	-	-	3.7	Down
M400013433	M400013433	-	-	-	-	-	-	-	3.7	Down
M200007064	M200007064	-	-	-	-	-	-	-	3.7	Up
XM_156082	F-box protein 40	-	-	-	-	-	3.6	Up	3.8	Up
M400010488	M400010488	-	-	-	-	-	3.5	Up	3.8	Up
M400009091	M400009091	-	-	-	-	-	-	-	3.8	Up
	Phosphatidylinositol glycan anchor biosynthesis, class Y									
NM_025574	Y	Pigy	-	-	-	-	-	-	3.8	Up
XM_144778	predicted gene, ENSMUSG00000076510	-	-	-	-	-	-	-	3.8	Up
NM_021893	CD274 antigen	Cd274	-	-	-	-	-	-	3.8	Up
M400014086	M400014086	-	-	-	-	-	-	-	3.9	Down
NM_021377	VPS10 domain receptor protein SORCS 1	Sorcs1	-	-	-	-	-	-	3.9	Up
M400007462	M400007462	-	-	-	-	-	-	-	3.9	Down
		1700024P16								
XM_161350	RIKEN cDNA 1700024P16 gene	Rik	-	-	-	-	-	-	3.9	Down
NM_011486, NM_213659, NM_213660										
M200012506	M200012506	-	-	-	-	-	-	-	4.0	Up
M400016506	M400016506	-	-	-	-	-	-	-	4.0	Down
M400018753	M400018753	-	-	-	-	-	-	-	4.1	Down
M400009574	M400009574	-	-	-	-	-	-	-	4.1	Down
NM_146677	Olfactory receptor 825	Olfr825	-	-	-	-	-	-	4.2	Down
M400014912	M400014912	-	-	-	-	-	-	-	4.2	Down
NM_018738	Interferon gamma induced GTPase	lgtp	-	-	-	-	-	-	4.2	Up
NM_007794, NM_181322										
M200000182	M200000182	-	-	-	-	-	-	-	4.2	Down
M400019157	M400019157	-	-	-	-	-	-	-	4.2	Down
M400012715	M400012715	-	-	-	-	-	-	-	4.3	Down
NM_177276	M400012401	-	-	-	-	-	-	-	4.3	Up
	DNA segment, Chr 2, Wayne State University 81, expressed									
NM_172660		D2Wsu81e	-	-	1.7	Down	-	-	-	-
NM_153807,	M200011599	-	-	-	1.6	Down	-	-	-	-

XM_485251										
NM_172528	Leucine rich repeat containing 1	Lrrc1	-	-	2.4	Down	-	-	-	-
NM_008469	Keratin 15	Krt15	-	-	2.4	Down	1.5	Up	-	-
NM_027185	Differentially expressed in FDCP 6	Def6	-	-	-	-	1.5	Up	-	-
NM_177057	RIKEN cDNA E230015B07 gene	-	-	-	-	-	1.5	Down	-	-
M400016440	M400016440	-	-	-	-	-	1.5	Up	-	-
NM_145952	TBC1D12: TBC1 domain family, member 12	Tbc1d12	-	-	-	-	1.5	Up	-	-
M400001556	M400001556	-	-	-	-	-	1.5	Up	-	-
NM_010567	Inositol polyphosphate phosphatase-like 1	Inpp1	-	-	-	-	1.5	Up	-	-
M400002331	M400002331	-	-	-	-	-	1.5	Up	-	-
NM_175226	Ring finger protein 139	Rnf139	-	-	-	-	1.5	Up	-	-
XM_485216	M400005746	-	-	-	-	-	1.5	Down	-	-
	Serine (or cysteine) peptidase inhibitor, clade B, member 6c	Serpinb6c	-	-	1.5	Down	1.6	Up	-	-
NM_148942	Angiogenin, ribonuclease A family, member 4	Ang4	-	-	-	-	1.6	Up	-	-
NM_177544	Angiogenin, ribonuclease A family, member 4	Ang4	-	-	-	-	1.6	Up	-	-
M400017224	M400017224	-	-	-	-	-	1.6	Up	-	-
NM_013475	Apolipoprotein H	ApoH	-	-	-	-	1.6	Up	-	-
NM_146231	zinc finger protein 825	-	-	-	-	-	1.6	Up	-	-
NM_016799	Serine/arginine repetitive matrix 1	Srrm1	-	-	-	-	1.6	Up	-	-
NM_008465	Karyopherin (importin) alpha 1	Kpna1	-	-	-	-	1.6	Up	-	-
NM_016907	Serine protease inhibitor, Kunitz type 1	Spint1	-	-	-	-	1.6	Up	-	-
NM_198410	Progesterone and adipoQ receptor family member VI	Paqr6	-	-	-	-	1.6	Up	-	-
NM_011619	Troponin T2, cardiac	Tnnt2	-	-	-	-	1.6	Up	-	-
NM_009001	RAB3A, member RAS oncogene family	Rab3a	-	-	-	-	1.6	Up	-	-
M400013968	M400013968	-	-	-	-	-	1.6	Up	-	-
	ATP-binding cassette, sub-family A (ABC1), member 8a	Abca8a	-	-	-	-	1.6	Up	-	-
NM_153145	8a	Abca8a	-	-	-	-	1.6	Up	-	-
M300007365	M300007365	-	-	-	-	-	1.6	Down	-	-
NM_011197	Prostaglandin F2 receptor negative regulator	Ptgfrn	-	-	-	-	1.6	Up	-	-
NM_011326	Sodium channel, nonvoltage-gated 1 gamma	Scnn1g	-	-	-	-	1.6	Up	-	-
NM_027769	Copine III	Cpne3	-	-	-	-	1.7	Up	-	-
		1700112C13								
NM_183103	RIKEN cDNA 1700112C13 gene	Rik	-	-	2.9	Down	1.7	Up	-	-
M300020799	M300020799	-	-	-	-	-	1.7	Up	-	-
M400008520	M400008520	-	-	-	-	-	1.7	Up	-	-
NM_020289	Olfactory receptor 544	Olfr544	-	-	-	-	1.7	Up	-	-
XM_136914	Gene model 221, (NCBI)	Gm221	-	-	-	-	1.7	Down	-	-
XM_484053	TAO kinase 1	-	-	-	-	-	1.7	Up	-	-
M400017768	M400017768	-	-	-	-	-	1.7	Up	-	-
NM_007583	Calcium channel, voltage-dependent, gamma subunit 2	Cacng2	-	-	2.2	Down	1.7	Down	-	-
M400012928	M400012928	-	-	-	-	-	1.7	Down	-	-
NM_144930	Expressed sequence AU018778	AU018778	-	-	-	-	1.7	Down	-	-
NM_177150	Centromere protein T	Cenpt	-	-	-	-	1.7	Up	-	-
M400010608	M400010608	-	-	-	-	-	1.7	Up	-	-
XM_484476	PHD finger protein 20-like 1	-	-	-	-	-	1.7	Up	-	-

NM_025656	Survivor of motor neuron protein interacting protein 1	Sip1	-	-	-	-	1.7	Down	-	-
NM_201226	Leucine rich repeat containing 47	Lrrc47	-	-	-	-	1.7	Up	-	-
M400008020	M400008020	-	-	-	-	-	1.7	Up	-	-
M200010626	M200010626	-	-	-	-	-	1.7	Up	-	-
NM_011317	KH domain containing, RNA binding, signal transduction associated 1	Khdrbs1	-	-	-	-	1.7	Up	-	-
NM_198167	Transmembrane protein 63b	Tmem63b	-	-	-	-	1.7	Up	-	-
M400015221	M400015221	-	-	-	-	-	1.8	Up	-	-
NM_133212	Toll-like receptor 8	Tlr8	-	-	-	-	1.8	Down	-	-
NM_178695	Proline rich Gla (G-carboxyglutamic acid) 4 (transmembrane)	Prrg4	-	-	-	-	1.8	Up	-	-
M400016592	M400016592	-	-	-	-	-	1.8	Up	-	-
NM_031185	A kinase (PRKA) anchor protein (gravin) 12	Akap12	-	-	-	-	1.8	Up	-	-
M400017236	M400017236	-	-	-	-	-	1.8	Up	-	-
NM_172725	RIKEN cDNA C330006K01 gene	C330006K01	-	-	-	-	-	-	-	-
M400015684	M400015684	Rik	-	-	-	1.6	Down	1.9	Down	-
NM_147045	Olfactory receptor 683	Olfr683	-	-	-	-	-	1.9	Up	-
NM_011143,										
XM_484409	M300019159	-	-	-	-	-	-	1.9	Up	-
NM_177397	ATPase, H+ transporting, lysosomal V1 subunit G3	Atp6v1g3	-	-	-	-	-	1.9	Down	-
NM_175751	Zinc finger protein 608	Zfp608	-	-	-	-	-	1.9	Up	-
NM_194341	AP1 gamma subunit binding protein 1	Ap1gbp1	-	-	-	-	-	1.9	Up	-
NM_026322	Methionine sulfoxide reductase A	Msra	-	-	-	-	-	2.0	Up	-
NM_010819	C-type lectin domain family 4, member d	Clec4d	-	-	-	-	-	2.0	Down	-
M400009128	M400009128	-	-	-	-	-	-	2.0	Up	-
M400015349	M400015349	-	-	-	-	-	-	2.0	Up	-
M400000348	M400000348	-	-	-	-	-	-	2.0	Up	-
M200011123	M200011123	-	-	-	-	-	-	2.0	Down	-
NM_028207	Dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	Dusp3	-	-	-	-	-	2.1	Up	-
NM_010493	Intercellular adhesion molecule 1	Icam1	-	-	-	-	-	2.1	Up	-
M400018202	M400018202	-	-	-	-	-	-	2.1	Up	-
M400008684	M400008684	-	-	-	-	-	-	2.1	Up	-
NM_133732	RIKEN cDNA 4931406C07 gene	4931406C07	-	-	-	-	-	-	-	-
NM_009963	Cryptochrome 2 (photolyase-like)	Rik	-	-	-	-	-	2.1	Up	-
M400017809	M400017809	Cry2	-	-	-	-	-	2.1	Up	-
NM_146229	Dynein cytoplasmic 1 light intermediate chain 1	-	-	-	-	-	-	2.1	Up	-
NM_053104,										
NM_175387	M300008835	Dync1li1	-	-	-	-	-	2.2	Up	-
M400002545	M400002545	-	-	-	-	-	-	2.2	Up	-
M400016109	M400016109	-	-	-	-	-	-	2.3	Up	-
NM_009565	Zinc finger and BTB domain containing 7B	Zbtb7b	-	-	-	-	-	2.3	Up	-
NM_146129	PDX1 C-terminal inhibiting factor 1	Pcif1	-	-	-	-	-	2.3	Up	-



NM_011423	M400011135	-	-	-	-	-	2.3	Up	-	-
M300005195	M300005195	-	-	-	-	-	2.3	Down	-	-
	Matrix extracellular phosphoglycoprotein with ASARM motif (bone)	Mepe	-	-	-	-	2.3	Down	-	-
NM_053172	M400015934	-	-	-	-	-	2.4	Up	-	-
M400015934	M400015934	-	-	-	-	-	2.4	Up	-	-
M200015120	M200015120	-	-	-	-	-	2.4	Down	-	-
NM_177737	expressed sequence AI854703	-	-	-	-	-	2.4	Up	-	-
NM_207270	Protein tyrosine phosphatase, receptor type, H	Ptprh	-	-	-	-	2.4	Down	-	-
XM_144837	cDNA sequence U29423	-	-	-	-	-	2.4	Down	-	-
M400001197	M400001197	-	-	-	-	-	2.5	Up	-	-
XM_484079	predicted gene, OTTMUSG00000002191	-	-	-	-	-	2.5	Down	-	-
	PRP40 pre-mRNA processing factor 40 homolog A (yeast)	Prpf40a	-	-	-	-	2.5	Down	-	-
NM_018785	Histone cluster 1, H2an	Hist1h2an	-	-	2.4	Up	2.5	Up	-	-
NM_178184	M400001777	-	-	-	-	-	2.5	Down	-	-
M400001777	M400001777	-	-	-	-	-	2.5	Down	-	-
NM_026394	Late cornified envelope 1F	Lce1f	-	-	1.7	Down	2.6	Up	-	-
M400012858	M400012858	-	-	-	-	-	2.6	Up	-	-
NM_008917	Palmitoyl-protein thioesterase 1	Ppt1	-	-	-	-	2.7	Down	-	-
M400001421	M400001421	-	-	-	-	-	2.8	Down	-	-
NM_028597	THO complex 3	Thoc3	-	-	-	-	2.8	Up	-	-
NM_009372	TG interacting factor 1	Tgif1	-	-	-	-	2.9	Down	-	-
XM_485377	expressed sequence AU014645	-	-	-	-	-	3.1	Down	-	-
NM_146604	Olfactory receptor 716	Olfr716	-	-	-	-	3.2	Down	-	-
NM_173395	CDNA sequence BC056923	BC056923	-	-	-	-	3.3	Down	-	-
M400002770	M400002770	-	-	-	-	-	3.3	Down	-	-
NM_011254	Retinol binding protein 1, cellular	Rbp1	-	-	-	-	3.5	Down	-	-
XM_142154	G protein-coupled receptor associated sorting protein 2	Gprasp2	-	-	-	-	3.6	Down	-	-
XM_356911	predicted gene, EG383189	-	-	-	-	-	3.6	Up	-	-
NM_174848	CDNA sequence BC043118	BC043118	-	-	-	-	3.6	Down	-	-
NM_009301	Seminal vesicle secretory protein 5	Svs5	-	-	-	-	3.7	Down	-	-
NM_175240	Transmembrane protein 162	Tmem162	-	-	-	-	3.8	Down	-	-
NM_173764	Transmembrane anterior posterior transformation 1	Tapt1	-	-	-	-	3.8	Down	-	-
XM_130312	titin	-	-	-	-	-	4.1	Down	-	-
NM_028259	Ribosomal protein S6 kinase, polypeptide 1	Rps6kb1	-	-	-	-	4.1	Down	-	-
		2400001E08	-	-	-	-			-	-
NM_025605	RIKEN cDNA 2400001E08 gene	Rik	-	-	-	-	4.2	Down	-	-
NM_001003	Clathrin, heavy polypeptide (Hc)	Cltc	-	-	2.2	Down	4.3	Down	-	-
908			-	-	-	-			-	-
NM_177054,	M300018505	-	-	-	-	-	4.3	Down	-	-
NM_199038	M300018505	-	-	-	-	-	4.3	Down	-	-
NM_025610	Asparaginase like 1	Asrgl1	-	-	1.5	Down	-	-	-	-
XM_141020	Fibrous sheath-interacting protein 2	Fsip2	-	-	1.5	Down	-	-	-	-
XM_354696	Brain-enriched guanylate kinase-associated	Begain	-	-	1.5	Down	-	-	-	-
M400005825	M400005825	-	-	-	1.5	Down	-	-	-	-
M400005964	M400005964	-	-	-	1.5	Down	-	-	-	-

NM_007388	Acid phosphatase 5, tartrate resistant	Acp5	-	-	1.5	Up	-	-	-	-
NM_147047	Olfactory receptor 618	Olfr618	-	-	1.5	Down	-	-	-	-
XM_487124	M40000382	-	-	-	1.5	Down	-	-	-	-
NM_007475	Acidic ribosomal phosphoprotein P0	Arbp	-	-	1.5	Down	-	-	-	-
NM_011528	Transaldolase 1	Taldo1	-	-	1.5	Down	-	-	-	-
M400015100	M400015100	-	-	-	1.5	Down	-	-	-	-
M400016519	M400016519	-	-	-	1.5	Down	-	-	-	-
M400013888	M400013888	-	-	-	1.5	Down	-	-	-	-
M400018989	M400018989	-	-	-	1.5	Down	-	-	-	-
NM_183297	Neurexophilin 4	Nxph4	-	-	1.5	Down	-	-	-	-
XM_355911	Proprotein convertase subtilisin/kexin type 6	Pcsk6	-	-	1.5	Up	-	-	-	-
NM_026912	Sorting nexin 15	Snx15	-	-	1.5	Down	-	-	-	-
NM_015811	Regulator of G-protein signaling 1	Rgs1	-	-	1.5	Down	-	-	-	-
NM_198295	Thioredoxin domain containing 10	Txndc10	-	-	1.5	Down	-	-	-	-
M400016710	M400016710	-	-	-	1.5	Down	-	-	-	-
NM_009873	Cyclin-dependent kinase 6	Cdk6	-	-	1.5	Down	-	-	-	-
NM_013793	Killer cell lectin-like receptor, subfamily A, member 1	Klra1	-	-	1.5	Down	-	-	-	-
NM_016969	Myeloid-associated differentiation marker	Myadm	-	-	1.5	Down	-	-	-	-
NM_023733	Carnitine O-octanoyltransferase	Crot	-	-	1.5	Down	-	-	-	-
	Beta-1,3-glucuronyltransferase 2									
NM_172124	(glucuronosyltransferase S)	B3gat2	-	-	1.5	Down	-	-	-	-
M400016626	M400016626	-	-	-	1.5	Down	-	-	-	-
M400004620	M400004620	-	-	-	1.5	Down	-	-	-	-
M400013102	M400013102	-	-	-	1.5	Down	-	-	-	-
NM_145834	Interleukin 17C	Il17c	-	-	1.5	Down	-	-	-	-
NM_028069	Mucin-like protocadherin	Mupcdh	-	-	1.5	Down	-	-	-	-
NM_029472	Glutathione S-transferase, theta 4	Gstt4	-	-	1.5	Down	-	-	-	-
NM_172476	Transmembrane channel-like gene family 7	Tmc7	-	-	1.5	Down	-	-	-	-
M400017416	M400017416	-	-	-	1.6	Down	-	-	-	-
NM_020285,										
NM_138631	M200009269	-	-	-	1.6	Down	-	-	-	-
NM_148922	Transformed mouse 3T3 cell double minute 1	Mdm1	-	-	1.6	Down	-	-	-	-
NM_011884	RNA guanylyltransferase and 5-phosphatase	Rngtt	-	-	1.6	Down	-	-	-	-
NM_145229	CDNA sequence AY074887	AY074887	-	-	1.6	Up	-	-	-	-
M400016305	M400016305	-	-	-	1.6	Down	-	-	-	-
M400001848	M400001848	-	-	-	1.6	Down	-	-	-	-
NM_172799	Tubulin tyrosine ligase-like family, member 6	Ttll6	-	-	1.6	Down	-	-	-	-
M400001492	M400001492	-	-	-	1.6	Down	-	-	-	-
NM_027025	Adenosine A3 receptor	Adora3	-	-	1.6	Down	-	-	-	-
XM_358375	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60	-	-	-	1.6	Up	-	-	-	-
M400009319	M400009319	-	-	-	1.6	Down	-	-	-	-
NM_028298	Zinc finger protein 655	Zfp655	-	-	1.6	Down	-	-	-	-
NM_145158	Elastin microfibril interfacier 2	Emilin2	-	-	1.6	Down	-	-	-	-
M400003691	M400003691	-	-	-	1.6	Up	-	-	-	-
M400001289	M400001289	-	-	-	1.6	Down	-	-	-	-

XM_131133	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 3	-	-	-	1.6	Down	-	-	-	-
M400002222	M400002222	-	-	-	1.6	Down	-	-	-	-
M400003000	M400003000	-	-	-	1.6	Down	-	-	-	-
XM_134745	coiled-coil domain containing 151	-	-	-	1.6	Down	-	-	-	-
NM_008481	Laminin, alpha 2	Lama2	-	-	1.6	Down	-	-	-	-
NM_022989	ADP-ribosylation factor-like 6 interacting protein 6	Arl6ip6	-	-	1.6	Down	-	-	-	-
NM_138683	R-spondin homolog (Xenopus laevis)	Rspo1	-	-	1.6	Down	-	-	-	-
M400018477	M400018477	-	-	-	1.6	Down	-	-	-	-
NM_145935	Glycine-N-acyltransferase	Glyat	-	-	1.6	Down	-	-	-	-
NM_027507,										
NM_030184	M200012684	-	-	-	1.6	Down	-	-	-	-
M400003266	M400003266	-	-	-	1.6	Down	-	-	-	-
M400006824	M400006824	-	-	-	1.6	Down	-	-	-	-
M400014668	M400014668	-	-	-	1.6	Down	-	-	-	-
M400012959	M400012959	-	-	-	1.6	Down	-	-	-	-
NM_009297	Suppressor of Ty 6 homolog (S. cerevisiae)	Supt6h	-	-	1.6	Down	-	-	-	-
NM_030614	Fibroblast growth factor 16	Fgf16	-	-	1.6	Down	-	-	-	-
XM_356366	RIKEN cDNA A830080D01 gene	-	-	-	1.6	Down	-	-	-	-
NM_028303	PDZ domain containing 11	Pdzd11	-	-	1.6	Down	-	-	-	-
M400016287	M400016287	-	-	-	1.6	Down	-	-	-	-
NM_016961,										
NM_207692	M300002149	-	-	-	1.6	Down	-	-	-	-
XM_130877	guanine monphosphate synthetase	-	-	-	1.6	Down	-	-	-	-
M400005466	M400005466	-	-	-	1.6	Down	-	-	-	-
NM_013884	Chondroitin sulfate proteoglycan 5	Cspg5	-	-	1.7	Down	-	-	-	-
NM_008737	Neuropilin 1	Nrp1	-	-	1.7	Up	-	-	-	-
NM_033574	Protocadherin gamma subfamily A, 10	Pcdhga12	-	-	1.7	Down	-	-	-	-
XM_127605	M400002210	-	-	-	1.7	Down	-	-	-	-
NM_177775	DNA segment, Chr 9, ERATO Doi 280, expressed	D9Ert280e	-	-	1.7	Down	-	-	-	-
M400006408	M400006408	-	-	-	1.7	Down	-	-	-	-
M400013586	M400013586	-	-	-	1.7	Down	-	-	-	-
M400013885	M400013885	-	-	-	1.7	Down	-	-	-	-
NM_022435	Trans-acting transcription factor 5	Sp5	-	-	1.7	Down	-	-	-	-
NM_011568	THO complex 4	Thoc4	-	-	1.7	Down	-	-	-	-
M400018604	M400018604	-	-	-	1.7	Down	-	-	-	-
NM_011322	Sodium channel, voltage-gated, type I, beta	Scn1b	-	-	1.7	Down	-	-	-	-
NM_009272	Spermidine synthase	Srm	-	-	1.7	Up	-	-	-	-
NM_023835	Tripartite motif-containing 12	Trim12	-	-	1.7	Down	-	-	-	-
M300006404	M300006404	-	-	-	1.7	Down	-	-	-	-
XM_486435	immunoglobulin kappa chain variable 4-71	-	-	-	1.7	Down	-	-	-	-
M400009214	M400009214	-	-	-	1.7	Up	-	-	-	-
		2310046K01								
NM_027172	RIKEN cDNA 2310046K01 gene	Rik	-	-	1.7	Down	-	-	-	-
NM_146671	Olfactory receptor 822	Olf822	-	-	1.7	Down	-	-	-	-

NM_008857	Protein kinase C, iota	Prkci	-	-	1.7	Down	-	-	-	-
M200009252	M200009252	-	-	-	1.7	Down	-	-	-	-
XM_155879,										
XM_358948	M400003089	-	-	-	1.7	Up	-	-	-	-
NM_153572	Katanin p60 subunit A-like 1	Katnal1	-	-	1.7	Down	-	-	-	-
M300005057	M300005057	-	-	-	1.7	Down	-	-	-	-
NM_010456	Homeo box A9	Hoxa9	-	-	1.7	Down	-	-	-	-
NM_177923	Histocompatibility 2, M region locus 10.2	H2-M10.2	-	-	1.7	Down	-	-	-	-
XM_356225	M400004319	-	-	-	1.7	Down	-	-	-	-
NM_144898	Misato homolog 1 (Drosophila)	Msto1	-	-	1.7	Down	-	-	-	-
M200008278	M200008278	-	-	-	1.7	Down	-	-	-	-
M400005813	M400005813	-	-	-	1.7	Up	-	-	-	-
NM_018787	Neuropeptide FF-amide peptide precursor	Npff	-	-	1.7	Down	-	-	-	-
NM_178744	Zinc finger and BTB domain containing 1	Zbtb1	-	-	1.7	Down	-	-	-	-
XM_130253	cytochrome b reductase 1	-	-	-	1.7	Down	-	-	-	-
NM_183143	CDNA sequence BC048679	BC048679	-	-	1.7	Down	-	-	-	-
XM_136366	Predicted gene, EG226601	EG226601	-	-	1.7	Down	-	-	-	-
NM_007588	Calcitonin receptor	Calcr	-	-	1.7	Down	-	-	-	-
M300004503	M300004503	-	-	-	1.7	Down	-	-	-	-
		2010311D03								
NM_133839	RIKEN cDNA 2010311D03 gene	Rik	-	-	1.7	Down	-	-	-	-
XM_129603	Tudor domain containing 5	Tdrd5	-	-	1.7	Down	-	-	-	-
XM_484151	RIKEN cDNA A430041B07 gene	-	-	-	1.7	Down	-	-	-	-
XM_484805	cytochrome P450, family 2, subfamily c, polypeptide 68	-	-	-	1.7	Up	-	-	-	-
	Solute carrier family 25 (mitochondrial carrier, brain), member 14	Slc25a14	-	-	1.7	Down	-	-	-	-
NM_011398										
XM_139040	M400004109	-	-	-	1.7	Up	-	-	-	-
M400005256	M400005256	-	-	-	1.8	Down	-	-	-	-
NM_011795	Complement component 1, q subcomponent-like 1	C1ql1	-	-	1.8	Down	-	-	-	-
XM_356602	AHNAK nucleoprotein 2	-	-	-	1.8	Up	-	-	-	-
NM_021384	Radical S-adenosyl methionine domain containing 2	Rsad2	-	-	1.8	Down	-	-	-	-
NM_182783	CDNA sequence BC030183	BC030183	-	-	1.8	Up	-	-	-	-
	A disintegrin-like and metalloproteinase (reprolysin type) with thrombospondin type 1 motif, 1	Adamts1	-	-	1.8	Down	-	-	-	-
NM_009621										
M300006489	M300006489	-	-	-	1.8	Down	-	-	-	-
NM_146228	ALS2 C-terminal like	Als2cl	-	-	1.8	Down	-	-	-	-
XM_110709,										
XM_359307	M300005845	-	-	-	1.8	Up	-	-	-	-
M400015148	M400015148	-	-	-	1.8	Down	-	-	-	-
XM_142305	RIKEN cDNA A630018P17 gene	-	-	-	1.8	Down	-	-	-	-
M400018194	M400018194	-	-	-	1.8	Down	-	-	-	-
M400001112	M400001112	-	-	-	1.8	Down	-	-	-	-
NM_172300	Ubiquitin-conjugating enzyme E2Z (putative)	Ube2z	-	-	1.8	Down	-	-	-	-
M400017644	M400017644	-	-	-	1.8	Down	-	-	-	-
XM_357872	RIKEN cDNA 2900075B16 gene	2900075B16	-	-	1.8	Down	-	-	-	-

M400008355	M400008355	Rik	-	-	-	1.8	Up	-	-	-	-
XM_133827	MYC-associated zinc finger protein (purine-binding transcription factor)		-	-	-	1.8	Down	-	-	-	-
NM_172994	Protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), gamma isoform	Ppp2r2c	-	-	-	1.8	Down	-	-	-	-
M400017110	M400017110		-	-	-	1.8	Down	-	-	-	-
M300004807	M300004807		-	-	-	1.8	Down	-	-	-	-
M400014857	M400014857		-	-	-	1.8	Up	-	-	-	-
NM_010410	Hypocretin	Hcrt	-	-	-	1.8	Down	-	-	-	-
M400010256	M400010256		-	-	-	1.8	Up	-	-	-	-
M200003188	M200003188		-	-	-	1.8	Down	-	-	-	-
NM_178337	Tubulin-specific chaperone e	Tbce	-	-	-	1.8	Down	-	-	-	-
NM_009332	Transcription factor 3	Tcf3	-	-	-	1.8	Down	-	-	-	-
M400015332	M400015332		-	-	-	1.8	Down	-	-	-	-
M300019696	M300019696		-	-	-	1.8	Down	-	-	-	-
M400004110	M400004110		-	-	-	1.8	Down	-	-	-	-
NM_145539	Transmembrane 4 superfamily member 4	Tm4sf4	-	-	-	1.8	Down	-	-	-	-
NM_153052	Granzyme N	Gzmn	-	-	-	1.9	Down	-	-	-	-
M400013528	M400013528		-	-	-	1.9	Down	-	-	-	-
M300009100	M300009100		-	-	-	1.9	Down	-	-	-	-
M400015932	M400015932		-	-	-	1.9	Down	-	-	-	-
NM_011867	Solute carrier family 26, member 4	Slc26a4	-	-	-	1.9	Down	-	-	-	-
NM_021467	Troponin I, skeletal, slow 1	Tnni1	-	-	-	1.9	Down	-	-	-	-
NM_021559	Zinc finger protein 191	Zfp191	-	-	-	1.9	Down	-	-	-	-
M400016721	M400016721		-	-	-	1.9	Down	-	-	-	-
M400018516	M400018516		-	-	-	1.9	Down	-	-	-	-
NM_030211	Potassium channel tetramerisation domain containing 18	Kctd18	-	-	-	1.9	Down	-	-	-	-
NM_023396	Reprimo, TP53 dependent G2 arrest mediator candidate	Rprm	-	-	-	1.9	Down	-	-	-	-
XM_112129,											
XM_290036	M400002632		-	-	-	1.9	Down	-	-	-	-
M200009797	M200009797		-	-	-	1.9	Down	-	-	-	-
NM_028965	Sorting nexin 11	Snx11	-	-	-	1.9	Down	-	-	-	-
M400005322	M400005322		-	-	-	1.9	Down	-	-	-	-
NM_026915	Lysozyme-like 4	Lyzl4	-	-	-	1.9	Down	-	-	-	-
NM_153805	Protein kinase N3	Pkn3	-	-	-	1.9	Down	-	-	-	-
NM_181854	Zinc finger protein 828	Zfp828	-	-	-	1.9	Down	-	-	-	-
NM_133753	ERBB receptor feedback inhibitor 1	Errfi1	-	-	-	1.9	Down	-	-	-	-
M400001453	M400001453		-	-	-	2.0	Down	-	-	-	-
NM_009154	Sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (	Sema5a	-	-	-	2.0	Down	-	-	-	-
NM_013915	Zinc finger protein 238	Zfp238	-	-	-	2.0	Down	-	-	-	-

M400004033	M400004033	-	-	-	2.0	Down	-	-	-	-
NM_023508	Phosducin-like 2	Pdcl2	-	-	2.0	Down	-	-	-	-
M400005757	M400005757	-	-	-	2.0	Down	-	-	-	-
XM_484258	M400003778	-	-	-	2.0	Down	-	-	-	-
NM_152823	Unc-5 homolog C (C. elegans)-like	Unc5cl	-	-	2.0	Down	-	-	-	-
M400001775	M400001775	-	-	-	2.0	Up	-	-	-	-
NM_183133	M400001908	-	-	-	2.0	Down	-	-	-	-
M300000978	M300000978	-	-	-	2.0	Down	-	-	-	-
NM_013527	Growth differentiation factor 7	Gdf7	-	-	2.0	Down	-	-	-	-
M400006812	M400006812	-	-	-	2.0	Down	-	-	-	-
NM_032394	Myosin VIIb	Myo7b	-	-	2.0	Down	-	-	-	-
XM_355044	gene model 944, (NCBI)	-	-	-	2.0	Down	-	-	-	-
NM_019935	OVO homolog-like 1 (Drosophila)	Ovol1	-	-	2.0	Down	-	-	-	-
M400003613	M400003613	-	-	-	2.0	Down	-	-	-	-
NM_025866	Cell division cycle associated 7	Cdca7	-	-	2.0	Down	-	-	-	-
NM_009679	Adaptor protein complex AP-2, mu1	Ap2m1	-	-	2.0	Down	-	-	-	-
NM_010200	Fibroblast growth factor 13	Fgf13	-	-	2.0	Up	-	-	-	-
NM_008314	5-hydroxytryptamine (serotonin) receptor 5A	Htr5a	-	-	2.0	Down	-	-	-	-
M400009384	M400009384	-	-	-	2.0	Down	-	-	-	-
M400016290	M400016290	-	-	-	2.0	Down	-	-	-	-
XM_355937	RIKEN cDNA 2010110P09 gene	-	-	-	2.0	Down	-	-	-	-
NM_011282	Ros1 proto-oncogene	Ros1	-	-	2.0	Down	-	-	-	-
XM_354889	keratin 81	-	-	-	2.0	Down	-	-	-	-
M400018636	M400018636	-	-	-	2.0	Down	-	-	-	-
XM_131888	GTP-binding protein 10 (putative)	-	-	-	2.0	Down	-	-	-	-
NM_019450	Interleukin 1 family, member 6	Il1f6	-	-	2.0	Down	-	-	-	-
M400002318	M400002318	-	-	-	2.0	Down	-	-	-	-
NM_145216	RAS-like, family 10, member A	Rasl10a	-	-	2.0	Down	-	-	-	-
NM_029537	Transmembrane protein 98	Tmem98	-	-	2.1	Down	-	-	-	-
M400005678	M400005678	-	-	-	2.1	Down	-	-	-	-
XM_129483	zinc finger, RAN-binding domain containing 3	-	-	-	2.1	Down	-	-	-	-
M300003550	M300003550	-	-	-	2.1	Down	-	-	-	-
NM_153418	CDNA sequence U46068	U46068	-	-	2.1	Up	-	-	-	-
NM_010104	Endothelin 1	Edn1	-	-	2.1	Down	-	-	-	-
NM_011835	Katanin p60 (ATPase-containing) subunit A1	Katna1	-	-	2.1	Down	-	-	-	-
NM_027028	RIKEN cDNA 1700008P20 gene	-	-	-	2.1	Down	-	-	-	-
XM_130487	Cystatin 12	Cst12	-	-	2.1	Down	-	-	-	-
NM_001003										
667	Keratin 77	Krt77	-	-	2.1	Up	-	-	-	-
		D330028D13								
NM_172727	RIKEN cDNA D330028D13 gene	Rik	-	-	2.1	Down	-	-	-	-
XM_354569	RIKEN cDNA 5033413D22 gene	-	-	-	2.1	Down	-	-	-	-
M400015920	M400015920	-	-	-	2.1	Down	-	-	-	-
NM_010143	Eph receptor B3	Ephb3	-	-	2.1	Down	-	-	-	-
NM_177045	Coiled-coil and C2 domain containing 1B	Cc2d1b	-	-	2.2	Down	-	-	-	-

NM_019748	SUMO1 activating enzyme subunit 1	Sae1	-	-	2.2	Down	-	-	-	-
NM_020333	Solute carrier family 12, member 5	Slc12a5	-	-	2.2	Down	-	-	-	-
NM_153170	Solute carrier family 36 (proton/amino acid symporter), member 2	Slc36a2	-	-	2.2	Down	-	-	-	-
M300015558	M300015558	-	-	-	2.2	Down	-	-	-	-
NM_001003										
960,NM_001003961,NM_001003963,										
NM_010068	M200016018	-	-	-	2.2	Down	-	-	-	-
XM_488563,										
XM_489917	M400013203	-	-	-	2.2	Down	-	-	-	-
	Solute carrier family 18 (vesicular monoamine), member 1	Slc18a1	-	-	2.2	Up	-	-	-	-
NM_153054	M400010473	-	-	-	2.2	Up	-	-	-	-
M400010473	M400010473	-	-	-	2.2	Up	-	-	-	-
NM_177009	SET and MYND domain containing 4	-	-	-	2.2	Down	-	-	-	-
M400008530	M400008530	-	-	-	2.2	Down	-	-	-	-
M400007862	M400007862	-	-	-	2.2	Up	-	-	-	-
NM_009624	Adenylate cyclase 9	Adcy9	-	-	2.2	Down	-	-	-	-
M400002994	M400002994	-	-	-	2.3	Down	-	-	-	-
M400014478	M400014478	-	-	-	2.3	Down	-	-	-	-
NM_012055	Asparagine synthetase	Asns	-	-	2.3	Down	-	-	-	-
		4930503E14								
NM_029131	RIKEN cDNA 4930503E14 gene	Rik	-	-	2.3	Down	-	-	-	-
NM_183270	Coiled-coil-helix-coiled-coil-helix domain containing 8	Chchd8	-	-	2.3	Down	-	-	-	-
NM_013526	Growth differentiation factor 6	Gdf6	-	-	2.3	Down	-	-	-	-
NM_016770	Folate hydrolase	Folh1	-	-	2.3	Down	-	-	-	-
NM_010254	Galanin receptor 2	Galr2	-	-	2.3	Down	-	-	-	-
M400017275	M400017275	-	-	-	2.3	Down	-	-	-	-
NM_011878	T-cell lymphoma invasion and metastasis 2	Tiam2	-	-	2.3	Down	-	-	-	-
	DCN1, defective in cullin neddylation 1, domain containing 3 (S. cerevisiae)	Dcun1d3	-	-	2.3	Down	-	-	-	-
NM_173408	Trichohyalin-like 1	Tchhl1	-	-	2.3	Down	-	-	-	-
NM_027762	Trichohyalin-like 1	Tchhl1	-	-	2.3	Down	-	-	-	-
NM_018826	Iroquois related homeobox 5 (Drosophila)	Irx5	-	-	2.3	Down	-	-	-	-
M400006724	M400006724	-	-	-	2.3	Down	-	-	-	-
M400001023	M400001023	-	-	-	2.4	Down	-	-	-	-
M400009410	M400009410	-	-	-	2.4	Up	-	-	-	-
NM_194462	A kinase (PRKA) anchor protein (yotiao) 9	Akap9	-	-	2.4	Down	-	-	-	-
XM_135029	CDNA sequence BC023892	BC023892	-	-	2.4	Down	-	-	-	-
NM_008977	Protein tyrosine phosphatase, non-receptor type 2	Ptpn2	-	-	2.4	Down	-	-	-	-
NM_009229	Syntrophin, basic 2	Sntpb2	-	-	2.4	Down	-	-	-	-
NM_010748	Lysosomal trafficking regulator	Lyst	-	-	2.4	Down	-	-	-	-
NM_013678	Surfeit gene 2	Surf2	-	-	2.4	Up	-	-	-	-
NM_027453	Basic transcription factor 3-like 4	Btf3l4	-	-	2.4	Down	-	-	-	-
M400019261	M400019261	-	-	-	2.5	Down	-	-	-	-

NM_181796	Glutathione S-transferase, pi 2	Gstp2	-	-	2.5	Up	-	-	-	-
XM_134088	RAB11 family interacting protein 1 (class I)	-	-	-	2.5	Down	-	-	-	-
M400002964	M400002964	-	-	-	2.5	Down	-	-	-	-
M400001789	M400001789	-	-	-	2.5	Down	-	-	-	-
M400014816	M400014816	-	-	-	2.5	Down	-	-	-	-
NM_177165	RIKEN cDNA F630111L10 gene	-	-	-	2.5	Up	-	-	-	-
		1110006G06								
NM_028661	RIKEN cDNA 1110006G06 gene	Rik	-	-	2.5	Down	-	-	-	-
M300003282	M300003282	-	-	-	2.5	Down	-	-	-	-
X56062	LHCA1	LHCA1	-	-	2.6	Down	-	-	-	-
M300015441	M300015441	-	-	-	2.6	Down	-	-	-	-
M300005681	M300005681	-	-	-	2.6	Down	-	-	-	-
XM_134736	zinc finger protein 26	-	-	-	2.6	Down	-	-	-	-
M200013499	M200013499	-	-	-	2.6	Down	-	-	-	-
		2010107E04								
NM_027360	RIKEN cDNA 2010107E04 gene	Rik	-	-	2.6	Up	-	-	-	-
NM_025285	Stathmin-like 2	Stmn2	-	-	2.6	Down	-	-	-	-
XM_489790	M400009045	-	-	-	2.7	Up	-	-	-	-
NM_015826	Doublesex and mab-3 related transcription factor 1	Dmrt1	-	-	2.7	Down	-	-	-	-
M400013658	M400013658	-	-	-	2.7	Down	-	-	-	-
NM_153779	Apoptosis-inducing factor, mitochondrion-associated 2	Aifm2	-	-	2.7	Down	-	-	-	-
NM_173023	Cation channel, sperm-associated, beta	Catsperb	-	-	2.7	Down	-	-	-	-
M300009172	M300009172	-	-	-	2.7	Down	-	-	-	-
NM_007656	CD82 antigen	Cd82	-	-	2.7	Down	-	-	-	-
	Protein phosphatase 1, regulatory (inhibitor) subunit 16B	Ppp1r16b	-	-	2.8	Down	-	-	-	-
NM_153089	Acetyl-Coenzyme A acyltransferase 1B	Acaa1b	-	-	2.8	Down	-	-	-	-
NM_146230	M400015058	-	-	-	2.8	Up	-	-	-	-
M400015058	M400015058	-	-	-	2.8	Up	-	-	-	-
M400017475	M400017475	-	-	-	2.8	Down	-	-	-	-
M400013628	M400013628	-	-	-	2.8	Down	-	-	-	-
NM_175217	Monocyte to macrophage differentiation-associated 2	Mmd2	-	-	2.8	Down	-	-	-	-
XM_284494	DEAD (Asp-Glu-Ala-Asp) box polypeptide 10	-	-	-	2.8	Down	-	-	-	-
M300004000	M300004000	-	-	-	2.9	Down	-	-	-	-
M400015504	M400015504	-	-	-	2.9	Down	-	-	-	-
M400003207	M400003207	-	-	-	2.9	Up	-	-	-	-
NM_198127	Abl-interactor 2	Abi2	-	-	3.0	Down	-	-	-	-
NM_007824	Cytochrome P450, family 7, subfamily a, polypeptide 1	Cyp7a1	-	-	3.0	Down	-	-	-	-
M400019480	M400019480	-	-	-	3.0	Down	-	-	-	-
M200015784	M200015784	-	-	-	3.0	Down	-	-	-	-
NM_009451	Tubulin, beta 4	Tubb4	-	-	3.0	Down	-	-	-	-
M400014741	M400014741	-	-	-	3.0	Down	-	-	-	-
NM_009802	Carbonic anhydrase 6	Car6	-	-	3.1	Down	-	-	-	-
NM_053165	C-type lectin domain family 2, member h	Clec2h	-	-	3.2	Down	-	-	-	-
NM_011170	Prion protein	Prnp	-	-	3.2	Down	-	-	-	-
M400015178	M400015178	-	-	-	3.2	Down	-	-	-	-



M400015661	M400015661	-	-	-	3.3	Down	-	-	-	-
XM_127972	PDZ domain containing 2	-	-	-	3.4	Down	-	-	-	-
XM_358375	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60	-	-	-	3.5	Up	-	-	-	-
NM_013530	Guanine nucleotide binding protein (G protein), beta 3	Gnb3	-	-	3.5	Down	-	-	-	-
XM_483891	M400007988	-	-	-	3.5	Down	-	-	-	-
XM_484472	M400003054	-	-	-	3.5	Down	-	-	-	-
NM_144842	Zinc finger, MYM-type 5	Zmym5	-	-	3.5	Down	-	-	-	-
		5830433M19								
NM_026368	RIKEN cDNA 5830433M19 gene	Rik	-	-	3.5	Down	-	-	-	-
M400007512	M400007512	-	-	-	3.5	Down	-	-	-	-
	Ubiquinol-cytochrome c reductase, Rieske iron-sulfur									
NM_025710	polypeptide 1	Uqcrfs1	-	-	3.5	Down	-	-	-	-
NM_153581	Glycoprotein m6a	Gpm6a	-	-	3.6	Down	-	-	-	-
NM_010795	Mannoside acetylglucosaminyltransferase 3	Mgat3	-	-	3.8	Down	-	-	-	-
M400007893	M400007893	-	-	-	3.9	Down	-	-	-	-
NM_028761	Poly(A)-specific ribonuclease (deadenylation nuclease)	Parn	-	-	4.0	Down	-	-	-	-
XM_133092	killer cell lectin-like receptor subfamily G, member 2	-	-	-	4.1	Down	-	-	-	-
XM_129817	RIKEN cDNA 4930408G06 gene	-	-	-	4.2	Down	-	-	-	-
NM_007718	Chemokine (C-C motif) receptor 1-like 1	Ccr11	-	-	4.3	Down	-	-	-	-
XM_125626	minichromosome maintenance complex component 9	-	1.5	Up	-	-	-	-	-	-
M400000207	M400000207	-	1.5	Up	-	-	-	-	-	-
NM_145968	T-cell activation Rho GTPase-activating protein	Tagap	1.5	Down	-	-	-	-	-	-
NM_133786	Structural maintenance of chromosomes 4	Smc4	1.5	Down	-	-	-	-	-	-
NM_026201	Cell division cycle and apoptosis regulator 1	Ccar1	1.6	Down	-	-	-	-	-	-
	Sema domain, immunoglobulin domain (Ig), short basic									
NM_011349	domain, secreted, (semaphorin) 3F	Sema3f	1.6	Up	-	-	-	-	-	-
XM_134865	pygopus 1	-	1.6	Up	-	-	-	-	-	-
NM_153422	Phosphodiesterase 5A, cGMP-specific	Pde5a	1.6	Up	-	-	-	-	-	-
NM_138671	NAD kinase	Nadk	1.6	Up	-	-	-	-	-	-
NM_009160	Surfactant associated protein D	Sftpd	1.6	Up	-	-	-	-	-	-
NM_023910	TSC22 domain family 4	Tsc22d4	1.7	Down	-	-	-	-	-	-
NM_010177	Fas ligand (TNF superfamily, member 6)	Fasl	1.7	Up	-	-	-	-	-	-
NM_025836	Mannose-6-phosphate receptor binding protein 1	M6prbp1	1.7	Down	-	-	-	-	-	-
NM_010556	Interleukin 3	Il3	1.7	Up	-	-	-	-	-	-
M400016527	M400016527	-	1.7	Up	-	-	-	-	-	-
M400001548	M400001548	-	1.8	Up	-	-	-	-	-	-
M400005384	M400005384	-	2.0	Up	-	-	-	-	-	-
M400002289	M400002289	-	2.0	Up	-	-	-	-	-	-
XM_135814	EF-hand domain (C-terminal) containing 2	-	2.0	Up	-	-	-	-	-	-
M200009890	M200009890	-	2.1	Up	-	-	-	-	-	-
NM_021347	Gasdermin A1	Gsdma1	2.2	Up	-	-	-	-	-	-
NM_146969	Olfactory receptor 1243	Olf1243	2.2	Up	-	-	-	-	-	-
NM_026720	Ankyrin repeat domain 13 family, member D	Ankrd13d	2.3	Up	-	-	-	-	-	-
NM_011072	Profilin 1	Pfn1	2.3	Down	-	-	-	-	-	-



## APPENDIX II

**Appendix II: Genes uniquely differentially regulated in the spleen of infected mice in response to infection with *F. tularensis* Schu4 and LVS.** Global transcriptional data from the spleens of infected mice were compared to uninfected mice, log transformed, and subjected to ANOVA and Benjamini and Hochberg false positive correction. Genes that were differentially regulated by 1.5 fold or more with a variance less than 0.05 were considered significant. Genes of interest are discussed in depth in Chapter 3.

Other ID	Gene Name	Gene ID	<i>Schu4</i> Infection								
			12	Direction	24	Direction	48	Direction	120	Direction	
NM_018743	1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosphatidic acid acyltransferase, zeta)	Agpat6	-	-	-	-	-	-	-	1.8	Down
NM_011853	2-5 oligoadenylate synthetase 1B	-	-	-	-	-	2.1	Down	-	2.0	Down
NM_145227	2-5 oligoadenylate synthetase 2	Oas2	-	-	-	-	-	-	-	2.4	Up
NM_011854	2-5 oligoadenylate synthetase-like 2	Oasl2	-	-	-	-	-	-	-	1.9	Down
NM_026172	2,4-dienoyl CoA reductase 1, mitochondrial	Decr1	-	-	1.7	Down	-	-	-	-	-
XM_127578	3-oxoacyl-ACP synthase, mitochondrial	-	-	-	-	-	-	-	-	1.5	Up
NM_009614	A disintegrin and metalloproteinase domain 15 (metargidin)	Adam15	-	-	-	-	-	-	-	2.0	Up
NM_031185	A kinase (PRKA) anchor protein (gravin) 12	Akap12	-	-	-	-	-	-	-	1.6	Up
XM_357160	absent in melanoma 2	-	-	-	-	-	-	-	-	3.0	Down
NM_153420	Acid phosphatase-like 2	Acpl2	-	-	-	-	-	-	-	2.3	Down
NM_009672	Acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	Anp32a	-	-	-	-	-	-	-	1.9	Down

NM_025271	Actin-like 7b	Actl7b	-	-	-	-	-	-	-	2.4	Down
NM_007498	Activating transcription factor 3	Atf3	-	-	-	-	-	-	-	2.6	Down
NM_146226	Acylpeptide hydrolase	Apeh	-	-	-	-	-	-	-	2.0	Down
NM_029505	Adaptor-related protein complex 3, mu 2 subunit	Ap3m2	-	-	-	-	-	-	-	2.2	Down
NM_0010054	Adhesion molecule, interacts with CXADR antigen 1	Amica1	-	-	-	-	-	-	-	3.2	Up
21	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited)	-	-	-	-	-	-	-	-	2.0	Down
XM_129376	ADP-ribosylation factor interacting protein 2	Arfp2	-	-	-	-	-	-	-	2.6	Up
NM_029802	ADP-ribosylation factor-like 5A	Arl5a	-	-	-	-	-	-	-	4.0	Up
NM_182994	ADP-ribosylation factor-like 5C	Arl5c	-	-	-	-	-	-	-	1.7	Up
NM_207231	Adrenomedullin	Adm	-	-	-	-	-	-	-	2.9	Up
NM_009627	Alanine-glyoxylate aminotransferase 2-like 2	Agxt2l2	-	-	1.7	Up	-	-	-	-	-
NM_028398	Aldehyde dehydrogenase 3 family, member B2	Aldh3b2	-	-	-	-	-	-	-	2.0	Down
XM_129134	Aldo-keto reductase family 1, member B8	Akr1b7	-	-	-	-	-	-	-	3.2	Down
NM_009731	Alpha fetoprotein	Afp	-	-	-	-	-	-	-	1.6	Down
NM_007423	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region gene 1 homolog (human)	Ammecr1	-	-	-	-	-	-	-	2.4	Down
NM_019496	Aminoacidase aminotransferase	Aadat	-	-	-	-	-	-	-	1.8	Down
NM_011834	amylo-1,6-glucosidase, 4-alpha-glucanotransferase	-	-	-	-	-	-	-	-	1.9	Down
XM_131166	Amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 12 (human)	Als2cr12	-	-	-	-	-	-	-	2.8	Down
NM_175370	Androgen binding protein epsilon	Abpe	-	-	-	-	-	-	-	1.7	Down
NM_207262	Androgen-binding protein eta	Apbh	-	-	-	-	-	-	-	3.3	Up
NM_020563	Angel homolog 1 (Drosophila)	Angel1	-	-	-	-	-	-	-	2.1	Down
NM_144524	Anillin, actin binding protein (scraps homolog, Drosophila)	Anln	-	-	-	-	-	-	-	2.2	Down
NM_028390	Ankyrin repeat and kinase domain containing 1	Ankk1	-	-	-	-	-	-	-	2.4	Down
NM_172922	Ankyrin repeat domain 1 (cardiac muscle)	Ankrd1	-	-	-	-	-	-	-	1.8	Down
NM_013468	Ankyrin repeat domain 22	Ankrd22	-	-	-	-	-	-	-	2.8	Up
NM_024204	Ankyrin repeat domain 27 (VPS9 domain)	Ankrd27	-	-	-	-	-	-	-	1.7	Down
NM_145633	ankyrin repeat domain 53	-	-	-	-	-	-	-	-	4.0	Down
XM_144855	Annexin A1	Anxa1	-	-	-	-	-	-	-	2.0	Up
NM_010730	Annexin A11	Anxa11	-	-	1.5	Up	1.5	Up	-	-	-
NM_013469	Anterior pharynx defective 1a homolog (C. elegans)	Aph1a	-	-	-	-	1.9	Up	-	1.9	Up
NM_146104	antigen identified by monoclonal antibody Ki 67	-	-	-	-	-	-	-	-	1.7	Down
XM_133912	Apolipoprotein C-I	Apoc1	-	-	-	-	-	-	-	2.3	Down
NM_007469	Apolipoprotein L 9a	Apol9a	1.8	Up	-	-	-	-	-	-	-
XM_128064	Apolipoprotein O	Apoo	-	-	-	-	-	-	-	1.6	Down
NM_026673	Apoptosis inhibitor 5	Api5	-	-	-	-	-	-	-	4.0	Down
NM_007466	Apoptosis-inducing, TAF9-like domain 1	Apitd1	-	-	-	-	-	-	-	2.0	Down
NM_027263	Aquaporin 3	Aqp3	-	-	-	-	-	-	-	2.2	Down
NM_016689	Arginase 1, liver	Arg1	-	-	-	-	-	-	-	3.1	Up
NM_007482											

NM_146205	Armadillo repeat containing 5	Armc5	-	-	-	-	-	-	2.3	Down
NM_019785	ARP10 actin-related protein 10 homolog (S. cerevisiae)	Actr10	-	-	-	-	-	-	2.3	Down
XM_128722	arrestin domain containing 5	-	-	-	-	-	-	-	4.3	Up
NM_016666	Aryl-hydrocarbon receptor-interacting protein	Aip	-	-	2.1	Up	-	-	-	-
NM_024184	ASF1 anti-silencing function 1 homolog B (S. cerevisiae)	Asf1b	-	-	-	-	-	-	2.6	Down
NM_026247	Asparagine-linked glycosylation 13 homolog (S. cerevisiae)	Alg13	-	-	-	-	-	-	2.4	Down
NM_026414	Aspartic peptidase, retroviral-like 1	Asprv1	-	-	-	-	-	-	2.3	Up
NM_007880	AT rich interactive domain 3A (Bright like)	Arid3a	-	-	-	-	1.7	Up	3.2	Up
NM_029654	ATG2 autophagy related 2 homolog B (S. cerevisiae)	Atg2b	-	-	-	-	-	-	1.5	Down
NM_138597	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	Atp5o	-	-	-	-	-	-	2.4	Up
NM_026458	ATP-binding cassette, sub-family A (ABC1), member 14	Abca14	-	-	1.9	Down	-	-	2.6	Down
NM_007379	ATP-binding cassette, sub-family A (ABC1), member 2	Abca2	-	-	-	-	2.0	Up	-	-
NM_013790	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	Abcc5	-	-	-	-	-	-	2.6	Down
NM_011994	ATP-binding cassette, sub-family D (ALD), member 2	Abcd2	-	-	-	-	-	-	2.4	Down
NM_174849	ATP/GTP binding protein-like 5	Agbl5	-	-	-	-	-	-	1.8	Up
NM_025504	ATP5S-like	Atp5sl	-	-	-	-	-	-	2.5	Down
NM_016745	ATPase, Ca++ transporting, ubiquitous	Atp2a3	-	-	-	-	1.9	Up	-	-
NM_172669	Autophagy/beclin 1 regulator 1	Ambra1	-	-	-	-	-	-	2.2	Up
XM_127501	B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB	-	-	-	-	-	-	-	2.9	Down
NM_009742	B-cell leukemia/lymphoma 2 related protein A1a	Bcl2a1a	-	-	-	-	-	-	2.2	Up
NM_007535	B-cell leukemia/lymphoma 2 related protein A1c	Bcl2a1c	-	-	-	-	-	-	1.7	Down
NM_025631	Bactericidal/permeability-increasing protein-like 1	Bpil1	-	-	-	-	-	-	1.8	Down
NM_144558	Basic, immunoglobulin-like variable motif containing	Bivm	-	-	-	-	-	-	1.8	Down
NM_153787	BCL2-associated transcription factor 1	Bclaf1	-	-	-	-	-	-	2.4	Down
NM_173404	Bone morphogenetic protein 3	Bmp3	-	-	-	-	-	-	2.3	Down
NM_174991	Brain-specific angiogenesis inhibitor 1	Bai1	-	-	-	-	-	-	2.6	Down
NM_199195	Branched chain ketoacid dehydrogenase E1, beta polypeptide	Bckdhb	-	-	-	-	1.8	Up	-	-
NM_023323	Brix domain containing 1	Bxdc1	-	-	-	-	-	-	1.7	Down
XM_129248	BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, (Mot1 homolog, S. cerevisiae)	-	-	-	-	-	-	-	2.0	Down
NM_007520	BTB and CNC homology 1	Bach1	-	-	-	-	-	-	1.7	Down
NM_009773	Budding uninhibited by benzimidazoles 1 homolog, beta (S. cerevisiae)	Bub1b	-	-	-	-	-	-	2.2	Down
NM_009594	C-abl oncogene 1, receptor tyrosine kinase	Abl1	-	-	-	-	-	-	1.9	Down
NM_008587	C-mer proto-oncogene tyrosine kinase	Mertk	-	-	-	-	-	-	1.9	Down
NM_027218	C-type lectin domain family 4, member b1	Clec4b1	-	-	-	-	-	-	3.2	Down
NM_028331	C1q and tumor necrosis factor related protein 6	C1qtnf6	-	-	-	-	-	-	2.4	Up
NM_026125	C1q domain containing 2	C1qdc2	-	-	-	-	-	-	1.7	Down
XM_283264	cadherin 10	-	-	-	-	-	-	-	1.6	Down
NM_174988	Cadherin 22	Cdh22	-	-	-	-	-	-	1.6	Down
NM_007665	Cadherin 3	Cdh3	-	-	1.9	Up	-	-	-	-

NM_009868	Cadherin 5	Cdh5	-	-	-	-	1.5	Up	-	-
XM_356089	Calcium and integrin binding family member 3	Cib3	-	-	-	-	-	-	1.7	Down
NM_009792	Calcium/calmodulin-dependent protein kinase II alpha	Camk2a	-	-	-	-	-	-	2.4	Down
NM_020036	Calmodulin 4	Calm4	-	-	-	-	-	-	1.6	Down
NM_133828	CAMP responsive element binding protein 1	Creb1	-	-	-	-	-	-	2.1	Down
NM_145365	CAMP responsive element binding protein 3-like 3	Creb3l3	-	-	-	-	-	-	3.3	Up
NM_009924	Cannabinoid receptor 2 (macrophage)	Cnr2	-	-	-	-	-	-	1.9	Down
NM_007599	Capping protein (actin filament), gelsolin-like	Capg	-	-	1.5	Up	-	-	-	-
NM_028117	Carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 14	Chst14	-	-	-	-	-	-	3.7	Up
NM_021439	Carbohydrate sulfotransferase 11	Chst11	-	-	-	-	2.1	Up	-	-
NM_021528	Carbohydrate sulfotransferase 12	Chst12	-	-	-	-	-	-	3.0	Up
NM_009799	Carbonic anhydrase 1	Car1	-	-	1.7	Up	-	-	-	-
NM_181588	Carboxymethylenebutenolidase-like (Pseudomonas)	Cmb1	-	-	-	-	-	-	2.5	Down
NM_023821	cardiomyopathy associated 5	-	-	-	2.0	Up	-	-	-	-
XM_283813	Cas scaffolding protein family member 4	-	-	-	-	-	2.4	Up	-	-
NM_009811	Caspase 6	Casp6	-	-	-	-	-	-	1.5	Down
NM_007744	Catechol-O-methyltransferase	Comt	-	-	-	-	-	-	2.2	Down
NM_009983	Cathepsin D	Ctsd	-	-	-	-	-	-	1.9	Down
NM_009883	CCAAT/enhancer binding protein (C/EBP), beta	Cebpb	-	-	-	-	-	-	2.7	Up
NM_028082	CCR4-NOT transcription complex, subunit 2	Cnot2	-	-	1.6	Up	-	-	-	-
NM_212484	CCR4-NOT transcription complex, subunit 6	Cnot6	-	-	-	-	-	-	3.5	Down
NM_009847	CD2-associated protein	Cd2ap	-	-	-	-	-	-	2.4	Down
NM_031162	CD247 antigen	Cd247	-	-	-	-	-	-	2.2	Down
XM_284241	CD27 antigen	-	-	-	-	-	-	-	1.6	Down
NM_021893	CD274 antigen	Cd274	-	-	-	-	-	-	1.8	Up
NM_009850	CD3 antigen, gamma polypeptide	Cd3g	-	-	-	-	-	-	1.8	Down
NM_199225	CD300C antigen	Cd300c	-	-	-	-	-	-	2.8	Down
NM_172050	CD300e antigen	Cd300e	-	-	-	-	-	-	3.9	Down
NM_019421	CD320 antigen	Cd320	-	-	-	-	-	-	2.1	Down
NM_009851	CD44 antigen	Cd44	-	-	-	-	-	-	3.1	Down
NM_009690	CD5 antigen-like	Cd5l	-	-	-	-	-	-	3.4	Down
NM_016904	CDC28 protein kinase 1b	Cks1b	-	-	-	-	-	-	2.9	Down
		Cdc42ep								
NM_027219	CDC42 effector protein (Rho GTPase binding) 1	1	-	-	-	-	1.5	Up	-	-
NM_025902	CDGSH iron sulfur domain 2	Cisd2	-	-	-	-	-	-	1.8	Up
		Cdk5rap								
NM_145990	CDK5 regulatory subunit associated protein 2	2	-	-	-	-	-	-	2.7	Down
NM_172407	CDKN2A interacting protein	Cdkn2aip	-	-	-	-	-	-	1.6	Down
		BC00388								
NM_198609	CDNA sequence BC003885	5	-	-	-	-	-	-	1.7	Up
XM_203523	cDNA sequence BC003940	-	-	-	-	-	-	-	2.2	Down
NM_133214	CDNA sequence BC017612	BC01761	-	-	-	-	-	-	1.6	Down

NM_0010014		2							
89	CDNA sequence BC021785	BC02178					1.5	Up	-
		5	-	-	-	-			-
		BC02268							
NM_145450	CDNA sequence BC022687	7	-	-	-	-	-	-	2.4
		BC02554							Up
NM_146215	CDNA sequence BC025546	6	-	-	-	-	-	-	1.8
		BC03018							Up
NM_182783	CDNA sequence BC030183	3	-	-	-	-	-	-	1.6
		BC03135							Up
NM_153584	CDNA sequence BC031353	3	-	-	-	-	-	-	1.9
		BC03174							Down
NM_146261	CDNA sequence BC031748	8	-	-	-	-	-	-	2.0
		BC03391							Down
NM_027498	CDNA sequence BC033915	5	-	-	-	-	-	-	1.6
		BC03703							Down
NM_153161	CDNA sequence BC037034	4	-	-	-	-	-	-	1.6
XM_132015	cDNA sequence BC037112	-	-	-	-	-	-	-	2.2
		BC03892							Down
NM_177878	CDNA sequence BC038925	5	-	-	-	-	-	-	2.3
XM_134537	cDNA sequence BC039210	-	-	-	-	-	-	-	1.6
		BC05019							Down
NM_201374	CDNA sequence BC050196	6	-	-	-	-	-	-	1.8
		BC05511							Down
NM_183182	CDNA sequence BC055111	1	-	-	-	-	-	-	1.5
		BC06828							Up
NM_173416	CDNA sequence BC068281	1	-	-	1.9	Down	-	-	2.0
NM_007659	Cell division cycle 2 homolog A (S. pombe)	Cdc2a	-	-	-	-	-	-	2.3
NM_007684	Centrin 3	Cetn3	-	-	-	-	1.6	Down	-
NM_172560	Centrobin, centrosomal BRCA2 interacting protein	Cntrob	-	-	-	-	-	-	2.8
NM_021886	Centromere protein H	Cenph	-	-	1.6	Up	-	-	Down
XM_135158	centrosomal protein 63	-	-	-	-	-	-	-	2.2
NM_172260	Centrosomal protein 68	Cep68	-	-	-	-	-	-	2.4
NM_175631	Cerebellin 4 precursor protein	Cbln4	-	-	-	-	-	-	1.7
	Ceroid lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeier-Vogt disease)	Cln3	-	-	1.9	Up	-	-	Down
NM_009907	Chemokine (C motif) ligand 1	Xcl1	-	-	-	-	-	-	2.5
NM_008510	Chemokine (C-C motif) ligand 3	Ccl3	-	-	-	-	-	-	3.0
NM_011337	Chemokine (C-C motif) ligand 3	Ccl3	-	-	-	-	-	-	Up
NM_009912	Chemokine (C-C motif) receptor 1	Ccr1	-	-	-	-	-	-	1.5
NM_007718	Chemokine (C-C motif) receptor 1-like 1	Ccr111	-	-	-	-	-	-	4.2
NM_009914	Chemokine (C-C motif) receptor 3	Ccr3	-	-	-	-	2.9	Up	-
NM_009917	Chemokine (C-C motif) receptor 5	Ccr5	-	-	-	-	1.6	Up	-
NM_019494	Chemokine (C-X-C motif) ligand 11	Cxcl11	-	-	-	-	-	-	4.1
									Up

NM_018866	Chemokine (C-X-C motif) ligand 13	Cxcl13	-	-	-	-	-	-	-	3.1	Up
NM_019568	Chemokine (C-X-C motif) ligand 14	Cxcl14	-	-	-	-	-	-	-	3.0	Down
NM_030712	Chemokine (C-X-C motif) receptor 6	Cxcr6	-	-	-	-	-	-	-	2.7	Down
NM_009142	Chemokine (C-X3-C motif) ligand 1	Cx3cl1	-	-	-	-	-	-	-	1.9	Down
NM_029313	chemokine-like factor	-	-	-	-	-	-	-	-	2.1	Down
NM_175752	Chimerin (chimaerin) 1	Chn1	-	-	-	-	-	-	-	2.0	Down
NM_007695	Chitinase 3-like 1	Chi3l1	-	-	-	-	1.8	Up	-	2.8	Up
NM_145126	Chitinase 3-like 4	Chi3l4	-	-	-	-	-	-	-	2.7	Up
NM_013491	Chloride channel 1	Clcn1	-	-	-	-	-	-	-	2.0	Up
NM_009890	Cholesterol 25-hydroxylase	Ch25h	-	-	-	-	-	-	-	2.1	Up
NM_023182	Chymotrypsin-like	Ctrl	-	-	2.5	Down	4.0	Up	-	-	-
NM_025583	Chymotrypsinogen B1	Ctrb1	2.6	Up	2.0	Down	-	-	-	-	-
NM_019815	Claudin 18	Cldn18	-	-	-	-	-	-	-	1.6	Down
NM_009903	Claudin 4	Cldn4	-	-	1.6	Up	-	-	-	-	-
NM_171826	Claudin domain containing 1	Cldnd1	-	-	-	-	-	-	-	1.9	Down
XM_133406	claudin domain containing 2	-	-	-	-	-	-	-	-	2.1	Down
NM_013492	Clusterin	Clu	-	-	-	-	-	-	-	2.3	Up
NM_010170	Coagulation factor II (thrombin) receptor-like 2	F2rl2	-	-	-	-	-	-	-	1.8	Down
NM_017478	Coatomer protein complex, subunit gamma 2	Copg2	-	-	-	-	-	-	-	3.5	Up
NM_019817	Coatomer protein complex, subunit zeta 1	Copz1	-	-	1.5	Up	1.7	Up	-	1.5	Up
NM_172582	Coenzyme Q6 homolog (yeast)	Coq6	-	-	-	-	-	-	-	1.5	Down
NM_026452	Coenzyme Q9 homolog (yeast)	Coq9	-	-	-	-	-	-	-	1.9	Down
NM_007688	Cofilin 2, muscle	Cfl2	-	-	-	-	-	-	-	1.8	Down
NM_025455	Coiled coil domain containing 28B	Ccdc28b	-	-	-	-	1.5	Up	-	-	-
NM_029339	Coiled-coil domain containing 101	Ccdc101	-	-	-	-	-	-	-	2.3	Down
XM_150129	coiled-coil domain containing 102A	-	-	-	-	-	-	-	-	1.8	Down
NM_025779	Coiled-coil domain containing 109B	Ccdc109	-	-	-	-	-	-	-	1.8	Down
NM_0010011	Coiled-coil domain containing 111	Ccdc111	-	-	-	-	-	-	-	1.8	Down
84	Coiled-coil domain containing 115	-	-	-	-	-	-	-	-	1.9	Down
XM_129811	coiled-coil domain containing 115	-	-	-	-	-	-	-	-	1.9	Down
NM_025351	Coiled-coil-helix-coiled-coil-helix domain containing 6	Chchd6	-	-	-	-	-	-	-	2.0	Down
NM_181391	Coiled-coil-helix-coiled-coil-helix domain containing 7	Chchd7	-	-	-	-	-	-	-	2.1	Down
NM_183270	Coiled-coil-helix-coiled-coil-helix domain containing 8	Chchd8	-	-	-	-	-	-	-	2.1	Down
NM_144901	Cold shock domain containing E1, RNA binding	Csde1	-	-	-	-	-	-	-	2.4	Down
NM_007743	Collagen, type I, alpha 2	Col1a2	-	-	-	-	-	-	-	2.0	Up
NM_009932	Collagen, type IV, alpha 2	Col4a2	-	-	-	-	-	-	-	3.0	Up
NM_007735	Collagen, type IV, alpha 4	Col4a4	-	-	-	-	-	-	-	1.9	Down
NM_198711	Collagen, type XXV, alpha 1	Col25a1	-	-	-	-	-	-	-	1.7	Down
NM_130449	Collectin sub-family member 12	Colec12	-	-	-	-	-	-	-	2.0	Up
NM_009971	Colony stimulating factor 3 (granulocyte)	Csf3	-	-	-	-	-	-	-	2.9	Up
NM_025417	COMM domain containing 4	Comm4	-	-	-	-	-	-	-	1.5	Down



NM_025536	COMM domain containing 5	Commd5	-	-	-	-	-	-	2.2	Up
NM_013484	Complement component 2 (within H-2S)	C2	-	-	-	-	-	-	2.0	Up
NM_016704	Complement component 6	C6	-	-	-	-	-	-	3.0	Down
NM_026225	Component of oligomeric golgi complex 6	Cog6	-	-	-	-	-	-	1.9	Up
NM_170684	Copine VII	Cpne7	-	-	-	-	1.7	Up	2.6	Up
NM_178379	COX10 homolog, cytochrome c oxidase assembly protein, heme A: farnesyltransferase (yeast)	Cox10	-	-	-	-	-	-	1.5	Down
NM_145409	CTF18, chromosome transmission fidelity factor 18 homolog (S. cerevisiae)	Chtf18	-	-	-	-	-	-	1.9	Down
NM_008411	CUB and zona pellucida-like domains 1	Cuzd1	-	-	-	-	2.4	Up	-	-
NM_024192	CUE domain containing 2	Cuedc2	-	-	-	-	-	-	2.0	Down
NM_009986	Cut-like homeobox 1	Cux1	-	-	-	-	1.7	Up	-	-
NM_007723	Cyclic nucleotide gated channel alpha 1	Cnga1	-	-	-	-	-	-	1.8	Down
NM_007630	Cyclin B2	Ccnb2	-	-	-	-	-	-	2.8	Down
XM_149022	cyclin Y-like 1	-	-	-	-	-	-	-	1.9	Down
NM_009871	Cyclin-dependent kinase 5, regulatory subunit (p35) 1	Cdk5r1	-	-	-	-	-	-	3.0	Down
XM_130487	Cystatin 12	Cst12	-	-	-	-	-	-	2.5	Down
NM_007793	Cystatin B	Cstb	-	-	-	-	-	-	2.3	Up
NM_172404	Cysteine conjugate-beta lyase 1	Ccbl1	-	-	-	-	-	-	1.7	Down
NM_144942	Cysteine sulfinic acid decarboxylase	Csad	-	-	-	-	2.4	Up	-	-
NM_020557	Cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial	Cmpk2	-	-	-	-	-	-	2.9	Up
XM_354691	cytochrome c oxidase, subunit VIIIc	-	-	-	-	-	-	-	1.7	Down
NM_009994	Cytochrome P450, family 1, subfamily b, polypeptide 1	Cyp1b1	-	-	-	-	1.5	Up	3.0	Up
NM_010000	Cytochrome P450, family 2, subfamily b, polypeptide 9	Cyp2b9	-	-	-	-	-	-	1.6	Down
NM_009995	Cytochrome P450, family 21, subfamily a, polypeptide 1	Cyp21a1	-	-	-	-	-	-	2.2	Down
NM_024264	Cytochrome P450, family 27, subfamily a, polypeptide 1	Cyp27a1	-	-	-	-	2.2	Up	4.1	Up
NM_010009	Cytochrome P450, family 27, subfamily b, polypeptide 1	Cyp27b1	-	-	-	-	-	-	1.6	Down
NM_018887	Cytochrome P450, family 39, subfamily a, polypeptide 1	Cyp39a1	-	-	-	-	-	-	1.8	Up
XM_130287	cytoskeleton associated protein 5	-	-	-	-	-	-	-	1.5	Down
NM_026378	DALR anticodon binding domain containing 3	Dalrd3	-	-	-	-	-	-	1.7	Down
NM_201227	DAN domain family, member 5	Dand5	-	-	-	-	-	-	2.0	Down
XM_284494	DEAD (Asp-Glu-Ala-Asp) box polypeptide 10	-	-	-	-	-	-	-	2.2	Down
NM_028074	DEAD (Asp-Glu-Ala-Asp) box polypeptide 42	Ddx42	-	-	-	-	-	-	2.0	Down
NM_007840	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	Ddx5	-	-	-	-	-	-	2.1	Down
NM_028041	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54	Ddx54	-	-	-	-	-	-	2.0	Down
XM_130301	death associated protein-like 1	-	-	-	-	-	-	-	2.1	Down
NM_031403	Debranching enzyme homolog 1 (S. cerevisiae)	Dbr1	-	-	-	-	-	-	2.5	Down
NM_183089	Defective in sister chromatid cohesion 1 homolog (S. cerevisiae)	Dscc1	-	-	-	-	-	-	2.1	Down
NM_207276	Defensin beta 21	Defb21	-	-	1.5	Up	-	-	-	-
NM_007866	Delta-like 3 (Drosophila)	Dll3	-	-	-	-	-	-	3.4	Up
XM_131083	DENN/MADD domain containing 2D	-	-	-	-	-	-	-	1.7	Down
NM_007832	Deoxycytidine kinase	Dck	-	-	-	-	2.3	Up	-	-

NM_013764	Deoxyguanosine kinase	Dguok	-	-	-	-	-	-	1.8	Down
NM_133964	Deoxyhypusine hydroxylase/monooxygenase	Dohh	-	-	-	-	-	-	2.0	Down
NM_009345	Deoxynucleotidyltransferase, terminal	Dntt	-	-	2.7	Up	-	-	-	-
NM_181682	Desmoglein 1 beta	Dsg1b	-	-	-	-	-	-	2.3	Down
XM_356085	DET1 and DDB1 associated 1	-	1.8	Up	-	-	-	-	-	-
NM_007879	Developmentally regulated GTP binding protein 1	Drg1	-	-	-	-	-	-	2.2	Down
NM_023232	Diablo homolog (Drosophila)	Diablo	-	-	-	-	-	-	1.5	Down
NM_178681	Diacylglycerol kinase, beta	Dgkb	-	-	-	-	-	-	1.8	Down
NM_010047	DiGeorge syndrome critical region gene 6	Dgcr6	-	-	-	-	-	-	3.4	Up
NM_172819	DIP2 disco-interacting protein 2 homolog B (Drosophila)	Dip2b	-	-	-	-	-	-	1.6	Up
NM_010074	Dipeptidylpeptidase 4	Dpp4	-	-	-	-	-	-	3.4	Down
NM_172624	Dipeptidylpeptidase 9	Dpp9	-	-	-	-	-	-	2.6	Down
NM_153530	DIS3 mitotic control homolog (S. cerevisiae)-like 2	Dis3l2	-	-	-	-	-	-	2.4	Up
NM_008921	DNA primase, p49 subunit	Prim1	-	-	-	-	-	-	2.2	Down
NM_008922	DNA primase, p58 subunit	Prim2	-	-	1.6	Up	-	-	-	-
NM_026579	DNA segment, Chr 10, Wayne State University 102, expressed	D10Wsu 102e	-	-	-	-	-	-	2.6	Down
NM_138598	DNA segment, Chr 11, Wayne State University 99, expressed	D11Wsu 99e	-	-	-	-	-	-	1.9	Down
NM_029758	DNA segment, Chr 12, ERATO Doi 553, expressed	D12Ert5 53e	-	-	-	-	-	-	2.7	Down
NM_199015	DNA segment, Chr 14, ERATO Doi 668, expressed	D14Ert6 68e	-	-	-	-	-	-	2.6	Up
NM_138582	DNA segment, Chr 17, human D6S56E 3	D17H6S 56E-3	-	-	-	-	2.1	Up	-	-
NM_172631	DNA segment, Chr 18, ERATO Doi 653, expressed	D18Ert6 53e	-	-	-	-	2.0	Up	-	-
NM_177467	DNA segment, Chr 6, ERATO Doi 160, expressed	-	-	-	-	-	-	-	1.7	Down
NM_018808	DnaJ (Hsp40) homolog, subfamily B, member 1	Dnajb1	-	-	-	-	-	-	2.7	Down
XM_135146	DnaJ (Hsp40) homolog, subfamily C, member 13	-	-	-	-	-	-	-	2.5	Up
NM_134081	DnaJ (Hsp40) homolog, subfamily C, member 9	Dnajc9	-	-	-	-	-	-	2.5	Down
NM_010071	Docking protein 2	Dok2	-	-	-	-	-	-	1.8	Down
NM_199322	DOT1-like, histone H3 methyltransferase (S. cerevisiae)	Dot1l	-	-	-	-	-	-	1.8	Down
NM_177577	Doublecortin domain containing 2a	Dcdc2a	-	-	-	-	-	-	3.4	Up
XM_355059	DTW domain containing 2	-	-	-	-	-	-	-	1.6	Up
NM_009342	Dynein light chain Tctex-type 1	Dynt1	-	-	-	-	-	-	1.7	Down
NM_025975	Dynein light chain Tctex-type 3	Dynt3	-	-	-	-	-	-	2.4	Down
XM_110968	dynein, axonemal, heavy chain 9	-	-	-	-	-	-	-	2.1	Up
NM_007893	E4F transcription factor 1	E4f1	-	-	-	-	-	-	1.7	Down
NM_019680	E74-like factor 4 (ets domain transcription factor)	Elf4	-	-	-	-	-	-	3.1	Up
NM_145951	Ecto-NOX disulfide-thiol exchanger 2	Enox2	-	-	-	-	-	-	1.5	Down
NM_026626	EF-hand calcium binding domain 2	Efcab2	-	-	-	-	-	-	3.1	Down

XM_355814	EF-hand calcium binding domain 4B	-	-	-	-	-	-	1.5	Down
NM_019397	EGF-like-domain, multiple 6	Egfl6	-	-	-	-	1.6	Up	-
NM_033612	Elastase 1, pancreatic	Ela1	-	-	-	-	3.2	Up	-
NM_015779	Elastase 2, neutrophil	Ela2	-	-	-	-	-	-	3.5
NM_007925	Elastin	Eln	-	-	-	-	-	-	1.7
NM_145158	Elastin microfibril interfacier 2	Emilin2	-	-	-	-	-	-	2.1
NM_145615	Electron transferring flavoprotein, alpha polypeptide	Etfa	-	-	-	-	-	-	1.8
NM_007965	Ena-vasodilator stimulated phosphoprotein	Evl	-	-	-	-	-	-	2.9
NM_172456	Endonuclease G-like 1	Endogl1	-	-	-	-	-	-	2.1
NM_023612	Endothelial cell-specific molecule 1	Esm1	-	-	-	-	-	-	1.6
NM_007971	Enhancer of zeste homolog 2 (Drosophila)	Ezh2	-	-	-	-	-	-	2.4
NM_007894	Eosinophil-associated, ribonuclease A family, member 1	Ear1	-	-	-	-	-	-	3.5
NM_053112	Eosinophil-associated, ribonuclease A family, member 10	Ear10	-	-	-	-	1.7	Down	1.9
NM_017388	Eosinophil-associated, ribonuclease A family, member 2	Ear2	-	-	-	-	-	-	4.1
NM_025613	EP300 interacting inhibitor of differentiation 1	Eid1	-	-	-	-	-	-	3.2
XM_204001	ephrin A3	-	-	-	2.3	Up	-	-	-
NM_022313	Era (G-protein)-like 1 (E. coli)	Eral1	-	-	-	-	1.5	Up	-
NM_145506	Erythrocyte protein band 4.1-like 5	Epb4.115	-	-	-	-	-	-	2.9
NM_019480	Estrogen receptor-binding fragment-associated gene 9	Ebag9	-	-	-	-	-	-	2.1
NM_023060	Eukaryotic elongation factor, selenocysteine-tRNA-specific	Eefsec	-	-	-	-	-	-	2.0
NM_026007	Eukaryotic translation elongation factor 1 gamma	Eef1g	-	-	-	-	-	-	1.7
NM_028659	Eukaryotic translation initiation factor 3, subunit K	Eif3k	-	-	-	-	-	-	1.5
NM_145380	Eukaryotic translation initiation factor 3, subunit M	Eif3m	-	-	-	-	2.4	Up	2.8
NM_007917	Eukaryotic translation initiation factor 4E	Eif4e	-	-	-	-	-	-	2.5
NM_198303	Eukaryotic translation initiation factor 5B	Eif5b	-	-	-	-	-	-	1.6
NM_026576	Ewings tumor-associated antigen 1	Etaa1	-	-	-	-	-	-	1.6
NM_015769	Excision repair cross-complementing rodent repair deficiency, complementation group 4	Erc4	-	-	-	-	-	-	2.4
NM_175353	Exocyst complex component 6	Exoc6	-	-	-	-	-	-	2.2
NM_012012	Exonuclease 1	Exo1	-	-	-	-	-	-	2.2
NM_176846	Exophilin 5	Exph5	-	-	-	-	-	-	2.3
NM_028274	Exosome component 6	Exosc6	-	-	-	-	-	-	2.4
NM_172379	Expressed sequence AA536717	AA536717	-	-	-	-	-	-	2.1
XM_354761	expressed sequence AA987161	-	-	-	-	-	-	-	2.0
NM_199146	Expressed sequence AI451617	AI451617	-	-	-	-	-	-	2.0
NM_177907	expressed sequence AI593442	-	-	-	-	-	-	-	2.9
NM_134067	Expressed sequence AW209491	AW209491	-	-	-	-	-	-	1.7
NM_145930	Expressed sequence AW549877	AW549877	-	-	-	-	-	-	2.2
NM_007957	Extraembryonic, spermatogenesis, homeobox 1	Esx1	-	-	-	-	-	-	3.4

NM_133940	F-box and leucine-rich repeat protein 14	Fbxl14	-	-	-	-	-	-	-	1.6	Down
NM_175206	F-box and leucine-rich repeat protein 22	Fbxl22	-	-	-	-	-	-	-	1.6	Down
NM_172721	F-box and WD-40 domain protein 8	Fbxw8	-	-	-	-	-	-	-	1.9	Down
NM_028049	F-box protein 22	Fbxo22	-	-	-	-	-	-	-	2.6	Down
NM_020593	F-box protein 3	Fbxo3	-	-	1.5	Down	-	-	-	2.6	Down
NM_025995	F-box protein 5	Fbxo5	-	-	-	-	-	-	-	3.3	Down
NM_017399	Fatty acid binding protein 1, liver	Fabp1	-	-	-	-	-	-	-	1.9	Down
NM_008375	Fatty acid binding protein 6, ileal (gastrotropin)	Fabp6	-	-	-	-	-	-	-	1.8	Down
NM_146094	Fatty acid desaturase 1	Fads1	-	-	-	-	-	-	-	1.9	Down
NM_173423	Fem-1 homolog c (C.elegans)	Fem1c	-	-	-	-	-	-	-	1.7	Down
NM_172673	FERM domain containing 5	Femd5	-	-	2.7	Down	-	-	-	2.5	Down
NM_153795	Fermitin family homolog 3 (Drosophila)	Fermt3	-	-	-	-	-	-	-	1.5	Down
NM_007996	Ferredoxin 1	Fdx1	1.6	Up	-	-	-	-	-	-	-
NM_010240	Ferritin light chain 1	Ftl1	-	-	-	-	-	-	-	2.3	Down
NM_145594	Fibrinogen-like protein 1	Fgl1	-	-	-	-	-	-	-	3.3	Up
NM_010200	Fibroblast growth factor 13	Fgf13	-	-	-	-	-	-	-	2.9	Down
XM_354975	fibronectin type III domain containing 1	-	-	-	-	-	1.9	Up	-	-	-
NM_007999	Flap structure specific endonuclease 1	Fen1	-	-	-	-	-	-	-	2.1	Down
NM_022009	Flightless I homolog (Drosophila)	Flii	-	-	-	-	-	-	-	1.8	Down
NM_029798	FLYWCH family member 2	Flywch2	-	-	-	-	2.1	Up	-	3.0	Up
NM_022888	Folate receptor 4 (delta)	Folr4	-	-	2.0	Up	-	-	-	-	-
NM_008045	Follicle stimulating hormone beta	Fshb	-	-	-	-	1.7	Up	-	-	-
NM_008038	formyl peptide receptor, related sequence 1	-	-	-	-	-	-	-	-	1.7	Up
NM_010235	Fos-like antigen 1	Fosl1	-	-	-	-	-	-	-	2.2	Up
NM_008055	Frizzled homolog 4 (Drosophila)	Fzd4	-	-	-	-	-	-	-	3.6	Up
NM_008057	Frizzled homolog 7 (Drosophila)	Fzd7	-	-	-	-	3.7	Up	-	-	-
XM_284144	frizzled homolog 9 (Drosophila)	-	-	-	-	-	-	-	-	1.6	Up
XM_131241	fucose-1-phosphate guanylyltransferase	-	-	-	-	-	-	-	-	2.0	Down
NM_134161	Fucosyltransferase 10	Fut10	-	-	-	-	-	-	-	1.7	Down
XM_203633	fucosyltransferase 11	-	-	-	-	-	-	-	-	2.1	Down
NM_026126	FUN14 domain containing 2	Fundc2	-	-	-	-	-	-	-	1.8	Down
NM_008761	FXYP domain-containing ion transport regulator 5	Fxyd5	-	-	-	-	-	-	-	2.8	Up
NM_008054	Fyn proto-oncogene	Fyn	-	-	-	-	-	-	-	2.8	Down
NM_148925	FYVE and coiled-coil domain containing 1	Fyco1	-	-	-	-	-	-	-	2.7	Down
XM_152907	G patch domain containing 8	-	-	-	1.9	Up	-	-	-	-	-
XM_130823	G protein-coupled receptor 160	Gpr160	-	-	-	-	-	-	-	2.7	Down
XM_136361	G protein-coupled receptor 161	-	-	-	-	-	-	-	-	1.6	Down
NM_013533	G protein-coupled receptor 162	Gpr162	-	-	-	-	-	-	-	2.0	Up
XM_142040	G protein-coupled receptor 174	-	-	-	-	-	-	-	-	1.6	Up
NM_011823	G protein-coupled receptor 34	Gpr34	-	-	-	-	-	-	-	3.1	Down
NM_175490	G protein-coupled receptor 75	Gpr75	-	-	-	-	-	-	-	1.8	Up

NM_147217	G protein-coupled receptor, family C, group 5, member C	Gprc5c	-	-	-	-	-	-	2.2	Down
NM_022427	G-protein coupled receptor 88	Gpr88	-	-	-	-	-	-	2.0	Down
NM_029522	G-protein signalling modulator 2 (AGS3-like, C. elegans)	Gpsm2	-	-	-	-	-	-	1.9	Down
NR_001462	G6B protein	-	-	-	-	-	-	-	1.5	Down
NM_199366	Galactose-3-O-sulfotransferase 2	Gal3st2	-	-	-	-	-	-	1.5	Up
NM_009752	Galactosidase, beta 1	Glb1	-	-	-	-	-	-	1.7	Down
NM_010253	Galanin	Gal	-	-	-	-	1.5	Up	-	-
NM_008082	Galanin receptor 1	Galr1	-	-	-	-	-	-	1.6	Down
NM_008073	Gamma-aminobutyric acid (GABA-A) receptor, subunit gamma 2	Gabrg2	-	-	-	-	-	-	1.7	Down
NM_008122	Gap junction protein, gamma 1	Gjc1	-	-	-	-	3.1	Up	-	-
NM_025466	Gastrokine 1	Gkn1	-	-	-	-	-	-	3.4	Up
NM_198101	Gem-interacting protein	Gmip	-	-	-	-	-	-	1.5	Down
XM_355369	gene model 1009, (NCBI)	-	-	-	-	-	-	-	2.0	Down
XM_357683	gene model 1418, (NCBI)	-	-	-	-	-	-	-	2.2	Up
NM_201366	Gene model 1631, (NCBI)	Gm1631	-	-	-	-	-	-	1.7	Down
XM_144113	gene model 436, (NCBI)	-	-	-	-	-	-	-	2.2	Up
NM_0010058										
54	Gene model 609, (NCBI)	Gm609	-	-	-	-	-	-	2.4	Up
XM_195647	gene model 660, (NCBI)	-	-	-	-	-	-	-	1.9	Down
XM_204104	gene model 693, (NCBI)	-	-	-	-	-	-	-	2.5	Down
XM_487218	gene model 804, (NCBI)	-	-	-	-	-	-	-	1.6	Up
XM_354695	gene model 896, (NCBI)	-	-	-	-	-	-	-	2.3	Up
XM_355044	gene model 944, (NCBI)	-	-	-	-	-	1.5	Up	-	-
XM_355058	gene model 949, (NCBI)	-	-	-	-	-	-	-	2.0	Down
NM_025294	Gene trap locus F3b	Gtlf3b	-	-	-	-	-	-	2.0	Down
NM_181392	General transcription factor IIH, polypeptide 5	Gtf2h5	-	-	-	-	-	-	1.8	Down
NM_010353	Germ cell-specific gene 2	Gsg2	-	-	-	-	-	-	1.8	Down
NM_022023	Glia maturation factor, beta	Gmfb	-	-	-	-	-	-	3.5	Down
NM_031184	GLIS family zinc finger 2	Glis2	-	-	-	-	1.7	Up	-	-
NM_008133	Glutamate dehydrogenase 1	Glud1	-	-	-	-	-	-	1.9	Down
NM_178602	Glutamate receptor, ionotropic, N-methyl D-aspartate-like 1A	Grin1a	-	-	-	-	-	-	2.2	Down
XM_196179	glutamate receptor, metabotropic 4	-	-	-	1.8	Down	-	-	-	-
NM_008160	Glutathione peroxidase 1	Gpx1	-	-	-	-	-	-	2.5	Up
NM_029555	Glutathione S-transferase kappa 1	Gstk1	-	-	-	-	-	-	3.2	Down
NM_013541	Glutathione S-transferase, pi 1	Gstp1	-	-	-	-	-	-	2.5	Up
NM_025638	Glycerophosphodiester phosphodiesterase domain containing 1	Gdpd1	-	-	-	-	-	-	2.8	Down
NM_026572	Glycine cleavage system protein H (aminomethyl carrier)	Gcsh	-	-	-	-	-	-	2.8	Down
NM_010369	Glycophorin A	Gypa	-	-	-	-	-	-	4.0	Down
NM_153581	Glycoprotein m6a	Gpm6a	-	-	-	-	-	-	2.5	Down
NM_008134	Glycosylation dependent cell adhesion molecule 1	Glycam1	-	-	-	-	2.0	Up	-	-
NM_173048	Golgi associated, gamma adaptin ear containing, ARF binding protein 3	Gga3	-	-	-	-	-	-	1.5	Down

NM_029793	Golgi autoantigen, golgin subfamily a, 1	Golga1	-	-	-	-	-	-	2.8	Down
NM_013542	Granzyme B	Gzmb	-	-	1.7	Down	-	-	-	-
AK014509	growth arrest specific 2	-	-	-	-	-	-	-	1.8	Down
NM_008108	Growth differentiation factor 3	Gdf3	-	-	-	-	-	-	1.6	Down
NM_008114	Growth factor independent 1B	Gfi1b	-	-	-	-	-	-	2.6	Down
NM_008117	Growth hormone	Gh	-	-	1.6	Up	-	-	-	-
NM_177330	Growth hormone secretagogue receptor	Ghsr	-	-	-	-	-	-	2.5	Up
NM_010276	GTP binding protein (gene overexpressed in skeletal muscle)	Gem	-	-	-	-	-	-	2.1	Up
NM_029000	GTPase, very large interferon inducible 1	Gvin1	-	-	-	-	-	-	2.0	Up
NM_023121	Guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 2	Gngt2	-	-	-	-	-	-	1.9	Down
NM_008190	Guanylate cyclase activator 2a (guanylin)	Guca2a	-	-	-	-	-	-	3.5	Down
NM_010385	H2-K region expressed gene 2	H2-Ke2	-	-	-	-	-	-	3.5	Up
NM_177688	H2A histone family, member J	H2afj	-	-	-	-	-	-	1.9	Down
NM_010436	H2A histone family, member X	H2afx	-	-	-	-	-	-	1.6	Down
NM_008235	Hairy and enhancer of split 1 (Drosophila)	Hes1	-	-	-	-	-	-	1.8	Down
NM_017370	Haptoglobin	Hp	-	-	-	-	-	-	3.0	Up
NM_144835	HEAT repeat containing 1	Heatr1	-	-	-	-	-	-	1.7	Down
NM_008303	Heat shock protein 1 (chaperonin 10)	Hspe1	-	-	-	-	-	-	2.7	Up
NM_010479	Heat shock protein 1A	Hspa1a	-	-	2.7	Up	-	-	-	-
XM_358383	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1	-	-	-	-	-	-	-	1.6	Up
NM_172473	HECT domain and ankyrin repeat containing, E3 ubiquitin protein ligase 1	Hace1	-	-	-	-	-	-	2.1	Down
NM_026101	Hect domain and RLD 4	Herc4	-	-	-	-	-	-	1.6	Down
XM_147710	hedgehog interacting protein-like 1	-	-	-	-	-	-	-	1.9	Down
NM_175256	HEG homolog 1 (zebrafish)	Heg1	-	-	-	-	-	-	2.2	Down
NM_008234	Helicase, lymphoid specific	Hells	-	-	-	-	-	-	2.5	Down
NM_198937	Hematological and neurological expressed 1-like	Hn1l	-	-	-	-	-	-	1.9	Up
NM_008245	Hematopoietically expressed homeobox	Hhex	-	-	-	-	-	-	2.5	Down
NM_008218	Hemoglobin alpha, adult chain 1	Hba-a1	-	-	-	-	-	-	2.6	Down
NM_008220	Hemoglobin, beta adult minor chain	Hbb-b1	-	-	-	-	-	-	4.3	Down
NM_016956	Hemoglobin, beta adult minor chain	Hbb-b1	-	-	-	-	-	-	3.4	Down
NM_175000	Hemoglobin, theta 1	Hbq1	-	-	-	-	-	-	1.7	Down
NM_134250	Hepatitis A virus cellular receptor 2	Havcr2	-	-	-	-	-	-	2.7	Down
XM_131076	hepatitis B virus x interacting protein	-	-	-	-	-	-	-	1.8	Down
NM_010448	Heterogeneous nuclear ribonucleoprotein A/B	Hnrnpab	-	-	-	-	-	-	2.7	Down
NM_028871	Heterogeneous nuclear ribonucleoprotein R	Hnrnpr	-	-	-	-	-	-	1.9	Down
NM_174998	Hippocalcin-like 4	Hpcal4	-	-	-	-	-	-	2.2	Up
NM_177635	Histocompatibility 2, M region locus 11	H2-M11	-	-	-	-	-	-	2.2	Down
NM_010397	Histocompatibility 2, T region locus 10	H2-T22	-	-	-	-	-	-	3.2	Up
NM_010398	Histocompatibility 2, T region locus 23	H2-D1	-	-	-	-	-	-	2.2	Up

NM_031367	Histocompatibility 28	H28	-	-	-	-	-	-	2.1	Down
NM_178187	Histone cluster 1, H2ae	Hist1h2ae	-	-	1.7	Up	-	-	-	-
NM_178184	Histone cluster 1, H2an	Hist1h2an	-	-	1.6	Up	-	-	2.2	Down
NM_178185	Histone cluster 1, H2ao	Hist1h2ao	-	-	1.9	Up	-	-	1.9	Down
NM_178194	Histone cluster 1, H2be	Hist1h2be	-	-	-	-	-	-	2.3	Down
NM_178207	Histone cluster 1, H3i	Hist1h3i	-	-	-	-	-	-	1.6	Down
NM_199198	Histone deacetylase 10	Hdac10	-	-	-	-	-	-	2.0	Down
NM_010450	Homeo box A11	Hoxa11	-	-	-	-	-	-	2.1	Down
NM_008268	Homeo box B5	Hoxb5	-	-	-	-	-	-	2.1	Down
NM_008272	Homeo box C9	Hoxc9	-	-	-	-	-	-	1.9	Down
NM_152134	Homer homolog 1 (Drosophila)	Homer1	-	-	-	-	-	-	2.1	Down
NM_015755	Hormonally upregulated Neu-associated kinase	Hunk	-	-	-	-	-	-	1.9	Down
NM_181821	Host cell factor C1 regulator 1 (XPO1-dependent)	Hcfc1r1	-	-	-	-	-	-	1.5	Down
NM_139269	HRAS like suppressor 3	Hrasls3	-	-	-	-	-	-	1.8	Down
NM_030127	HtrA serine peptidase 3	Htra3	-	-	-	-	-	-	1.6	Down
NM_007772	Human immunodeficiency virus type I enhancer binding protein 1	Hivep1	-	-	-	-	-	-	3.4	Down
NM_146001	Huntingtin interacting protein 1	Hip1	-	-	-	-	-	-	1.9	Down
NM_177900	Hyaluronan and proteoglycan link protein 4	Hapln4	-	-	-	-	3.4	Up	-	-
NM_008317	Hyaluronoglucosaminidase 1	Hyal1	-	-	-	-	-	-	1.7	Up
NM_016763	Hydroxysteroid (17-beta) dehydrogenase 10	Hsd17b10	-	-	-	-	-	-	1.6	Down
NM_053262	Hydroxysteroid (17-beta) dehydrogenase 11	Hsd17b11	-	-	-	-	-	-	1.7	Up
NM_008288	Hydroxysteroid 11-beta dehydrogenase 1	Hsd11b1	-	-	-	-	-	-	1.6	Up
NM_024255	Hydroxysteroid dehydrogenase like 2	Hsd12	-	-	-	-	-	-	1.8	Down
XM_355503	hypothetical LOC381535	-	-	-	-	-	3.8	Up	-	-
NM_183305	hypothetical protein A430057O09	-	-	-	-	-	-	-	1.6	Down
NM_013556	Hypoxanthine guanine phosphoribosyl transferase 1	Hprt1	-	-	-	-	-	-	4.0	Down
NM_133662	Immediate early response 3	Ier3	-	-	-	-	-	-	2.2	Up
NM_198610	Immunoglobulin superfamily, member 21	Igsf21	-	-	-	-	-	-	1.8	Down
XM_203589	immunoglobulin heavy variable V1-64	-	-	-	-	-	-	-	1.6	Down
XM_138377	immunoglobulin heavy variable V1-77	-	-	-	-	-	-	-	3.1	Up
NM_152839	Immunoglobulin joining chain	Igj	-	-	-	-	-	-	3.2	Down
XM_144852	immunoglobulin kappa chain complex	-	-	-	-	-	-	-	3.0	Up
XM_355782	immunoglobulin kappa chain variable 12-41	-	-	-	2.6	Up	-	-	-	-
NM_177915	Immunoglobulin superfamily, member 1	Igsf1	-	-	-	-	-	-	1.9	Down
NM_177642	immunoglobulin-like and fibronectin type III domain containing 1	-	-	-	-	-	-	-	3.3	Down
NM_028260	IMP1 inner mitochondrial membrane peptidase-like (S. cerevisiae)	Immp1l	-	-	-	-	-	-	3.1	Down

NM_146152	Importin 13	Ipo13	-	-	-	-	-	-	-	1.9	Down
NR_001463	inactive X specific transcripts	-	-	-	-	-	-	-	-	1.6	Down
NM_023626	Inhibitor of growth family, member 3	Ing3	-	-	-	-	-	-	-	1.9	Down
NM_199056	Inositol 1,3,4,5,6-pentakisphosphate 2-kinase	Ippk	-	-	-	-	-	-	-	2.0	Down
NM_173027	Inositol hexaphosphate kinase 3	Ihpk3	-	-	-	-	-	-	-	1.5	Down
NM_031156	Insulin degrading enzyme	Ide	-	-	-	-	-	-	-	2.3	Down
NM_008387	Insulin II	Ins2	-	-	-	-	1.6	Up	-	-	-
NM_153526	Insulin induced gene 1	Insig1	-	-	-	-	-	-	-	1.7	Down
NM_027421	Integrator complex subunit 2	Ints2	-	-	-	-	-	-	-	2.0	Down
NM_176843	Integrator complex subunit 5	Ints5	-	-	-	-	1.7	Up	-	-	-
NM_008399	Integrin alpha E, epithelial-associated	Itgae	-	-	-	-	-	-	-	3.6	Up
NM_207217	Integrin alpha FG-GAP repeat containing 3	Itfg3	-	-	-	-	-	-	-	3.1	Up
NM_010584	Intelectin 1 (galactofuranose binding)	Itln1	-	-	-	-	-	-	-	1.7	Down
NM_018746	Inter alpha-trypsin inhibitor, heavy chain 4	Itih4	-	-	-	-	-	-	-	1.6	Up
NM_172471	Inter-alpha (globulin) inhibitor H5	Itih5	-	-	-	-	-	-	-	2.1	Down
NM_008327	Interferon activated gene 202B	Ifi202b	-	-	-	-	-	-	-	4.2	Up
NM_172648	Interferon activated gene 205	Ifi205	-	-	-	-	-	-	-	3.5	Up
NM_010510	Interferon beta 1, fibroblast	Ifnb1	-	-	-	-	-	-	-	2.2	Up
NM_010999	Interferon gamma inducible protein 47	Olfir56	-	-	-	-	-	-	-	3.7	Up
NM_030694	Interferon induced transmembrane protein 2	Ifitm2	-	-	-	-	1.6	Up	-	4.1	Up
NM_025378	Interferon induced transmembrane protein 3	Ifitm3	-	-	-	-	-	-	-	3.3	Up
NM_178757	Interferon regulatory factor 2 binding protein 1	Irf2bp1	-	-	-	-	-	-	-	1.9	Down
NM_153511	Interleukin 1 family, member 9	Il1f9	-	-	-	-	-	-	-	2.6	Up
NM_010555	Interleukin 1 receptor, type II	Il1r2	-	-	-	-	1.5	Up	-	-	-
NM_008348	Interleukin 10 receptor, alpha	Il10ra	-	-	-	-	-	-	-	1.6	Down
NM_008355	Interleukin 13	Il13	-	-	-	-	-	-	-	2.1	Up
NM_008356	Interleukin 13 receptor, alpha 2	Il13ra2	-	-	-	-	-	-	-	2.0	Down
NM_008365	Interleukin 18 receptor 1	Il18r1	-	-	-	-	-	-	-	2.1	Down
NM_008368	Interleukin 2 receptor, beta chain	Il2rb	-	-	-	-	-	-	-	2.2	Down
NM_008374	Interleukin 9 receptor	Il9r	-	-	-	-	-	-	-	1.7	Down
NM_010587	Intersectin 1 (SH3 domain protein 1A)	Itns1	-	-	-	-	-	-	-	1.7	Down
NM_019987	Intestinal cell kinase	Ick	-	-	-	-	-	-	-	2.7	Up
XM_145005	IQ motif and Sec7 domain 3	-	-	-	-	-	-	-	-	1.7	Down
NM_015783	ISG15 ubiquitin-like modifier	Isg15	-	-	-	-	-	-	-	2.4	Up
NM_010492	Islet cell autoantigen 1	Ica1	-	-	-	-	-	-	-	4.0	Up
NM_198653	Isoleucine-tRNA synthetase 2, mitochondrial	Iars2	-	-	-	-	-	-	-	3.1	Down
NM_030887	Jun dimerization protein 2	Jdp2	-	-	-	-	-	-	-	1.9	Up
NM_010645	Kallikrein 1-related peptidase b1	Kik1b1	-	-	-	-	-	-	-	2.2	Up
NM_010640	Kallikrein 1-related peptidase b11	Kik1b11	-	-	-	-	-	-	-	3.6	Up
NM_010643	Kallikrein 1-related peptidase b24	Kik1b24	-	-	-	-	-	-	-	2.5	Up
NM_008693	Kallikrein 1-related peptidase b3	Kik1b3	-	-	-	-	-	-	-	2.6	Up



NM_008455	Kallikrein B, plasma 1	Cyp4v3	-	-	-	-	-	-	1.7	Down
NM_174865	Kallikrein related-peptidase 15	Klk15	-	-	-	-	1.6	Up	-	-
NM_010655	Karyopherin (importin) alpha 2	Kpna2	-	-	-	-	-	-	2.6	Down
NM_008467	Karyopherin (importin) alpha 4	Kpna4	-	-	-	-	-	-	1.8	Down
NM_153572	Katanin p60 subunit A-like 1	Katnal1	-	-	-	-	-	-	2.0	Down
XM_130293	kelch repeat and BTB (POZ) domain containing 10	-	-	-	-	-	-	-	1.8	Down
NM_172565	Kelch-like 11 (Drosophila)	Klhl11	-	-	-	-	-	-	2.3	Down
NM_019956	Keratin 71	Krt71	-	-	-	-	-	-	3.7	Up
NM_130873	Keratin associated protein 16-4	Krtap16-4	-	-	-	-	-	-	2.3	Down
NM_027844	Keratin associated protein 5-2	Krtap5-2	-	-	-	-	-	-	2.6	Down
NM_177155	Killer cell lectin-like receptor family I member 2	Klri2	-	-	-	-	-	-	2.7	Down
NM_013794	Killer cell lectin-like receptor, subfamily A, member 16	Klra16	-	-	3.2	Down	-	-	3.3	Down
XM_141392	kinesin family member 16B	-	-	-	-	-	-	-	2.1	Up
XM_193936	kinesin family member 20B	-	-	-	-	-	-	-	1.9	Down
NM_010629	Kinesin-associated protein 3	Kifap3	-	-	-	-	-	-	1.7	Down
XM_132322	kinetochore associated 1	-	-	-	-	-	-	-	2.4	Down
NM_031180	Klotho beta KRR1, small subunit (SSU) processome component, homolog (yeast)	Klb	-	-	-	-	-	-	1.7	Up
NM_178610	Kruppel-like factor 15	Krr1	-	-	-	-	-	-	2.1	Down
NM_023184	Kynureninase (L-kynurenine hydrolase)	Klf15	-	-	-	-	-	-	2.1	Down
NM_027552	Kynureninase (L-kynurenine hydrolase)	Kynu	-	-	-	-	-	-	1.7	Down
NM_145443	L-2-hydroxyglutarate dehydrogenase	L2hgdh	-	-	-	-	-	-	1.6	Down
NM_008522	Lactotransferrin	Ltf	-	-	-	-	2.1	Up	-	-
NM_138647	LAG1 homolog, ceramide synthase 1	Gdf1	-	-	-	-	-	-	2.7	Up
NM_008482	Laminin B1 subunit 1	Lamb1-1	-	-	-	-	-	-	2.0	Down
NM_008480	Laminin, alpha 1	Lama1	-	-	-	-	-	-	2.8	Down
XM_140451	Laminin, alpha 3	Lama3	-	-	1.8	Up	-	-	-	-
NM_008485	Laminin, gamma 2	Lamc2	-	-	-	-	1.5	Up	-	-
NM_178069	Large subunit GTPase 1 homolog (S. cerevisiae)	Lsg1	-	-	-	-	-	-	1.7	Down
NM_027137	Late cornified envelope 1D	Lce1d	-	-	-	-	-	-	2.2	Up
NM_0010055	Lemur tyrosine kinase 3	Lmtk3	-	-	-	-	-	-	1.6	Up
NM_025304	Leucine carboxyl methyltransferase 1	Lcmt1	-	-	-	-	-	-	1.8	Down
NM_028915	Leucine rich repeat and coiled-coil domain containing 1	Lrrcc1	-	-	-	-	-	-	2.5	Down
NM_030562	Leucine rich repeat and fibronectin type III domain containing 1	Lrfn1	-	-	-	-	-	-	1.7	Down
NM_178714	Leucine rich repeat and fibronectin type III domain containing 5	Lrfn5	-	-	-	-	-	-	1.8	Up
NM_153542	Leucine rich repeat containing 20	Lrrc20	-	-	-	-	-	-	1.9	Down
NM_175124	Leucine rich repeat containing 28	Lrrc28	-	-	-	-	-	-	2.1	Down
NM_029796	Leucine-rich alpha-2-glycoprotein 1	Lrg1	-	-	-	-	-	-	3.5	Up
NM_025808	Leucine-zipper-like transcriptional regulator, 1	Lztr1	-	-	-	-	-	-	1.6	Down
NM_013532	Leukocyte immunoglobulin-like receptor, subfamily B, member 4	Lilrb4	-	-	-	-	-	-	2.7	Up

NM_010734	Leukocyte specific transcript 1	Lst1	-	-	-	-	-	-	2.3	Down
NM_008519	Leukotriene B4 receptor 1	Ltb4r1	-	-	-	-	1.7	Up	-	-
X56062	LHCA1	LHCA1	-	-	-	-	-	-	2.3	Down
NM_020295	limb region 1	-	-	-	-	-	3.6	Up	-	-
NM_173756	Lin-52 homolog (C. elegans)	Lin52	-	-	-	-	-	-	2.6	Down
NM_008280	Lipase, hepatic	Lipc	-	-	-	-	-	-	1.9	Down
NM_172950	Lipin 1	Lpin1	-	-	-	-	-	-	2.8	Down
NM_177763	Lipoma HMGIC fusion partner-like protein 4	Lhfpl4	-	-	-	-	-	-	1.5	Down
NM_030695	LPS-responsive beige-like anchor	Lrba	-	-	-	-	-	-	1.7	Down
AF159803	LTP6 (Lipid transfer protein 6); lipid binding	LTP6	-	-	-	-	-	-	2.7	Down
NM_028190	Luc7 homolog (S. cerevisiae)-like	Luc7l	-	-	-	-	-	-	1.6	Down
NM_008497	Luteinizing hormone beta	Lhb	-	-	-	-	-	-	2.3	Down
NM_025281	Ly1 antibody reactive clone	Lyar	-	-	-	-	-	-	2.1	Down
NM_010738	Lymphocyte antigen 6 complex, locus A	Ly6a	-	-	-	-	-	-	2.4	Up
NM_008530	Lymphocyte antigen 6 complex, locus F	Ly6f	-	-	-	-	-	-	2.6	Up
NM_027366	Lymphocyte antigen 6 complex, locus G6E	Ly6g6e	-	-	-	-	-	-	3.9	Down
NM_020498	Lymphocyte antigen 6 complex, locus I	Ly6i	-	-	-	-	-	-	2.7	Up
NM_029627	Lymphocyte antigen 6 complex, locus K	Ly6k	-	-	-	-	-	-	3.1	Up
NM_010703	Lymphoid enhancer binding factor 1	Lef1	-	-	-	-	-	-	2.4	Down
NM_010735	Lymphotoxin A	Lta	-	-	-	-	1.5	Up	-	-
NM_030257	LysM, putative peptidoglycan-binding, domain containing 3	Lysmd3	-	-	-	-	-	-	2.6	Down
NM_146106	Lysophospholipase-like 1	Lyplal1	-	-	-	-	-	-	2.0	Down
NM_013590	Lysozyme 1	Lyz1	-	-	-	-	-	-	3.7	Down
NM_026092	Lysozyme-like 1	Lyzl1	-	-	-	-	-	-	2.9	Down
NM_016756,										
NM_183417	M200000037	-	-	-	-	-	-	-	1.9	Down
M200002559	M200002559	-	-	-	-	-	-	-	4.0	Up
M200003620	M200003620	-	-	-	-	-	-	-	2.2	Down
M200003667	M200003667	-	2.6	Up	-	-	-	-	-	-
M200003682	M200003682	-	-	-	-	-	-	-	1.7	Down
M200004621	M200004621	-	-	-	-	-	-	-	2.6	Down
M200004835	M200004835	-	-	-	-	-	-	-	2.2	Up
M200004929	M200004929	-	-	-	-	-	-	-	2.7	Down
M200005306	M200005306	-	-	-	-	-	-	-	1.5	Down
NM_133885,										
NM_173350	M200005519	-	-	-	-	-	-	-	1.7	Down
M200005540	M200005540	-	-	-	-	-	1.6	Up	-	-
M200005555	M200005555	-	-	-	2.3	Up	-	-	-	-
M200006178	M200006178	-	-	-	2.3	Up	-	-	-	-
M200006198	M200006198	-	-	-	-	-	-	-	1.7	Down
M200006392	M200006392	-	-	-	-	-	-	-	2.4	Down
NM_176996,	M200006414	-	-	-	-	-	-	-	1.9	Down



NM_0010039												
60,NM_0010												
03961,NM_0												
01003963,N												
M_010068	M200016018	-	-	-	-	-	-	-	-	-	2.2	Down
NM_0010018												
06,NM_0075												
65	M200016261	-	-	-	-	-	-	-	-	-	3.2	Down
M2NC00001												
0	M2NC000010	-	-	-	-	-	-	-	-	-	2.7	Down
M300000005	M300000005	-	-	-	-	-	-	1.8	Down	-	3.3	Down
NM_011852,												
NM_145211	M300000160	-	-	-	-	-	-	-	-	-	2.6	Up
M300000168	M300000168	-	-	-	-	-	-	-	-	-	2.5	Down
M300000454	M300000454	-	-	-	-	-	-	-	-	-	3.3	Up
NM_008681,												
NM_010884	M300000638	-	-	-	-	-	-	-	-	-	2.0	Up
M300000787	M300000787	-	-	-	-	-	-	-	-	-	1.6	Down
M300000817	M300000817	-	-	-	-	-	-	-	-	-	2.0	Up
M300001410	M300001410	-	-	-	-	-	-	-	-	-	2.4	Up
M300001422	M300001422	-	-	-	-	-	-	-	-	-	1.6	Up
M300001561	M300001561	-	-	-	-	-	-	-	-	-	1.7	Down
M300001614	M300001614	-	-	-	-	-	-	-	-	-	2.0	Down
NM_013634,												
NM_134027	M300001640	-	-	-	-	-	-	-	-	-	2.1	Down
M300001658	M300001658	-	-	-	-	-	-	-	-	-	2.0	Down
M300001857	M300001857	-	-	-	-	-	-	-	-	-	2.3	Down
M300001935	M300001935	-	-	-	-	-	-	-	-	-	1.6	Down
M300001943	M300001943	-	-	-	-	-	-	-	-	-	2.3	Down
NM_0010037												
17,NM_1754												
89	M300002055	-	-	-	-	-	-	-	-	-	2.4	Down
NM_016961,												
NM_207692	M300002149	-	-	-	-	-	-	-	-	-	2.8	Down
NM_145136,												
NM_146386	M300002238	-	-	-	-	2.0	Up	-	-	-	-	-
M300002259	M300002259	-	-	-	-	-	-	1.5	Up	-	-	-
M300002279	M300002279	-	-	-	-	-	-	-	-	-	3.0	Up
M300002294	M300002294	-	-	-	-	-	-	-	-	-	1.5	Down
M300002347	M300002347	-	-	-	-	-	-	-	-	-	1.8	Up
M300002686	M300002686	-	-	-	-	-	-	-	-	-	2.1	Down
M300002735	M300002735	-	-	-	-	-	-	-	-	-	3.4	Down
M300002779	M300002779	-	-	-	-	-	-	-	-	-	4.0	Down

M300002800	M300002800	-	-	-	-	-	-	-	-	2.1	Down
M300002883	M300002883	-	-	-	-	-	-	-	-	2.3	Up
XM_127605	M300002950	-	-	-	-	-	-	-	-	2.0	Up
M300002961	M300002961	-	-	-	-	-	-	-	-	2.0	Down
M300002988	M300002988	-	-	-	-	-	-	-	-	2.5	Down
NM_175341,											
NM_207515	M300003107	-	-	-	-	-	-	3.1	Up	-	-
M300003149	M300003149	-	-	-	-	1.6	Up	-	-	-	-
M300003301	M300003301	-	-	-	-	1.6	Up	-	-	2.1	Up
M300003385	M300003385	-	-	-	-	-	-	-	-	2.9	Down
XM_156257,											
XM_358863	M300003424	-	-	-	-	-	-	-	-	1.5	Down
NM_007757,											
XM_489571	M300003479	-	-	-	-	2.3	Up	1.7	Up	-	-
M300003482	M300003482	-	-	-	-	-	-	1.8	Up	-	-
M300003550	M300003550	-	-	-	-	-	-	-	-	3.9	Down
M300003562	M300003562	-	-	-	-	-	-	-	-	3.6	Down
M300003632	M300003632	-	-	-	-	-	-	-	-	1.7	Down
NM_0010036											
68,NM_0168											
79	M300003641	-	-	-	-	-	-	-	-	2.7	Down
M300003740	M300003740	-	-	-	-	-	-	2.9	Up	-	-
M300003809	M300003809	-	-	-	-	-	-	-	-	1.9	Down
M300003896	M300003896	-	-	-	-	-	-	-	-	2.4	Up
M300004118	M300004118	-	-	-	-	-	-	-	-	1.9	Down
M300004163	M300004163	-	-	-	-	3.8	Down	-	-	-	-
M300004173	M300004173	-	-	-	-	-	-	-	-	1.6	Down
M300004212	M300004212	-	-	-	-	-	-	-	-	1.5	Down
XM_488529	M300004366	-	-	-	-	-	-	-	-	3.2	Down
M300004372	M300004372	-	-	-	-	-	-	-	-	2.7	Up
M300004390	M300004390	-	-	-	-	-	-	-	-	2.3	Up
M300004646	M300004646	-	-	-	-	-	-	-	-	1.7	Down
M300004833	M300004833	-	-	-	-	-	-	-	-	2.4	Down
M300004849	M300004849	-	-	-	-	-	-	-	-	1.5	Down
M300004950	M300004950	-	-	-	-	-	-	-	-	1.5	Down
M300004997	M300004997	-	-	-	-	-	-	-	-	1.7	Down
M300005150	M300005150	-	-	-	-	-	-	-	-	1.7	Down
M300005213	M300005213	-	-	-	-	-	-	-	-	1.6	Down
M300005297	M300005297	-	-	-	-	-	-	-	-	1.6	Down
M300005361	M300005361	-	-	-	-	-	-	-	-	4.1	Up
NM_026563,											
NM_030155	M300005383	-	-	-	-	-	-	-	-	2.1	Down

M300005395	M300005395	-	-	-	-	-	-	-	-	3.0	Down
M300005461	M300005461	-	-	-	-	-	-	-	-	3.1	Up
M300005501	M300005501	-	-	-	-	-	-	-	-	2.8	Up
NM_138750, NM_178047	M300005608	-	-	-	-	-	-	-	-	2.1	Down
M300005674	M300005674	-	-	-	-	-	-	-	-	3.8	Up
M300005734	M300005734	-	-	-	-	-	-	-	-	1.6	Down
M300005774	M300005774	-	-	-	-	-	-	1.5	Up	1.6	Up
M300005787	M300005787	-	-	-	-	-	-	-	-	3.7	Down
M300006211	M300006211	-	-	-	-	-	-	-	-	1.5	Down
XM_484659	M300006321	-	-	-	-	-	-	-	-	3.8	Down
M300006591	M300006591	-	-	-	-	-	-	-	-	1.8	Down
M300006810	M300006810	-	-	-	-	-	-	-	-	1.7	Up
M300006863	M300006863	-	-	-	-	-	-	-	-	1.8	Down
XM_485742	M300006898	-	-	-	-	-	-	-	-	1.6	Down
NM_153094, NM_181064	M300007038	-	-	-	-	-	-	-	-	2.0	Down
M300007120	M300007120	-	-	-	-	2.0	Up	-	-	-	-
M300007209	M300007209	-	-	-	-	-	-	-	-	1.6	Down
M300007280	M300007280	-	-	-	-	-	-	-	-	2.3	Up
M300007287	M300007287	-	-	-	-	-	-	-	-	1.6	Down
M300007516	M300007516	-	-	-	-	-	-	-	-	1.6	Down
M300007572	M300007572	-	-	-	-	-	-	-	-	2.3	Down
NM_010839, XM_489852	M300007605	-	-	1.6	Up	1.5	Up	-	-	-	-
M300007610	M300007610	-	-	-	-	-	-	-	-	2.4	Down
XM_289923, XM_489850	M300007701	-	-	-	-	-	-	-	-	3.1	Down
M300007849	M300007849	-	-	-	-	-	-	-	-	1.8	Down
M300008202	M300008202	-	-	-	-	-	-	-	-	2.6	Down
NM_0010012 95,NM_1725 19	M300008240	-	-	-	-	-	-	-	-	1.7	Down
M300008304	M300008304	-	-	-	-	-	-	-	-	2.0	Down
XM_486257	M300008344	-	-	-	-	-	-	-	-	1.8	Down
NM_144554, NM_175093	M300008400	-	-	-	-	-	-	-	-	1.6	Down
NM_172134, XM_488563, XM_489917	M300008443	-	-	-	-	-	-	-	-	1.6	Down
NM_144889, NM_212446	M300008487	-	-	1.6	Up	1.9	Up	-	-	-	-
M300008571	M300008571	-	-	-	-	-	-	-	-	3.4	Up

M300008575	M300008575	-	-	-	-	-	-	-	-	1.9	Down
M300009034	M300009034	-	-	-	-	-	-	-	-	1.6	Up
M300009073	M300009073	-	-	-	-	-	-	-	-	1.6	Up
M300009127	M300009127	-	-	-	-	-	-	-	-	1.7	Down
M300009172	M300009172	-	-	-	-	-	-	-	-	1.6	Down
M300009373	M300009373	-	-	-	-	-	-	-	-	1.6	Down
M300009411	M300009411	-	-	-	-	-	-	-	-	2.5	Up
M300009505	M300009505	-	-	-	-	-	-	-	-	3.2	Up
M300009788	M300009788	-	-	-	-	-	-	-	-	2.6	Up
M300009816	M300009816	-	-	-	-	-	-	1.9	Up	-	-
M300009924	M300009924	-	-	-	-	1.6	Up	1.6	Up	-	-
NM_172052, NM_178771	M300010181	-	-	-	-	-	-	-	-	1.6	Down
M300010346	M300010346	-	-	-	-	-	-	-	-	2.7	Up
M300010882	M300010882	-	-	-	-	-	-	-	-	1.7	Down
XM_354943, XM_489511	M300011265	-	-	-	-	-	-	-	-	1.7	Down
M300011719	M300011719	-	-	-	-	-	-	-	-	1.7	Down
M300011880	M300011880	-	-	-	-	-	-	-	-	1.6	Down
NM_153564, NM_212440	M300012578	-	-	-	-	-	-	-	-	2.3	Up
M300012623	M300012623	-	-	-	-	-	-	-	-	2.2	Down
M300013071	M300013071	-	-	-	-	-	-	-	-	1.8	Up
M300013112	M300013112	-	-	-	-	-	-	-	-	2.2	Down
M300013133	M300013133	-	-	-	-	-	-	-	-	3.2	Down
XM_194023	M300013483	-	-	-	-	-	-	-	-	1.5	Up
M300014011	M300014011	-	-	-	-	-	-	-	-	2.4	Up
M300014365	M300014365	-	-	-	-	-	-	-	-	1.8	Down
NM_153384, NM_153385, NM_153386	M300014909	-	-	-	-	1.9	Down	-	-	2.6	Down
NM_0010028 98,NM_1984 05	M300015179	-	-	-	-	-	-	-	-	2.8	Down
M300015195	M300015195	-	-	-	-	-	-	-	-	2.8	Up
M300016267	M300016267	-	-	-	-	-	-	-	-	2.1	Up
NM_146328, XM_489777	M300017001	-	-	-	-	-	-	2.7	Up	-	-
M300017202	M300017202	-	-	-	-	-	-	-	-	2.8	Up
M300017395	M300017395	-	-	-	-	-	-	1.6	Up	-	-
M300019464	M300019464	-	-	-	-	-	-	-	-	3.0	Down
M300019647	M300019647	-	-	-	-	-	-	-	-	1.6	Down

NM_198016	M300019706	-	-	-	-	-	-	-	-	2.4	Down
M300019893	M300019893	-	-	-	-	-	-	-	-	3.0	Up
M300020122	M300020122	-	-	-	-	-	-	-	-	3.1	Up
M300020516	M300020516	-	-	-	-	-	-	-	-	1.6	Down
M300020531	M300020531	-	-	-	-	-	-	-	-	2.5	Down
M300021519	M300021519	-	-	-	-	-	-	-	-	2.0	Down
M300021573	M300021573	-	-	-	-	-	-	-	-	2.1	Down
M300021838	M300021838	-	-	-	-	-	-	-	-	1.9	Up
M300021883	M300021883	-	-	-	-	-	-	-	-	1.6	Down
M400000013	M400000013	-	-	-	-	-	-	-	-	3.3	Up
M400000061	M400000061	-	-	-	-	-	-	-	-	2.1	Up
M400000085	M400000085	-	-	-	-	-	-	-	-	2.0	Down
M400000127	M400000127	-	-	-	-	-	-	-	-	2.0	Down
M400000168	M400000168	-	-	-	-	-	-	-	-	2.4	Up
M400000224	M400000224	-	-	-	-	-	-	-	-	1.8	Up
M400000229	M400000229	-	-	-	-	-	-	-	-	2.3	Down
M400000336	M400000336	-	-	-	-	-	-	-	-	1.5	Up
M400000345	M400000345	-	-	-	-	-	-	-	-	3.3	Up
NM_013552,											
NM_013552	M400000383	-	-	-	-	-	-	-	-	3.8	Down
M400000458	M400000458	-	-	-	-	-	-	-	-	4.2	Up
M400000478	M400000478	-	-	-	-	-	-	-	-	1.8	Down
M400000488	M400000488	-	-	-	-	-	-	-	-	3.0	Down
M400000540	M400000540	-	-	-	-	-	-	-	-	1.8	Down
XM_358756,											
XM_489505	M400000583	-	-	-	-	-	-	-	-	2.9	Down
M400000585	M400000585	-	-	-	-	-	-	-	-	3.1	Up
M400000611	M400000611	-	-	-	-	-	-	-	-	1.6	Up
M400000637	M400000637	-	-	-	-	-	-	-	-	1.8	Down
M400000826	M400000826	-	-	-	-	-	-	-	-	2.4	Down
M400000836	M400000836	-	-	-	-	-	-	-	-	2.2	Up
M400000841	M400000841	-	-	-	-	-	-	-	-	1.7	Down
M400000869	M400000869	-	-	-	-	-	-	-	-	2.0	Down
M400000879	M400000879	-	-	-	-	-	-	-	-	1.8	Down
M400000968	M400000968	-	-	-	-	-	-	-	-	2.9	Down
M400001023	M400001023	-	-	-	-	-	-	-	-	2.3	Down
M400001094	M400001094	-	-	-	-	-	-	-	-	3.5	Down
M400001111	M400001111	-	-	-	-	-	-	-	-	2.6	Down
M400001112	M400001112	-	-	-	-	-	-	-	-	2.7	Down
M400001117	M400001117	-	-	-	-	-	-	-	-	2.5	Down
NM_008228,											
XM_485447	M400001120	-	-	-	-	-	-	-	-	2.0	Down



M400001131	M400001131	-	-	-	-	-	-	-	-	2.4	Up
M400001153	M400001153	-	-	-	-	-	-	3.6	Up	-	-
M400001190	M400001190	-	-	-	-	-	-	-	-	2.0	Down
M400001312	M400001312	-	-	-	-	-	-	-	-	1.5	Down
M400001321	M400001321	-	-	-	-	1.7	Up	-	-	-	-
M400001349	M400001349	-	-	-	-	1.9	Down	-	-	-	-
M400001388	M400001388	-	-	-	-	-	-	-	-	2.0	Up
M400001492	M400001492	-	-	-	-	-	-	-	-	1.5	Down
M400001533	M400001533	-	-	-	-	1.8	Up	-	-	-	-
M400001701	M400001701	-	-	-	-	-	-	-	-	1.8	Down
M400001706	M400001706	-	-	-	-	-	-	-	-	2.4	Down
M400001729	M400001729	-	-	-	-	-	-	-	-	2.8	Down
M400001757	M400001757	-	-	-	-	-	-	-	-	2.3	Down
M400001758	M400001758	-	-	-	-	-	-	-	-	2.7	Down
XM_487979	M400001759	-	-	-	-	2.8	Down	-	-	-	-
M400001777	M400001777	-	-	-	-	2.8	Down	-	-	2.2	Down
M400001789	M400001789	-	-	-	-	2.2	Up	-	-	-	-
M400001842	M400001842	-	-	-	-	1.6	Up	-	-	-	-
M400001952	M400001952	-	2.0	Up	-	-	-	1.7	Up	-	-
M400002037	M400002037	-	-	-	-	-	-	-	-	2.3	Down
M400002040	M400002040	-	-	-	-	-	-	-	-	1.6	Down
M400002073	M400002073	-	-	-	-	-	-	-	-	1.8	Down
XM_485388	M400002150	-	-	-	-	-	-	-	-	2.2	Down
M400002187	M400002187	-	-	-	-	-	-	-	-	2.0	Down
M400002281	M400002281	-	-	-	-	-	-	-	-	2.7	Down
M400002298	M400002298	-	-	-	-	-	-	-	-	1.6	Down
M400002300	M400002300	-	-	-	-	-	-	-	-	1.5	Down
M400002312	M400002312	-	-	-	-	-	-	-	-	2.1	Down
M400002318	M400002318	-	-	-	-	-	-	-	-	2.1	Down
M400002344	M400002344	-	-	-	-	-	-	-	-	3.9	Up
M400002424	M400002424	-	-	-	-	-	-	-	-	2.4	Down
M400002472	M400002472	-	-	-	-	1.6	Up	-	-	-	-
M400002488	M400002488	-	-	-	-	-	-	-	-	1.9	Down
XM_355197,		-	-	-	-	-	-	-	-	-	-
XM_355305	M400002495	-	-	-	-	1.6	Down	-	-	1.7	Down
M400002705	M400002705	-	-	-	-	-	-	-	-	1.7	Down
M400002751	M400002751	-	-	-	-	-	-	-	-	1.9	Down
M400002765	M400002765	-	-	-	-	-	-	-	-	1.6	Down
XM_487325	M400002791	-	-	-	-	-	-	-	-	1.6	Down
M400002796	M400002796	-	-	-	-	-	-	-	-	2.5	Down
M400002821	M400002821	-	-	-	-	-	-	-	-	2.3	Down

XM_489304	M400002880	-	-	-	1.7	Up	-	-	-	-
M400002889	M400002889	-	-	-	-	-	-	-	2.4	Up
M400002893	M400002893	-	-	-	-	-	-	-	2.3	Down
M400002921	M400002921	-	-	-	-	-	-	-	2.2	Down
M400002941	M400002941	-	-	-	-	-	-	-	1.7	Down
M400002949	M400002949	-	-	-	-	-	-	-	1.6	Down
M400002970	M400002970	-	-	-	-	-	-	-	1.9	Down
XM_145268,										
XM_355758	M400002995	-	-	-	-	-	-	-	1.8	Down
M400003005	M400003005	-	-	-	-	-	-	-	1.7	Down
M400003017	M400003017	-	-	-	-	-	-	-	2.1	Down
M400003032	M400003032	-	-	-	-	-	-	-	1.5	Up
XM_136824	M400003035	-	-	-	-	-	-	-	1.6	Down
NM_023871,										
XM_354669,										
XM_486488	M400003074	-	-	-	-	-	-	-	2.2	Down
M400003173	M400003173	-	-	-	-	-	-	-	1.9	Down
XM_135707,										
XM_485815	M400003210	-	-	-	-	-	-	-	2.3	Down
M400003250	M400003250	-	-	-	-	-	-	-	3.1	Up
XM_136032	M400003253	-	-	-	-	-	-	-	2.2	Up
M400003261	M400003261	-	-	-	-	-	-	-	1.9	Down
M400003321	M400003321	-	-	-	-	-	-	-	2.3	Down
M400003333	M400003333	-	-	-	-	-	-	-	2.3	Down
M400003344	M400003344	-	-	-	-	-	-	-	1.6	Down
M400003379	M400003379	-	-	-	2.3	Up	-	-	-	-
M400003381	M400003381	-	-	-	-	-	-	-	2.1	Down
XM_358393	M400003385	-	-	-	-	-	-	-	2.1	Up
XM_110173,										
XM_148072,										
XM_359273	M400003409	-	-	-	-	-	-	-	3.2	Up
M400003421	M400003421	-	-	-	-	-	-	-	1.8	Down
M400003454	M400003454	-	-	-	-	-	-	-	1.7	Up
M400003468	M400003468	-	-	-	-	-	-	-	1.8	Down
XM_143622	M400003506	-	-	-	-	-	-	-	1.7	Down
M400003518	M400003518	-	-	-	-	-	-	-	2.7	Down
M400003532	M400003532	-	-	-	-	-	-	-	3.6	Down
M400003604	M400003604	-	-	-	-	-	-	-	2.2	Down
M400003644	M400003644	-	-	-	-	-	-	-	3.0	Up
M400003673	M400003673	-	-	-	-	-	-	-	2.0	Down
M400003677	M400003677	-	-	-	-	-	-	-	3.1	Down
M400003679	M400003679	-	-	-	-	-	-	-	1.7	Down

M400003691	M400003691	-	-	-	-	-	-	-	-	1.8	Down
M400003720	M400003720	-	1.6	Up	3.1	Up	-	-	-	-	-
M400003747	M400003747	-	-	-	-	-	-	-	-	3.5	Down
M400003768	M400003768	-	-	-	-	-	-	-	-	3.7	Up
XM_485613	M400003779	-	-	-	-	-	-	-	-	2.6	Down
XM_155973,											
XM_358755	M400003857	-	-	-	-	-	-	-	-	3.2	Up
M400003876	M400003876	-	-	-	-	-	-	-	-	1.8	Up
M400003999	M400003999	-	-	-	-	-	-	-	-	1.5	Down
M400004013	M400004013	-	-	-	-	-	-	-	-	2.3	Down
M400004022	M400004022	-	-	-	1.9	Up	-	-	-	2.0	Up
M400004023	M400004023	-	-	-	2.2	Up	-	-	-	-	-
M400004029	M400004029	-	-	-	-	-	-	-	-	1.7	Up
M400004059	M400004059	-	-	-	-	-	-	-	-	2.2	Up
M400004071	M400004071	-	-	-	-	-	-	-	-	3.1	Up
M400004081	M400004081	-	-	-	-	-	-	-	-	1.6	Down
M400004100	M400004100	-	-	-	-	-	-	-	-	2.7	Down
M400004105	M400004105	-	-	-	-	-	-	-	-	1.6	Down
M400004152	M400004152	-	-	-	-	-	-	-	-	2.4	Down
NM_172776,											
XM_486383	M400004172	-	-	-	-	-	-	-	-	1.5	Up
M400004211	M400004211	-	-	-	-	-	-	-	-	2.1	Down
M400004246	M400004246	-	-	-	-	-	-	-	-	1.6	Down
M400004302	M400004302	-	-	-	-	-	-	-	-	2.3	Down
XM_356225	M400004319	-	-	-	-	-	-	-	-	2.4	Down
M400004378	M400004378	-	-	-	-	-	-	-	-	1.5	Down
M400004422	M400004422	-	-	-	-	-	-	-	-	1.5	Up
M400004443	M400004443	-	-	-	-	-	-	-	-	2.7	Down
M400004462	M400004462	-	-	-	-	-	2.8	Up	-	-	-
XM_356948	M400004535	-	-	-	-	-	-	-	-	1.7	Up
M400004574	M400004574	-	-	-	-	-	-	-	-	2.0	Down
M400004578	M400004578	-	-	-	-	-	-	-	-	1.5	Down
XM_207780,											
XM_489724	M400004640	-	-	-	-	-	-	-	-	1.8	Down
M400004692	M400004692	-	-	-	-	-	-	-	-	1.6	Down
M400004693	M400004693	-	-	-	-	-	-	-	-	3.8	Up
M400004793	M400004793	-	-	-	-	-	-	-	-	1.6	Down
M400004817	M400004817	-	-	-	1.5	Down	-	-	-	3.0	Down
M400004859	M400004859	-	-	-	-	-	-	-	-	1.7	Down
M400004861	M400004861	-	-	-	-	-	-	-	-	3.1	Up
M400004930	M400004930	-	-	-	-	-	-	-	-	2.2	Down
M400004947	M400004947	-	-	-	-	-	-	-	-	1.7	Down

M400005016	M400005016	-	-	-	-	-	-	-	-	1.7	Up
M400005024	M400005024	-	-	-	-	-	-	-	-	3.3	Up
M400005031	M400005031	-	-	-	-	-	-	-	-	1.9	Up
M400005042	M400005042	-	-	-	-	-	-	-	-	3.7	Up
XM_142911	M400005043	-	-	-	-	-	-	-	-	1.6	Up
M400005066	M400005066	-	-	-	-	-	-	-	-	2.0	Down
NM_007534, NM_007536	M400005072	-	-	-	-	-	-	-	-	2.7	Up
NM_030886, NM_198010	M400005085	-	-	-	-	-	-	-	-	1.8	Down
M400005162	M400005162	-	-	-	-	-	-	-	-	2.4	Down
M400005163	M400005163	-	-	-	-	-	-	-	-	2.0	Up
M400005195	M400005195	-	-	-	-	-	-	-	-	2.6	Down
M400005271	M400005271	-	1.8	Up	-	-	-	-	-	-	-
M400005285	M400005285	-	-	-	1.5	Up	-	-	-	2.8	Up
NM_019743, XM_486450	M400005288	-	-	-	-	-	-	-	-	2.5	Up
M400005384	M400005384	-	-	-	-	-	-	-	-	1.8	Up
M400005394	M400005394	-	-	-	-	-	-	-	-	3.9	Down
NM_175267	M400005484	-	-	-	-	-	-	-	-	2.1	Down
M400005487	M400005487	-	-	-	-	-	-	-	-	1.6	Down
M400005494	M400005494	-	-	-	-	-	-	-	-	2.7	Down
M400005630	M400005630	-	-	-	-	-	-	-	-	1.6	Down
M400005672	M400005672	-	-	-	-	-	-	-	-	3.0	Up
M400005690	M400005690	-	-	-	-	-	-	-	-	2.2	Up
XM_135033	M400005691	-	-	-	-	-	-	-	-	1.6	Down
M400005698	M400005698	-	-	-	1.6	Down	-	-	-	-	-
M400005776	M400005776	-	-	-	-	-	1.8	Up	-	-	-
M400005791	M400005791	-	1.6	Up	-	-	-	-	-	1.6	Up
M400005803	M400005803	-	-	-	-	-	-	-	-	2.3	Down
M400005810	M400005810	-	-	-	-	-	1.8	Down	-	2.4	Down
M400005838	M400005838	-	-	-	-	-	-	-	-	1.6	Down
M400005855	M400005855	-	-	-	-	-	-	-	-	2.6	Up
XM_487057	M400005867	-	-	-	-	-	-	-	-	1.7	Down
M400005878	M400005878	-	-	-	-	-	-	-	-	2.0	Down
M400005881	M400005881	-	-	-	-	-	-	-	-	3.2	Up
M400005890	M400005890	-	-	-	-	-	-	-	-	3.8	Up
XM_485768	M400005935	-	-	-	-	-	-	-	-	3.2	Up
M400005945	M400005945	-	-	-	-	-	-	-	-	2.8	Down
M400005950	M400005950	-	-	-	-	-	-	-	-	1.6	Down
M400005966	M400005966	-	-	-	-	-	-	-	-	2.2	Down
M400005979	M400005979	-	-	-	-	-	-	-	-	2.1	Up

XM_356745	M400005980	-	-	-	-	-	-	-	-	2.2	Up
M400005994	M400005994	-	-	-	-	-	-	-	-	1.5	Down
M400006009	M400006009	-	-	-	-	-	-	-	-	1.7	Down
M400006057	M400006057	-	-	-	-	-	-	-	-	2.3	Down
M400006058	M400006058	-	-	-	-	-	-	-	-	2.6	Down
XM_485704	M400006077	-	-	-	-	-	-	-	-	1.5	Down
M400006162	M400006162	-	-	-	-	-	-	-	-	1.5	Down
M400006223	M400006223	-	-	-	-	-	-	-	-	2.5	Down
XM_355888	M400006235	-	-	-	-	-	-	-	-	2.0	Down
M400006255	M400006255	-	-	-	-	-	-	-	-	1.6	Down
NM_145360,											
NM_177960	M400006262	-	-	-	-	-	-	-	-	1.9	Up
XM_136698	M400006270	-	-	-	-	-	-	-	-	1.7	Down
M400006293	M400006293	-	-	-	-	-	-	-	-	3.3	Up
M400006308	M400006308	-	-	-	-	-	-	-	-	2.2	Down
M400006325	M400006325	-	-	-	-	-	-	-	-	1.9	Down
M400006331	M400006331	-	-	-	-	-	-	-	-	1.5	Down
M400006337	M400006337	-	-	-	-	-	-	-	-	2.1	Down
M400006361	M400006361	-	-	-	-	-	-	-	-	1.9	Down
M400006366	M400006366	-	-	-	-	-	-	-	-	3.3	Down
M400006381	M400006381	-	-	-	-	-	-	-	-	1.7	Up
M400006391	M400006391	-	-	-	-	-	-	-	-	2.7	Up
M400006407	M400006407	-	-	-	-	-	-	-	-	1.6	Down
M400006421	M400006421	-	-	-	-	-	-	-	-	2.0	Down
XM_487301	M400006443	-	-	-	-	-	-	-	-	2.4	Down
M400006474	M400006474	-	-	-	-	1.7	Up	-	-	-	-
M400006491	M400006491	-	-	-	-	-	-	-	-	2.4	Down
M400006510	M400006510	-	-	-	-	-	-	-	-	2.2	Down
M400006515	M400006515	-	-	-	-	-	-	-	-	1.8	Down
M400006545	M400006545	-	-	-	-	-	-	-	-	1.6	Down
M400006569	M400006569	-	-	-	-	-	-	-	-	1.9	Down
M400006579	M400006579	-	-	-	-	-	-	-	-	1.5	Down
M400006592	M400006592	-	-	-	-	-	-	-	-	1.8	Down
M400006597	M400006597	-	-	-	-	-	-	-	-	1.7	Down
M400006616	M400006616	-	-	-	-	-	-	-	-	1.6	Down
M400006634	M400006634	-	-	-	-	-	-	-	-	1.7	Down
M400006669	M400006669	-	-	-	-	-	-	-	-	2.0	Down
M400006693	M400006693	-	-	-	-	-	-	-	-	2.0	Down
XM_487586,											
XM_487587	M400006699	-	-	-	-	-	-	-	-	2.1	Down
M400006702	M400006702	-	-	-	-	-	-	-	-	1.7	Down
XM_357358,	M400006717	-	-	-	-	-	-	-	-	1.7	Down

XM_485274,										
XM_487745										
XM_486211	M400006726	-	-	-	-	-	-	-	-	1.6 Up
M400006737	M400006737	-	-	-	-	-	-	-	-	1.7 Up
M400006813	M400006813	-	-	-	-	-	-	-	-	1.7 Down
M400006819	M400006819	-	-	-	-	-	-	-	-	2.4 Down
M400006835	M400006835	-	-	-	-	-	-	-	-	1.7 Down
M400006837	M400006837	-	-	-	-	-	-	-	-	2.4 Down
M400006841	M400006841	-	-	-	-	-	-	-	-	1.6 Down
M400006853	M400006853	-	-	-	-	-	-	-	-	1.7 Down
M400006864	M400006864	-	-	-	-	-	-	-	-	1.6 Down
M400006865	M400006865	-	-	-	-	-	-	-	-	1.9 Down
M400006868	M400006868	-	2.4	Up	-	1.9	Up	-	-	-
M400006871	M400006871	-	-	-	-	-	-	-	-	2.6 Down
M400006900	M400006900	-	-	-	-	-	-	-	-	1.6 Down
M400006936	M400006936	-	-	-	-	-	-	-	-	2.0 Down
M400006943	M400006943	-	-	-	-	-	-	-	-	1.9 Down
M400006949	M400006949	-	-	-	-	-	-	-	-	1.7 Down
M400007055	M400007055	-	-	-	-	-	-	-	-	1.7 Down
M400007058	M400007058	-	-	-	-	-	-	-	-	-
M400007073	M400007073	-	-	-	-	3.0	Down	-	-	-
M400007119	M400007119	-	-	-	-	-	-	-	-	1.9 Down
M400007121	M400007121	-	-	-	-	-	-	-	-	2.0 Down
M400007127	M400007127	-	-	-	-	-	-	-	-	1.8 Down
M400007132	M400007132	-	-	-	-	-	-	-	-	1.9 Down
M400007140	M400007140	-	-	-	-	-	-	-	-	2.8 Up
M400007143	M400007143	-	-	-	-	-	-	-	-	1.7 Down
M400007143	M400007143	-	-	-	-	-	-	-	-	2.1 Down
M400007185	M400007185	-	-	-	-	-	-	-	-	1.6 Down
M400007191	M400007191	-	-	-	-	-	-	-	-	1.6 Down
XM_359359	M400007229	-	-	-	-	-	-	-	-	2.7 Down
M400007251	M400007251	-	-	-	-	-	-	-	-	1.7 Down
XM_486504	M400007312	-	-	-	-	-	-	-	-	1.5 Up
XM_485233	M400007333	-	-	-	-	-	-	-	-	1.5 Down
M400007353	M400007353	-	-	-	-	-	-	-	-	2.0 Down
M400007393	M400007393	-	-	-	-	-	-	-	-	1.6 Down
M400007417	M400007417	-	-	-	-	-	-	-	-	2.1 Down
XM_487801	M400007424	-	-	-	-	-	-	1.9	Down	2.9 Down
M400007428	M400007428	-	-	-	-	-	-	-	-	1.7 Down
M400007443	M400007443	-	-	-	-	-	-	-	-	2.5 Up
M400007477	M400007477	-	-	-	-	-	-	-	-	1.6 Down
XM_484324	M400007481	-	-	-	-	-	-	-	-	2.0 Down

XM_486835	M400007489	-	-	-	-	-	-	-	-	1.8	Down
M400007501	M400007501	-	-	-	-	-	-	-	-	1.7	Down
M400007505	M400007505	-	-	-	-	-	-	-	-	1.8	Down
M400007536	M400007536	-	-	-	-	-	-	-	-	2.5	Down
XM_109346	M400007537	-	-	-	-	-	-	-	-	1.6	Down
XM_488279	M400007542	-	-	-	-	1.8	Up	-	-	-	-
NM_175216	M400007553	-	-	-	-	-	-	-	-	1.6	Down
M400007571	M400007571	-	-	-	-	-	-	-	-	2.9	Down
M400007575	M400007575	-	-	-	-	-	-	-	-	2.2	Down
XM_488248	M400007577	-	-	-	-	-	-	-	-	2.0	Down
M400007584	M400007584	-	-	-	-	-	-	-	-	2.1	Down
M400007597	M400007597	-	-	-	-	-	-	-	-	2.1	Down
M400007602	M400007602	-	-	-	-	-	-	-	-	1.8	Down
M400007608	M400007608	-	-	-	-	-	-	-	-	3.0	Down
M400007624	M400007624	-	-	-	-	-	-	-	-	1.7	Down
M400007634	M400007634	-	1.6	Up	-	-	-	-	-	-	-
M400007650	M400007650	-	-	-	-	-	-	-	-	1.7	Down
M400007655	M400007655	-	-	-	-	-	-	-	-	1.7	Down
M400007703	M400007703	-	-	-	-	-	-	-	-	3.0	Down
M400007719	M400007719	-	-	-	-	-	-	-	-	2.5	Down
M400007754	M400007754	-	-	-	-	-	-	-	-	2.0	Down
M400007767	M400007767	-	-	-	-	-	-	-	-	2.1	Down
M400007790	M400007790	-	-	-	-	-	-	-	-	2.0	Down
M400007803	M400007803	-	-	-	-	-	-	-	-	1.6	Down
M400007832	M400007832	-	-	-	-	-	-	-	-	2.4	Down
M400007833	M400007833	-	-	-	-	-	-	-	-	1.8	Down
M400007857	M400007857	-	-	-	-	-	-	-	-	2.1	Down
M400007868	M400007868	-	-	-	-	1.9	Up	-	-	-	-
M400007885	M400007885	-	-	-	-	-	-	-	-	1.5	Down
M400007958	M400007958	-	-	-	-	-	-	1.5	Down	1.5	Down
XM_484103	M400008005	-	-	-	-	-	-	-	-	2.1	Down
M400008008	M400008008	-	-	-	-	-	-	-	-	3.0	Up
M400008011	M400008011	-	-	-	-	-	-	-	-	2.4	Down
M400008020	M400008020	-	-	-	-	-	-	-	-	3.5	Up
M400008048	M400008048	-	-	-	-	-	-	-	-	1.6	Down
M400008055	M400008055	-	-	-	-	-	-	-	-	1.7	Down
M400008060	M400008060	-	-	-	-	-	-	-	-	1.7	Down
M400008070	M400008070	-	2.0	Up	-	2.2	Up	-	-	-	-
M400008076	M400008076	-	2.1	Up	-	2.2	Up	-	-	-	-
NM_009819,											
NM_145732	M400008093	-	-	-	-	-	-	-	-	1.7	Down

M400008105	M400008105	-	-	-	-	-	-	-	-	1.9	Down
M400008129	M400008129	-	-	-	-	-	-	-	-	1.5	Down
XM_487957	M400008141	-	1.7	Up	-	-	-	-	-	-	-
XM_143511	M400008172	-	1.6	Up	-	-	-	-	-	-	-
M400008190	M400008190	-	-	-	-	-	-	-	-	2.0	Down
XM_484668	M400008195	-	-	-	-	-	-	-	-	1.6	Down
M400008204	M400008204	-	-	-	-	-	-	-	-	2.4	Up
M400008231	M400008231	-	-	-	-	-	-	-	-	2.4	Down
M400008251	M400008251	-	-	-	3.6	Up	-	-	-	-	-
M400008254	M400008254	-	-	-	-	-	-	-	-	1.9	Down
M400008259	M400008259	-	-	-	1.8	Up	-	-	-	-	-
XM_486667	M400008261	-	-	-	-	-	-	-	-	1.7	Up
M400008310	M400008310	-	-	-	2.1	Down	-	-	-	1.7	Down
XM_138781	M400008367	-	-	-	-	-	-	-	-	1.6	Down
M400008405	M400008405	-	-	-	-	-	3.9	Up	-	-	-
M400008459	M400008459	-	-	-	-	-	-	-	-	1.8	Down
M400008462	M400008462	-	-	-	1.9	Up	-	-	-	-	-
M400008488	M400008488	-	-	-	-	-	-	-	-	2.6	Up
XM_489530	M400008509	-	-	-	-	-	-	-	-	3.1	Up
M400008517	M400008517	-	-	-	-	-	-	-	-	2.2	Down
M400008538	M400008538	-	-	-	-	-	-	-	-	1.5	Down
M400008546	M400008546	-	-	-	-	-	-	-	-	3.0	Down
M400008548	M400008548	-	-	-	-	-	-	-	-	4.1	Up
M400008552	M400008552	-	-	-	-	-	-	-	-	1.7	Down
M400008593	M400008593	-	-	-	-	-	-	-	-	3.1	Down
M400008598	M400008598	-	-	-	-	-	-	-	-	2.4	Down
M400008640	M400008640	-	-	-	-	-	1.7	Down	-	2.1	Down
M400008685	M400008685	-	-	-	-	-	2.4	Up	-	-	-
M400008700	M400008700	-	-	-	-	-	-	-	-	1.6	Down
NM_009665,											
XM_483892	M400008706	-	-	-	-	-	-	-	-	2.0	Down
M400008754	M400008754	-	-	-	-	-	-	-	-	2.0	Down
M400008771	M400008771	-	-	-	-	-	-	-	-	2.6	Down
M400008789	M400008789	-	-	-	-	-	-	-	-	2.1	Up
M400008795	M400008795	-	-	-	-	-	-	-	-	2.4	Down
M400008820	M400008820	-	-	-	-	-	-	-	-	1.5	Down
M400008826	M400008826	-	-	-	-	-	-	-	-	2.5	Down
M400008833	M400008833	-	-	-	-	-	-	-	-	1.9	Down
M400008849	M400008849	-	-	-	-	-	-	-	-	1.8	Down
M400008895	M400008895	-	-	-	-	-	-	-	-	1.6	Down
M400008932	M400008932	-	-	-	-	-	-	-	-	2.1	Down



M400008971	M400008971	-	-	-	-	-	-	-	-	2.0	Down
M400008973	M400008973	-	-	-	-	-	-	-	-	1.7	Down
M400008986	M400008986	-	-	-	-	-	-	-	-	1.6	Down
M400009021	M400009021	-	-	-	-	-	-	-	-	1.7	Down
M400009049	M400009049	-	-	-	-	-	-	-	-	1.8	Down
M400009050	M400009050	-	-	-	-	-	-	-	-	2.0	Down
M400009062	M400009062	-	-	-	-	-	-	1.6	Down	-	-
M400009086	M400009086	-	-	-	-	-	-	-	-	1.7	Down
M400009095	M400009095	-	-	-	-	-	-	-	-	2.2	Down
M400009115	M400009115	-	-	-	-	-	-	-	-	2.0	Down
M400009138	M400009138	-	-	-	-	-	-	-	-	2.1	Down
M400009151	M400009151	-	-	-	-	-	-	-	-	3.0	Down
M400009162	M400009162	-	-	-	-	-	-	-	-	1.6	Down
M400009164	M400009164	-	-	-	-	-	-	-	-	1.6	Down
M400009192	M400009192	-	-	-	-	-	-	-	-	2.1	Down
M400009193	M400009193	-	-	-	-	-	-	-	-	1.9	Down
M400009206	M400009206	-	-	-	-	-	-	-	-	1.8	Down
M400009228	M400009228	-	-	-	-	-	-	-	-	1.5	Down
M400009252	M400009252	-	-	-	-	-	-	-	-	3.1	Down
M400009262	M400009262	-	-	-	-	1.6	Up	-	-	-	-
XM_355466,											
XM_486561	M400009264	-	-	-	-	-	-	-	-	2.6	Down
M400009274	M400009274	-	-	-	-	-	-	-	-	1.7	Down
M400009287	M400009287	-	-	-	-	-	-	-	-	2.2	Down
M400009306	M400009306	-	-	-	-	-	-	-	-	1.6	Down
M400009353	M400009353	-	-	-	-	-	-	-	-	2.1	Down
M400009362	M400009362	-	-	-	-	-	-	-	-	2.1	Down
M400009384	M400009384	-	-	-	-	-	-	-	-	1.7	Down
M400009386	M400009386	-	-	-	-	-	-	-	-	2.3	Down
M400009401	M400009401	-	-	-	-	-	-	-	-	2.1	Down
M400009410	M400009410	-	-	-	-	-	-	-	-	2.1	Down
M400009435	M400009435	-	-	-	-	-	-	-	-	1.7	Down
M400009453	M400009453	-	-	-	-	-	-	-	-	2.1	Down
NM_010646,											
NM_010647,											
NM_024470	M400009462	-	-	-	-	-	-	1.9	Up	1.8	Down
NM_207547,											
XM_485887	M400009478	-	-	-	-	-	-	-	-	1.7	Down
M400009501	M400009501	-	-	-	-	-	-	-	-	1.7	Down
M400009508	M400009508	-	-	-	-	-	-	1.6	Up	-	-
M400009524	M400009524	-	-	-	-	-	-	-	-	4.2	Up
M400009534	M400009534	-	-	-	-	-	-	-	-	3.8	Up

M400009552	M400009552	-	-	-	-	-	-	-	-	1.7	Down
M400009590	M400009590	-	-	-	-	-	-	-	-	1.7	Down
M400009631	M400009631	-	-	-	-	-	-	-	-	1.5	Down
M400009709	M400009709	-	-	-	-	-	-	-	-	1.9	Down
XM_135659	M400009733	-	-	-	-	-	-	-	-	2.3	Down
M400009776	M400009776	-	-	-	-	-	-	-	-	2.3	Down
M400009787	M400009787	-	-	-	-	-	-	-	-	2.2	Down
M400009800	M400009800	-	-	-	-	-	-	-	-	2.2	Down
M400009804	M400009804	-	-	-	-	-	-	-	-	2.5	Down
M400009829	M400009829	-	-	-	-	-	-	-	-	1.7	Up
M400009846	M400009846	-	-	-	-	-	-	-	-	1.7	Down
M400009851	M400009851	-	-	-	-	-	-	-	-	1.6	Down
M400009852	M400009852	-	-	-	-	-	-	-	-	2.0	Down
M400009857	M400009857	-	-	-	-	-	-	-	-	2.0	Down
M400009881	M400009881	-	-	-	-	-	-	-	-	2.0	Down
M400009882	M400009882	-	-	-	-	-	-	-	-	1.5	Down
XM_487217	M400009936	-	-	-	-	1.8	Up	-	-	2.7	Up
M400009959	M400009959	-	-	-	-	-	-	-	-	1.7	Down
M400009983	M400009983	-	-	-	-	-	-	-	-	1.5	Down
M400009988	M400009988	-	-	-	-	-	-	-	-	1.5	Down
M400009993	M400009993	-	-	-	-	-	-	-	-	2.2	Down
M400010030	M400010030	-	-	-	-	-	-	-	-	1.7	Down
M400010047	M400010047	-	-	-	-	-	-	-	-	1.9	Down
M400010049	M400010049	-	-	-	-	-	-	-	-	2.2	Up
M400010054	M400010054	-	-	-	-	-	-	-	-	2.0	Down
M400010071	M400010071	-	1.8	Up	-	-	-	-	-	-	-
M400010072	M400010072	-	2.2	Up	-	-	-	-	-	1.7	Up
M400010074	M400010074	-	-	-	-	-	-	-	-	4.3	Up
M400010106	M400010106	-	-	-	-	-	-	-	-	2.2	Down
M400010112	M400010112	-	-	-	-	-	-	-	-	2.2	Down
M400010136	M400010136	-	-	-	-	-	-	-	-	2.4	Down
M400010154	M400010154	-	-	-	-	-	-	-	-	1.6	Down
M400010159	M400010159	-	-	-	-	-	-	-	-	2.1	Down
M400010184	M400010184	-	-	-	-	-	-	-	-	2.2	Down
M400010233	M400010233	-	-	-	-	-	-	-	-	1.7	Down
M400010237	M400010237	-	-	-	-	-	-	-	-	3.2	Down
M400010243	M400010243	-	-	-	-	-	-	-	-	2.2	Down
M400010255	M400010255	-	-	-	-	-	-	-	-	1.7	Down
M400010278	M400010278	-	-	-	-	-	-	-	-	1.7	Down
M400010297	M400010297	-	-	-	-	-	-	-	-	1.6	Down
M400010356	M400010356	-	-	-	-	-	-	-	-	2.8	Down

M400010371	M400010371	-	-	-	-	-	3.7	Up	-	-
M400010392	M400010392	-	-	-	-	-	-	-	3.0	Down
M400010410	M400010410	-	-	-	-	-	-	-	2.3	Down
M400010434	M400010434	-	-	-	-	-	-	-	1.6	Up
M400010435	M400010435	-	-	-	-	-	-	-	2.5	Up
M400010460	M400010460	-	-	-	-	1.6	Down	-	-	-
M400010473	M400010473	-	-	-	-	-	-	-	2.2	Down
M400010526	M400010526	-	-	-	-	-	-	-	3.0	Down
M400010561	M400010561	-	-	-	-	-	-	-	1.5	Down
M400010567	M400010567	-	-	-	-	-	-	-	1.7	Down
M400010636	M400010636	-	-	-	-	-	2.5	Down	1.6	Down
M400010643	M400010643	-	-	-	-	-	2.1	Down	2.5	Down
M400010795 _60	M400010795_60	-	-	-	-	-	-	-	1.8	Down
M400010795 _70	M400010795_70	-	-	-	-	-	-	-	1.7	Down
M400010795 _90	M400010795_90	-	-	-	-	-	-	-	1.6	Up
NM_008907, XM_356177, XM_485997	M400010868	-	-	-	-	-	-	-	1.6	Down
NM_009486, NM_009487	M400010938	-	-	-	-	-	-	-	2.7	Up
M400011004	M400011004	-	-	-	-	1.8	Down	-	3.1	Up
NM_173366	M400012263	-	-	-	-	-	-	-	2.7	Down
M400012299	M400012299	-	-	-	-	-	-	-	2.5	Down
NM_175395	M400012309	-	-	-	-	-	-	-	1.5	Down
NM_175690	M400012328	-	-	-	-	-	-	-	1.9	Down
M400012344	M400012344	-	-	-	-	-	-	-	1.7	Down
NM_177252	M400012398	-	-	-	-	-	-	-	2.2	Down
NM_178186, NM_178187, NM_178188, NM_178189	M400012458	-	-	-	-	1.9	Up	-	1.9	Down
NM_013549, NM_178212	M400012465	-	-	-	-	-	-	-	2.2	Down
NM_178881	M400012501	-	-	-	-	-	-	-	2.4	Down
NM_178927	M400012512	-	-	-	-	-	-	-	2.0	Down
M400012535	M400012535	-	-	-	-	-	-	-	2.2	Down
M400012696	M400012696	-	-	-	-	-	-	-	2.3	Down
M400012715	M400012715	-	-	-	-	-	-	-	2.3	Down
M400012721	M400012721	-	-	-	-	-	-	-	3.0	Down
M400012744	M400012744	-	-	-	-	-	-	-	2.6	Down

M400012806	M400012806	-	-	-	-	-	-	-	-	2.4	Down
M400012836	M400012836	-	-	-	-	-	-	1.6	Up	-	-
M400012838	M400012838	-	-	-	-	1.5	Up	-	-	-	-
M400012849	M400012849	-	-	-	-	-	-	-	-	2.5	Down
M400012857	M400012857	-	-	-	-	-	-	-	-	1.6	Down
M400012861	M400012861	-	-	-	-	-	-	-	-	2.2	Down
M400012863	M400012863	-	-	-	-	-	-	-	-	3.4	Up
M400012879	M400012879	-	-	-	-	-	-	-	-	2.0	Down
M400012904	M400012904	-	-	-	-	-	-	-	-	2.7	Down
M400012918	M400012918	-	-	-	-	2.2	Down	-	-	-	-
M400012928	M400012928	-	-	-	-	-	-	-	-	1.7	Down
M400012933	M400012933	-	-	-	-	-	-	-	-	1.6	Down
M400012934	M400012934	-	-	-	-	-	-	-	-	2.3	Down
M400012954	M400012954	-	-	-	-	-	-	-	-	3.1	Up
M400012968	M400012968	-	-	-	-	-	-	-	-	2.3	Down
M400012970	M400012970	-	-	-	-	-	-	-	-	2.4	Down
M400012972	M400012972	-	-	-	-	-	-	-	-	2.0	Down
M400012984	M400012984	-	-	-	-	-	-	-	-	2.5	Down
M400012990	M400012990	-	-	-	-	-	-	-	-	2.6	Down
M400012996	M400012996	-	-	-	-	1.9	Down	-	-	4.0	Down
M400013005	M400013005	-	-	-	-	-	-	-	-	1.9	Down
M400013010	M400013010	-	-	-	-	-	-	-	-	2.6	Down
M400013012	M400013012	-	-	-	-	-	-	-	-	2.0	Down
M400013018	M400013018	-	-	-	-	-	-	-	-	2.3	Down
M400013019	M400013019	-	-	-	-	-	-	-	-	1.6	Down
M400013028	M400013028	-	-	-	-	-	-	-	-	2.1	Down
M400013035	M400013035	-	-	-	-	-	-	-	-	3.0	Down
M400013039	M400013039	-	-	-	-	-	-	-	-	1.9	Down
M400013046	M400013046	-	-	-	-	-	-	-	-	1.5	Down
M400013052	M400013052	-	-	-	-	-	-	-	-	2.1	Down
M400013063	M400013063	-	-	-	-	-	-	-	-	2.8	Down
M400013068	M400013068	-	-	-	-	-	-	-	-	1.7	Down
XM_484493,											
XM_485090	M400013071	-	-	-	-	-	-	-	-	2.7	Down
M400013081	M400013081	-	-	-	-	-	-	-	-	3.1	Down
M400013082	M400013082	-	-	-	-	-	-	1.7	Up	1.8	Up
M400013087	M400013087	-	-	-	-	-	-	-	-	1.8	Down
M400013111	M400013111	-	-	-	-	-	-	-	-	1.8	Down
M400013117	M400013117	-	-	-	-	-	-	-	-	2.4	Down
M400013122	M400013122	-	-	-	-	-	-	-	-	1.6	Down
M400013129	M400013129	-	-	-	-	-	-	-	-	1.7	Down

M400013172	M400013172	-	-	-	-	-	-	-	-	1.8	Up
M400013175	M400013175	-	-	-	-	-	-	-	-	2.2	Down
M400013179	M400013179	-	-	-	-	2.2	Down	-	-	-	-
M400013200	M400013200	-	-	-	-	-	-	-	-	1.9	Down
M400013206	M400013206	-	-	-	-	-	-	-	-	2.0	Down
M400013219	M400013219	-	-	-	-	-	-	-	-	1.5	Down
M400013230	M400013230	-	-	-	-	-	-	-	-	1.8	Down
M400013237	M400013237	-	-	-	-	-	-	-	-	1.6	Down
M400013241	M400013241	-	-	-	-	-	-	-	-	3.1	Down
M400013243	M400013243	-	-	-	-	-	-	-	-	1.9	Down
M400013260	M400013260	-	-	-	-	1.7	Up	-	-	-	-
M400013283	M400013283	-	-	-	-	-	-	-	-	2.3	Down
M400013284	M400013284	-	-	-	-	-	-	-	-	2.5	Down
M400013309	M400013309	-	-	-	-	-	-	-	-	1.5	Down
M400013313	M400013313	-	-	-	-	-	-	-	-	1.8	Up
M400013318	M400013318	-	-	-	-	-	-	-	-	1.8	Down
M400013330	M400013330	-	-	-	-	-	-	-	-	1.6	Down
M400013337	M400013337	-	-	-	-	-	-	-	-	2.3	Down
M400013343	M400013343	-	-	-	-	-	-	-	-	1.7	Down
M400013355	M400013355	-	-	-	-	-	-	-	-	1.5	Down
M400013361	M400013361	-	-	-	-	-	-	-	-	2.0	Down
M400013384	M400013384	-	-	-	-	-	-	-	-	2.7	Down
M400013403	M400013403	-	-	-	-	-	-	-	-	1.7	Down
M400013412	M400013412	-	-	-	-	-	-	-	-	2.2	Down
M400013415	M400013415	-	-	-	-	2.2	Down	-	-	2.4	Down
M400013451	M400013451	-	-	-	-	-	-	-	-	2.3	Down
M400013454	M400013454	-	-	-	-	-	-	-	-	2.2	Down
M400013455	M400013455	-	-	-	-	-	-	-	-	2.4	Down
M400013486	M400013486	-	-	-	-	1.7	Down	-	-	-	-
M400013544	M400013544	-	-	-	-	-	-	-	-	1.9	Down
M400013550	M400013550	-	-	-	-	-	-	-	-	2.1	Down
M400013577	M400013577	-	-	-	-	-	-	-	-	1.8	Up
M400013587	M400013587	-	-	-	-	-	-	-	-	2.7	Down
M400013604	M400013604	-	-	-	-	-	-	-	-	2.3	Down
M400013648	M400013648	-	-	-	-	-	-	-	-	1.5	Down
M400013653	M400013653	-	-	-	-	-	-	-	-	1.6	Down
M400013682	M400013682	-	-	-	-	-	-	-	-	3.8	Down
M400013713	M400013713	-	-	-	-	-	-	-	-	1.6	Down
M400013717	M400013717	-	-	-	-	-	-	-	-	2.1	Down
M400013736	M400013736	-	-	-	-	-	-	-	-	2.1	Down
M400013759	M400013759	-	-	-	-	-	-	-	-	2.9	Down

M400013783	M400013783	-	-	-	-	-	-	-	-	3.1	Down
XM_488527	M400013784	-	-	-	-	-	-	-	-	2.0	Down
M400013793	M400013793	-	-	-	-	-	-	-	-	2.2	Down
M400013794	M400013794	-	-	-	-	-	-	-	-	1.8	Down
M400013795	M400013795	-	-	-	-	-	-	-	-	2.3	Down
M400013802	M400013802	-	-	-	-	-	-	-	-	1.6	Down
M400013820	M400013820	-	-	-	-	-	-	-	-	2.1	Down
M400013824	M400013824	-	-	-	-	-	-	-	-	1.8	Up
M400013825	M400013825	-	-	-	-	-	-	-	-	1.9	Down
M400013828	M400013828	-	-	-	-	-	-	-	-	1.7	Down
M400013840	M400013840	-	-	-	-	-	-	-	-	2.5	Down
M400013888	M400013888	-	-	-	-	-	-	-	-	2.0	Down
M400013899	M400013899	-	-	-	-	-	-	-	-	2.8	Down
M400013902	M400013902	-	-	-	-	-	-	-	-	2.0	Down
M400013931	M400013931	-	-	-	-	-	-	-	-	2.4	Down
M400013935	M400013935	-	-	-	-	-	-	-	-	2.8	Down
M400013960	M400013960	-	-	-	-	-	-	-	-	1.8	Down
M400013961	M400013961	-	-	-	-	-	-	-	-	2.0	Down
M400013966	M400013966	-	-	-	-	-	-	-	-	2.2	Down
M400013967	M400013967	-	-	-	-	-	-	-	-	3.0	Down
M400013997	M400013997	-	-	-	-	-	-	-	-	1.6	Down
M400014010	M400014010	-	-	-	-	-	-	-	-	1.8	Down
M400014063	M400014063	-	-	-	-	-	-	-	-	2.2	Down
M400014068	M400014068	-	-	-	-	-	-	-	-	2.0	Down
M400014076	M400014076	-	-	-	-	-	-	2.5	Up	-	-
M400014087	M400014087	-	-	-	-	-	-	-	-	2.1	Up
M400014145	M400014145	-	-	-	-	-	-	-	-	1.9	Down
M400014163	M400014163	-	-	-	-	-	-	-	-	2.0	Down
M400014178	M400014178	-	-	-	-	-	-	-	-	2.1	Down
M400014241	M400014241	-	-	-	-	-	-	-	-	1.6	Down
M400014253	M400014253	-	-	-	-	-	-	-	-	2.6	Down
M400014267	M400014267	-	-	-	-	-	-	-	-	2.3	Down
M400014327	M400014327	-	-	-	-	-	-	-	-	2.0	Down
M400014333	M400014333	-	-	-	-	-	-	-	-	1.7	Up
M400014355	M400014355	-	-	-	-	-	-	-	-	1.7	Up
M400014375	M400014375	-	-	-	-	-	-	-	-	1.7	Down
M400014382	M400014382	-	-	-	-	-	-	-	-	1.6	Down
M400014385	M400014385	-	-	-	-	-	-	-	-	1.8	Up
M400014399	M400014399	-	-	-	-	-	-	-	-	2.3	Down
M400014420	M400014420	-	-	-	-	-	-	-	-	2.1	Down
M400014430	M400014430	-	-	-	-	1.7	Up	-	-	-	-

M400014490	M400014490	-	-	-	-	-	-	-	-	2.9	Down
M400014495	M400014495	-	-	-	-	-	-	-	-	2.7	Down
XM_488664	M400014510	-	-	-	-	-	-	-	-	2.9	Down
M400014538	M400014538	-	-	-	-	-	-	-	-	1.9	Down
M400014561	M400014561	-	-	-	-	-	-	-	-	2.0	Down
M400014565	M400014565	-	-	-	-	-	-	-	-	1.9	Down
M400014582	M400014582	-	-	-	-	-	-	-	-	3.6	Up
M400014584	M400014584	-	-	-	-	-	-	-	-	2.3	Down
M400014597	M400014597	-	-	-	-	-	-	-	-	1.6	Down
M400014659	M400014659	-	-	-	-	-	-	-	-	1.9	Up
M400014669	M400014669	-	-	-	-	-	-	-	-	2.4	Up
M400014672	M400014672	-	-	-	-	-	-	-	-	2.4	Down
M400014704	M400014704	-	-	-	-	1.6	Down	-	-	-	-
M400014738	M400014738	-	-	-	-	-	-	-	-	1.7	Down
M400014792	M400014792	-	-	-	-	-	-	-	-	2.0	Down
M400014810	M400014810	-	-	-	-	-	-	-	-	3.5	Down
M400014828	M400014828	-	-	-	-	-	-	-	-	1.7	Down
M400014833	M400014833	-	-	-	-	-	-	-	-	1.6	Up
M400014839	M400014839	-	-	-	-	-	-	-	-	1.6	Down
M400014854	M400014854	-	-	-	-	-	-	-	-	3.2	Down
M400014875	M400014875	-	-	-	-	-	-	-	-	1.9	Down
M400014902	M400014902	-	-	-	-	-	-	-	-	3.0	Down
M400014920	M400014920	-	-	-	-	-	-	2.7	Up	-	-
M400014924	M400014924	-	-	-	-	-	-	-	-	2.0	Down
M400014933	M400014933	-	-	-	-	1.8	Down	-	-	3.7	Down
M400014958	M400014958	-	-	-	-	-	-	-	-	1.5	Down
M400014959	M400014959	-	-	-	-	-	-	-	-	1.5	Down
M400014976	M400014976	-	-	-	-	-	-	-	-	2.7	Down
M400014990	M400014990	-	-	-	-	-	-	2.0	Up	-	-
M400014994	M400014994	-	-	-	-	-	-	-	-	2.6	Down
M400015091	M400015091	-	-	-	-	-	-	-	-	3.8	Down
M400015106	M400015106	-	-	-	-	-	-	-	-	1.7	Down
M400015121	M400015121	-	-	-	-	-	-	-	-	2.6	Down
M400015190	M400015190	-	-	-	-	-	-	-	-	1.5	Down
M400015222	M400015222	-	-	-	-	-	-	-	-	2.5	Down
M400015238	M400015238	-	-	-	-	-	-	-	-	1.5	Down
M400015250	M400015250	-	-	-	-	-	-	-	-	3.1	Down
M400015282	M400015282	-	-	-	-	1.6	Down	-	-	-	-
M400015306	M400015306	-	-	-	-	-	-	-	-	2.5	Down
M400015350	M400015350	-	-	-	-	-	-	-	-	2.0	Down
M400015379	M400015379	-	-	-	-	-	-	-	-	1.7	Down

M400015380	M400015380	-	-	-	-	-	-	-	-	1.5	Down
M400015427	M400015427	-	-	-	-	-	-	-	-	2.3	Down
M400015435	M400015435	-	-	-	-	-	-	-	-	2.3	Down
M400015475	M400015475	-	-	-	-	-	-	-	-	2.3	Down
M400015480	M400015480	-	-	-	-	-	-	-	-	1.6	Down
M400015599	M400015599	-	-	-	-	-	-	-	-	1.6	Down
M400015611	M400015611	-	-	-	-	-	-	-	-	1.6	Down
M400015628	M400015628	-	-	-	-	2.1	Down	-	-	1.8	Down
M400015638	M400015638	-	-	-	-	-	-	3.9	Up	-	-
M400015673	M400015673	-	-	-	-	1.7	Down	-	-	-	-
M400015686	M400015686	-	-	-	-	-	-	-	-	2.2	Down
M400015718	M400015718	-	-	-	-	-	-	-	-	1.5	Down
M400015754	M400015754	-	-	-	-	-	-	-	-	1.9	Down
M400015776	M400015776	-	-	-	-	-	-	-	-	2.4	Up
M400015779	M400015779	-	-	-	-	-	-	-	-	2.3	Down
M400015795	M400015795	-	-	-	-	-	-	-	-	1.5	Down
M400015867	M400015867	-	-	-	-	-	-	-	-	3.8	Down
M400015911	M400015911	-	-	-	-	-	-	-	-	4.3	Up
M400015914	M400015914	-	-	-	-	-	-	-	-	1.6	Down
M400016009	M400016009	-	-	-	-	-	-	-	-	2.3	Down
M400016015	M400016015	-	-	-	-	-	-	-	-	1.7	Down
M400016047	M400016047	-	-	-	-	-	-	-	-	2.8	Down
M400016094	M400016094	-	-	-	-	2.3	Down	-	-	-	-
M400016146	M400016146	-	-	-	-	-	-	-	-	2.1	Down
M400016148	M400016148	-	-	-	-	-	-	-	-	3.0	Up
M400016186	M400016186	-	-	-	-	-	-	-	-	1.8	Down
M400016290	M400016290	-	-	-	-	-	-	-	-	2.2	Down
M400016301	M400016301	-	-	-	-	-	-	-	-	2.7	Down
M400016373	M400016373	-	-	-	-	-	-	-	-	2.8	Down
M400016376	M400016376	-	-	-	-	-	-	-	-	2.8	Down
M400016377	M400016377	-	-	-	-	-	-	-	-	2.1	Down
M400016489	M400016489	-	-	-	-	-	-	-	-	2.6	Down
M400016494	M400016494	-	-	-	-	-	-	-	-	1.9	Down
M400016551	M400016551	-	-	-	-	-	-	-	-	2.6	Down
M400016583	M400016583	-	-	-	-	-	-	-	-	1.5	Down
M400016602	M400016602	-	-	-	-	-	-	-	-	1.6	Down
M400016617	M400016617	-	-	-	-	-	-	-	-	3.8	Up
M400016620	M400016620	-	-	-	-	-	-	-	-	2.1	Down
M400016627	M400016627	-	-	-	-	-	-	-	-	1.9	Down
M400016637	M400016637	-	-	-	-	-	-	-	-	1.9	Down
M400016664	M400016664	-	-	-	-	-	-	-	-	2.2	Up



M400016692	M400016692	-	-	-	-	-	-	-	-	2.0	Down
M400016704	M400016704	-	-	-	-	-	-	-	-	3.3	Up
M400016757	M400016757	-	-	-	-	-	-	-	-	2.1	Down
M400016814	M400016814	-	-	-	-	-	-	-	-	2.7	Down
M400016846	M400016846	-	-	-	-	-	-	-	-	3.6	Down
M400016917	M400016917	-	-	-	-	-	-	-	-	2.4	Down
M400016939	M400016939	-	-	-	-	-	-	-	-	3.0	Down
M400016999	M400016999	-	-	-	-	-	-	-	-	1.6	Down
M400017071	M400017071	-	-	-	-	-	-	-	-	1.5	Down
M400017120	M400017120	-	-	-	-	-	-	-	-	3.5	Down
M400017139	M400017139	-	-	-	-	-	-	-	-	1.8	Up
M400017231	M400017231	-	-	-	-	-	-	-	-	1.7	Down
M400017245	M400017245	-	-	-	-	-	-	-	-	2.4	Down
M400017290	M400017290	-	-	-	-	2.4	Down	-	-	2.6	Down
M400017306	M400017306	-	-	-	-	-	-	-	-	2.6	Up
M400017321	M400017321	-	-	-	-	-	-	-	-	2.5	Up
M400017379	M400017379	-	-	-	-	-	-	-	-	2.7	Down
M400017404	M400017404	-	-	-	-	-	-	-	-	1.6	Down
M400017490	M400017490	-	-	-	-	-	-	-	-	3.1	Up
M400017512	M400017512	-	-	-	-	-	-	1.7	Up	-	-
M400017618	M400017618	-	-	-	-	-	-	-	-	2.4	Down
M400017732	M400017732	-	-	-	-	1.7	Down	-	-	-	-
M400017767	M400017767	-	-	-	-	1.7	Down	-	-	3.2	Down
M400017940	M400017940	-	-	-	-	-	-	-	-	3.6	Down
M400017969	M400017969	-	-	-	-	1.5	Down	-	-	2.4	Down
M400017976	M400017976	-	-	-	-	-	-	-	-	1.5	Up
M400017986	M400017986	-	-	-	-	-	-	-	-	1.7	Down
M400018002	M400018002	-	-	-	-	-	-	-	-	1.7	Down
M400018006	M400018006	-	-	-	-	1.9	Down	-	-	-	-
M400018009	M400018009	-	-	1.8	Down	-	-	-	-	-	-
M400018077	M400018077	-	-	-	-	-	-	-	-	2.0	Down
M400018093	M400018093	-	-	-	-	-	-	-	-	2.3	Down
M400018201	M400018201	-	-	-	-	-	-	-	-	1.6	Down
M400018211	M400018211	-	-	-	-	-	-	-	-	1.7	Down
M400018232	M400018232	-	-	-	-	-	-	2.9	Up	-	-
M400018236	M400018236	-	-	-	-	-	-	-	-	1.7	Down
M400018307	M400018307	-	-	-	-	-	-	-	-	1.6	Down
M400018333	M400018333	-	-	-	-	-	-	-	-	2.2	Down
M400018390	M400018390	-	-	-	-	-	-	-	-	2.4	Down
M400018401	M400018401	-	-	1.9	Down	-	-	-	-	-	-
M400018432	M400018432	-	-	-	-	-	-	-	-	1.7	Down

M400018443	M400018443	-	-	-	-	-	-	-	-	2.3	Down
M400018449	M400018449	-	-	-	-	-	-	-	-	1.7	Down
M400018475	M400018475	-	-	-	-	1.7	Up	-	-	2.2	Up
M400018523	M400018523	-	-	-	-	-	-	2.3	Up	-	-
M400018556	M400018556	-	-	-	-	-	-	2.2	Down	-	-
M400018621	M400018621	-	-	-	-	-	-	-	-	3.5	Down
M400018662	M400018662	-	-	-	-	-	-	-	-	2.6	Down
M400018769	M400018769	-	2.4	Down	-	-	-	-	-	-	-
M400018789	M400018789	-	-	-	-	-	-	1.9	Up	-	-
M400018830	M400018830	-	-	-	-	-	-	1.5	Up	-	-
M400018845	M400018845	-	-	-	-	-	-	-	-	1.9	Down
XM_488665	M400018881	-	-	-	-	-	-	-	-	2.3	Down
M400018901	M400018901	-	-	-	-	-	-	-	-	1.7	Down
M400018909	M400018909	-	-	-	-	-	-	2.2	Up	-	-
M400018911	M400018911	-	-	-	-	2.8	Down	-	-	-	-
M400018942	M400018942	-	-	-	-	-	-	-	-	2.1	Down
M400018971	M400018971	-	-	-	-	-	-	-	-	2.4	Down
M400018995	M400018995	-	-	-	-	-	-	-	-	1.7	Down
M400019045	M400019045	-	-	-	-	-	-	-	-	2.5	Up
M400019057	M400019057	-	-	-	-	-	-	-	-	2.4	Down
M400019137	M400019137	-	-	-	-	-	-	-	-	3.0	Down
M400019150	M400019150	-	-	-	-	-	-	-	-	1.5	Down
M400019156	M400019156	-	-	-	-	-	-	-	-	1.8	Down
M400019172	M400019172	-	-	-	-	-	-	-	-	1.6	Down
M400019188	M400019188	-	-	-	-	-	-	-	-	1.7	Up
M400019232	M400019232	-	-	-	-	1.6	Down	-	-	-	-
M400019238	M400019238	-	-	-	-	-	-	-	-	2.1	Down
M400019245	M400019245	-	-	-	-	-	-	-	-	2.6	Down
M400019300	M400019300	-	-	-	-	-	-	-	-	2.1	Down
M400019364	M400019364	-	-	-	-	-	-	-	-	2.3	Down
M400019411	M400019411	-	-	-	-	-	-	-	-	2.2	Down
M400019417	M400019417	-	-	-	-	-	-	-	-	2.0	Down
M400019459	M400019459	-	-	-	-	-	-	-	-	1.7	Down
M400019461	M400019461	-	-	-	-	-	-	1.6	Up	-	-
M400019470	M400019470	-	-	-	-	-	-	-	-	1.6	Down
M400019484	M400019484	-	-	-	-	-	-	2.5	Up	3.4	Up
M400019516	M400019516	-	-	-	-	-	-	-	-	1.9	Down
M400019520	M400019520	-	-	-	-	-	-	-	-	3.3	Up
NM_194336	Macrophage activation 2 like LOC626578	Mpa2l	-	-	-	1.6	Down	-	-	-	-
NM_019499	MAD2 (mitotic arrest deficient, homolog)-like 1 (yeast)	Mad2l1	-	-	-	-	-	-	-	2.8	Down
NM_025952	Magnesium transporter 1	Magt1	1.7	Down	-	-	-	-	-	2.5	Down

NM_172499	Major facilitator superfamily domain containing 9 MAK10 homolog, amino-acid N-acetyltransferase subunit, ( <i>S. cerevisiae</i> )	Mfsd9	-	-	-	-	-	-	-	1.8	Down
NM_030153	MAM domain containing 4	Mak10	-	-	-	-	-	-	-	2.1	Down
XM_355317	Mammary tumor virus receptor 2	Mtvr2	-	-	2.0	Up	-	-	-	-	-
NM_181452	Mannose receptor, C type 1	Mrc1	-	-	-	-	-	-	-	1.7	Down
NM_008625	Mannoside acetylglucosaminyltransferase 1	Mgat1	-	-	-	-	-	-	-	1.7	Down
NM_010794	MAP kinase-activated protein kinase 2	Mapkapk2	-	-	-	-	-	-	-	1.9	Up
NM_007928	MAP/microtubule affinity-regulating kinase 2	Mark2	-	-	-	-	-	-	-	4.2	Up
NM_010790	Maternal embryonic leucine zipper kinase	Melk	-	-	-	-	-	-	-	2.2	Down
NM_010808	Matrix metalloproteinase 24	Mmp24	-	-	-	-	-	-	-	2.3	Down
NM_013599	Matrix metalloproteinase 9	Mmp9	-	-	-	-	-	-	-	1.9	Down
NM_010751	MAX dimerization protein 1	Mxd1	-	-	-	-	-	-	-	1.9	Up
NM_016662	Max dimerization protein 3	Mxd3	-	-	-	-	-	-	-	1.7	Down
NM_013720	MAX gene associated	Mga	-	-	-	-	-	-	-	1.5	Down
NM_011513	Mediator complex subunit 22 Mediator of RNA polymerase II transcription, subunit 10 homolog ( <i>NUT2, S. cerevisiae</i> )	Med22	-	-	-	-	-	-	-	1.6	Down
NM_138596	Mediator of RNA polymerase II transcription, subunit 11 homolog ( <i>S. cerevisiae</i> )	Med10	-	-	2.3	Up	-	-	-	-	-
NM_025397	Melanoma antigen, family B, 2	Med11	-	-	-	-	-	-	-	2.1	Up
NM_031171	Membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5)	Mageb2	-	-	-	-	-	-	-	1.9	Down
NM_019579	Membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6)	Mpp5	-	-	-	-	-	-	-	1.9	Down
NM_019939	Membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	Mpp6	-	-	-	-	-	-	-	3.1	Down
XM_128966	Membrane-spanning 4-domains, subfamily A, member 8A	-	-	-	-	-	-	-	-	2.0	Down
NM_022430	meningioma 1	Ms4a8a	-	-	-	-	-	-	-	1.6	Up
XM_485667	Methionine-tRNA synthetase	-	-	-	-	-	-	-	-	2.8	Down
NM_013602	methylmalonyl CoA epimerase	Mt1	-	-	-	-	-	-	-	4.1	Up
NM_144800	metastasis suppressor 1	Mtss1	-	-	-	-	-	-	-	1.7	Up
NM_016804	Metaxin 2	Mtx2	-	-	-	-	-	-	-	2.1	Up
NM_0010039	Methionine-tRNA synthetase	Mars	-	-	-	-	-	-	-	2.3	Down
13	MFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	-	-	-	-	-	-	-	-	2.0	Down
XM_133510	Microtubule-associated protein 1 light chain 3 beta	Mfng	-	-	-	-	3.9	Up	-	-	-
NM_008595	Misato homolog 1 ( <i>Drosophila</i> )	Map1lc3b	-	-	-	-	-	-	-	3.8	Up
NM_026160	Mitochondrial methionyl-tRNA formyltransferase	Msto1	-	-	-	-	-	-	-	1.9	Down
NM_144898	Mitochondrial ribosomal protein L11	Mtfmt	-	-	-	-	-	-	-	1.8	Down
NM_027134	Mitochondrial ribosomal protein L2	Mrpl11	-	-	-	-	-	-	-	3.1	Up
NM_025553		Mrpl2	-	-	-	-	-	-	-	2.1	Down
NM_025302			-	-	-	-	-	-	-		

NM_025796	Mitochondrial ribosomal protein L33	Mrpl33	-	-	-	-	-	-	2.0	Up
NM_025474	Mitochondrial ribosomal protein S14	Mrps14	-	-	-	-	-	-	2.8	Down
NM_025434	Mitochondrial ribosomal protein S28	Mrps28	-	-	-	-	-	-	2.0	Down
NM_010270	Mitochondrial ribosomal protein S33	Mrps33	-	-	-	-	-	-	2.2	Down
NM_025369	Mitochondrial ribosomal protein S36	Mrps36	-	-	-	-	-	-	2.7	Down
NM_145433	Mitochondrial rRNA methyltransferase 1 homolog (S. cerevisiae)	Mrm1	-	-	-	-	-	-	2.1	Down
NM_172135	Mitochondrial transcription termination factor	Mterf	-	-	-	-	-	-	1.7	Down
NM_175374	Mitochondrial translational release factor 1-like	Mtrf1l	-	-	-	-	-	-	1.7	Down
NM_011943	Mitogen-activated protein kinase kinase 6	Map2k6	-	-	-	-	-	-	1.9	Down
NM_011948	Mitogen-activated protein kinase kinase kinase 4	Map3k4	-	-	-	-	-	-	2.1	Down
NM_008580	Mitogen-activated protein kinase kinase 5	Map3k5	-	-	-	-	-	-	1.7	Down
NM_177395	Mitogen-activated protein kinase kinase kinase 9	Map3k9	-	-	-	-	-	-	2.3	Down
XM_356104	mixed lineage kinase domain-like	-	-	-	-	-	-	-	3.2	Up
XM_284098	MOB1, Mps One Binder kinase activator-like 1A (yeast)	-	-	-	-	-	-	-	2.2	Down
NM_177448	Monoacylglycerol O-acyltransferase 2	Mogat2	-	-	-	-	-	-	1.7	Down
NM_013605	Mucin 1, transmembrane	Muc1	-	-	-	-	1.9	Up	-	-
NM_139063	Muted	Muted	-	-	-	-	-	-	1.8	Down
NM_178054	muted	-	-	-	-	-	-	-	1.6	Down
NM_133250	MutY homolog (E. coli)	Mutyh	-	-	-	-	-	-	1.8	Up
XM_133827	MYC-associated zinc finger protein (purine-binding transcription factor)	-	-	-	-	-	-	-	1.7	Down
NM_0010018										
80	Myelin protein zero-like 1	Mpzl1	-	-	-	-	-	-	2.4	Down
NM_008666	Myelin transcription factor 1-like	Myt1l	-	-	-	-	-	-	3.0	Down
XM_355579	myeloid/lymphoid or mixed-lineage leukemia 3	-	-	-	-	-	-	-	2.8	Down
NM_201600	Myosin Vb	Myo5b	-	-	-	-	-	-	1.7	Down
NM_172742	Myotubularin related protein 10	Mtmr10	-	-	-	-	-	-	1.8	Down
NM_178728	N-acyl phosphatidylethanolamine phospholipase D	Napepld	-	-	-	-	-	-	1.6	Down
NM_025898	N-ethylmaleimide sensitive fusion protein attachment protein alpha	Napa	-	-	-	-	-	-	1.6	Down
NM_181569	N-methylpurine-DNA glycosylase	Mpg	-	-	-	-	-	-	1.6	Down
NM_010884	N-myc downstream regulated gene 1	-	-	-	-	-	-	-	3.6	Up
NM_008708	N-myristoyltransferase 2	Nmt2	-	-	-	-	-	-	2.2	Down
NM_010941	NAD(P) dependent steroid dehydrogenase-like	Nsdhl	-	-	2.0	Up	-	-	-	-
NM_020282	NAD(P)H dehydrogenase, quinone 2	Nqo2	-	-	-	-	-	-	1.8	Down
NM_019443	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1	Ndufa1	-	-	-	-	-	-	2.1	Down
NM_026614	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5	Ndufa5	-	-	-	-	-	-	1.9	Down
NM_026610	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 4	Ndufb4	-	-	-	-	-	-	2.3	Down
NM_025316	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5	Ndufb5	-	-	-	-	-	-	2.2	Down
NM_028186	Naked cuticle 2 homolog (Drosophila)	Nkd2	-	-	-	-	-	-	1.9	Up
NM_023294	NDC80 homolog, kinetochore complex component (S. cerevisiae)	Ndc80	-	-	-	-	-	-	1.9	Down
NM_008682	Neural precursor cell expressed, developmentally down-regulated gene 1	Nedd1	-	-	-	-	-	-	2.6	Down

NM_029447	Neurolysin (metallopeptidase M3 family)	Nln	-	-	-	-	-	-	2.0	Down
NM_008742	Neurotrophin 3	Ntf3	-	-	-	-	-	-	1.7	Down
NM_008668	Ngfi-A binding protein 2	Nab2	-	-	-	-	-	-	1.6	Down
NM_022988	Ngg1 interacting factor 3-like 1 (S. pombe)	Nif3l1	-	-	-	-	-	-	3.0	Down
NM_025623	Nipsnap homolog 3A (C. elegans)	Nipsnap3								
NM_010927	Nitric oxide synthase 2, inducible, macrophage	a	-	-	-	-	-	-	2.1	Down
XM_144267	NK1 transcription factor related, locus 1 (Drosophila)	Nos2	-	-	-	-	1.5	Down	2.4	Down
NM_010870	NLR family, apoptosis inhibitory protein 5	-	-	-	-	-	-	-	1.9	Down
XM_197335	NLR family, CARD domain containing 4	Naip5	-	-	-	-	-	-	2.5	Down
NM_177690	NLR family, pyrin domain containing 2	-	-	-	-	-	-	-	2.1	Down
NM_146171	Non-SMC condensin I complex, subunit D2	Nlrp2	-	-	-	-	-	-	1.7	Down
NM_133762	Non-SMC condensin II complex, subunit G2	Ncapd2	-	-	-	-	-	-	2.7	Down
NM_017373	Nuclear factor, interleukin 3, regulated	Ncapg2	-	-	-	-	-	-	2.0	Down
NM_013745	Nuclear fragile X mental retardation protein interacting protein 1	Nfil3	-	-	-	-	-	-	1.9	Up
NM_010881	Nuclear receptor coactivator 1	Nufip1	-	-	-	-	-	-	2.0	Down
NM_013839	Nuclear receptor subfamily 1, group H, member 3	Ncoa1	-	-	-	-	-	-	2.2	Down
NM_010264	Nuclear receptor subfamily 6, group A, member 1	Nr1h3	-	-	-	-	-	-	3.2	Down
XM_142191	nuclear RNA export factor 3	Nr6a1	-	-	2.1	Up	-	-	-	-
NM_016773	Nucleobindin 2	-	-	-	-	-	-	-	2.7	Up
NM_026578	Nucleolar protein family A, member 1 (H/ACA small nucleolar RNPs)	Nucb2	-	-	1.6	Down	-	-	-	-
NM_016714	Nucleoporin 50	Nola1	-	-	2.2	Up	-	-	-	-
NM_183392	Nucleoporin 54	Nup50	-	-	-	-	-	-	3.0	Down
NM_0010029	Nucleoporin 85	Nup54	-	-	-	-	-	-	2.0	Up
NM_011956	Nucleotide binding protein 2	Nup85	-	-	-	-	-	-	2.2	Down
NM_026341	Nudix (nucleoside diphosphate linked moiety X)-type motif 13	Nubp2	1.6	Up	1.6	Up	-	-	-	-
NM_029385	Nudix (nucleoside diphosphate linked moiety X)-type motif 16	Nudt13	-	-	-	-	-	-	1.8	Down
NM_026623	Nudix (nucleoside diphosphate linked moiety X)-type motif 21	Nudt16	-	-	-	-	-	-	1.9	Down
NM_019837	Nudix (nucleotide diphosphate linked moiety X)-type motif 3	Nudt21	-	-	-	-	-	-	1.8	Down
NM_008598	O-6-methylguanine-DNA methyltransferase	Nudt3	-	-	-	-	-	-	2.0	Up
NM_028091	O-sialoglycoprotein endopeptidase-like 1	Mgmt	-	-	-	-	-	-	1.6	Down
NM_146569	Olfactory receptor 1014	Ormdl1	-	-	-	-	-	-	2.1	Down
NM_207142	Olfactory receptor 1036	Olfr1014	-	-	1.6	Up	-	-	-	-
NM_146847	Olfactory receptor 1090	Olfr1036	-	-	-	-	-	-	1.7	Down
NM_146351	Olfactory receptor 1133	Olfr1090	-	-	-	-	-	-	1.9	Down
NM_146902	Olfactory receptor 1221	Olfr1133	-	-	-	-	-	-	2.5	Down
NM_146476	Olfactory receptor 1254	Olfr1221	-	-	-	-	-	-	3.2	Down
NM_146401	Olfactory receptor 1305	Olfr1254	-	-	-	-	-	-	1.8	Down
NM_146448	Olfactory receptor 1317	Olfr1305	-	-	-	-	1.6	Up	3.3	Up
NM_146533	Olfactory receptor 1367	Olfr1317	-	-	-	-	-	-	1.5	Up
NM_207253	Olfactory receptor 1371	Olfr1367	-	-	-	-	-	-	2.0	Down
		Olfr1371	-	-	-	-	-	-	1.6	Down

NM_146467	Olfactory receptor 1388	Olfr1388	-	-	-	-	1.8	Down	-	-
NM_146471	Olfactory receptor 1393	Olfr1393	-	-	-	-	-	-	2.3	Down
NM_146651	Olfactory receptor 1403	Olfr1403	-	-	-	-	-	-	1.8	Down
NM_146491	Olfactory receptor 1410	Olfr1410	-	-	-	-	-	-	1.7	Down
NM_146704	Olfactory receptor 1446	Olfr1446	-	-	-	-	-	-	2.2	Down
NM_146303	Olfactory receptor 1449	Olfr1449	-	-	-	-	-	-	3.3	Up
NM_146692	Olfactory receptor 1454	Olfr1454	-	-	-	-	-	-	2.1	Down
NM_207575	Olfactory receptor 1480	Olfr1480	-	-	-	-	-	-	1.5	Down
NM_146345	Olfactory receptor 1491	Olfr1491	-	-	-	-	-	-	1.9	Up
XM_146788	Olfactory receptor 150	Olfr150	-	-	-	-	-	-	2.9	Up
NM_146618	Olfactory receptor 297	Olfr297	-	-	-	-	-	-	2.4	Down
NM_146443	Olfactory receptor 382	Olfr382	-	-	-	-	-	-	2.0	Down
NM_146708	Olfactory receptor 402	Olfr402	-	-	-	-	-	-	1.9	Down
NM_146296	Olfactory receptor 437	Olfr437	-	-	-	-	-	-	1.5	Down
NM_147064	Olfactory receptor 449	Olfr449	-	-	-	-	-	-	2.4	Up
NM_146736	Olfactory receptor 491	Olfr491	-	-	-	-	-	-	1.7	Down
NM_146909	Olfactory receptor 51	Olfr51	-	-	-	-	-	-	1.6	Down
NM_146520	Olfactory receptor 536	Olfr536	-	-	1.6	Up	2.0	Up	2.8	Up
NM_146812	Olfactory receptor 620	Olfr620	-	-	-	-	-	-	2.1	Down
NM_147120	Olfactory receptor 638	Olfr638	-	-	-	-	-	-	2.3	Down
NM_147096	Olfactory receptor 666	Olfr666	-	-	-	-	-	-	2.0	Up
NM_147059	Olfactory receptor 668	Olfr668	-	-	-	-	-	-	1.8	Down
NM_146556	Olfactory receptor 798	Olfr798	-	-	-	-	-	-	1.8	Down
NM_146677	Olfactory receptor 825	Olfr825	-	-	-	-	-	-	2.7	Down
NM_146676	Olfactory receptor 826	Olfr826	-	-	-	-	-	-	1.7	Down
NM_146300	Olfactory receptor 827	Olfr827	-	-	1.9	Down	-	-	1.6	Down
NM_146522	Olfactory receptor 854	Olfr854	-	-	-	-	-	-	1.7	Down
NM_146424	Olfactory receptor 888	Olfr888	-	-	-	-	-	-	1.7	Down
NM_146804	Olfactory receptor 905	Olfr905	-	-	-	-	-	-	1.5	Up
NM_146811	Olfactory receptor 910	Olfr910	-	-	-	-	-	-	1.9	Down
XM_485604	on-SMC condensin I complex, subunit G	-	-	-	-	-	-	-	2.7	Down
NM_008106	Opsin 1 (cone pigments), medium-wave-sensitive (color blindness, deutan)	Opn1mw	-	-	-	-	-	-	4.1	Up
NM_008768	Orosomucoid 1	Orm1	-	-	-	-	-	-	2.9	Up
NM_145460	Oxidoreductase NAD-binding domain containing 1	Oxnad1	-	-	-	-	-	-	2.5	Down
NM_176840	Oxysterol binding protein-like 11	Osbpl11	-	-	-	-	-	-	3.2	Down
XM_111790	p21 (CDKN1A)-activated kinase 6	-	-	-	-	-	-	-	1.5	Down
NM_178939	P53 and DNA damage regulated 1	Pdrg1	1.8	Up	-	-	-	-	-	-
NM_011041	Paired box gene 9	Pax9	-	-	-	-	-	-	1.8	Down
NM_011093	Paired-Ig-like receptor A6	Lilrb3	-	-	-	-	-	-	3.0	Up
NM_026925	Pancreatic lipase	Pnlip	-	-	-	-	2.3	Up	-	-

NM_011128	Pancreatic lipase-related protein 2	Pnliprp2	-	-	-	-	-	-	1.7	Up
NM_001002005	Pannexin 2	Panx2	-	-	-	-	-	-	1.8	Down
NM_130887	Papilin, proteoglycan-like sulfated glycoprotein	Papln	-	-	-	-	-	-	3.2	Up
NM_025682	Paraspeckle protein 1	Pspc1	-	-	-	-	-	-	1.7	Down
NM_080850	PAS domain containing serine/threonine kinase	Pask	-	-	-	-	-	-	2.2	Down
NM_146239	PCTAIRE-motif protein kinase 2	Pctk2	-	-	-	-	-	-	1.7	Down
NM_023209	PDZ binding kinase	Pbk	-	-	-	-	-	-	1.6	Down
NM_144868	Pecanex-like 3 (Drosophila)	Pcnx13	-	-	-	-	2.2	Up	4.2	Up
XM_127497	pentatricopeptide repeat domain 2	-	-	-	-	-	-	-	2.0	Down
NM_173180	Peptidase (mitochondrial processing) alpha	Pmpca	-	-	-	-	-	-	1.9	Down
NM_011060	Peptidyl arginine deiminase, type III	Padi3	-	-	-	-	-	-	3.6	Up
NM_008835	per-hexamer repeat gene 4	-	-	-	2.4	Down	-	-	2.0	Down
NM_011073	Perforin 1 (pore forming protein)	Prf1	-	-	-	-	1.7	Up	-	-
NM_012021	Peroxiredoxin 5	Prdx5	-	-	-	-	-	-	3.1	Up
NM_007453	Peroxiredoxin 6	Prdx6	-	-	-	-	-	-	3.4	Up
NM_172705	PHD finger protein 13	Phf13	-	-	-	-	-	-	3.4	Up
NM_029404	PHD finger protein 14	Phf14	-	-	-	-	-	-	2.1	Down
NM_138755	PHD finger protein 21A	Phf21a	-	-	-	-	-	-	1.6	Down
NM_011811	Phenylalanyl-tRNA synthetase, beta subunit	Farsb	-	-	-	-	-	-	2.4	Down
NM_008838	Phosphatidylinositol glycan anchor biosynthesis, class F	Pigf	-	-	-	-	-	-	2.2	Down
XM_485660	phosphatidylinositol glycan anchor biosynthesis, class G	-	-	-	-	-	1.6	Up	-	-
NM_011822	Phosphatidylinositol glycan anchor biosynthesis, class Q	Pigq	-	-	-	-	1.5	Up	-	-
NM_025574	Phosphatidylinositol glycan anchor biosynthesis, class Y	Pigy	-	-	-	-	-	-	4.1	Up
NM_008851	Phosphatidylinositol membrane-associated 1	Pitpnm1	-	-	-	-	1.8	Up	-	-
NM_008847	Phosphatidylinositol-4-phosphate 5-kinase, type 1 alpha	Pip5k1a	-	-	1.6	Up	-	-	-	-
NM_008846	Phosphatidylinositol-4-phosphate 5-kinase, type 1 beta	Pip5k1b	-	-	-	-	-	-	3.3	Up
NM_177298	Phosphatidylserine decarboxylase	Pisd	-	-	-	-	-	-	1.8	Up
NM_008826	Phosphofructokinase, liver, B-type	Pfkl	-	-	-	-	-	-	1.9	Down
XM_203853	phosphohistidine phosphatase 1	-	-	-	-	-	-	-	2.2	Down
NM_031376	Phosphoinositide-3-kinase adaptor protein 1	Pik3ap1	-	-	-	-	-	-	2.2	Down
NM_016915	Phospholipase A2, group VI	Pla2g6	1.6	Up	-	-	-	-	-	-
NM_019588	Phospholipase C, epsilon 1	Plce1	-	-	-	-	-	-	1.7	Down
NM_026784	Phosphomevalonate kinase	Pmvk	-	-	-	-	-	-	1.8	Down
NM_011063	Phosphoprotein enriched in astrocytes 15A	Pea15a	-	-	-	-	-	-	1.6	Up
NM_010256	Phosphoribosylglycinamide formyltransferase	Gart	-	-	-	-	-	-	1.9	Down
NM_133900	Phosphoserine phosphatase	Psph	-	-	-	-	-	-	2.2	Down
NM_008891	Pinin	Pnn	-	-	-	-	-	-	2.2	Down
NM_021311	Piwi-like homolog 1 (Drosophila)	Piwil1	-	-	-	-	-	-	2.2	Down
NM_008902	Placental protein 11 related	Pp11r	-	-	-	-	-	-	2.8	Up
NM_011113	Plasminogen activator, urokinase receptor	Plaur	-	-	-	-	-	-	3.0	Up

NM_183034	Pleckstrin homology domain containing, family M (with RUN domain) member 1	Plekhm1	-	-	-	-	-	-	-	1.7	Down
XM_485870	PNMA-like 2	-	-	-	-	-	-	-	-	1.8	Down
XM_146604	podocan-like 1	-	-	-	-	-	-	-	-	2.1	Down
NM_152804	Polo-like kinase 2 (Drosophila)	Plk2	-	-	-	-	-	-	-	2.1	Up
NM_011865	Poly(rC) binding protein 1	Pcbp1	-	-	-	-	-	-	-	2.4	Down
NM_153783	Polyamine oxidase (exo-N4-amino)	Paox	-	-	-	-	-	-	-	3.5	Down
NM_029508	Polycomb group ring finger 5	Pcgf5	-	-	-	-	-	-	-	2.4	Up
NM_198600	Polymerase (DNA directed) sigma	Pols	-	-	-	-	-	-	-	1.6	Up
NM_008892	Polymerase (DNA directed), alpha 1	Pola1	-	-	-	-	-	-	-	2.7	Down
NM_011131	Polymerase (DNA directed), delta 1, catalytic subunit	Pold1	-	-	-	-	-	-	-	2.1	Down
NM_011133	Polymerase (DNA directed), epsilon 2 (p59 subunit)	Pole2	-	-	-	-	-	-	-	1.7	Down
NM_021498	Polymerase (DNA directed), epsilon 3 (p17 subunit)	Pole3	-	-	-	-	-	-	-	2.7	Up
NM_027196	Polymerase (DNA-directed), delta 4	Pold4	-	-	1.6	Up	-	-	-	-	-
XM_283153	polymerase (RNA) III (DNA directed) polypeptide G	-	-	-	-	-	-	-	-	1.5	Down
NM_019550	Polypyrimidine tract binding protein 2	Ptbp2	-	-	-	-	-	-	-	1.9	Down
NM_027008	Potassium channel tetramerisation domain containing 5	Kctd5	-	-	-	-	-	-	-	1.6	Down
NM_027782	Potassium channel tetramerisation domain containing 6	Kctd6	-	-	-	-	-	-	-	1.9	Down
NM_134073	Potassium channel tetramerisation domain containing 9	Kctd9	-	-	-	-	-	-	-	1.9	Down
NM_008430	Potassium channel, subfamily K, member 1	Kcnk1	-	-	-	-	-	-	-	2.7	Down
NM_008428	Potassium inwardly-rectifying channel, subfamily J, member 8	Kcnj8	-	-	-	-	-	-	-	1.9	Down
NM_028231	Potassium large conductance calcium-activated channel, subfamily M, beta member 2	Kcnmb2	-	-	-	-	-	-	-	1.8	Up
NM_020574	Potassium voltage-gated channel, Isk-related subfamily, gene 3	Kcne3	-	-	-	-	-	-	-	2.3	Down
NM_019697	Potassium voltage-gated channel, Shal-related family, member 2	Kcnd2	-	-	-	-	-	-	-	1.8	Down
XM_143960	potassium voltage-gated channel, subfamily Q, member 4	-	-	-	-	-	-	-	-	2.0	Down
XM_204027	PR domain containing 2, with ZNF domain	-	-	-	1.5	Up	-	-	-	-	-
XM_125812	PR domain containing 4	-	-	-	-	-	-	-	-	1.7	Down
NM_016983	Pre-B lymphocyte gene 2	Vpreb2	-	-	-	-	-	-	-	1.9	Down
NM_009514	Pre-B lymphocyte gene 3	Vpreb3	-	-	2.5	Up	-	-	-	-	-
NM_030555	pre-B-cell leukemia homeobox 4	-	-	-	-	-	-	-	-	1.8	Down
XM_488677	predicted gene, 328235	-	-	-	-	-	-	-	-	1.6	Down
XM_138356	predicted gene, EG211331	-	-	-	-	-	-	-	-	2.5	Up
XM_143402	predicted gene, EG212727	-	-	-	-	-	-	-	-	1.6	Down
XM_125109	predicted gene, EG214738	-	-	-	-	-	-	-	-	1.7	Down
NM_175010	predicted gene, EG224180	-	-	-	-	-	-	-	-	3.4	Up
XM_140295	predicted gene, EG225416	-	-	-	-	-	-	-	-	2.0	Down
NM_183166	Predicted gene, EG233164	EG233164	-	-	-	-	-	-	-	1.8	Up
XM_135671	Predicted gene, EG236451	EG236451	-	-	-	-	-	-	-	1.9	Up
XM_137275	predicted gene, EG237433	-	-	-	-	-	-	-	-	3.9	Down



XM_146438	predicted gene, EG244595	-	-	-	-	-	-	-	-	1.9	Down
XM_195619	predicted gene, EG272350	-	-	-	-	-	-	-	-	1.8	Down
XM_286185	predicted gene, EG328825	-	-	-	-	-	-	-	-	1.6	Down
NM_177849	predicted gene, EG329541	-	-	-	2.2	Up	-	-	-	-	-
XM_282816	predicted gene, EG330731	-	-	-	-	-	-	-	-	2.1	Down
		EG33094									
XM_284504	Predicted gene, EG330948	8	-	-	-	-	-	-	-	2.0	Down
XM_355960	predicted gene, EG381936	-	-	-	-	-	-	-	-	1.7	Down
XM_356468	predicted gene, EG382371	-	-	-	-	-	-	-	-	1.6	Down
		EG38284									
XM_356704	Predicted gene, EG382843	3	-	-	-	-	-	-	-	2.3	Down
XM_356994	predicted gene, EG383341	-	-	-	-	-	-	-	-	2.0	Up
		EG38462									
XM_357752	Predicted gene, EG384622	2	-	-	-	-	-	-	-	4.3	Up
XM_357875	predicted gene, EG384813	-	-	-	-	-	-	-	-	2.7	Down
XM_483898	predicted gene, EG432460	-	-	-	-	-	-	-	-	1.6	Down
XM_484650	predicted gene, EG433125	-	-	-	-	-	-	-	-	2.2	Down
XM_488079	predicted gene, EG436008	-	-	-	2.4	Down	-	-	-	-	-
NM_027015	Predicted gene, ENSMUSG00000050621	Rps27	1.6	Up	1.9	Up	-	-	-	-	-
XM_144778	predicted gene, ENSMUSG00000076510	-	1.6	Up	-	-	-	-	-	-	-
XM_485781	predicted gene, ENSMUSG00000076563	-	-	-	-	-	-	-	-	3.1	Up
XM_485782	predicted gene, ENSMUSG00000076576	-	-	-	-	-	-	-	-	1.8	Up
		OTTMUS									
		G000000									
XM_485359	Predicted gene, OTTMUSG00000004549	04549	-	-	-	-	-	-	-	1.6	Down
XM_487797	predicted gene, OTTMUSG00000007008	-	-	-	-	-	-	-	-	2.4	Up
		OTTMUS									
		G000000									
XM_485426	Predicted gene, OTTMUSG00000009006	09006	-	-	-	-	-	-	-	2.5	Down
XM_487833	predicted gene, OTTMUSG00000010747	-	-	-	-	-	-	-	-	2.2	Down
XM_357407	predicted gene, OTTMUSG00000011077	-	-	-	-	-	-	-	-	2.1	Down
XM_485004	predicted gene, OTTMUSG00000013031	-	-	-	2.6	Up	-	-	-	-	-
		OTTMUS									
		G000000									
NM_177843	Predicted gene, OTTMUSG00000016703	16703	-	-	-	-	-	-	-	1.5	Down
NM_011964	Pregnancy specific glycoprotein 19	Psg19	-	-	1.9	Up	-	-	-	-	-
XM_128979	PRELI domain containing 2	-	-	-	-	-	-	-	-	1.6	Down
NM_019501	Prenyl (solanesyl) diphosphate synthase, subunit 1	Pdss1	-	-	-	-	-	-	-	1.5	Down
NM_011050	Programmed cell death 4	Pdcd4	-	-	-	-	-	-	-	2.7	Down
NM_008831	Prohibitin	Phb	-	-	-	-	-	-	-	1.9	Down
XM_149933	proline rich 12	-	-	3.7	Up	-	-	-	-	-	-
NM_019455	Prostaglandin D2 synthase 2, hematopoietic	Ptgds2	-	-	-	-	-	-	-	1.9	Down

NM_029614	Protease, serine, 23	Prss23	-	-	-	-	1.9	Up	-	-
NM_008949	Proteasome (prosome, macropain) 26S subunit, ATPase 3, interacting protein	Psmc3ip	-	-	-	-	-	-	1.9	Down
NM_011189	Proteasome (prosome, macropain) 28 subunit, alpha	Psme1	-	-	-	-	-	-	2.0	Up
NM_011967	Proteasome (prosome, macropain) subunit, alpha type 5	Psmas5	-	-	-	-	1.5	Down	-	-
NM_013585	Proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2)	Psmb9	-	-	-	-	-	-	1.8	Up
XM_126809	protein disulfide isomerase associated 6	-	-	-	-	-	-	-	1.6	Down
NM_178900	Protein kinase D2	Prkd2	-	-	-	-	-	-	1.7	Down
NM_008863	Protein kinase inhibitor beta, cAMP dependent, testis specific	Pkib	-	-	-	-	-	-	1.8	Up
NM_008924	Protein kinase, cAMP dependent regulatory, type II alpha	Prkar2a	-	-	-	-	-	-	1.7	Down
NM_029632	Protein phosphatase 1, regulatory (inhibitor) subunit 11	Ppp1r11	-	-	-	-	-	-	1.6	Up
NM_175523	Protein phosphatase 1K (PP2C domain containing)	Ppm1k	-	-	-	-	-	-	1.9	Down
NM_172994	Protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), gamma isoform	Ppp2r2c	-	-	-	-	-	-	2.1	Down
NM_008913	Protein phosphatase 3, catalytic subunit, alpha isoform	Ppp3ca	-	-	-	-	2.0	Up	-	-
NM_182939	Protein phosphatase 4, regulatory subunit 2	Ppp4r2	-	-	1.6	Down	-	-	-	-
NM_153594	Protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2	Pcmt2	-	-	-	-	-	-	1.7	Up
NM_008920	Proteoglycan 2, bone marrow	Prg2	-	-	-	-	-	-	2.3	Down
XM_142105	protocadherin 11 X-linked	-	-	-	-	-	-	-	2.5	Down
NM_033590	Protocadherin gamma subfamily A, 10	Pcdhga1 2	-	-	-	-	-	-	2.7	Down
NM_033595	Protocadherin gamma subfamily A, 10	Pcdhga1 2	-	-	-	-	-	-	1.5	Down
NM_033585	Protocadherin gamma subfamily A, 2	Pcdhga2	-	-	-	-	-	-	1.8	Down
NM_008911	Protoporphyrinogen oxidase	Ppox	-	-	1.7	Up	-	-	-	-
NM_145478	Proviral integration site 3	Pim3	-	-	-	-	-	-	2.2	Up
NM_028281	Pterin 4 alpha carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) 2	Pcbd2	-	-	-	-	-	-	2.4	Down
NM_007982	PTK2 protein tyrosine kinase 2	Ptk2	-	-	1.5	Up	-	-	-	-
NM_008989	Purine rich element binding protein A	Pura	-	-	-	-	-	-	1.9	Down
NM_028808	Purinergic receptor P2Y, G-protein coupled 13	P2ry13	-	-	-	-	1.8	Up	3.0	Up
NM_008791	Purkinje cell protein 4	Pcp4	1.6	Up	-	-	-	-	-	-
NM_144795	Pyrraline-5-carboxylate reductase 1	Pycr1	-	-	-	-	-	-	1.6	Down
NM_133705	Pyrraline-5-carboxylate reductase family, member 2	Pycr2	-	-	-	-	-	-	1.6	Down
NM_172665	Pyruvate dehydrogenase kinase, isoenzyme 1	Pdk1	-	-	-	-	-	-	2.1	Down
NM_145630	Pyruvate dehydrogenase kinase, isoenzyme 3	Pdk3	-	-	-	-	-	-	1.8	Down
NM_013631	Pyruvate kinase liver and red blood cell	Pklr	-	-	-	-	-	-	1.6	Down
NM_133686	Quinolate phosphoribosyltransferase	Qprt	-	-	-	-	-	-	1.9	Down
NM_138683	R-spondin homolog (Xenopus laevis)	Rspo1	-	-	-	-	-	-	2.5	Down
NM_011231	RAB geranylgeranyl transferase, b subunit	Rabggtb	-	-	-	-	-	-	2.3	Down

NM_024436	RAB22A, member RAS oncogene family	Rab22a	-	-	-	-	-	-	2.3	Down
NM_029494	RAB30, member RAS oncogene family	Rab30	-	-	-	-	-	-	2.0	Down
NM_028238	Rab38, member of RAS oncogene family	Rab38	-	-	-	-	-	-	1.9	Down
NM_175562	RAB39, member RAS oncogene family	Rab39	-	-	-	-	-	-	4.1	Down
NM_144875	RAB7, member RAS oncogene family-like 1	Rab711	-	-	-	-	-	-	1.5	Down
NM_011233	RAD17 homolog (S. pombe)	Rad17	-	-	-	-	-	-	2.8	Up
NM_009041	Radixin	Rdx	-	-	-	-	-	-	1.9	Down
NM_023884	Ral GEF with PH domain and SH3 binding motif 2	Ralgps2	-	-	-	-	-	-	3.5	Down
NM_021536	Ras homolog gene family, member T1	Rhot1	-	-	-	-	-	-	1.8	Down
NM_013716	Ras-GTPase-activating protein SH3-domain binding protein 1	G3bp1	-	-	-	-	-	-	1.5	Down
NM_178593	RCSD domain containing 1	Rcsd1	-	-	-	-	-	-	1.9	Down
NM_009043	Regenerating islet-derived 2	Reg2	-	-	-	-	1.8	Up	-	-
NM_134083	Regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 2	Rcbtb2	-	-	-	-	-	-	3.9	Down
NM_019492	Regulator of G-protein signaling 3	Rgs3	-	-	-	-	-	-	2.1	Down
NM_026653	Replication protein A1	Rpa1	-	-	-	-	-	-	3.5	Down
NM_198023	REST corepressor 1	Rcor1	-	-	-	-	-	-	1.5	Down
NM_009037	Reticulocalbin 1	Rcn1	-	-	-	-	2.7	Up	-	-
NM_133669	Retinitis pigmentosa 2 homolog (human)	Rp2h	-	-	2.0	Down	1.5	Down	4.3	Down
NM_009029	Retinoblastoma 1	Rb1	-	-	-	-	-	-	1.7	Down
NM_021557	Retinol dehydrogenase 11	Rdh11	-	-	-	-	-	-	2.8	Down
NM_011270	Rh blood group, D antigen	Rhd	-	-	-	-	-	-	3.8	Down
XM_130033	Rho GTPase activating protein 21	-	-	-	-	-	-	-	2.2	Up
NM_138630	Rho GTPase activating protein 4	Arhgap4	-	-	-	-	-	-	2.0	Down
NM_008488	Rho guanine nucleotide exchange factor (GEF) 1	Arhgef1	-	-	-	-	-	-	1.6	Down
XM_356099	ribonuclease H2, large subunit	-	-	-	-	-	-	-	1.7	Down
NM_026616	Ribonuclease H2, subunit C	Rnaseh2c	-	-	-	-	-	-	2.9	Down
XM_130010	ribonuclease P/MRP 38 subunit (human)	-	-	-	-	-	-	-	1.5	Down
NM_007447	Ribonuclease, RNase A family 4	Rnase4	-	-	-	-	-	-	4.1	Up
NM_011271	Ribonuclease, RNase A family, 1 (pancreatic)	Rnase1	-	-	2.8	Down	3.9	Up	3.4	Up
NM_009076	Ribosomal protein L12	Rpl12	-	-	-	-	-	-	3.2	Up
NM_025586	Ribosomal protein L15	Rpl15	-	-	-	-	-	-	2.6	Up
NM_009082	Ribosomal protein L29	Rpl29	-	-	2.1	Up	-	-	-	-
NM_019865	Ribosomal protein L36a	Rpl36a	-	-	-	-	-	-	1.9	Up
NM_025589	Ribosomal protein L36a-like	Rpl36al	-	-	-	-	-	-	1.8	Down
NM_023372	Ribosomal protein L38	Rpl38	-	-	-	-	-	-	2.0	Up
NM_170669	Ribosomal protein S15a	Rps15a	-	-	-	-	-	-	2.2	Down
NM_028259	Ribosomal protein S6 kinase, polypeptide 1	Rps6kb1	-	-	-	-	-	-	2.6	Up
NM_178916	Rieske (Fe-S) domain containing	Rfesd	-	-	-	-	-	-	1.9	Down
NM_025319	RIKEN cDNA 0610009B22 gene	0610009B22Rik	1.6	Up	-	-	-	-	-	-

NM_026757	RIKEN cDNA 0610010K14 gene	0610010 K14Rik	-	-	1.9	Up	-	-	-	-
NM_026995	RIKEN cDNA 0710008K08 gene	0710008 K08Rik	-	-	-	-	-	-	1.6	Down
NM_183249	RIKEN cDNA 1100001G20 gene	1100001 G20Rik	-	-	-	-	-	-	3.4	Up
NM_025377	RIKEN cDNA 1110001A07 gene	1110001 A07Rik	-	-	-	-	-	-	1.7	Down
NM_019772	RIKEN cDNA 1110004F10 gene	1110004 F10Rik	-	-	-	-	-	-	3.5	Down
NM_176902	RIKEN cDNA 1110014K08 gene	1110014 K08Rik	-	-	-	-	-	-	1.6	Down
NM_025411	RIKEN cDNA 1110049F12 gene	1110049 F12Rik	-	-	-	-	-	-	1.9	Down
NM_025427	RIKEN cDNA 1190002H23 gene	1190002 H23Rik	-	-	1.7	Up	-	-	-	-
NM_175125	RIKEN cDNA 1500011K16 gene	-	-	-	-	-	-	-	1.6	Down
NM_177132	RIKEN cDNA 1520401A03 gene	-	-	-	-	-	-	-	2.4	Up
NM_029306	RIKEN cDNA 1700012B09 gene	1700012 B09Rik	-	-	-	-	-	-	1.6	Up
NM_183266	RIKEN cDNA 1700020N01 gene	-	-	-	-	-	-	-	2.0	Up
XM_355444	RIKEN cDNA 1700021C14 gene	-	-	-	-	-	-	-	1.9	Up
XM_355303	RIKEN cDNA 1700029F09 gene	-	-	-	-	-	-	-	1.7	Down
NM_025856	RIKEN cDNA 1700029G01 gene	1700029 G01Rik	-	-	-	-	-	-	2.0	Down
NM_028494	RIKEN cDNA 1700034I23 gene	1700034I 23Rik	-	-	-	-	-	-	1.7	Down
NM_025308	RIKEN cDNA 1810007E14 gene	-	-	-	-	-	-	-	2.4	Down
XM_358452	RIKEN cDNA 1810011H11 gene	1810011 H11Rik	-	-	-	-	-	-	2.9	Down
NM_028795	RIKEN cDNA 1810018F18 gene	-	-	-	1.9	Down	-	-	2.0	Down
XM_109683	RIKEN cDNA 1810027O10 gene	-	-	-	1.7	Up	-	-	-	-
XM_110690	RIKEN cDNA 1810033B17 gene	-	-	-	-	-	-	-	3.7	Up
XM_128169	RIKEN cDNA 1810041L15 gene	1810041 L15Rik	-	-	-	-	-	-	1.6	Down
XM_355363	RIKEN cDNA 1810053B01 gene	-	-	-	-	-	-	-	1.8	Down
NM_025912	RIKEN cDNA 2010011I20 gene	2010011I 20Rik	-	-	-	-	-	-	1.7	Down
NM_025946	RIKEN cDNA 2010100O12 gene	2010100 O12Rik	-	-	-	-	-	-	2.4	Down
NM_028111	RIKEN cDNA 2010109K11 gene	-	-	-	-	-	-	-	2.0	Down
XM_355890	RIKEN cDNA 2210412E05 gene	2210412 E05Rik	-	-	-	-	-	-	1.7	Down
XM_149530	RIKEN cDNA 2300002D11 gene	-	-	-	-	-	-	-	3.5	Up

NM_175148	RIKEN cDNA 2300002M23 gene	2300002 M23Rik	-	-	-	-	-	-	-	3.6	Up
NM_025511	RIKEN cDNA 2310005N03 gene	2310005 N03Rik	-	-	-	-	-	-	-	2.4	Down
NM_025509	RIKEN cDNA 2310008M10 gene	2310008 M10Rik	-	-	-	-	-	-	-	1.6	Down
NM_023516	RIKEN cDNA 2310016C08 gene	2310016 C08Rik	-	-	-	-	-	-	-	3.5	Up
XM_355883	RIKEN cDNA 2310022K01 gene	2310022 K01Rik	-	-	-	-	-	-	-	1.7	Down
NM_026509	RIKEN cDNA 2310039E09 gene	2310039 E09Rik	-	-	-	-	-	-	-	1.9	Up
NM_027342	RIKEN cDNA 2310056P07 gene	2310056 P07Rik	1.7	Up	-	-	-	-	-	-	-
XM_128627	RIKEN cDNA 2310061I04 gene	-	-	-	-	-	-	-	-	1.7	Down
NM_133677	RIKEN cDNA 2310061J03 gene	-	-	-	-	-	-	-	-	1.6	Down
NM_023215	RIKEN cDNA 2500003M10 gene	2500003 M10Rik	-	-	-	-	-	-	-	2.4	Down
XM_131720	RIKEN cDNA 2610002D18 gene	-	-	-	-	-	-	-	-	1.6	Down
NM_146084	RIKEN cDNA 2610024E20 gene	2610024 E20Rik	-	-	-	-	-	-	-	1.7	Down
NM_027420	RIKEN cDNA 2610034B18 gene	2610034 B18Rik	-	-	-	-	-	-	-	2.2	Down
NM_026476	RIKEN cDNA 2610101N10 gene	2610101 N10Rik	-	-	-	-	-	-	-	2.1	Down
NM_175157	RIKEN cDNA 2610204G22 gene	-	-	-	-	-	-	-	-	1.9	Down
NM_026620	RIKEN cDNA 2610510H03 gene	2610510 H03Rik	-	-	-	-	-	-	-	2.8	Down
XM_484798	RIKEN cDNA 2700046G09 gene	-	-	-	-	-	-	-	-	2.5	Up
NM_026528	RIKEN cDNA 2700060E02 gene	2700060 E02Rik	-	-	-	-	-	-	-	1.9	Down
NM_028314	RIKEN cDNA 2700097O09 gene	2700097 O09Rik	-	-	-	-	-	-	-	2.2	Down
NM_175179	RIKEN cDNA 2810002O09 gene	2810002 O09Rik	-	-	-	-	-	-	-	2.3	Down
NM_173382	RIKEN cDNA 2810046L04 gene	2810046 L04Rik	-	-	-	-	-	-	-	1.7	Down
NM_026062	RIKEN cDNA 2900024C23 gene	2900024 C23Rik	-	-	-	-	-	-	-	2.7	Down
XM_125510	RIKEN cDNA 3110003A17 gene	-	-	-	-	-	-	-	-	2.2	Down
NM_026622	RIKEN cDNA 3110057O12 gene	3110057 O12Rik	-	-	-	-	-	-	-	3.8	Up
NM_027532	RIKEN cDNA 3200002M19 gene	3200002 M19Rik	-	-	-	-	-	-	-	1.8	Down

NM_027510	RIKEN cDNA 3830403N18 gene	3830403 N18Rik	-	-	-	-	-	-	2.0	Down
NM_198651	RIKEN cDNA 4430402I18 gene	4430402I 18Rik	-	-	2.9	Up	-	-	-	-
NM_172500	RIKEN cDNA 4831426I19 gene	4831426I 19Rik	-	-	-	-	-	-	1.5	Down
XM_129740	RIKEN cDNA 4921511C04 gene	-	-	-	-	-	-	-	1.5	Down
XM_130219	RIKEN cDNA 4930402F06 gene	-	-	-	-	-	-	-	1.8	Down
NM_178098	RIKEN cDNA 4930486L24 gene	4930486 L24Rik	-	-	-	-	-	-	1.9	Up
XM_284734	RIKEN cDNA 4930524E20 gene	-	-	-	-	-	-	-	2.1	Down
XM_485433	RIKEN cDNA 4930544O15 gene	4930544 O15Rik	-	-	-	-	-	-	1.9	Up
NM_029235	RIKEN cDNA 4930556L07 gene	-	2.2	Down	-	-	-	-	3.2	Down
XM_355249	RIKEN cDNA 4930562F07 gene	-	-	-	-	-	-	-	1.6	Down
XM_130220	RIKEN cDNA 4930568D16 gene	4930568 D16Rik	-	-	-	-	-	-	1.6	Up
NM_027089	RIKEN cDNA 4930579C15 gene	4930579 C15Rik	-	-	-	-	-	-	3.0	Up
NM_026358	RIKEN cDNA 4930583H14 gene	4930583 H14Rik	-	-	-	-	-	-	1.7	Up
NM_133732	RIKEN cDNA 4931406C07 gene	4931406 C07Rik	-	-	-	-	-	-	2.4	Down
NM_172741	RIKEN cDNA 4931406P16 gene	4931406 P16Rik	-	-	-	-	-	-	2.2	Down
NM_183104	RIKEN cDNA 4931429L15 gene	-	-	-	-	-	-	-	2.9	Up
NM_026339	RIKEN cDNA 4932415G12 gene	-	-	-	-	-	-	-	2.1	Down
NM_024203	RIKEN cDNA 4932442K08 gene	4932442 K08Rik	-	-	-	-	-	-	1.7	Down
NM_028739	RIKEN cDNA 4933404G15 gene	-	-	-	-	-	-	-	2.6	Down
XM_354798	RIKEN cDNA 4933413J09 gene	4933413 J09Rik	-	-	-	-	-	-	1.8	Down
NM_183100	RIKEN cDNA 5430414B19 gene	-	-	-	-	-	-	-	1.5	Down
NM_174847	RIKEN cDNA 5830404H04 gene	5830404 H04Rik	-	-	-	-	-	-	2.0	Down
NM_029082	RIKEN cDNA 5830411J07 gene	-	-	-	1.7	Down	-	-	-	-
XM_358531	RIKEN cDNA 5830416P10 gene	-	-	-	-	-	-	-	1.5	Down
NM_026368	RIKEN cDNA 5830433M19 gene	5830433 M19Rik	-	-	2.6	Down	-	-	-	-
NM_177359	RIKEN cDNA 6030490I01 gene	6030490I 01Rik	-	-	-	-	-	-	1.9	Down
NM_134022	RIKEN cDNA 6330403K07 gene	6330403 K07Rik	-	-	-	-	-	-	2.4	Down
NM_176962	RIKEN cDNA 6330416L07 gene	6330416	2.0	Up	-	-	-	-	-	-

		L07Rik											
XM_205477	RIKEN cDNA 6330545A04 gene	-	-	-	-	-	-	-	-	2.3	Down		
		6330578											
NM_198006	RIKEN cDNA 6330578E17 gene	E17Rik	-	-	-	-	-	-	-	1.5	Down		
		6430604											
NM_175560	RIKEN cDNA 6430604K15 gene	K15Rik	-	-	-	-	-	-	-	1.8	Down		
		6430706											
NM_198652	RIKEN cDNA 6430706D22 gene	D22Rik	-	-	-	-	-	-	-	2.1	Down		
		8230402											
NM_177755	RIKEN cDNA 8230402K04 gene	K04Rik	-	-	-	-	-	-	-	2.5	Down		
		9030425											
NM_133733	RIKEN cDNA 9030425E11 gene	E11Rik	-	-	-	-	-	-	-	2.3	Up		
XM_484126	RIKEN cDNA 9030624G23 gene	-	-	-	-	-	-	-	-	1.8	Down		
NM_177146	RIKEN cDNA 9330175E14 gene	-	-	-	2.1	Down	-	-	-	3.1	Down		
		9530008											
NM_175417	RIKEN cDNA 9530008L14 gene	L14Rik	-	-	-	-	-	-	-	1.8	Up		
XM_144080	RIKEN cDNA 9530096D07 gene	-	-	-	-	-	-	-	-	1.9	Down		
XM_194000	RIKEN cDNA 9630050M13 gene	-	-	-	-	-	-	-	-	2.2	Down		
		9930111											
NM_173434	RIKEN cDNA 9930111J21 gene	J21Rik	-	-	-	-	-	-	-	1.7	Down		
NM_030005	RIKEN cDNA A030005K14 gene	-	-	-	-	-	-	-	-	1.6	Down		
NM_020591	RIKEN cDNA A030009H04 gene	-	-	-	-	-	-	-	-	1.6	Down		
NM_177228	RIKEN cDNA A130004G07 gene	-	-	-	-	-	-	-	-	1.6	Up		
XM_354697	RIKEN cDNA A230065H16 gene	-	-	-	-	-	-	1.8	Up	-	-		
NM_207529	RIKEN cDNA A430093F15 gene	-	-	-	-	-	-	-	-	2.3	Down		
		A430110											
NM_173008	RIKEN cDNA A430110N23 gene	N23Rik	-	-	-	-	-	-	-	1.8	Down		
		A530064											
NM_178796	RIKEN cDNA A530064D06 gene	D06Rik	-	-	-	-	-	-	-	1.9	Up		
		A630033											
NM_175442	RIKEN cDNA A630033H20 gene	H20Rik	-	-	-	-	-	-	-	1.8	Down		
NM_183214	RIKEN cDNA A830019P07 gene	-	-	-	-	-	-	-	-	2.4	Up		
		B020004											
XM_484380	RIKEN cDNA B020004C17 gene	C17Rik	-	-	-	-	-	-	-	2.4	Down		
		B230206											
NM_177280	RIKEN cDNA B230206H07 gene	H07Rik	-	-	-	-	-	-	-	2.8	Up		
		C030011											
NM_174868	RIKEN cDNA C030011O14 gene	O14Rik	-	-	-	-	-	-	-	2.5	Down		
NM_176897	RIKEN cDNA C530043A13 gene	-	-	-	-	-	-	-	-	1.7	Down		
		D030016											
NM_177240	RIKEN cDNA D030016E14 gene	E14Rik	1.7	Down	-	-	-	-	-	-	-		
XM_283282	RIKEN cDNA D330001F17 gene	-	-	-	-	-	-	-	-	2.3	Up		
XM_357326	RIKEN cDNA D630013G24 gene	-	-	-	-	-	-	-	-	1.6	Down		
NM_016698	Ring finger protein 10	Rnf10	-	-	-	-	-	1.7	Up	-	-		

NM_009543	Ring finger protein 103	Rnf103	-	-	-	-	-	-	-	1.5	Down
NM_153503	Ring finger protein 113A1	Rnf113a	1	-	-	-	-	-	-	2.2	Down
NM_028019	Ring finger protein 135	Rnf135	-	-	-	-	-	-	-	2.0	Down
NM_080561	Ring finger protein 216	Rnf216	-	-	-	-	-	-	-	1.6	Down
XM_135065	ring finger protein 7	-	-	-	-	-	-	-	-	2.7	Down
NM_027266	RNA (guanine-9-) methyltransferase domain containing 3	Rg9mtd3	-	-	-	-	-	-	-	1.9	Down
NM_019869	RNA binding motif protein 14	Rbm14	-	-	-	-	-	-	-	1.7	Down
NM_152824	RNA binding motif protein 17	Rbm17	-	-	-	-	-	-	-	2.7	Up
NM_176838	RNA binding motif protein 35b	Rbm35b	-	-	-	-	-	-	-	1.8	Down
NM_009032	RNA binding motif protein 4	Rbm4	-	-	2.4	Up	-	-	-	-	-
NM_173376	RNA binding motif protein, X-linked 2	Rbmx2	-	-	-	-	-	-	-	1.7	Down
NM_011884	RNA guanylyltransferase and 5-phosphatase	Rngtt	-	-	-	-	-	-	-	2.0	Down
NM_011304	RuvB-like protein 2	Ruvbl2	-	-	1.8	Up	-	-	-	-	-
NM_025637	RWD domain containing 3	Rwdd3	-	-	-	-	-	-	-	1.8	Up
NM_016740	S100 calcium binding protein A11 (calgizzarin)	S100a11	-	-	-	-	-	-	-	2.0	Up
NM_011313	S100 calcium binding protein A6 (calcyclin)	S100a6	-	-	-	-	-	-	-	3.5	Up
NM_013650	S100 calcium binding protein A8 (calgranulin A)	S100a8	-	-	-	-	-	-	-	3.3	Up
NM_175303	Sal-like 4 (Drosophila)	Sall4	-	-	-	-	-	-	-	2.1	Down
NM_023380	SAM domain, SH3 domain and nuclear localization signals, 1	Samsn1	-	-	-	-	-	-	-	2.2	Up
NM_172894	SAPS domain family, member 1	Saps1	-	-	-	-	-	-	-	1.7	Down
NM_175347	Sarcalumenin	Srl	-	-	-	-	-	-	-	2.4	Down
NM_011892	Sarcoglycan, gamma (dystrophin-associated glycoprotein)	Sgcg	-	-	-	-	-	-	-	1.5	Down
NM_011407	Schlafen 1	Slfn1	-	-	-	-	-	-	-	1.8	Up
NM_011410	Schlafen 4	Slfn4	-	-	-	-	-	-	-	2.4	Up
NM_009132	Scinderin	Scin	-	-	-	-	-	-	-	2.5	Up
NM_144520	SEC14-like 2 (S. cerevisiae)	Sec14l2	-	-	-	-	-	-	-	2.1	Down
NM_021305	Sec61, alpha subunit 2 (S. cerevisiae)	Sec61a2	-	-	-	-	-	-	-	2.3	Down
NM_011343	SEC61, gamma subunit	Sec61g	-	-	-	-	-	-	-	1.8	Up
NM_009242	Secreted acidic cysteine rich glycoprotein	Sparc	-	-	-	-	-	-	-	1.8	Up
NM_009263	Secreted phosphoprotein 1	Spp1	-	-	-	-	-	-	-	3.3	Up
XM_148959	secretin receptor	-	-	-	-	-	-	-	-	1.7	Down
NM_054038	Secretoglobin, family 3A, member 2	Scgb3a2	-	-	-	-	-	-	-	3.0	Up
NM_011886	Secretory carrier membrane protein 3	Scamp3	-	-	-	-	-	-	-	1.9	Up
NM_175400	Selenophosphate synthetase 1	Sephs1	-	-	-	-	-	-	-	1.9	Down
NM_053267	Selenoprotein M	Selm	-	-	-	-	-	-	-	3.2	Up
NM_013759	Selenoprotein X 1	Sepx1	-	-	-	-	-	-	-	1.5	Up
NM_009152	Sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	Sema3a	-	-	-	-	-	-	-	2.1	Up
NM_172490	Sep (O-phosphoserine) tRNA:Sec (selenocysteine) tRNA synthase	Sepsecs	-	-	-	-	-	-	-	2.4	Down
NM_011157	Serglycin	Srgn	-	-	-	-	-	-	-	3.2	Up
NM_009245	Serine (or cysteine) peptidase inhibitor, clade A, member 1c	Serpina1	-	-	-	-	-	-	-	1.7	Down



		c							
NM_198028	Serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 10	Serpinb10	-	-	-	-	-	-	1.8 Down
		Serpinb3							
NM_201363	Serine (or cysteine) peptidase inhibitor, clade B, member 3C	c	-	-	-	-	-	-	1.6 Down
NM_009825	Serine (or cysteine) peptidase inhibitor, clade H, member 1	Serpinh1	-	-	1.9	Up	-	-	2.9 Up
		Serpina1							
NM_009244	Serine (or cysteine) peptidase inhibitor, clade A, member 1b	b	-	-	1.6	Up	-	-	-
NM_028230	Serine hydroxymethyltransferase 2 (mitochondrial)	Shmt2	-	-	1.7	Up	-	-	-
NM_016795	Serine/arginine-rich protein specific kinase 1	Srpk1	-	-	-	-	-	-	2.0 Down
NM_021420	Serine/threonine kinase 4	Stk4	-	-	-	-	-	-	2.8 Down
NM_011318	Serum amyloid P-component	Apcs	-	-	-	-	-	-	1.7 Down
NM_138741	Serum deprivation response	Sdpr	-	-	-	-	-	-	3.5 Down
NM_177009	SET and MYND domain containing 4	-	-	-	-	-	-	-	2.1 Down
NM_080793	SET domain containing (lysine methyltransferase) 7	Setd7	-	-	-	-	-	-	2.5 Up
NM_011367	Sex hormone binding globulin	Shbg	-	-	1.8	Up	-	-	-
NM_028232	Shugoshin-like 1 (S. pombe)	Sgol1	-	-	-	-	-	-	2.6 Down
NM_172900	Sialic acid binding Ig-like lectin G	Siglecg	-	-	-	-	-	-	1.9 Down
NM_172257	SID1 transmembrane family, member 2	Sidt2	-	-	-	-	-	-	2.5 Up
NM_026911	Signal peptidase complex subunit 1 homolog (S. cerevisiae)	Spcs1	-	-	-	-	-	-	3.4 Up
NM_025527	Signal recognition particle 19	Srp19	1.6	Up	-	-	-	-	1.6 Up
XM_127048	similar to Down-regulated in nephrectomized rat kidney #3	-	-	-	-	-	-	-	1.6 Down
XM_139220	similar to insulinoma protein (rig)	-	-	-	-	-	-	-	2.1 Up
XM_488191	similar to matrilin 1, cartilage matrix protein	-	-	-	-	-	-	-	1.7 Down
XM_139922	similar to OBOX3	-	-	-	-	-	-	-	1.6 Up
NM_009276	simple repeat sequence-containing transcript	-	-	-	-	-	-	-	1.6 Up
NM_009119	Sin3-associated polypeptide 18	Sap18	-	-	-	-	-	-	2.1 Down
NM_011381	Sine oculis-related homeobox 3 homolog (Drosophila)	Six3	-	-	-	-	-	-	3.3 Up
NM_013929	SIVA1, apoptosis-inducing factor	Siva1	-	-	-	-	-	-	2.5 Down
XM_129445	SLIT-ROBO Rho GTPase activating protein 2	-	-	-	-	-	-	-	2.6 Down
NM_025531	Slowmo homolog 2 (Drosophila)	Slmo2	-	-	-	-	-	-	2.7 Down
NM_026506	Small nuclear ribonucleoprotein polypeptide G	Snrpg	-	-	-	-	-	-	2.6 Down
NM_011468	Small proline-rich protein 2A	Sprr2a	-	-	-	-	-	-	1.6 Down
NM_011475	Small proline-rich protein 2I	Sprr2i	-	-	-	-	1.6	Up	-
NM_011476	small proline-rich protein 2J	-	-	-	1.8	Down	-	-	-
NM_033568	SNF8, ESCRT-II complex subunit, homolog (S. cerevisiae)	Snf8	-	-	-	-	-	-	2.0 Down
NM_026008	sodium channel and clathrin linker 1	-	-	-	-	-	-	-	1.9 Down
XM_355332	sodium channel, voltage-gated, type III, alpha	-	-	-	-	-	-	-	2.3 Down
NM_146255	Solute carrier family 1 (glutamate transporter), member 7	Slc1a7	-	-	-	-	-	-	2.1 Down
	Solute carrier family 10 (sodium/bile acid cotransporter family), member 6	Slc10a6	-	-	-	-	2.7	Up	-
NM_029415									
NM_024254	Solute carrier family 12, member 6	Slc12a6	-	-	-	-	-	-	2.0 Down

NM_030696	Solute carrier family 16 (monocarboxylic acid transporters), member 3	Slc16a3	-	-	-	-	-	-	2.2	Up
NM_172523	Solute carrier family 18 (vesicular monoamine), member 2	Slc18a2	-	-	-	-	-	-	2.0	Down
NM_011400	Solute carrier family 2 (facilitated glucose transporter), member 1	Slc2a1	-	-	-	-	-	-	3.1	Up
NM_019741	Solute carrier family 2 (facilitated glucose transporter), member 5	Slc2a5	-	-	-	-	-	-	2.5	Up
NM_172659	Solute carrier family 2 (facilitated glucose transporter), member 6	Slc2a6	-	-	-	-	-	-	2.6	Up
NM_145559	Solute carrier family 2 (facilitated glucose transporter), member 9	Slc2a9	-	-	-	-	-	-	1.8	Down
NM_009203	Solute carrier family 22 (organic anion/cation transporter), member 12	Slc22a12	-	-	-	-	-	-	1.7	Down
NM_020520	Solute carrier family 25 (mitochondrial carnitine/acylcarnitine translocase), member 20	Slc25a20	1.5	Up	-	-	-	-	-	-
NM_011398	Solute carrier family 25 (mitochondrial carrier, brain), member 14	Slc25a14	-	-	-	-	-	-	2.0	Down
NM_175194	Solute carrier family 25 (mitochondrial carrier, Graves disease autoantigen), member 16	Slc25a16	-	-	-	-	-	-	2.0	Down
NM_172577	Solute carrier family 25 (mitochondrial oxodicarboxylate carrier), member 21	Slc25a21	-	-	-	-	-	-	1.6	Down
NM_026232	Solute carrier family 25, member 30	Slc25a30	-	-	1.5	Up	-	-	-	-
NM_011867	Solute carrier family 26, member 4	Slc26a4	-	-	-	-	-	-	2.4	Down
XM_128932	solute carrier family 27 (fatty acid transporter), member 6	-	-	-	-	-	-	-	1.7	Down
NM_023596	Solute carrier family 29 (nucleoside transporters), member 3	Slc29a3	-	-	-	-	-	-	1.5	Down
NM_008577	Solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	Slc3a2	-	-	-	-	-	-	3.6	Up
NM_178651	Solute carrier family 30 (zinc transporter), member 9	Slc30a9	-	-	-	-	-	-	2.1	Down
NM_080854	Solute carrier family 34 (sodium phosphate), member 3	Slc34a3	-	-	-	-	-	-	2.5	Down
NM_078484	Solute carrier family 35 (UDP-galactose transporter), member A2	Slc35a2	-	-	-	-	-	-	1.9	Down
NM_020258	Solute carrier family 37 (glycerol-3-phosphate transporter), member 2	Slc37a2	-	-	-	-	-	-	2.3	Down
XM_130259	solute carrier family 43, member 1	-	-	-	-	-	1.9	Up	-	-
NM_152808	Solute carrier family 44, member 2	Slc44a2	-	-	-	-	-	-	1.7	Up
NM_021053	Solute carrier family 46, member 2	Slc46a2	-	-	-	-	-	-	1.6	Up
NM_053248	Solute carrier family 5 (sodium iodide symporter), member 5	Slc5a5	-	-	-	-	-	-	2.7	Down
NM_133987	Solute carrier family 6 (neurotransmitter transporter, creatine), member 8	Slc6a8	-	-	-	-	-	-	2.2	Up
NM_011405	Solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	Slc7a7	-	-	-	-	-	-	2.4	Down
XM_134478	solute carrier family 7, member 6 opposite strand	-	-	-	-	-	-	-	1.5	Down
NM_172468	Sorting nexin family member 30	Snx30	-	-	-	-	-	-	2.2	Down
NM_022316	SPARC related modular calcium binding 1	Smoc1	-	-	-	-	2.1	Up	-	-
NM_026282	SPC24, NDC80 kinetochore complex component, homolog (S. cerevisiae)	Spc24	-	-	-	-	-	-	1.8	Down
NM_026293	Sperm acrosome associated 1	Spaca1	-	-	-	-	-	-	2.6	Down
NM_009261	Spermatid perinuclear RNA binding protein	Strbp	-	-	-	-	-	-	1.7	Down
NM_011518	Spleen tyrosine kinase	Syk	-	-	-	-	-	-	1.8	Down
NM_026175	Splicing factor 3a, subunit 1	Sf3a1	-	-	-	-	-	-	2.0	Down

NM_031179	Splicing factor 3b, subunit 1	Sf3b1	-	-	-	-	-	-	1.8	Down
NM_133953	Splicing factor 3b, subunit 3	Sf3b3	-	-	-	-	-	-	2.2	Up
NM_025573	Splicing factor, arginine/serine rich 9	Sfrs9	-	-	-	-	-	-	2.7	Down
NM_009169	Split hand/foot malformation (ectrodactyly) type 1	Shfm1	-	-	-	-	-	-	1.6	Down
NM_001001144	SREBF chaperone	Scap	-	-	-	-	-	-	1.8	Up
NM_009234	SRY-box containing gene 11	Sox11	-	-	-	-	-	-	1.8	Down
NM_011446	SRY-box containing gene 7	Sox7	-	-	1.6	Up	-	-	-	-
NM_009181	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 2	St8sia2	-	-	-	-	-	-	1.5	Down
NM_029019	StAR-related lipid transfer (START) domain containing 6	Stard6	-	-	-	-	-	-	1.7	Down
NM_009293	Steroid sulfatase	Sts	-	-	-	-	-	-	2.0	Down
NM_016737	Stress-induced phosphoprotein 1	Stip1	-	-	-	-	-	-	1.9	Up
XM_132038	stromal interaction molecule 2	-	-	-	-	-	-	-	2.4	Down
NM_153808	Structural maintenance of chromosomes 5	Smc5	-	-	-	-	-	-	1.6	Down
NM_019879	Succinate-CoA ligase, GDP-forming, alpha subunit	Suclg1	-	-	-	-	-	-	2.9	Down
NM_011506	Succinate-Coenzyme A ligase, ADP-forming, beta subunit	Sucla2	-	-	-	-	-	-	2.3	Down
NM_145937	Sulfatase modifying factor 1	Sumf1	-	-	-	-	-	-	1.7	Down
NM_019748	SUMO1 activating enzyme subunit 1	Sae1	-	-	-	-	-	-	1.7	Down
NM_028151	Superkiller viralicidic activity 2-like 2 ( <i>S. cerevisiae</i> )	Skiv2l2	-	-	-	-	-	-	2.5	Down
NM_153153	Supervillin	Svil	-	-	-	-	-	-	2.3	Down
		Suv420h2	-	-	-	-	-	-	2.2	Down
NM_146177	Suppressor of variegation 4-20 homolog 2 ( <i>Drosophila</i> )	Suz12	-	-	-	-	-	-	2.2	Down
NM_199196	Suppressor of zeste 12 homolog ( <i>Drosophila</i> )	Suz12	-	-	-	-	-	-	2.2	Down
NM_013678	Surfeit gene 2	Surf2	-	-	1.7	Up	-	-	1.7	Up
NM_172429	Survival motor neuron domain containing 1	Smndc1	-	-	-	-	-	-	2.9	Down
XM_149659	SV2 related protein	-	-	-	-	-	-	-	2.3	Down
NM_028052	Synaptoporin	Synpr	-	-	-	-	-	-	2.4	Down
NM_009222	Synaptosomal-associated protein 23	Snap23	-	-	-	-	-	-	3.1	Down
NM_023348	Synaptosomal-associated protein 29	Snap29	-	-	-	-	-	-	2.2	Down
NM_016663	Synaptotagmin III	Syt3	-	-	-	-	-	-	3.8	Up
NM_031394	Synaptotagmin-like 2	Sytl2	-	-	-	-	-	-	1.8	Down
NM_011521	Syndecan 4	Sdc4	-	-	-	-	-	-	2.3	Up
NM_028769	Synovial apoptosis inhibitor 1, synoviolin	Syvn1	-	-	-	-	1.7	Up	3.2	Up
XM_203312	Syntaxin 11	Stx11	-	-	-	-	-	-	2.1	Up
NM_024414	Syntaxin 1B	Stx1b	-	-	-	-	-	-	1.5	Down
NM_019829	Syntaxin 5A	Stx5a	-	-	-	-	-	-	2.4	Up
NM_021433	Syntaxin 6	Stx6	-	-	-	-	-	-	1.7	Down
NM_001001320	T-box 10	Tbx10	-	-	-	-	-	-	1.8	Down
NM_019507	T-box 21	Tbx21	-	-	-	-	-	-	1.5	Down
NM_177342	TAF5 RNA polymerase II, TATA box binding protein (TBP)-associated factor	Taf5	-	-	-	-	-	-	1.8	Down

NM_146092	TAF6-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor	Taf6l	-	-	-	-	-	-	-	1.5	Down
XM_484053	TAO kinase 1	-	-	-	-	-	-	-	-	2.9	Up
NM_145556	TAR DNA binding protein	Tardbp	-	-	-	-	-	-	-	3.0	Down
NM_031867	Taste receptor, type 1, member 1	Tas1r1	-	-	-	-	2.3	Up	-	-	-
NM_199154	Taste receptor, type 2, member 107	Tas2r107	-	-	-	-	-	-	-	1.6	Down
NM_207021	Taste receptor, type 2, member 117	Tas2r117	-	-	-	-	-	-	-	1.8	Down
NM_181276	Taste receptor, type 2, member 136	Tas2r136	-	-	-	-	-	-	-	1.9	Down
NM_172443	TBC1 domain family, member 16	Tbc1d16	-	-	-	-	-	-	-	1.7	Down
NM_145705	Terf1 (TRF1)-interacting nuclear factor 2	Tinf2	-	-	-	-	-	-	-	1.5	Down
NM_031382	Testis expressed gene 16	Tex16	-	-	-	-	-	-	-	2.5	Up
NM_198292	Testis expressed gene 2	Tex2	-	-	-	-	-	-	-	2.7	Up
NM_019784	Testis expressed gene 21	Tex21	-	-	-	-	1.7	Down	-	1.5	Down
XM_139378	testis-specific protein, Y-encoded-like 5	-	-	-	-	-	-	-	-	3.0	Down
NM_145363	Tetraspanin 10	Tspan10	-	-	-	-	-	-	-	1.9	Down
NM_025982	Tetraspanin 31	Tspan31	-	-	-	-	-	-	-	2.4	Up
NM_025978	Tetratricopeptide repeat domain 14	Ttc14	-	-	-	-	-	-	-	3.8	Down
XM_130319	tetratricopeptide repeat domain 21B	-	-	-	-	-	-	-	-	2.0	Down
NM_177625	Tetratricopeptide repeat domain 5	Ttc5	-	-	-	-	-	-	-	1.6	Down
NM_019913	Thioredoxin 2	Txn2	-	-	-	-	-	-	-	3.3	Up
XM_130523	thioredoxin domain containing 13	-	-	-	-	-	1.6	Up	-	3.4	Up
NM_153552	THO complex 1	Thoc1	-	-	-	-	-	-	-	3.2	Down
NM_172438	THO complex 5	Thoc5	-	-	-	-	-	-	-	2.8	Up
NM_172444	Thrombospondin, type I, domain containing 4	Thsd4	-	-	-	-	-	-	-	1.9	Down
NM_009375	Thyroglobulin	Tg	-	-	-	-	-	-	-	2.3	Up
NM_011639	Thyroid hormone receptor interactor 6	Trip6	-	-	-	-	-	-	-	2.2	Up
NM_011595	Tissue inhibitor of metalloproteinase 3	Timp3	-	-	-	-	-	-	-	2.5	Up
NM_011632	Tnf receptor-associated factor 3	Traf3	-	-	-	-	-	-	-	3.3	Up
NM_205819	Toll-like receptor 11	Tlr11	-	-	-	-	-	-	-	2.2	Down
NM_153137	TRAF3 interacting protein 3	Traf3ip3	-	-	-	-	-	-	-	2.2	Down
NM_175114	Trafficking protein, kinesin binding 1	Trak1	-	-	-	-	-	-	-	2.0	Up
NM_009328	Transcription factor 15	Tcf15	-	-	-	-	-	-	-	1.9	Down
NM_011545	Transcription factor 21	Tcf21	-	-	2.4	Up	-	-	-	-	-
NM_009332	Transcription factor 3	Tcf3	-	-	-	-	-	-	-	2.3	Down
NM_172562	Transcriptional adaptor 2 (ADA2 homolog, yeast)-like	Tada2l	-	-	-	-	-	-	-	2.0	Down
NM_020507	Transducer of ERBB2, 2	Tob2	-	-	-	-	-	-	-	2.8	Down
NM_173378	Transformation related protein 53 binding protein 2	Trp53bp2	-	-	-	-	-	-	-	2.6	Down
NM_178871	transforming growth factor beta regulated gene 3	-	-	-	-	-	-	-	-	1.9	Down
NM_013897	Translocase of inner mitochondrial membrane 8 homolog b (yeast)	Timm8b	-	-	-	-	-	-	-	2.0	Down
NM_172282	Transmembrane and coiled-coil domains 3	Tmco3	-	-	-	-	-	-	-	1.9	Down
NM_134020	Transmembrane emp24 protein transport domain containing 4	Tmed4	-	-	-	-	-	-	-	2.8	Up

NM_146260	Transmembrane inner ear	Tmie	-	-	-	-	-	-	2.4	Down
NM_153776	Transmembrane protein 121	Tmem12 1	-	-	-	-	-	-	2.1	Down
NM_025480	Transmembrane protein 128	Tmem12 8	-	-	-	-	-	-	1.8	Down
NM_172885	Transmembrane protein 132D	Tmem13 2d	-	-	1.8	Up	-	-	-	-
NM_144916	Transmembrane protein 150	Tmem15 0	-	-	-	-	1.8	Up	-	-
NM_026321	Transmembrane protein 157	Tmem15 7	-	-	-	-	-	-	2.2	Down
XM_128954	Transmembrane protein 173	Tmem17 3	-	-	-	-	-	-	3.0	Down
NM_030018	Transmembrane protein 50B	Tmem50 b	-	-	-	-	-	-	1.8	Down
NM_025382	Transmembrane protein 57	Tmem57	-	-	-	-	2.0	Up	-	-
NM_175502	Transmembrane protein 74	Tmem74	-	-	-	-	-	-	3.0	Down
NM_026519	Transmembrane protein 85	Tmem85	-	-	2.7	Down	-	-	-	-
NM_021406	Triggering receptor expressed on myeloid cells 1	Trem1	-	-	-	-	-	-	2.9	Up
NM_172623	Triggering receptor expressed on myeloid cells-like 4	Trem14	-	-	-	-	-	-	3.2	Down
NM_177742	Tripartite motif family-like 1	Trim1	1.7	Up	-	-	-	-	-	-
NM_053084	Tripartite motif-containing 32	Trim32	-	-	-	-	-	-	3.4	Up
NM_201373	Tripartite motif-containing 56	Trim56	-	-	-	-	1.9	Up	-	-
NM_175113	TRNA methyltransferase 6 homolog (S. cerevisiae)	Trmt6	-	-	-	-	-	-	2.9	Up
NM_199033	TRNA splicing endonuclease 2 homolog (SEN2, S. cerevisiae)	Tsen2	-	-	-	-	-	-	3.0	Down
NM_021883	Tropomodulin 1	Tmod1	-	-	-	-	3.8	Up	-	-
NM_025537	Ts translation elongation factor, mitochondrial	Tsfm	-	-	-	-	-	-	2.7	Down
NM_198617	TSPY-like 3	Tspyl3	-	-	-	-	-	-	1.9	Down
NM_009321	Tubulin cofactor a	Tbca	-	-	-	-	-	-	1.8	Up
NM_172799	Tubulin tyrosine ligase-like family, member 6	Ttl6	-	-	-	-	-	-	1.7	Up
NM_011654	Tubulin, alpha 1B	Tuba1b	-	-	-	-	-	-	3.3	Down
NM_009447	Tubulin, alpha 4A	Tuba4a	-	-	-	-	-	-	2.4	Down
NM_009450	Tubulin, beta 2a	Tubb2a	-	-	-	-	-	-	2.7	Down
NM_009451	Tubulin, beta 4	Tubb4	-	-	-	-	-	-	2.4	Down
NM_011656	Tuftelin 1	Tuft1	-	-	-	-	-	-	1.7	Down
NM_018783	Tuftelin interacting protein 11	Tfip11	-	-	-	-	-	-	1.7	Down
NM_027206	Tumor necrosis factor, alpha-induced protein 8-like 2	Tnfai82	-	-	-	-	-	-	1.9	Down
NM_009429	Tumor protein, translationally-controlled 1	Tpt1	-	-	-	-	-	-	1.7	Up
NM_008971	Twinfilin, actin-binding protein, homolog 1 (Drosophila)	Twf1	-	-	1.6	Up	-	-	-	-
NM_009536	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	Ywhae	-	-	-	-	-	-	1.6	Down
NM_018871	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide	Ywhag	-	-	-	-	-	-	2.3	Up

NM_018793	Tyrosine kinase 2	Tyk2	-	-	-	-	-	-	2.0	Down
NM_176860	Ubiquitin associated and SH3 domain containing, B	Ubash3b	-	-	-	-	-	-	2.2	Down
NM_011909	Ubiquitin specific peptidase 18	Usp18	-	-	-	-	-	-	3.0	Up
NM_027804	Ubiquitin specific peptidase 19	Usp19	-	-	-	-	-	-	3.1	Up
XM_110937	ubiquitin specific peptidase 32	-	-	-	-	-	-	-	1.8	Down
XM_126772	Ubiquitin specific peptidase 36	Usp36	-	-	1.8	Up	-	-	-	-
NM_0010039	18	Usp7	-	-	-	-	-	-	1.7	Up
NM_019668	Ubiquitin-conjugating enzyme E2A, RAD6 homolog (S. cerevisiae)	Ube2a	-	-	-	-	-	-	1.8	Down
NM_026785	Ubiquitin-conjugating enzyme E2C	Ube2c	-	-	-	-	-	-	1.6	Down
NM_145420	Ubiquitin-conjugating enzyme E2D 1, UBC4/5 homolog (yeast)	Ube2d1	1.7	Up	-	-	-	-	-	-
NM_053215	UDP glucuronosyltransferase 2 family, polypeptide B37	Ugt2b37	-	-	-	-	-	-	2.3	Down
NM_198899	UDP-glucose ceramide glucosyltransferase-like 1	Ugcgl1	-	-	-	-	1.8	Up	-	-
NM_172855	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 5	Galnt5	-	-	-	-	-	-	1.7	Down
NM_172451	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6	Galnt6	-	-	-	-	-	-	1.9	Down
NM_026449	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 5	Galntl5	-	-	-	-	-	-	1.9	Up
NM_009469	Unc-51 like kinase 1 (C. elegans)	Ulk1	-	-	-	-	-	-	1.7	Down
NM_009482	Undifferentiated embryonic cell transcription factor 1	Utf1	-	-	-	-	-	-	2.0	Up
XM_110787	UPF3 regulator of nonsense transcripts homolog B (yeast)	-	-	-	-	-	-	-	2.8	Down
NM_023211	Upregulated during skeletal muscle growth 5	Usmg5	-	-	-	-	-	-	2.0	Up
NM_009471	Uridine monophosphate synthetase	Umps	-	-	-	-	-	-	2.6	Down
NM_009476	Uroplakin 2	Upk2	-	-	-	-	-	-	1.8	Down
NM_009479	Uroporphyrinogen III synthase	Uros	-	-	-	-	-	-	1.9	Down
XM_125867	UTP20, small subunit (SSU) processome component, homolog (yeast)	Utp20	-	-	-	-	-	-	2.0	Down
NM_021387	V-set and transmembrane domain containing 2B	Vstm2b	-	-	-	-	-	-	2.1	Down
NM_025783	Vacuolar protein sorting 24 (yeast)	Vps24	-	-	-	-	-	-	2.5	Down
NM_025842	Vacuolar protein sorting 28 (yeast)	Vps28	-	-	1.6	Up	-	-	-	-
NM_033560	Vacuolar protein sorting 37A (yeast)	Vps37a	-	-	-	-	-	-	1.7	Down
NM_126165	Vacuolar protein sorting 4a (yeast)	Vps4a	-	-	2.0	Up	-	-	-	-
NM_009506	Vascular endothelial growth factor C	Vegfc	-	-	-	-	1.5	Up	-	-
NM_012037	Vesicle amine transport protein 1 homolog (T californica)	Vat1	-	-	-	-	1.6	Up	-	-
NM_016862	Vesicle transport through interaction with t-SNAREs homolog 1A (yeast)	Vti1a	-	-	-	-	-	-	1.6	Down
NM_207544	Vomer nasal 1 receptor, D11	V1rd11	-	-	-	-	-	-	1.9	Down
NM_030736	Vomer nasal 1 receptor, D14	V1rd14	-	-	-	-	-	-	1.6	Down
NM_134221	Vomer nasal 1 receptor, I4	V1ri4	-	-	-	-	-	-	1.6	Down
NM_199306	WD and tetratricopeptide repeats 1	Wdtdc1	-	-	1.7	Up	-	-	-	-
NM_027963	WD repeat domain 16	Wdr16	-	-	-	-	-	-	2.0	Down

NM_172445	WD repeat domain 37	Wdr37	-	-	2.2	Up	-	-	-	-
XM_128124	WD repeat domain 67	-	-	-	-	-	-	-	3.1	Down
NM_178909	WD repeat domain 92	Wdr92	-	-	-	-	-	-	1.5	Down
NM_026044	WD40 repeat domain 85	Wdr85	-	-	-	-	-	-	1.9	Down
NM_025375	Williams Beuren syndrome chromosome region 22	Wbscr22	-	-	-	-	-	-	2.3	Down
NM_033572	Williams-Beuren syndrome chromosome region 16 homolog (human)	Wbscr16	-	-	-	-	-	-	2.3	Down
NM_145218	Williams-Beuren syndrome chromosome region 17 homolog (human)	Wbscr17	-	-	-	-	-	-	1.6	Up
NM_175394	Wilms tumour 1-associating protein	Wtap	-	-	-	-	-	-	2.0	Down
NM_0010044	36									
	Wings apart-like homolog (Drosophila)	Wapal	-	-	-	-	-	-	1.9	Down
XM_282903	WNT1 inducible signaling pathway protein 3	-	-	-	-	-	-	-	1.7	Down
NM_133784	WW domain containing transcription regulator 1	Wwtr1	-	-	-	-	-	-	1.6	Down
NM_031493	X-linked lymphocyte-regulated 5C	Xlr5c	-	-	-	-	-	-	1.8	Down
NM_011725	X-linked lymphocyte-regulated complex	Xlr	-	-	-	-	-	-	2.4	Down
NM_019926	X-linked myotubular myopathy gene 1	Mtm1	-	-	-	-	-	-	2.1	Down
	X-ray repair complementing defective repair in Chinese hamster cells									
NM_009533	5	Xrcc5	-	-	-	-	-	-	1.8	Down
NM_011723	Xanthine dehydrogenase	Xdh	-	-	-	-	-	-	2.2	Up
XM_282966	XIAP associated factor 1	-	-	-	-	-	-	-	3.1	Up
NM_023784	Yip1 domain family, member 7	Yipf7	-	-	-	-	-	-	1.6	Up
XM_284281	Yip1 interacting factor homolog B (S. cerevisiae)	-	-	-	-	-	-	-	2.7	Down
NM_145393	YTH domain family 2	Ythdf2	-	-	-	-	-	-	3.5	Down
NM_177622	Zinc finger protein 595	Zfp595	-	-	-	-	-	-	1.7	Down
NM_133206	Zinc and ring finger 1	Znrf1	-	-	1.8	Up	-	-	-	-
XM_127016	zinc finger and BTB domain containing 25	-	-	-	-	-	-	-	1.6	Down
NM_009570	Zinc finger protein 1, Y linked	Zfy1	-	-	-	-	-	-	1.9	Down
NM_177681	Zinc finger protein 12	Zfp12	-	-	-	-	-	-	3.3	Down
NM_011981	Zinc finger protein 260	Zfp260	-	-	-	-	-	-	2.3	Up
NM_146175	Zinc finger protein 282	Zfp282	-	-	-	-	-	-	3.0	Down
XM_128374	zinc finger protein 294	-	-	-	-	-	-	-	2.3	Down
NM_183185	Zinc finger protein 300	Zfp300	-	-	-	-	-	-	3.3	Down
NM_017467	Zinc finger protein 316	Zfp316	-	-	-	-	-	-	2.2	Down
XM_131700	zinc finger protein 362	-	-	-	-	-	-	-	1.5	Down
NM_175494	Zinc finger protein 367	Zfp367	-	-	-	-	-	-	2.7	Down
NM_020589	Zinc finger protein 467	Zfp467	-	-	-	-	-	-	1.5	Down
NM_145459	Zinc finger protein 503	Zfp503	-	-	-	-	1.8	Up	-	-
NM_011762	Zinc finger protein 59	Zfp59	-	-	-	-	-	-	1.8	Down
NM_178707	Zinc finger protein 592	Zfp592	-	-	-	-	-	-	1.5	Down
NM_177226	Zinc finger protein 629	Zfp629	-	-	-	-	-	-	2.1	Down
NM_025884	Zinc finger protein 830	Zfp830	-	-	-	-	-	-	2.0	Down
NM_011764	Zinc finger protein 90	Zfp90	-	-	-	-	-	-	2.0	Down
NM_009575	Zinc finger protein of the cerebellum 3	Zic3	-	-	-	-	-	-	1.8	Down

NM_011768	Zinc finger protein X-linked	Zfx	-	-	2.6	Down	-	-	3.4	Down
NM_016683	Zinc finger with KRAB and SCAN domains 5	Zkscan5	-	-	-	-	-	-	1.8	Down
NM_028287	Zinc finger with UFM1-specific peptidase domain	Zufsp	-	-	-	-	-	-	2.5	Up
NM_026846	Zinc finger, AN1 type domain 2B	Zfand2b	1.6	Up	-	-	-	-	-	-
NM_172735	Zinc finger, C3HC type 1	Zc3hc1	-	-	1.8	Up	-	-	-	-
NM_199309	Zinc finger, DHHC domain containing 19	Zdhhc19	-	-	-	-	4.2	Up	-	-
NM_144887	Zinc finger, DHHC domain containing 5	Zdhhc5	-	-	2.2	Up	-	-	-	-
NM_030081	Zinc finger, FYVE domain containing 20	Zfyve20	-	-	-	-	-	-	2.1	Down
XM_355521	zinc finger, MYM-type 4	-	-	-	-	-	-	-	1.6	Down
NM_011741	Zonadhesin	Zan	-	-	-	-	-	-	1.7	Down
NM_030260	ZXD family zinc finger C	Zxdc	-	-	-	-	-	-	1.9	Down

Other ID	Gene Name	Gene ID	<i>LVS Infection</i>							
			12	Direction	24	Direction	48	Direction	120	Direction
NM_018862	1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha)	Agpat1	-	-	-	-	-	-	2.9	Up
NM_026212	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta)	Agpat2	-	-	-	-	1.7	Up	2.0	Up
NM_053014	1-acylglycerol-3-phosphate O-acyltransferase 3	Agpat3	-	-	-	-	1.6	Up	-	-
NM_145209	2-5 oligoadenylate synthetase-like 1	Oasl1	-	-	-	-	1.7	Up	-	-
NM_172733	2-deoxyribose-5-phosphate aldolase homolog (C. elegans)	Dera	-	-	-	-	1.9	Up	-	-
NM_008309	5-hydroxytryptamine (serotonin) receptor 1D	Htr1d	-	-	-	-	-	-	3.3	Up
NM_008315	5-hydroxytryptamine (serotonin) receptor 7	Htr7	-	-	-	-	-	-	2.5	Up
XM_138431	5-methyltetrahydrofolate-homocysteine methyltransferase	-	-	-	-	-	-	-	1.7	Up
NM_172480	5-methyltetrahydrofolate-homocysteine methyltransferase reductase	Mtrr	-	-	-	-	-	-	2.3	Up
XM_112246	5-nucleotidase, cytosolic IA	-	-	-	-	-	-	-	1.6	Up
NM_026561	5-nucleotidase, cytosolic III-like	Nt5c3l	-	-	-	-	1.9	Up	-	-
NM_010840	5,10-methylenetetrahydrofolate reductase	Mthfr	-	-	-	-	-	-	2.8	Up
NM_015807	5,3-nucleotidase, cytosolic	Nt5c	-	-	-	-	1.9	Up	-	-
NM_134029	5,3-nucleotidase, mitochondrial	Nt5m	-	-	-	-	1.7	Up	-	-
NM_025396	6-phosphogluconolactonase	Pgl3	-	-	-	-	-	-	1.5	Down
NM_007856	7-dehydrocholesterol reductase	Dhcr7	-	-	-	-	-	-	2.5	Up
NM_0010072	20	-	-	-	-	-	-	-	-	-
NM_010086	A disintegrin and metallopeptidase domain 22	Adam22	-	-	-	-	-	-	2.7	Up
NM_153397	A disintegrin and metallopeptidase domain 24 (testase 1)	Adam24	-	-	-	-	1.6	Down	-	-
NM_007404	A disintegrin and metallopeptidase domain 32	Adam32	-	-	-	-	-	-	2.3	Up
NM_0010013	A disintegrin and metallopeptidase domain 9 (meltrin gamma)	Adam9	-	-	-	-	-	-	1.8	Down
22	A disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 13	Adamts1	-	-	-	-	-	-	3.1	Up
XM_137117	a disintegrin-like and metallopeptidase (reprolysin type) with	3	-	-	-	-	-	-	3.4	Up



	thrombospondin type 1 motif, 14												
NM_172053	A disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 16	Adamts1	6	-	-	-	-	-	-	-	-	1.7	Up
XM_133542	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 17	-	-	-	-	-	-	-	-	-	-	3.1	Up
NM_175643	A disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 2	Adamts2	-	-	-	-	-	-	-	-	-	1.7	Up
NM_019921	A kinase (PRKA) anchor protein 10	Akap10	-	-	-	-	-	2.0	Up	-	-	-	-
XM_486648	A kinase (PRKA) anchor protein 14	-	-	-	-	-	-	-	-	-	-	3.1	Up
XM_138063	A kinase (PRKA) anchor protein 5	-	-	-	-	-	-	-	-	-	-	1.7	Up
NM_024465	Abhydrolase domain containing 12	Abhd12	-	-	-	-	-	-	-	-	-	2.4	Down
NM_018811	Abhydrolase domain containing 2	Abhd2	-	-	-	-	-	-	-	-	-	2.4	Up
XM_131754	Absent in melanoma 1-like	Aim1l	-	-	-	-	-	-	-	-	-	1.6	Up
NM_009338	Acetyl-Coenzyme A acetyltransferase 2	Acat2	-	-	-	-	-	-	-	-	-	1.6	Down
XM_109883	acetyl-Coenzyme A carboxylase alpha	-	-	-	-	-	-	-	-	-	-	2.1	Up
NM_133904	Acetyl-Coenzyme A carboxylase beta	Acacb	-	-	-	-	-	-	-	-	-	2.5	Up
NM_153416	Achalasia, adrenocortical insufficiency, alacrimia	Aaas	-	-	-	-	-	1.8	Up	-	-	-	-
NM_134052	Acireductone dioxygenase 1	Adi1	-	-	-	-	-	2.0	Up	-	-	-	-
XM_355744	ACN9 homolog (S. cerevisiae)	-	-	-	-	-	-	1.6	Up	-	-	-	-
NM_198649	Actin binding LIM protein family, member 3	Ablim3	-	-	-	-	-	-	-	-	-	1.8	Up
NM_146102	Actin filament associated protein 1-like 2	Afap1l2	-	-	-	-	-	-	-	-	-	2.6	Up
NM_019767	Actin related protein 2/3 complex, subunit 1A	Arpc1a	-	-	-	-	-	-	-	-	-	2.2	Down
XM_129773	actin related protein 2/3 complex, subunit 2	-	-	-	-	-	-	-	-	-	-	1.6	Down
NM_175497	Actin, beta-like 2	Actbl2	-	-	-	-	-	-	-	-	-	3.6	Up
NM_019426	Activating transcription factor 7 interacting protein	Atf7ip	-	-	-	-	-	2.9	Up	-	-	-	-
NM_007396	Activin receptor IIA	Acvr2a	-	-	-	-	-	-	-	-	-	3.9	Up
NM_007397	Activin receptor IIB	Acvr2b	-	-	-	-	-	1.7	Up	-	-	2.9	Up
XM_126946	acyl-CoA thioesterase 6	-	-	-	-	-	-	-	-	-	-	2.3	Up
NM_028250	Acyl-Coenzyme A binding domain containing 6	Acbd6	-	-	-	-	-	1.6	Up	-	-	-	-
NM_172678	Acyl-Coenzyme A dehydrogenase family, member 9	Acad9	-	-	-	-	-	-	-	-	-	1.8	Down
NM_021475	ADAM-like, decysin 1	Adamdec	1	-	-	-	-	-	-	-	-	2.2	Down
XM_130065	ADAMTS-like 2	-	-	-	-	-	-	-	-	-	-	2.1	Up
XM_194370	ADAMTS-like 3	Adamtsl3	-	-	-	-	-	-	-	-	-	2.3	Up
NM_027915	Adaptor-related protein complex 2, beta 1 subunit	Ap2b1	-	-	-	-	-	1.8	Up	-	-	-	-
NM_009350	Adenosine deaminase domain containing 1 (testis specific)	Adad1	-	-	-	-	-	-	-	-	-	2.5	Up
NM_013925	Adenosine deaminase, tRNA-specific 1	Adat1	-	-	-	-	-	-	-	-	-	1.7	Up
NM_138305	Adenylate cyclase 3	Adcy3	-	-	-	-	-	1.7	Down	-	-	-	-
NM_007405	Adenylate cyclase 6	Adcy6	-	-	-	-	-	-	-	-	-	1.7	Up
NM_009625	Adenylate cyclase activating polypeptide 1	Adcyap1	-	-	-	-	-	-	-	-	-	2.3	Up
NM_197985	Adiponectin receptor 2	Adipor2	-	-	-	-	-	-	-	-	-	1.6	Down
NM_007479	ADP-ribosylation factor 4	Arf4	-	-	-	-	-	2.2	Up	-	-	-	-

NM_007481	ADP-ribosylation factor 6	Arf6	-	-	-	-	1.5	Up	-	-
NM_177337	ADP-ribosylation factor-like 11	Arl11	-	-	-	-	2.1	Up	2.5	Up
NM_177305	ADP-ribosylation factor-like 4C	Arl4c	-	-	-	-	-	-	1.9	Up
NM_019665	ADP-ribosylation factor-like 6	Arl6	-	-	1.6	Down	-	-	-	-
NM_022989	ADP-ribosylation factor-like 6 interacting protein 6	Arl6ip6	-	-	-	-	-	-	2.0	Down
NM_007490	ADP-ribosyltransferase 2a	Art2a	-	-	-	-	-	-	1.8	Up
NM_181728	ADP-ribosyltransferase 3	Art3	-	-	-	-	1.6	Up	-	-
NM_007491	ADP-ribosyltransferase 5	Art5	-	-	-	-	-	-	2.1	Up
NM_007417	Adrenergic receptor, alpha 2a	Adra2a	-	-	-	-	1.6	Up	-	-
NM_007418	Adrenergic receptor, alpha 2c	Adra2c	-	-	-	-	-	-	2.1	Up
NM_009635	Advillin	Avil	-	-	-	-	-	-	2.1	Up
NM_133919	AF4/FMR2 family, member 1	Aff1	-	-	-	-	-	-	1.9	Up
NM_008032	AF4/FMR2 family, member 2	Aff2	-	-	-	-	-	-	2.4	Up
XM_128950	AFG3(ATPase family gene 3)-like 2 (yeast)	-	-	-	-	-	-	-	2.0	Down
NM_021604	Agtrin	Agm	-	-	-	-	-	-	2.4	Up
XM_356602	AHNAK nucleoprotein 2	-	-	-	-	-	-	-	2.2	Up
XM_131202	alcohol dehydrogenase 6A (class V)	-	-	-	-	-	-	-	2.4	Up
NM_027406	Aldehyde dehydrogenase 1 family, member L1	Aldh111	-	-	1.6	Down	-	-	-	-
NM_026316	Aldehyde dehydrogenase 3 family, member B1	Aldh3b1	-	-	-	-	2.5	Up	-	-
NM_178713	Aldehyde dehydrogenase 8 family, member A1	Aldh8a1	-	-	-	-	-	-	2.0	Up
NM_007437	Aldehyde dehydrogenase family 3, subfamily A2	Aldh3a2	-	-	-	-	-	-	2.9	Down
NM_134042	Aldehyde dehydrogenase family 6, subfamily A1	Aldh6a1	-	-	-	-	1.9	Up	-	-
NM_030611	Aldo-keto reductase family 1, member C6	Akr1c6	-	-	-	-	-	-	1.7	Up
NM_007438	Aldolase A, fructose-bisphosphate	Aldoa	-	-	-	-	-	-	1.8	Down
XM_132400	alkB, alkylation repair homolog 4 (E. coli)	-	-	-	-	-	1.7	Up	-	-
NM_007443	Alpha 1 microglobulin/bikunin	Ambp	-	-	-	-	-	-	2.2	Up
XM_128290	alpha-1-B glycoprotein	-	-	-	-	-	-	-	1.8	Up
NM_054085	Alpha-kinase 3	Alpk3	-	-	-	-	1.5	Down	-	-
NM_029638	Amiloride binding protein 1 (amine oxidase, copper-containing)	Abp1	-	-	-	-	-	-	3.4	Up
NM_183022	Amiloride-sensitive cation channel 4, pituitary	Accn4	-	-	-	-	-	-	3.1	Up
NM_013930	Aminoadipate-semialdehyde synthase	Aass	-	-	-	-	-	-	2.8	Up
NM_009653	Aminolevulinic acid synthase 2, erythroid	Alas2	-	-	-	-	-	-	1.9	Up
NM_009704	Amphiregulin	Areg	-	-	-	-	-	-	2.1	Up
NM_008569	Anaphase promoting complex subunit 1	Anapc1	-	-	-	-	-	-	4.0	Up
NM_194338	androgen binding protein gamma	-	-	-	-	-	-	-	1.9	Up
NM_146110	Angio-associated migratory protein	Aamp	-	-	-	-	-	-	2.9	Down
NM_177544	Angiogenin, ribonuclease A family, member 4	Ang4	-	-	-	-	-	-	2.0	Up
NM_153319	Angiomotin	Amot	-	-	-	-	-	-	2.3	Up
XM_134711	angiomotin-like 1	-	-	-	-	-	-	-	1.9	Up
NM_028333	Angiopoietin-like 1	Angptl1	-	-	-	-	-	-	1.8	Up
NM_175086	Angiotensin II receptor, type 1b	Agtr1b	-	-	-	-	-	-	1.6	Up

XM_130845	ankrin repeat domain 50	-	-	-	-	-	-	2.7	Up
NM_176980	Ankyrin and armadillo repeat containing	Ankar	-	-	-	-	-	2.9	Up
XM_357954	Ankyrin repeat and death domain containing 1A	Ankdd1a	-	-	-	-	-	1.5	Up
NM_172756	Ankyrin repeat and LEM domain containing 1	Ankle1	-	-	1.6	Down	-	-	-
NM_172850	Ankyrin repeat and MYND domain containing 1	Ankmy1	-	-	-	-	-	1.9	Up
NM_139152	Ankyrin repeat and SOCS box-containing 18	Asb18	-	-	-	-	-	1.7	Up
NM_023048	Ankyrin repeat and SOCS box-containing protein 4	Asb4	-	-	-	-	-	2.2	Up
NM_133346	Ankyrin repeat and SOCS box-containing protein 6	Asb6	-	-	-	-	-	1.9	Up
NM_026720	Ankyrin repeat domain 13 family, member D	Ankrd13d	-	-	-	-	-	2.3	Up
NM_020033	Ankyrin repeat domain 2 (stretch responsive muscle)	Ankrd2	-	-	-	-	1.8	Up	-
XM_129028	Ankyrin repeat domain 29	Ankrd29	-	-	-	-	-	1.8	Up
NM_175455	Ankyrin repeat domain 34B	Ankrd34b	-	-	-	-	-	2.3	Up
NM_027799	Ankyrin repeat domain 40	Ankrd40	-	-	-	-	2.0	Up	-
XM_355251	Ankyrin repeat domain 45	Ankrd45	-	-	-	-	-	2.8	Up
NM_027211	Annexin A13	Anxa13	-	-	-	-	-	2.2	Up
NM_013900	Antigen p97 (melanoma associated) identified by monoclonal antibodies 133.2 and 96.5	Mfi2	-	-	-	-	-	1.9	Up
NM_194357	Antimicrobial peptide RYA3	RP23-244H7.9	-	-	-	-	-	3.3	Up
NM_080434	Apolipoprotein A-V	Apoa5	-	-	-	-	-	2.7	Up
NM_009696	Apolipoprotein E	ApoE	-	-	-	-	2.0	Up	-
NM_177744	Apolipoprotein L 11a	Apol10a	-	-	-	-	-	2.9	Up
NM_175178	Apoptosis-inducing factor, mitochondrion-associated 3	Aifm3	-	-	-	-	-	2.2	Up
NM_029943	Apurinic/apyrimidinic endonuclease 2	Apex2	-	-	-	-	-	1.7	Up
NM_009702	Aquarius	Aqr	-	-	-	-	-	2.2	Up
NM_009660	Arachidonate 15-lipoxygenase	Alox15	-	-	-	-	-	1.6	Up
NM_009661	Arachidonate 8-lipoxygenase	Alox8	-	-	-	-	-	1.9	Up
NM_145985	Archain 1	Arcn1	-	-	-	-	1.6	Up	-
NM_029103	Arginine-rich, mutated in early stage tumors	Armet	-	-	-	-	-	1.6	Down
NM_025822	Arginine/serine-rich coiled-coil 1	Rsrc1	-	-	-	-	1.6	Up	2.0
NM_025936	Arginyl-tRNA synthetase	Rars	-	-	-	-	-	2.1	Down
NM_026139	Armadillo repeat containing, X-linked 2	Armxc2	-	-	-	-	-	2.1	Down
NM_146243	ARP2 actin-related protein 2 homolog (yeast)	Actr2	-	-	-	-	-	2.9	Down
NM_020577	Arsenic (+3 oxidation state) methyltransferase	As3mt	-	-	-	-	-	2.3	Down
NM_009709	Aryl hydrocarbon receptor nuclear translocator	Arnt	-	-	-	-	-	1.9	Up
NM_025541	ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	Asf1a	-	-	-	-	-	2.8	Down
NM_009714	Asialoglycoprotein receptor 1	Asgr1	-	-	-	-	-	2.1	Up
NM_012055	Asparagine synthetase	Asns	1.5	Up	-	-	-	-	-
NM_024178	Asparagine-linked glycosylation 14 homolog (yeast)	Alg14	-	-	-	-	-	3.3	Up
NM_025442	Asparagine-linked glycosylation 5 homolog (yeast, dolichyl-phosphate beta-glucosyltransferase)	Alg5	-	-	-	-	-	2.7	Down
NM_028386	Aspartate beta-hydroxylase domain containing 2	Asphd2	-	-	-	-	-	2.1	Up

NM_133723	Aspartate-beta-hydroxylase	Asph	-	-	-	-	-	-	2.5	Up
NM_019689	AT rich interactive domain 3B (Bright like)	Arid3b	-	-	-	-	-	-	1.8	Up
NM_009125	Ataxin 2	Atxn2	-	-	-	-	-	-	2.0	Up
XM_354666	ataxin 7-like 1	-	-	-	-	-	-	-	1.8	Up
NM_007500	Atonal homolog 1 (Drosophila)	Atoh1	-	-	-	-	-	-	2.5	Up
NM_145427	ATP synthase mitochondrial F1 complex assembly factor 2	Atpaf2	-	-	-	-	1.7	Up	-	-
NM_009725	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1	Atp5f1	-	-	-	-	-	-	3.0	Down
NM_026468	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2	Atp5g2	-	-	-	-	-	-	2.0	Down
NM_025313	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	Atp5d	-	-	-	-	-	-	2.0	Down
NM_147219	ATP-binding cassette, sub-family A (ABC1), member 5	Abca5	-	-	1.5	Down	-	-	-	-
NM_147218	ATP-binding cassette, sub-family A (ABC1), member 6	Abca6	-	-	-	-	-	-	2.6	Up
NM_011075	ATP-binding cassette, sub-family B (MDR/TAP), member 1B	Abcb1b	-	-	-	-	-	-	3.2	Up
NM_172912	ATP-binding cassette, sub-family C (CFTR/MRP), member 12	Abcc12	-	-	-	-	-	-	2.8	Up
NM_013854	ATP-binding cassette, sub-family F (GCN20), member 1	Abcf1	-	-	-	-	-	-	2.4	Down
NM_009593	ATP-binding cassette, sub-family G (WHITE), member 1	Abcg1	-	-	-	-	-	-	1.6	Down
NM_030239	ATP-binding cassette, sub-family G (WHITE), member 3	Abcg3	-	-	-	-	-	-	2.7	Down
NM_172902	ATP/GTP binding protein-like 1	Agbl1	-	-	-	-	2.0	Up	-	-
NM_133224	ATPase type 13A1	Atp13a1	-	-	-	-	1.7	Up	-	-
XM_148700	ATPase type 13A3	-	-	-	-	-	-	-	2.8	Up
NM_175650	ATPase type 13A5	Atp13a5	-	-	-	-	-	-	3.2	Up
NM_177236	ATPase, Ca++ transporting, plasma membrane 3	Atp2b3	-	-	-	-	-	-	2.6	Up
NM_001001488	ATPase, class I, type 8B, member 1	Atp8b1	-	-	-	-	-	-	3.8	Up
NM_007509	ATPase, H+ transporting, lysosomal V1 subunit B2	Atp6v1b2	-	-	-	-	1.6	Up	-	-
NM_013415	ATPase, Na+/K+ transporting, beta 2 polypeptide	Atp1b2	-	-	-	-	-	-	2.0	Up
NM_007502	ATPase, Na+/K+ transporting, beta 3 polypeptide	Atp1b3	-	-	-	-	-	-	2.4	Down
NM_009720	ATX1 (antioxidant protein 1) homolog 1 (yeast)	Atox1	-	-	-	-	1.9	Up	-	-
NM_011787	Autocrine motility factor receptor	Amfr	-	-	-	-	-	-	2.3	Down
NM_025770	Autophagy-related 10 (yeast)	Atg10	-	-	-	-	-	-	1.9	Down
NM_009733	Axin 1	Axin1	-	-	-	-	-	-	1.9	Down
NM_033601	B-cell leukemia/lymphoma 3	Bcl3	-	-	-	-	-	-	3.1	Up
NM_012060	B-cell receptor-associated protein 31	Bcap31	-	-	-	-	-	-	1.6	Down
NM_009770	B-cell translocation gene 3	Btg3	-	-	-	-	-	-	2.7	Down
NM_177850	Bactericidal permeability increasing protein	Bpi	-	-	-	-	-	-	1.7	Up
NM_025833	BAI1-associated protein 2-like 1	Baiap2l1	-	-	-	-	-	-	2.4	Up
NM_181316	Bardet-Biedl syndrome 9	Bbs9	-	-	-	-	-	-	2.0	Down
NM_019446	BarH-like 1 (Drosophila)	Barhl1	-	-	-	-	-	-	1.9	Up
NM_207275	Barrier to autointegration factor 2	Banf2	-	-	-	-	-	-	2.2	Up
NM_011498	Basic helix-loop-helix domain containing, class B2	Bhlhb2	-	-	-	-	-	-	2.0	Down

NM_025824	Basic leucine zipper and W2 domains 1	Bzw1	-	-	-	-	-	-	2.3	Down
NM_145455	Basic transcription factor 3	Btf3	-	-	-	-	-	-	1.6	Down
NM_007562	Basonuclin 1	Bnc1	-	-	-	-	-	-	2.2	Up
NM_007567	Bassoon	Bsn	-	-	-	-	-	-	2.6	Up
XM_148990	BAT2 domain containing 1	-	-	-	-	-	-	-	2.5	Up
NM_133234	Bcl-2 binding component 3	Bbc3	-	-	-	-	-	-	2.3	Up
NM_007523	BCL2-antagonist/killer 1	Bak1	-	-	-	-	-	-	2.5	Up
NM_009736	Bcl2-associated athanogene 1	Bag1	-	-	-	-	-	-	1.6	Down
NM_009743	Bcl2-like 1	Bcl2l1	-	-	-	-	-	-	2.2	Up
NM_013479	Bcl2-like 10	Bcl2l10	-	-	-	-	-	-	2.3	Up
NM_019584	Beclin 1, autophagy related	Becn1	-	-	-	-	2.1	Up	-	-
NM_172449	Benzodiazapine receptor associated protein 1	Bzrap1	-	-	-	-	-	-	1.7	Up
XM_356501	bestrophin 3	-	-	-	-	-	-	-	1.7	Up
NM_145933	Beta galactoside alpha 2,6 sialyltransferase 1	St6gal1	-	-	-	-	-	-	4.1	Down
NM_172829	Beta galactoside alpha 2,6 sialyltransferase 2	St6gal2	-	-	1.6	Down	-	-	-	-
NM_008081	Beta-1,4-N-acetyl-galactosaminyl transferase 2	B4galnt2	-	-	-	-	-	-	3.2	Down
NM_009735	Beta-2 microglobulin	B2m	-	-	-	-	1.5	Up	-	-
NM_011792	Beta-site APP cleaving enzyme 1	Bace1	-	-	-	-	-	-	1.6	Up
NM_007568	Betacellulin, epidermal growth factor family member	Btc	-	-	-	-	-	-	2.8	Up
NM_016668	Betaine-homocysteine methyltransferase	Bhmt	-	-	-	-	-	-	2.9	Up
NM_007542	Biglycan	Bgn	-	-	-	-	-	-	1.6	Down
NM_144923	Biliverdin reductase B (flavin reductase (NADPH))	Blvrb	-	-	-	-	1.6	Up	2.0	Up
XM_193940	Biogenesis of lysosome-related organelles complex-1, subunit 2	Bloc1s2	-	-	-	-	-	-	2.4	Down
NM_025295	Biotinidase	Btd	-	-	-	-	2.1	Up	2.9	Up
NM_178645	Bleomycin hydrolase	Blmh	-	-	-	-	-	-	1.8	Down
NM_009759	BMX non-receptor tyrosine kinase	Bmx	-	-	-	-	-	-	1.6	Up
NM_027444	Bobby sox homolog (Drosophila)	Bbx	-	-	-	-	-	-	1.6	Up
NM_175103	BolA-like 2 (E. coli)	Bola2	-	-	-	-	-	-	2.3	Up
NM_009766	Bombesin-like receptor 3	Brs3	-	-	-	-	2.2	Up	-	-
NM_007561	Bone morphogenic protein receptor, type II (serine/threonine kinase)	Bmpr2	-	-	-	-	-	-	2.5	Up
NM_007539	Bradykinin receptor, beta 1	Bdkrb1	-	-	-	-	-	-	1.6	Up
NM_009747	Bradykinin receptor, beta 2	Bdkrb2	-	-	-	-	-	-	2.4	Up
NM_027395	Brain abundant, membrane attached signal protein 1	Basp1	-	-	1.5	Up	-	-	-	-
NM_153781	Brain glycogen phosphorylase	Pygb	-	-	-	-	1.8	Up	-	-
NM_178309	BRCA1 interacting protein C-terminal helicase 1	Brip1	-	-	-	-	-	-	2.4	Up
NM_145125	Bromodomain and WD repeat domain containing 1	Brwd1	-	-	-	-	-	-	2.9	Up
NM_020508	Bromodomain containing 4	Brd4	-	-	-	-	-	-	2.7	Up
NM_175235	Bruno-like 6, RNA binding protein (Drosophila)	Bruno6	-	-	1.5	Down	-	-	-	-
NM_133889	BSD domain containing 1	Bsdc1	-	-	1.9	Up	-	-	-	-
NM_177472	BTB (POZ) domain containing 12	Btbd12	-	-	-	-	-	-	2.9	Up
NM_183314	BTB (POZ) domain containing 16	-	-	-	-	-	-	-	1.8	Up

NM_013502	C-terminal binding protein 1	Ctbp1	-	-	-	-	-	-	2.5	Down
XM_132881	C-type lectin domain family 12, member B	Clec12b	-	-	-	-	-	-	2.2	Up
NM_153506	C-type lectin domain family 2, member e	Clec2e	-	-	-	-	-	-	2.0	Up
NM_053165	C-type lectin domain family 2, member h	Clec2h	-	-	-	-	-	-	2.8	Up
NM_007662	Cadherin 15	Cdh15	-	-	-	-	-	-	2.4	Up
XM_354862	cadherin 18	-	-	-	-	-	-	-	2.1	Up
NM_023370	Cadherin 23 (otocadherin)	Cdh23	-	-	-	-	-	-	1.9	Up
NM_199470	Cadherin-like 24	Cdh24	-	-	-	-	-	-	3.8	Up
NM_198656	Cadherin-like 26	Cdh26	-	-	-	-	-	-	2.0	Up
NM_009886	Cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila)	Celsr1	-	-	-	-	-	-	2.1	Up
NM_001004177	Cadherin, EGF LAG seven-pass G-type receptor 2 (flamingo homolog, Drosophila)	Celsr2	-	-	-	-	-	-	2.1	Up
NM_080437	Cadherin, EGF LAG seven-pass G-type receptor 3 (flamingo homolog, Drosophila)	Celsr3	-	-	-	-	-	-	2.5	Up
XM_131990	Calcium and integrin binding family member 4	Cib4	-	-	-	-	1.5	Up	3.1	Up
NM_144822	Calcium binding atopy-related autoantigen 1	Cbara1	-	-	-	-	2.5	Up	-	-
NM_013877	Calcium binding protein 5	Cabp5	-	-	-	-	-	-	2.2	Up
NM_019582	Calcium channel, voltage-dependent, alpha 1F subunit	Cacna1f	-	-	1.9	Down	-	-	-	-
NM_023116	Calcium channel, voltage-dependent, beta 2 subunit	Cacnb2	-	-	-	-	-	-	3.5	Up
NM_007582	Calcium channel, voltage-dependent, gamma subunit 1	Cacng1	-	-	-	-	-	-	1.7	Up
NM_133183	Calcium channel, voltage-dependent, gamma subunit 6	Cacng6	-	-	-	-	-	-	2.4	Up
XM_358335	calcium channel, voltage-dependent, L type, alpha 1S subunit	-	-	-	-	-	-	-	1.9	Up
NM_009782	Calcium channel, voltage-dependent, R type, alpha 1E subunit	Cacna1e	-	-	-	-	-	-	1.5	Up
NM_138585	Calcium homeostasis endoplasmic reticulum protein	Cherp	-	-	-	-	-	-	2.0	Up
NM_023813	Calcium/calmodulin-dependent protein kinase II, delta	Camk2d	-	-	-	-	-	-	1.7	Down
NM_009793	Calcium/calmodulin-dependent protein kinase IV	Camk4	-	-	-	-	1.5	Up	2.8	Up
NM_029341	Calcyphosine-like	Capsl	-	-	-	-	-	-	2.5	Up
NM_009790	Calmodulin 1	Calm1	-	-	-	-	-	-	4.1	Down
XM_129477	calmodulin regulated spectrin-associated protein 1-like 1	-	-	-	-	-	-	-	4.1	Up
NM_027416	Calmodulin-like 3	Calml3	-	-	-	-	-	-	3.2	Up
XM_193876	calpain 11	-	-	-	-	-	-	-	1.8	Up
NM_007725	Calponin 2	Cnn2	-	-	1.8	Up	-	-	1.8	Down
NM_013497	CAMP responsive element binding protein 3	Creb3	-	-	-	-	-	-	4.1	Up
AK036658	Cannabinoid receptor 2 (macrophage)	Cnr2	-	-	-	-	1.7	Up	-	-
NM_019953	Canopy 2 homolog (zebrafish)	Cnpy2	-	-	-	-	1.6	Up	-	-
NM_178612	Canopy 4 homolog (zebrafish)	Cnpy4	-	-	-	-	-	-	1.5	Up
NM_009990	CAP-GLY domain containing linker protein 2	Clip2	-	-	-	-	-	-	2.9	Up
XM_129769	carbamoyl-phosphate synthetase 1	-	-	-	-	-	-	-	2.7	Up
NM_023525	Carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase	Cad	-	-	-	-	2.4	Up	1.6	Up
NM_030558	Carbonic anhydrase 15	Car15	-	-	-	-	-	-	1.7	Up

NM_009885	Carboxyl ester lipase	Cel	-	-	-	-	-	-	1.8	Up
NM_145603	Carboxylesterase 2	Ces2	-	-	-	-	-	-	1.6	Up
NM_177834	Carboxypeptidase A6	Cpa6	-	-	1.9	Down	-	-	-	-
NM_030703	Carboxypeptidase N, polypeptide 1	Cpn1	-	-	-	-	-	-	3.6	Up
XM_357710	carcinoembryonic antigen-related cell adhesion molecule 3	-	-	-	-	-	-	-	2.2	Up
NM_007760	Carnitine acetyltransferase	Crat	-	-	-	-	-	-	2.4	Up
NM_023733	Carnitine O-octanoyltransferase	Crot	-	-	-	-	-	-	2.8	Down
NM_013495	Carnitine palmitoyltransferase 1a, liver	Cpt1a	-	-	-	-	-	-	2.2	Down
NM_009948	Carnitine palmitoyltransferase 1b, muscle	Cpt1b	-	-	-	-	2.4	Up	-	-
NM_153679	Carnitine palmitoyltransferase 1c	Cpt1c	-	-	-	-	-	-	2.9	Up
NM_007784	Casein alpha s1	Csn1s1	-	-	-	-	-	-	2.5	Up
NM_146087	Casein kinase 1, alpha 1	Csnk1a1	-	-	-	-	1.9	Up	2.9	Up
NM_011802	Caseinolytic peptidase X (E.coli)	Clpx	-	-	-	-	-	-	2.6	Down
NM_018761	Catenin (cadherin associated protein), alpha-like 1	Ctnnal1	-	-	-	-	-	-	1.5	Up
NM_019541	Cathepsin 8	Cts8	-	-	-	-	-	-	2.2	Up
NM_007800	Cathepsin G	Ctsg	-	-	-	-	-	-	4.1	Up
NM_009984	Cathepsin L	Ctsl	-	-	-	-	-	-	3.2	Down
NM_139301	Cation channel of sperm 1	Catsper1	-	-	1.7	Down	-	-	-	-
NM_010828	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	Cited2	-	-	-	-	-	-	2.7	Up
NM_009882	CCAAT/enhancer binding protein zeta	-	-	-	-	-	-	-	2.6	Down
NM_016877	CCR4-NOT transcription complex, subunit 4	Cnot4	-	-	-	-	1.5	Up	-	-
NM_133655	CD 81 antigen	Cd81	-	-	-	-	1.5	Up	2.0	Down
NM_016898	CD164 antigen	Cd164	-	-	-	-	-	-	2.6	Down
NM_009844	CD19 antigen	Cd19	-	-	-	-	2.7	Up	-	-
NM_013486	CD2 antigen	Cd2	-	-	-	-	-	-	1.7	Down
NM_130904	CD209d antigen	Cd209d	-	-	-	-	-	-	2.7	Up
NM_130905	CD209e antigen	Cd209e	-	-	-	-	-	-	1.6	Up
XM_284386	CD209f antigen	Cd209f	-	-	-	-	-	-	2.3	Up
XM_284376	CD209g antigen	Cd209g	-	-	-	-	1.8	Up	2.8	Up
NM_009845	CD22 antigen	Cd22	-	-	-	-	2.3	Up	-	-
NM_021293	CD33 antigen	Cd33	-	-	-	-	-	-	3.4	Down
NM_013488	CD4 antigen	Cd4	-	-	-	-	-	-	1.9	Up
NM_010581	CD47 antigen (Rh-related antigen, integrin-associated signal transducer)	Cd47	-	-	-	-	-	-	3.1	Down
NM_007650	CD5 antigen	Cd5	-	-	-	-	2.4	Up	1.7	Up
NM_010016	CD55 antigen	Cd55	-	-	-	-	-	-	2.4	Down
NM_007652	CD59a antigen	Cd59a	-	-	-	-	-	-	2.8	Up
NM_009853	CD68 antigen	Cd68	-	-	-	-	2.3	Up	-	-
XM_140553	CDC42 binding protein kinase gamma (DMPK-like)	Cdc42bp g	-	-	-	-	-	-	1.9	Up
NM_026772	CDC42 effector protein (Rho GTPase binding) 2	Cdc42ep	-	-	-	-	1.6	Up	-	-

NM_134007	CDGSH iron sulfur domain 1	2	Cisd1	-	-	-	-	-	-	2.0	Down
NM_030248	CDK5 regulatory subunit associated protein 3	3	Cdk5rap	-	-	-	-	2.8	Up	-	-
NM_029976	CDKN2A interacting protein N-terminal like		Cdkn2aip	-	-	-	-	-	-	1.5	Down
XM_128528	CDNA sequence BC003965		nl	-	-	-	-	-	-	3.1	Down
XM_131217	cDNA sequence BC007180		BC00396	-	-	-	-	-	-	1.7	Up
NM_198171	CDNA sequence BC015286		BC01528	-	-	-	-	-	-	1.8	Up
NM_144832	CDNA sequence BC017643		6	-	-	-	-	-	-	1.9	Down
NM_177761	cDNA sequence BC022713		BC01764	-	-	-	-	-	-	1.9	Up
NM_145357	cDNA sequence BC023105		3	-	-	-	-	-	-	2.0	Up
NM_153562	CDNA sequence BC023814		BC02381	-	-	-	-	-	-	2.3	Up
NM_199200	CDNA sequence BC025575		4	-	-	-	-	-	-	2.2	Up
NM_172378	CDNA sequence BC026439		BC02557	-	-	-	-	-	-	3.5	Up
NM_183192	cDNA sequence BC027582		5	-	-	-	-	2.2	Up	1.9	Up
XM_134244	cDNA sequence BC028663		BC02643	-	-	-	-	-	-	2.6	Up
NM_153557	CDNA sequence BC029214		9	-	-	-	-	-	-	3.2	Up
XM_140041	cDNA sequence BC032203		4	-	-	-	-	-	-	3.1	Up
NM_178117	cDNA sequence BC035947		-	-	-	-	-	-	-	4.1	Up
NM_207161	CDNA sequence BC048355		BC02921	-	-	-	-	-	-	1.7	Up
NM_178776	CDNA sequence BC049715		4	-	-	-	-	-	-	2.3	Up
XM_110973	cDNA sequence BC050078		5	-	-	-	-	-	-	2.4	Up
NM_020609	cDNA sequence BC051019		BC04835	-	-	-	-	2.3	Up	2.7	Up
NM_182636	CDNA sequence BC052055		5	-	-	-	-	-	-	2.0	Up
NM_198301	CDNA sequence BC052328		BC05232	-	-	-	-	-	-	2.5	Down
NM_177822	CDNA sequence BC052484		8	-	-	-	-	-	-	2.0	Up
NM_183321	CDNA sequence BC053749		BC05248	-	-	-	-	-	-	4.1	Up
NM_0010014	CDNA sequence BC056474		4	-	-	-	-	1.7	Up	-	-
93	CDNA sequence BC057371		9	-	-	-	-	-	-	2.0	Up
NM_177572	CDNA sequence BC057371		BC05647	-	-	-	-	-	-	2.0	Up
			4	-	-	-	-	-	-	2.0	Up
			BC05737	-	-	-	-	-	-	2.0	Up



		1							
		BC05755							
NM_172502	CDNA sequence BC057552	2	-	-	-	-	1.6	Up	-
NM_198603	cDNA sequence BC060267	-	-	-	-	-	-	-	2.8 Up
		BC06063							
NM_198625	CDNA sequence BC060632	2	-	-	-	-	-	-	3.1 Up
		BC06210							
NM_182841	CDNA sequence BC062109	9	-	-	-	-	-	-	1.7 Up
		BC06212							
NM_199062	CDNA sequence BC062127	7	-	-	-	-	-	-	2.1 Up
XM_485102	cDNA sequence BC067047	-	-	-	-	-	-	-	2.8 Up
XM_137156	cDNA sequence BC072620	-	-	-	-	-	-	-	2.6 Up
NM_183223	cDNA sequence BC107364	-	-	-	-	-	-	-	2.2 Up
NM_0010013		BC11709							
32	CDNA sequence BC1179090	0	-	-	-	-	-	-	3.3 Up
XM_144837	cDNA sequence U29423	-	-	-	-	-	-	-	1.7 Up
NM_153418	CDNA sequence U46068	U46068	-	-	-	-	-	-	1.9 Up
NM_173370	CDP-diacylglycerol synthase 1	Cds1	-	-	-	-	-	-	1.9 Up
		Ceacam1							
NM_026087	CEA-related cell adhesion molecule 12	2	-	-	-	-	-	-	1.5 Up
		Ceacam1							
NM_027210	CEA-related cell adhesion molecule 13	3	-	-	-	-	-	-	1.8 Up
NM_178721	Cell adhesion molecule 2	Cadm2	-	-	-	-	-	-	2.5 Up
XM_138861	Cell division cycle 20 homolog B (S. cerevisiae)	Cdc20b	-	-	-	-	-	-	2.5 Up
NM_139291	Cell division cycle 26	Cdc26	-	-	-	-	-	-	2.3 Down
NM_029158	Cellular nucleic acid binding protein 2	Cnbp2	-	-	-	-	-	-	2.4 Up
NM_007759	Cellular retinoic acid binding protein II	Crabp2	-	-	-	-	-	-	2.9 Up
NM_019405	Centrin 2	Cetn2	-	-	-	-	3.0	Up	-
NM_007682	Centromere protein B	Cenpb	-	-	-	-	-	-	1.6 Up
NM_145924	Centromere protein I	Cenpi	-	-	-	-	-	-	1.6 Up
NM_025495	Centromere protein P	Cenpp	1.7	Up	-	-	-	-	-
XM_129509	Centrosomal protein 350	Cep350	-	-	-	-	-	-	3.9 Up
NM_028959	Centrosomal protein 72	Cep72	-	-	-	-	-	-	2.9 Up
NM_146014	Cerebral cavernous malformation 2 homolog (human)	Ccm2	-	-	-	-	1.6	Up	1.8 Down
XM_127882	ceroid-lipofuscinosis, neuronal 5	-	-	-	-	-	-	-	2.5 Down
NM_007636	Chaperonin subunit 2 (beta)	Cct2	-	-	-	-	1.8	Up	-
NM_007637	Chaperonin subunit 5 (epsilon)	Cct5	-	-	-	-	2.0	Up	-
NM_009840	Chaperonin subunit 8 (theta)	Cct8	-	-	-	-	-	-	1.6 Down
NM_011798	Chemokine (C motif) receptor 1	Xcr1	-	-	-	-	1.5	Up	-
NM_011329	Chemokine (C-C motif) ligand 1	Ccl1	-	-	-	-	-	-	2.0 Up
NM_011333	Chemokine (C-C motif) ligand 2	Ccl2	-	-	-	-	-	-	2.6 Up
NM_020279	Chemokine (C-C motif) ligand 28	Ccl28	-	-	-	-	-	-	3.2 Up

NM_013653	Chemokine (C-C motif) ligand 5	Ccl5	-	-	-	-	-	-	2.8	Down
NM_013654	Chemokine (C-C motif) ligand 7	Ccl7	-	-	-	-	-	-	2.5	Up
NM_011338	Chemokine (C-C motif) ligand 9	Ccl9	-	-	-	-	-	-	2.0	Down
NM_007721	Chemokine (C-C motif) receptor 10	Ccr10	-	-	-	-	-	-	3.0	Up
NM_145700	Chemokine (C-C motif) receptor-like 1	Ccr11	-	-	-	-	-	-	2.0	Up
NM_008176	Chemokine (C-X-C motif) ligand 1	Cxcl1	-	-	-	-	-	-	1.9	Up
NM_153576	Chemokine (C-X-C motif) ligand 17	Cxcl17	-	-	-	-	-	-	1.7	Up
NM_009910	Chemokine (C-X-C motif) receptor 3	Cxcr3	-	-	-	-	-	-	1.8	Up
XM_484016	Chibby homolog 3 (Drosophila)	Cby3	-	-	-	-	-	-	3.5	Up
NM_023186	Chitinase, acidic	Chia	-	-	-	-	-	-	1.7	Up
NM_017474	Chloride channel calcium activated 3	Clca3	-	-	-	-	-	-	3.0	Up
NM_023671	Chloride channel, nucleotide-sensitive, 1A	Clns1a	-	-	-	-	1.9	Up	-	-
NM_144807	Choline phosphotransferase 1	Chpt1	-	-	-	-	-	-	2.2	Down
NM_133869	Choline/ethanolaminephosphotransferase 1	Cept1	-	-	-	-	-	-	2.2	Down
NM_203491	Cholinergic receptor, muscarinic 2, cardiac	Chrm2	-	-	1.5	Down	-	-	-	-
NM_033269	Cholinergic receptor, muscarinic 3, cardiac	Chrm3	-	-	-	-	-	-	2.4	Up
NM_145129	Cholinergic receptor, nicotinic, alpha polypeptide 3	Chrna3	-	-	-	-	-	-	2.0	Up
NM_172753	Chondroitin sulfate N-acetylgalactosaminyltransferase 1	Csgalnac t1	-	-	-	-	-	-	1.9	Up
NM_139134	Chondrolectin	Chodl	-	-	-	-	-	-	2.6	Up
NM_031258	Chordin-like 1	Chrdl1	-	-	-	-	-	-	3.3	Up
NM_029814	Chromatin modifying protein 5	Chmp5	-	-	-	-	-	-	2.4	Down
NM_007623	Chromobox homolog 2 (Drosophila Pc class)	Cbx2	-	-	-	-	-	-	1.8	Up
XM_196334	chromodomain helicase DNA binding protein 5	-	-	-	-	-	-	-	3.1	Up
NM_026444	Citrate synthase	Cs	-	-	-	-	1.6	Up	-	-
NM_027945	Citrate synthase like	Csl	-	-	-	-	-	-	2.7	Up
NM_026036	CKLF-like MARVEL transmembrane domain containing 6	Cmtm6	-	-	-	-	1.6	Up	-	-
NM_133978	CKLF-like MARVEL transmembrane domain containing 7	Cmtm7	-	-	1.8	Up	-	-	3.2	Up
NM_027294	CKLF-like MARVEL transmembrane domain containing 8	Cmtm8	-	-	-	-	-	-	4.1	Up
NM_173861	CKT2 protein	Ckt2	-	-	-	-	-	-	1.8	Up
NM_178669	Clarín 3	Clrn3	-	-	1.7	Up	-	-	2.1	Up
XM_109767	clathrin interactor 1	-	-	-	-	-	-	-	2.1	Up
NM_016760	Clathrin, light polypeptide (Lca)	Clta	-	-	-	-	2.9	Up	-	-
NM_181490	Claudin 17	Cldn17	-	-	-	-	-	-	1.6	Up
NM_027998	Claudin 23	Cldn23	-	-	-	-	-	-	2.5	Up
NM_029078	Cleavage and polyadenylation factor subunit homolog (S. cerevisiae)	Pcf11	-	-	-	-	-	-	1.6	Down
NM_133840	CLP1, cleavage and polyadenylation factor I subunit, homolog (S. cerevisiae)	Clp1	-	-	-	-	-	-	2.2	Down
NM_146047	CLPTM1-like	Clptm11	-	-	-	-	-	-	1.5	Down
NM_028071	Coactosin-like 1 (Dictyostelium)	Cotl1	-	-	-	-	2.3	Up	-	-
NM_010169	Coagulation factor II (thrombin) receptor	F2r	-	-	-	-	-	-	2.7	Down
NM_010171	Coagulation factor III	F3	-	-	-	-	-	-	1.6	Up

XM_135893	coagulation factor IX	-	-	-	-	-	-	1.9	Up
NM_010172	Coagulation factor VII	F7	-	-	-	-	-	1.8	Up
NM_028066	Coagulation factor XI	F11	-	-	-	-	-	1.5	Up
NM_201244	Coatomer protein complex, subunit gamma	Copg	-	-	-	-	-	3.6	Up
NM_177025	Cobl-like 1	Cobl1	-	-	-	-	-	3.5	Up
NM_178686	Coiled-coil domain containing 100	Ccdc100	2.0	Down	-	-	-	-	-
XM_129746	coiled-coil domain containing 150	-	-	-	-	-	-	1.9	Up
NM_024462	Coiled-coil domain containing 23	Ccdc23	-	-	-	-	2.7	Up	-
NM_029212	Coiled-coil domain containing 33	Ccdc33	-	-	-	-	2.0	Up	3.1
XM_486258	Coiled-coil domain containing 36	Ccdc36	-	-	-	-	-	-	1.6
NM_175488	Coiled-coil domain containing 38	Ccdc38	-	-	-	-	-	-	3.4
NM_175430	Coiled-coil domain containing 40	Ccdc40	-	-	-	-	-	-	1.8
NM_025918	Coiled-coil domain containing 43	Ccdc43	-	-	-	-	-	-	1.9
NM_025602	Coiled-coil domain containing 59	Ccdc59	-	-	-	-	-	-	1.8
XM_132334	coiled-coil domain containing 62	-	-	-	-	-	-	-	2.6
XM_132372	coiled-coil domain containing 64	-	-	-	-	-	-	-	2.9
NM_153784	Coiled-coil domain containing 64B	Ccdc64b	-	-	-	-	-	-	1.7
NM_181816	Coiled-coil domain containing 67	Ccdc67	-	-	-	-	-	-	2.4
NM_180958	Coiled-coil domain containing 79	Ccdc79	-	-	-	-	1.9	Up	-
NM_181577	Coiled-coil domain containing 85A	Ccdc85a	-	-	-	-	-	-	2.6
NM_028381	Coiled-coil domain containing 94	Ccdc94	-	-	-	-	1.5	Up	2.7
NM_172405	Coiled-coil domain containing 98	Ccdc98	-	-	-	-	-	-	1.6
NM_145473	Cold shock domain containing C2, RNA binding	Csdc2	-	-	-	-	-	-	2.9
NM_015734	Collagen, type V, alpha 1	Col5a1	1.5	Up	-	-	-	-	-
XM_484897	collagen, type VI, alpha 3	-	-	-	-	-	-	-	2.3
NM_007730	Collagen, type XII, alpha 1	Col12a1	-	-	-	-	2.2	Up	3.4
NM_007733	Collagen, type XIX, alpha 1	Col19a1	-	-	-	-	-	-	3.4
XM_283054	collectin sub-family member 11	-	-	-	-	-	-	-	1.7
NM_009970	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)	-	-	-	-	-	-	-	2.7
NM_007780	Colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)	Csf2rb	-	-	-	-	-	-	2.1
NM_175095	COMM domain containing 2	Commd2	-	-	-	-	1.5	Up	-
NM_147778	COMM domain containing 3	Commd3	-	-	-	-	-	-	2.0
NM_133850	COMM domain containing 7	Commd7	-	-	-	-	3.1	Up	-
NM_013499	Complement component (3b/4b) receptor 1-like	Cr1l	-	-	-	-	-	-	2.3
NM_007573	Complement component 1, q subcomponent binding protein	C1qbp	-	-	-	-	-	-	2.0
NM_009777	Complement component 1, q subcomponent, beta polypeptide	C1qb	-	-	1.7	Up	2.0	Up	-
NM_007574	Complement component 1, q subcomponent, C chain	C1qc	-	-	2.2	Up	2.8	Up	-
NM_009779	Complement component 3a receptor 1	C3ar1	-	-	-	-	1.6	Down	-
XM_130127	complement component 8, gamma subunit	-	-	-	-	-	-	-	2.7
NM_009888	Complement component factor h	Cfh	-	-	-	-	1.6	Up	1.7

NM_145493	Complexin 4	Cplx4	-	-	-	-	-	-	2.3	Up
NM_139229	Component of oligomeric golgi complex 8	Cog8	-	-	-	-	1.9	Up	-	-
NM_007770	Cone-rod homeobox containing gene	Crx	-	-	-	-	-	-	3.4	Up
NM_0010043	Contactin associated protein-like 2	Cntnap2	-	-	-	-	-	-	1.8	Up
57	contactin associated protein-like 3	-	-	-	-	-	-	-	2.8	Up
XM_138666	COP9 (constitutive photomorphogenic) homolog, subunit 2	-	-	-	-	-	-	-	-	-
NM_009939	(Arabidopsis thaliana)	Cops2	-	-	-	-	-	-	1.7	Down
NM_012003	COP9 (constitutive photomorphogenic) homolog, subunit 7a	Cops7a	-	-	-	-	1.7	Up	-	-
NM_153166	(Arabidopsis thaliana)	Copine5	-	-	-	-	-	-	1.6	Up
NM_172496	Copine V	Cpne5	-	-	-	-	-	-	3.7	Up
NM_009920	Cordon-bleu	Cobl	-	-	-	-	-	-	3.7	Up
NM_028408	Cornichon homolog 2 (Drosophila)	Cnih2	-	-	-	-	-	-	2.1	Up
NM_009898	Cornichon homolog 3 (Drosophila)	Cnih3	-	-	1.5	Down	-	-	-	-
NM_178893	Coronin, actin binding protein 1A	Coro1a	-	-	-	-	2.1	Up	-	-
NM_198408	Coronin, actin binding protein 2A	Coro2a	-	-	-	-	-	-	1.6	Up
NM_144874	Corticotropin releasing hormone binding protein	Crhbp	-	-	-	-	-	-	3.7	Up
NM_007685	COX15 homolog, cytochrome c oxidase assembly protein (yeast)	Cox15	-	-	-	-	1.6	Up	-	-
NM_133239	Cripto, FRL-1, cryptic family 1	Cfc1	-	-	-	-	-	-	2.0	Up
NM_007776	Crumbs homolog 1 (Drosophila)	Crb1	-	-	1.6	Down	-	-	-	-
NM_027010	Crystallin, gamma D	Crygd	-	-	-	-	-	-	2.8	Up
NM_153076	Crystallin, gamma F	Crygf	-	-	1.9	Down	-	-	-	-
NM_146034	Crystallin, gamma N	Crygn	-	-	-	-	-	-	3.0	Up
NM_010160	CTAGE family, member 5	Ctage5	-	-	-	-	-	-	2.5	Down
XM_145875	CUG triplet repeat, RNA binding protein 2	Cugbp2	-	-	-	-	-	-	1.9	Down
NM_009828	cyclic nucleotide gated channel alpha 4	-	-	-	-	-	-	-	1.7	Up
NM_172301	Cyclin A1	Ccna1	-	-	-	-	-	-	2.0	Up
NM_007631	Cyclin A2	Ccna2	2.1	Up	-	-	-	-	1.7	Down
NM_007633	Cyclin B1	Ccnb1	1.8	Up	-	-	-	-	-	-
NM_007634	Cyclin C	Ccnc	-	-	-	-	1.6	Up	-	-
XM_354606	Cyclin D1	Ccnd1	-	-	-	-	1.9	Up	-	-
NM_009832	Cyclin E1	Ccne1	-	-	-	-	1.9	Up	-	-
NM_027165	Cyclin F	Ccnf	-	-	-	-	-	-	2.3	Up
XM_285518	cyclin J-like	-	-	-	-	-	-	-	1.5	Up
NM_173369	Cyclin K	Ccnk	-	-	-	-	-	-	2.6	Up
XM_283777	cyclin-dependent kinase 3	-	-	-	-	-	-	-	2.4	Up
NM_028623	cyclin-dependent kinase-like 4	-	-	-	-	-	-	-	1.7	Up
NM_007792	cylicin, basic protein of sperm head cytoskeleton 1	-	-	-	-	-	2.0	Down	2.0	Up
	Cylindromatosis (turban tumor syndrome)	Cyld	-	-	-	-	-	-	1.7	Down
	cystatin 11	-	-	-	-	-	-	-	3.1	Up
	Cystatin E/M	Cst6	-	-	-	-	-	-	1.5	Up
	Cysteine and glycine-rich protein 2	Csrp2	-	-	-	-	-	-	1.6	Down

NM_181417	Cysteine and glycine-rich protein 2 binding protein	Csrp2bp	-	-	-	-	-	-	3.1	Up
NM_173763	Cysteine conjugate-beta lyase 2	Ccb12	-	-	-	-	-	-	1.6	Down
NM_028850	Cysteine-rich hydrophobic domain 2	Chic2	-	-	-	-	-	-	3.4	Down
NM_009638	Cysteine-rich secretory protein 1	Crisp1	-	-	-	-	1.6	Up	2.2	Up
NM_009639	Cysteine-rich secretory protein 3	Crisp3	-	-	-	-	2.4	Up	-	-
NM_153407	Cysteine-serine-rich nuclear protein 2	Csrnp2	-	-	-	-	-	-	2.4	Up
XM_134026	cysteinyl-tRNA synthetase 2 (mitochondrial)(putative)	-	-	-	-	-	-	-	2.7	Up
NM_031251	Cystinosis, nephropathic	Ctns	-	-	-	-	-	-	2.9	Up
NM_007806	Cytochrome b-245, alpha polypeptide	Cyba	-	-	-	-	-	-	2.1	Down
NM_024195	Cytochrome b5 reductase 4	Cyb5r4	-	-	-	-	-	-	2.8	Down
NM_009941	Cytochrome c oxidase subunit IV isoform 1	Cox4i1	-	-	-	-	1.6	Up	-	-
NM_183406	Cytochrome c oxidase subunit VIb polypeptide 2	Cox6b2	-	-	-	-	-	-	1.5	Up
NM_183405	Cytochrome c oxidase subunit VIb polypeptide 2	Cox6b2	-	-	-	-	-	-	2.6	Up
NM_007747	Cytochrome c oxidase, subunit Va	Cox5a	-	-	-	-	2.0	Up	-	-
NM_007751	Cytochrome c oxidase, subunit VIIIb	Cox8b	-	-	-	-	-	-	1.6	Up
NM_025567	Cytochrome c-1	Cyc1	-	-	-	-	1.6	Up	-	-
NM_009997	Cytochrome P450, family 2, subfamily a, polypeptide 4	Cyp2a4	-	-	-	-	-	-	1.7	Up
XM_145466	cytochrome P450, family 2, subfamily b, polypeptide 23	-	-	-	-	-	-	-	1.5	Up
NM_134144	Cytochrome P450, family 2, subfamily c, polypeptide 50	Cyp2c50	-	-	-	-	-	-	2.6	Up
XM_484805	cytochrome P450, family 2, subfamily c, polypeptide 68	-	-	-	-	-	-	-	2.0	Up
NM_010006	Cytochrome P450, family 2, subfamily d, polypeptide 12	Cyp2d9	-	-	-	-	-	-	2.3	Up
NM_133695	cytochrome P450, family 2, subfamily d, polypeptide 13	-	2.1	Up	-	-	-	-	-	-
NM_010005	Cytochrome P450, family 2, subfamily d, polypeptide 22	Cyp2d22	-	-	-	-	-	-	2.5	Up
NM_029562	Cytochrome P450, family 2, subfamily d, polypeptide 26	Cyp2d26	-	-	-	-	-	-	1.8	Up
NM_145548	Cytochrome P450, family 2, subfamily j, polypeptide 13	Cyp2j13	-	-	-	-	1.9	Up	3.9	Up
XM_131188	cytochrome P450, family 2, subfamily u, polypeptide 1	-	-	-	-	-	-	-	2.3	Up
NM_007819	Cytochrome P450, family 3, subfamily a, polypeptide 13	Cyp3a13	-	-	-	-	-	-	3.2	Up
NM_010010	Cytochrome P450, family 46, subfamily a, polypeptide 1	Cyp46a1	-	-	-	-	-	-	2.7	Up
NM_007824	Cytochrome P450, family 7, subfamily a, polypeptide 1	Cyp7a1	-	-	-	-	-	-	1.7	Up
NM_010012	Cytochrome P450, family 8, subfamily b, polypeptide 1	Cyp8b1	-	-	-	-	-	-	2.4	Up
NM_018827	Cytokine receptor-like factor 1	Crif1	-	-	-	-	-	-	1.5	Up
NM_016715	Cytokine receptor-like factor 2	Crif2	-	-	-	-	-	-	2.1	Down
NM_133769	Cytoplasmic FMR1 interacting protein 2	Cyfp2	-	-	-	-	-	-	2.5	Down
NM_175342	Cytoplasmic polyadenylated homeobox	Cphx	-	-	-	-	-	-	3.1	Up
NM_198300	Cytoplasmic polyadenylation element binding protein 3	Cpeb3	-	-	-	-	-	-	2.1	Up
NM_011585	Cytotoxic granule-associated RNA binding protein 1	Tia1	-	-	-	-	-	-	2.4	Down
NM_025314	D-tyrosyl-tRNA deacylase 1 homolog (S. cerevisiae)	Dtd1	-	-	-	-	1.5	Up	-	-
NM_011262	D4, zinc and double PHD fingers family 2	Dpf2	-	-	-	-	1.9	Up	-	-
NM_015735	Damage specific DNA binding protein 1	Ddb1	-	-	-	-	2.1	Up	-	-
NM_172826	Dapper homolog 2, antagonist of beta-catenin (xenopus)	Dact2	-	-	-	-	-	-	3.1	Up
NM_173408	DCN1, defective in cullin neddylation 1, domain containing 3 (S.	Dcun1d3	-	-	-	-	-	-	2.1	Up

	cerevisiae)									
NM_176845	DDHD domain containing 1	Ddhd1	-	-	-	-	1.9	Up	2.0	Up
NM_134040	DEAD (Asp-Glu-Ala-Asp) box polypeptide 1	Ddx1	-	-	-	-	-	-	2.1	Down
NM_026409	DEAD (Asp-Glu-Ala-Asp) box polypeptide 55	Ddx55	-	-	-	-	-	-	1.7	Down
NM_018769	Deafness, autosomal dominant 5 homolog (human)	Dfna5h	-	-	-	-	-	-	1.6	Up
NM_026191	DEAH (Asp-Glu-Ala-His) box polypeptide 40	Dhx40	-	-	-	-	-	-	2.3	Down
NM_033606	DEAQ RNA-dependent ATPase	Dqx1	-	-	-	-	-	-	1.9	Up
NM_027030	Decapping enzyme, scavenger	Dcps	-	-	-	-	-	-	1.5	Down
NM_007833	Decorin	Dcn	-	-	-	-	-	-	2.0	Down
NM_033374	Dedicator of cyto-kinesis 2	Dock2	-	-	-	-	-	-	2.2	Down
NM_153413	Dedicator of cyto-kinesis 3	Dock3	-	-	-	-	-	-	3.0	Up
NM_026082	Dedicator of cytokinesis 7	Dock7	-	-	-	-	1.6	Up	-	-
NM_010015	defender against cell death 1	-	-	-	-	-	1.7	Up	-	-
NM_145157	Defensin beta 19	Defb19	-	-	-	-	-	-	2.3	Up
NM_176950	Defensin beta 20	Defb20	-	-	-	-	-	-	2.1	Up
XM_485085	defensin beta 36	-	-	-	-	-	-	-	2.6	Up
NM_207658	Defensin related cryptdin 21	Defcr22	-	-	-	-	-	-	3.9	Up
NM_007845	Defensin related cryptdin, related sequence 10	Defcr-rs10	-	-	-	-	-	-	1.6	Up
NM_007848	Defensin related cryptdin, related sequence 7	Defcr-rs7	-	-	-	-	-	-	1.9	Up
NM_027790	Dehydrogenase/reductase member 2	Dhrs2	-	-	-	-	-	-	2.7	Up
NM_007860	Deiodinase, iodothyronine, type I	Dio1	-	-	-	-	-	-	3.1	Up
NM_010050	Deiodinase, iodothyronine, type II	Dio2	-	-	-	-	-	-	1.5	Up
NM_010021	Deleted in azoospermia-like	Dazl	-	-	-	-	-	-	1.8	Up
NM_173419	Deleted in lymphocytic leukemia, 7	Dleu7	-	-	-	-	-	-	3.2	Up
NM_030714	Deltex 3 homolog (Drosophila)	Dtx3	-	-	-	-	-	-	1.6	Up
NM_177857	DENN/MADD domain containing 2C	Dennd2c	-	-	-	-	-	-	2.1	Up
XM_134902	DENN/MADD domain containing 4A	-	-	-	-	-	-	-	2.7	Down
NM_026603	Density-regulated protein	Denr	-	-	-	-	1.6	Up	1.8	Up
NM_133763	Deoxynucleotidyltransferase, terminal, interacting protein 1	Dnttip1	-	-	-	-	-	-	1.8	Down
NM_010061	Deoxyribonuclease I	Dnase1	-	-	-	-	-	-	1.8	Up
NM_007857	Desert hedgehog	Dhh	-	-	1.7	Down	-	-	-	-
NM_010043	Desmin	Des	-	-	-	-	-	-	1.5	Up
NM_013505	Desmocollin 2	Dsc2	-	-	-	-	1.6	Up	-	-
XM_484705	desmoglein 1 alpha	-	-	-	-	-	-	-	2.1	Up
NM_181680	Desmoglein 1 gamma	Dsg1c	-	-	-	-	-	-	2.0	Up
NM_030596	Desmoglein 3	Dsg3	-	-	-	-	-	-	1.6	Up
NM_181564	Desmoglein 4	Dsg4	-	-	-	-	-	-	2.0	Up
NM_019771	Destrin	Dstn	-	-	-	-	-	-	2.4	Down
NM_007887	Deubiquitinating enzyme 1	Dub1	-	-	-	-	-	-	2.5	Up
NM_201409	Deubiquitinating enzyme 1a	Dub1a	-	-	-	-	-	-	2.5	Up

NM_0010015													
59	Deubiquitinating enzyme 2a	Dub2a	-	-	-	-	-	-	-	-	-	1.7	Up
NM_207533	Developing brain homeobox 2	Dbx2	-	-	-	-	-	2.3	Up	-	-	3.8	Up
NM_0010043													
64	Development and differentiation enhancing factor 2	Ddef2	-	-	-	-	-	-	-	-	-	2.8	Up
NM_028610	Developmental pluripotency associated 4	Dppa4	-	-	-	-	-	-	-	-	-	1.8	Up
NM_177914	Diacylglycerol kinase kappa	Dgkk	-	-	-	-	-	-	-	-	-	1.6	Up
NM_019505	Diacylglycerol kinase, epsilon	Dgke	-	-	-	-	-	-	-	-	-	2.2	Up
NM_177746	Diacylglycerol O-acyltransferase 2-like 4	Dgat2l4	-	-	-	-	-	-	-	-	-	2.3	Up
NM_026428	Dicarbonyl L-xylulose reductase	Dcxr	-	-	-	-	-	-	-	-	-	1.6	Down
NM_145592	Dickkopf homolog 4 ( <i>Xenopus laevis</i> )	Dkk4	-	-	-	-	-	-	-	-	-	1.6	Up
XM_193873	diffuse panbronchiolitis critical region 1 (human)	-	-	-	-	-	-	-	-	-	-	3.3	Up
NM_022722	Dihydropyrimidinase	Dpys	-	-	-	-	-	-	-	-	-	1.7	Up
XM_134309	dihydrouridine synthase 2-like (SMM1, <i>S. cerevisiae</i> )	-	-	-	-	-	-	-	-	-	-	1.8	Up
NM_026993	Dimethylarginine dimethylaminohydrolase 1	Ddah1	-	-	-	-	-	1.8	Up	-	-	-	-
XM_484214	DIP2 disco-interacting protein 2 homolog C ( <i>Drosophila</i> )	-	-	-	-	-	-	-	-	-	-	1.7	Up
NM_007876	Dipeptidase 1 (renal)	Dpep1	-	-	-	-	-	-	-	-	-	1.9	Up
NM_031843	Dipeptidylpeptidase 7	Dpp7	-	-	-	-	-	1.8	Up	-	-	-	-
NM_177259	Disabled homolog 1 ( <i>Drosophila</i> )	Dab1	-	-	-	-	-	-	-	-	-	3.2	Up
NM_007584	Discoidin domain receptor family, member 1	Ddr1	-	-	-	-	-	-	-	-	-	2.3	Up
NM_007864	Discs, large homolog 4 ( <i>Drosophila</i> )	Dlg4	-	-	-	-	-	-	-	-	-	2.5	Up
NM_172464	Dishevelled associated activator of morphogenesis 1	Daam1	-	-	-	-	-	-	-	-	-	2.8	Up
NM_170596	disrupted in schizophrenia 1	-	-	-	-	-	-	-	-	-	-	1.6	Up
NM_007867	Distal-less homeobox 4	Dlx4	-	-	-	-	-	-	-	-	-	3.5	Up
NM_198854	Distal-less homeobox 5	Dlx5	-	-	-	-	-	-	-	-	-	2.2	Up
NM_178118	DIX domain containing 1	Dixdc1	-	-	-	-	-	-	-	-	-	3.4	Up
XM_358382	Dmx-like 2	-	-	-	-	-	-	-	-	-	-	2.4	Up
NM_007859	DNA fragmentation factor, beta subunit	Dffb	-	-	-	-	-	-	-	-	-	2.0	Up
NM_181857	DNA polymerase N	Poln	-	-	-	-	-	1.6	Up	-	-	2.4	Up
NM_028027	DNA segment, Chr 10, ERATO Doi 610, expressed	D10Erttd6 10e	1.6	Down	-	-	-	-	-	-	-	-	-
NM_145422	DNA segment, Chr 10, Wayne State University 52, expressed	D10Wsu 52e	-	-	-	-	-	-	-	-	-	1.8	Down
NM_198420	DNA segment, Chr 15, Wayne State University 169, expressed	D15Wsu 169e	-	-	-	-	-	-	-	-	-	1.6	Up
NM_029648	DNA segment, Chr 19, ERATO Doi 737, expressed	D19Erttd7 37e	-	-	-	-	-	-	-	-	-	1.9	Up
NM_145528	DNA segment, Chr 2, ERATO Doi 391, expressed	D2Erttd39 1e	-	-	-	-	-	1.6	Up	-	-	-	-
XM_143175	DNA segment, Chr 3, ERATO Doi 254, expressed	-	-	-	-	-	-	-	-	-	-	2.9	Up
NM_025667	DNA segment, Chr 4, ERATO Doi 196, expressed	D4Erttd19 6e	-	-	-	-	-	-	-	-	-	2.0	Down
XM_485595	DNA segment, Chr 5, ERATO Doi 579, expressed	-	-	-	-	-	-	-	-	-	-	1.7	Up

NM_007837	DNA-damage inducible transcript 3	Ddit3	-	-	-	-	-	-	2.2	Down
NM_008299	DnaJ (Hsp40) homolog, subfamily B, member 3	Dnajb3	-	-	-	-	-	-	3.6	Up
NM_025926	DnaJ (Hsp40) homolog, subfamily B, member 4	Dnajb4	-	-	1.5	Down	-	-	2.7	Down
NM_019874	DnaJ (Hsp40) homolog, subfamily B, member 5	Dnajb5	-	-	-	-	1.6	Up	1.8	Up
NM_021317	DnaJ (Hsp40) homolog, subfamily B, member 7	Dnajb7	-	-	-	-	-	-	3.1	Up
NM_024181	DnaJ (Hsp40) homolog, subfamily C, member 10	Dnajc10	-	-	-	-	-	-	1.7	Down
NM_016775	DnaJ (Hsp40) homolog, subfamily C, member 5	Dnajc5	-	-	-	-	2.0	Up	-	-
NM_019795	DnaJ (Hsp40) homolog, subfamily C, member 7	Dnajc7	-	-	-	-	-	-	2.2	Down
NM_007875	Dolichyl-phosphate (UDP-N-acetylglucosamine) acetylglucosaminophosphotransferase 1 (GlcNAc-1-P transferase)	Dpagt1	-	-	-	-	-	-	1.8	Down
NM_013503	Dopamine receptor 5	Drd5	-	-	-	-	-	-	3.1	Up
NM_183389	Double homeobox B-like	Duxbl	-	-	-	-	-	-	2.3	Up
NM_026106	Down-regulator of transcription 1	Dr1	-	-	-	-	-	-	3.0	Down
NM_027136	DPH1 homolog (S. cerevisiae)	Dph1	-	-	-	-	-	-	1.7	Up
NM_026992	DPH4 homolog (JJJ3, S. cerevisiae)	Dph4	-	-	-	-	2.0	Up	-	-
NM_019813	Drebrin 1	Dbn1	-	-	-	-	-	-	1.7	Up
NM_011932	Dual adaptor for phosphotyrosine and 3-phosphoinositides 1	Dapp1	-	-	-	-	-	-	1.5	Down
NM_028099	Dual specificity phosphatase 11 (RNA/RNP complex 1-interacting)	Dusp11	-	-	-	-	-	-	2.7	Down
NM_029352	Dual specificity phosphatase 9	Dusp9	-	-	-	-	-	-	2.3	Up
NM_027151	Dynactin 2	Dctn2	-	-	-	-	2.4	Up	-	-
XM_355934	Dynein, axonemal, heavy chain 3	Dnahc3	-	-	-	-	-	-	2.2	Up
XM_287612	dynein, axonemal, heavy chain 6	-	-	-	2.2	Down	-	-	1.7	Up
NM_013811	Dynein, axonemal, heavy chain 8	Dnahc8	-	-	-	-	-	-	3.6	Up
NM_010081	dystonin	-	-	-	-	-	-	-	2.5	Up
XM_149937	E2F transcription factor 8	-	-	-	-	-	2.2	Up	4.1	Up
NM_007920	E74-like factor 1	Elf1	-	-	-	-	3.1	Up	2.7	Up
NM_010095	Early B-cell factor 2	Ebf2	-	-	-	-	-	-	1.9	Up
NM_007913	Early growth response 1	Egr1	-	-	-	-	-	-	1.9	Down
NM_020596	Early growth response 4	Egr4	-	-	-	-	-	-	2.2	Up
NM_007900	Ect2 oncogene	Ect2	2.0	Up	-	-	-	-	-	-
NM_175540	Ectodysplasin A2 isoform receptor	Eda2r	-	-	-	-	-	-	2.3	Up
NM_015744	Ectonucleotide pyrophosphatase/phosphodiesterase 2	Enpp2	-	-	-	-	-	-	2.3	Down
NM_199016	Ectonucleotide pyrophosphatase/phosphodiesterase 4	Enpp4	-	-	-	-	-	-	2.4	Down
NM_028643	EF hand domain family A1	Efha1	-	-	-	-	-	-	1.6	Down
XM_129694	EF-hand domain (C-terminal) containing 1	Efhc1	-	-	1.8	Down	-	-	-	-
NM_053208	EGL nine homolog 2 (C. elegans)	Egln2	-	-	-	-	-	-	1.5	Down
NM_053255	ElaC homolog 1 (E. coli)	Elac1	-	-	-	-	2.1	Up	2.2	Up
NM_182840	Elastin microfibril interfacer 3	Emilin3	-	-	-	-	-	-	3.7	Up
NM_010485	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)	Elavl1	-	-	-	-	1.8	Up	-	-
NM_010488	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 4 (Hu antigen D)	Elavl4	-	-	-	-	-	-	1.5	Up



NM_025794	Electron transferring flavoprotein, dehydrogenase	Etfdh	-	-	-	-	-	-	1.9	Up
NM_013508	ELK3, member of ETS oncogene family	Elk3	-	-	-	-	-	-	2.2	Up
NM_028932	ELL associated factor 1	Eaf1	-	-	-	-	-	-	2.0	Up
NM_011431	Elongation factor Tu GTP binding domain containing 2	Eftud2	-	-	-	-	1.8	Up	-	-
NM_134255	ELOVL family member 5, elongation of long chain fatty acids (yeast)	Elovl5	-	-	-	-	-	-	3.3	Down
NM_010330	Embigin	Emb	-	-	-	-	-	-	1.8	Down
NM_010132	Empty spiracles homolog 2 (Drosophila)	Emx2	-	-	-	-	-	-	1.8	Up
NM_010135	Enabled homolog (Drosophila)	Enah	-	-	-	-	-	-	1.7	Up
NM_017468	Enamelin	Enam	-	-	-	-	-	-	1.8	Up
NM_028013	Endonuclease domain containing 1	Endod1	-	-	-	-	-	-	3.7	Up
NM_030711	Endoplasmic reticulum aminopeptidase 1	Erap1	-	-	-	-	-	-	2.0	Down
NM_019561	Endosulfine alpha	Ensa	-	-	1.8	Down	-	-	-	-
NM_007903	Endothelin 3	Edn3	-	-	-	-	-	-	2.1	Up
NM_007904	Endothelin receptor type B	Ednrb	-	-	-	-	-	-	1.6	Up
NM_007970	Enhancer of zeste homolog 1 (Drosophila)	Ezh1	-	-	-	-	2.1	Up	-	-
NM_016772	Enoyl coenzyme A hydratase 1, peroxisomal	Ech1	-	-	-	-	-	-	1.5	Down
NM_053113	Eosinophil-associated, ribonuclease A family, member 11	Ear11	-	-	-	-	-	-	1.8	Up
NM_017389	Eosinophil-associated, ribonuclease A family, member 14	Ear4	-	-	-	-	1.8	Up	-	-
NM_053111	Eosinophil-associated, ribonuclease A family, member 6	Ear6	-	-	-	-	-	-	1.6	Up
NM_198425	EP300 interacting inhibitor of differentiation 2	Eid2	-	-	1.7	Up	-	-	-	-
NM_134065	Ependymin related protein 1 (zebrafish)	Epdr1	-	-	-	-	-	-	2.5	Up
NM_010143	Eph receptor B3	Ephb3	-	-	-	-	-	-	2.6	Up
NM_010111	Ephrin B2	Efnb2	-	-	-	-	-	-	2.3	Up
NM_007912	Epidermal growth factor receptor	Egfr	-	-	-	-	-	-	2.0	Up
NM_183031	Epstein-Barr virus induced gene 2	Ebi2	-	-	-	-	2.6	Up	-	-
NM_138677	ER degradation enhancer, mannosidase alpha-like 1	Edem1	-	-	-	-	-	-	2.2	Down
XM_193956	ER degradation enhancer, mannosidase alpha-like 3	-	-	-	-	-	-	-	2.1	Up
NM_013848	Erythroblast membrane-associated protein	Ermap	-	-	2.4	Down	-	-	-	-
NM_183428	Erythrocyte protein band 4.1	Epb4.1	-	-	-	-	2.2	Up	2.5	Up
NM_133867	ESP8-like 3	Eps8l3	-	-	-	-	-	-	2.0	Up
NM_207687	Espin	Espn	-	-	-	-	-	-	1.5	Up
XM_149072	espin-like	-	-	-	-	-	-	-	2.5	Up
NM_007954	Esterase 1	Es1	-	-	-	-	-	-	1.6	Up
NM_007956	Estrogen receptor 1 (alpha)	Esr1	-	-	-	-	-	-	2.3	Up
NM_172545	Euchromatic histone methyltransferase 1	Ehmt1	-	-	-	-	-	-	1.6	Down
NM_018796	Eukaryotic translation elongation factor 1 beta 2	Eef1b2	-	-	-	-	-	-	3.1	Down
NM_012010	Eukaryotic translation initiation factor 2, subunit 3, structural gene X-linked	Eif2s3x	-	-	-	-	-	-	2.6	Up
NM_012011	Eukaryotic translation initiation factor 2, subunit 3, structural gene Y-linked	Eif2s3y	-	-	1.6	Down	-	-	-	-
NM_153178	Eukaryotic translation initiation factor 2C, 2	Eif2c2	-	-	-	-	-	-	1.9	Up
NM_133916	Eukaryotic translation initiation factor 3, subunit B	Eif3b	-	-	-	-	-	-	1.5	Down

NM_146200	Eukaryotic translation initiation factor 3, subunit C	Eif3c	-	-	-	-	-	-	2.6	Down
NM_008388	Eukaryotic translation initiation factor 3, subunit E	Eif3e	-	-	-	-	-	-	3.5	Down
NM_145139	Eukaryotic translation initiation factor 3, subunit E interacting protein	Eif3eip	-	-	-	-	-	-	2.1	Down
NM_025344	Eukaryotic translation initiation factor 3, subunit F	Eif3f	-	-	-	-	-	-	2.4	Down
NM_013507	Eukaryotic translation initiation factor 4, gamma 2	Eif4g2	-	-	-	-	-	-	1.9	Down
NM_181582	Eukaryotic translation initiation factor 5A	Eif5a	-	-	-	-	1.7	Up	1.7	Down
NM_177586	Eukaryotic translation initiation factor 5A2	Eif5a2	-	-	1.7	Down	-	-	-	-
NM_144866	Eukaryotic translation termination factor 1	Etf1	-	-	-	-	-	-	2.9	Down
NM_133658	Excision repair cross-complementing rodent repair deficiency, complementation group 3	Ercc3	-	-	-	-	-	-	1.5	Down
XM_132150	exocyst complex component 1	-	-	-	-	-	-	-	1.7	Down
NM_172857	Exonuclease 3-5 domain-like 1	Exdl1	-	-	-	-	-	-	2.1	Up
NM_027698	Exonuclease domain containing 1	Exod1	-	-	-	-	2.4	Up	3.1	Up
NM_144886	Exosome component 2	Exosc2	-	-	-	-	1.9	Up	-	-
NM_010163	Exostoses (multiple) 2	Ext2	-	-	-	-	-	-	2.2	Down
XM_141626	expressed sequence AA414768	-	-	-	-	-	-	-	3.2	Up
XM_127129	expressed sequence AI132487	-	-	-	-	-	1.5	Down	-	-
XM_284742	expressed sequence AV320801	-	-	-	-	-	-	-	3.0	Up
NM_134096	Expressed sequence AW049604	AW049604	-	-	-	-	-	-	2.7	Up
NM_153540	Expressed sequence C85492	C85492	-	-	-	-	-	-	2.4	Up
NM_133790	expressed sequence R74862	-	-	-	-	-	1.6	Up	-	-
NM_009510	Ezrin	Ezr	-	-	1.5	Up	-	-	-	-
NM_177076	F-box and leucine-rich repeat protein 13	Fbxl13	-	-	-	-	-	-	2.1	Up
XM_128716	F-box and leucine-rich repeat protein 17	-	-	-	-	-	-	-	2.0	Down
NM_178674	F-box and leucine-rich repeat protein 21	Fbxl21	-	-	-	-	1.7	Up	3.7	Up
NM_172988	F-box and leucine-rich repeat protein 4	Fbxl4	-	-	-	-	2.1	Up	-	-
NM_015821	F-box and leucine-rich repeat protein 8	Fbxl8	-	-	-	-	1.9	Up	2.5	Up
XM_126264	F-box and WD-40 domain protein 10	-	-	-	-	-	-	-	1.8	Up
NM_015793	F-box and WD-40 domain protein 14	Fbxw14	-	-	-	-	-	-	1.9	Up
XM_110248	F-box protein 11	-	-	-	-	-	-	-	2.5	Down
NM_176848	F-box protein 2	Fbxo2	-	-	-	-	-	-	1.5	Up
NM_175530	F-box protein 46	Fbxo46	-	-	-	-	-	-	2.0	Up
NM_015797	F-box protein 6	Fbxo6	-	-	-	-	1.6	Up	-	-
NM_015791	F-box protein 8	Fbxo8	-	-	-	-	2.7	Up	-	-
NM_145946	Fanconi anemia, complementation group I	Fanci	-	-	-	-	-	-	2.0	Up
NM_177244	FAST kinase domains 1	Fastkd1	-	-	-	-	-	-	2.1	Up
NM_011936	Fat mass and obesity associated	Fto	-	-	-	-	-	-	1.7	Down
XM_194446	FAT tumor suppressor homolog 3 (Drosophila)	-	-	-	-	-	-	-	1.6	Up
XM_356226	FAT tumor suppressor homolog 3 (Drosophila)	-	-	-	-	-	-	-	2.1	Up
NM_007980	Fatty acid binding protein 2, intestinal	Fabp2	-	-	-	-	1.7	Up	2.8	Up
NM_026143	Fatty acyl CoA reductase 1	Far1	-	-	-	-	-	-	2.7	Up

NM_183222	Fc receptor-like 5	Fcrl5	-	-	-	-	2.2	Up	3.4	Up
NM_010189	Fc receptor, IgG, alpha chain transporter FCF1 small subunit (SSU) processome component homolog (S. cerevisiae)	Fcgrt	-	-	-	-	2.4	Up	-	-
NM_028632	FCH and double SH3 domains 1	Fcf1	-	-	-	-	1.8	Up	-	-
NM_175684	fer-1-like 5 (C. elegans)	Fchsd1	-	-	-	-	1.6	Up	3.1	Up
XM_136730	FERM domain containing 3	-	-	-	-	-	-	-	1.7	Up
NM_172869	Ferredoxin reductase	Frmd3	-	-	-	-	-	-	1.8	Up
NM_007997	Fibroblast growth factor 17	Fdxr	-	-	-	-	-	-	2.7	Up
NM_008004	Fibroblast growth factor 18	Fgf17	-	-	-	-	-	-	1.5	Up
NM_008005	Fibroblast growth factor 21	Fgf18	-	-	-	-	-	-	2.3	Up
NM_020013	Fibroblast growth factor 3	Fgf21	-	-	-	-	-	-	2.4	Up
NM_008007	Fibroblast growth factor 7	Fgf3	-	-	-	-	-	-	1.7	Up
NM_008008	Fibroblast growth factor 8	Fgf7	-	-	-	-	-	-	2.2	Up
NM_010205	Fibroblast growth factor receptor 3	Fgf8	-	-	-	-	-	-	2.1	Up
NM_008010	Fibulin 7	Fgfr3	-	-	-	-	-	-	2.3	Up
NM_024237	Ficolin A	Fbln7	-	-	-	-	-	-	1.6	Up
NM_007995	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived)	Fcna	-	-	-	-	-	-	2.9	Down
NM_007990	Fission 1 (mitochondrial outer membrane) homolog (yeast)	Fau	-	-	-	-	-	-	1.9	Down
NM_025562	Fizzy/cell division cycle 20 related 1 (Drosophila)	Fis1	-	-	-	-	-	-	1.5	Down
NM_019757	FK506 binding protein 14	Fzr1	-	-	-	-	-	-	2.0	Up
NM_153573	Flt3 interacting zinc finger protein 1	Fkbp14	-	-	-	-	-	-	3.3	Up
NM_011813	FLYWCH-type zinc finger 1	Fiz1	-	-	-	-	-	-	2.7	Up
NM_153791	Follistatin-like 4	Flywch1	-	-	-	-	-	-	2.3	Up
NM_177059	Follistatin-like 5	Fstl4	-	-	-	-	-	-	2.2	Up
NM_178673	Forkhead box A2	Fstl5	-	-	-	-	-	-	1.8	Up
NM_010446	Forkhead box B1	Foxa2	-	-	-	-	-	-	1.8	Up
NM_022378	Forkhead box C1	Foxb1	-	-	-	-	-	-	2.4	Up
NM_008592	Forkhead box D4	Foxc1	-	-	-	-	-	-	2.1	Up
NM_008022	Forkhead box G1	Foxd4	-	-	-	-	-	-	1.5	Up
NM_008241	Forkhead box H1	Foxg1	-	-	-	-	-	-	1.7	Up
NM_007989	Forkhead box N2	Foxh1	-	-	1.5	Down	-	-	-	-
NM_180974	Forkhead box P3	Foxn2	-	-	-	-	-	-	2.9	Up
NM_054039	forkhead-associated (FHA) phosphopeptide binding domain 1	Foxp3	2.1	Up	-	-	-	-	-	-
NM_028429	Formin-like 3	-	-	-	-	-	-	-	2.1	Up
NM_011711	formyl peptide receptor, related sequence 7	Fmnl3	-	-	-	-	-	-	3.6	Up
NM_177317	Four jointed box 1 (Drosophila)	-	-	-	-	-	-	-	1.7	Up
NM_010218	Fragile X mental retardation gene 1, autosomal homolog	Fjx1	-	-	-	-	-	-	1.8	Up
NM_008053	Fragile X mental retardation, autosomal homolog 2	Fxr1	-	-	-	-	-	-	1.8	Down
NM_011814	Fras1 related extracellular matrix protein 1	Fxr2	-	-	-	-	-	-	2.9	Up
NM_177863	Free fatty acid receptor 2	Frem1	-	-	-	-	-	-	3.3	Up
NM_146187		Ffar2	-	-	-	-	-	-	1.6	Down

NM_022721	Frizzled homolog 5 (Drosophila)	Fzd5	-	-	-	-	-	-	1.6	Up
NM_024243	Fucosidase, alpha-L- 1, tissue	Hmgcl	-	-	-	-	-	-	2.3	Up
NM_139234	FYVE, RhoGEF and PH domain containing 4	Fgd4	-	-	-	-	1.6	Down	1.7	Up
NM_177266	G elongation factor, mitochondrial 2	Gfm2	-	-	-	-	-	-	2.2	Up
NM_173747	G patch domain and KOW motifs	Gpkow	-	-	-	-	1.8	Up	-	-
XM_128679	G protein-coupled receptor 115	-	-	-	1.7	Down	-	-	2.0	Down
NM_181752	G protein-coupled receptor 135	Gpr135	-	-	2.0	Down	-	-	-	-
NM_031999	G protein-coupled receptor 137B	Gpr137b	-	-	-	-	-	-	3.4	Up
XM_146103	G protein-coupled receptor 139	-	-	-	-	-	-	-	2.1	Up
XM_142008	G protein-coupled receptor 15-like	-	-	-	-	-	-	-	1.9	Up
NM_173398	G protein-coupled receptor 171	Gpr171	-	-	-	-	-	-	1.6	Down
NM_182806	G protein-coupled receptor 18	Gpr18	-	-	-	-	1.6	Up	-	-
NM_008158	G protein-coupled receptor 27	Gpr27	-	-	-	-	-	-	1.6	Up
NM_175668	G protein-coupled receptor 4	Gpr4	-	-	-	-	2.1	Up	1.6	Up
NM_018882	G protein-coupled receptor 56	Gpr56	-	-	-	-	-	-	1.6	Up
NM_199058	G protein-coupled receptor 6	Gpr6	-	-	-	-	1.7	Up	-	-
NM_178712	G protein-coupled receptor 64	Gpr64	-	-	-	-	2.4	Up	3.2	Up
NM_175520	G protein-coupled receptor 81	Gpr81	-	-	-	-	-	-	2.5	Up
NM_026229	G protein-coupled receptor 89	Gpr89	-	-	-	-	-	-	1.8	Up
NM_019497	G protein-coupled receptor kinase 4	Grk4	-	-	-	-	-	-	2.4	Up
NM_011938	G protein-coupled receptor kinase 6	Grk6	-	-	-	-	-	-	2.1	Up
NM_181444	G protein-coupled receptor, family C, group 5, member A	Gprc5a	-	-	-	-	-	-	1.9	Up
NM_022420	G protein-coupled receptor, family C, group 5, member B	Gprc5b	-	-	-	-	-	-	1.7	Up
NM_053118	G protein-coupled receptor, family C, group 5, member D	Gprc5d	-	-	-	-	1.7	Up	2.2	Up
NM_153071	G protein-coupled receptor, family C, group 6, member A	Gprc6a	-	-	-	-	-	-	2.2	Up
NM_012014	G protein-regulated inducer of neurite outgrowth 1	Gprin1	-	-	-	-	-	-	2.0	Up
NM_008151	G-protein coupled receptor 12	Gpr12	-	-	-	-	-	-	1.7	Up
NM_027543	G-protein coupled receptor 173	Gpr173	-	-	-	-	-	-	2.0	Up
NM_008154	G-protein coupled receptor 3	Gpr3	-	-	1.7	Down	-	-	-	-
NM_008152	G-protein coupled receptor 65	Gpr65	-	-	-	-	-	-	1.6	Down
NM_016722	Galactosamine (N-acetyl)-6-sulfate sulfatase	Galns	-	-	-	-	-	-	1.8	Up
XM_284152	galactose-3-O-sulfotransferase 4	-	-	-	-	-	-	-	2.2	Up
NM_146017	Gamma-aminobutyric acid (GABA-A) receptor, pi	Gabrp	-	-	-	-	-	-	2.6	Up
NM_010250	Gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 1	Gabra1	-	-	-	-	-	-	2.1	Up
NM_010251	Gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 4	Gabra4	-	-	-	-	-	-	2.0	Up
NM_008074	Gamma-aminobutyric acid (GABA-A) receptor, subunit gamma 3	Gabrg3	-	-	-	-	-	-	2.9	Up
XM_143750	gamma-aminobutyric acid (GABA) B receptor 2	-	-	-	-	-	-	-	2.0	Up
NM_019749	Gamma-aminobutyric acid receptor associated protein	Gabarap	-	-	-	-	2.7	Up	-	-
NM_027819	Gamma-glutamyltransferase 6	Ggt6	-	-	-	-	-	-	1.9	Up
NM_010268	ganglioside-induced differentiation-associated-protein 10	-	-	1.5	Down	-	-	-	-	-
NM_008121	Gap junction membrane channel protein alpha 5	Gja5	-	-	-	-	-	-	1.8	Up

NM_010290	Gap junction protein, delta 2	Gjd2	-	-	-	-	-	-	1.6	Up
NM_008177	Gastrin releasing peptide receptor	Grpr	-	-	-	-	-	-	2.6	Up
NM_015739	Gastrulation brain homeobox 1	Gbx1	-	-	-	-	-	-	3.2	Up
NM_008089	GATA binding protein 1	Gata1	2.2	Up	-	-	-	-	-	-
NM_133708	GDP-mannose pyrophosphorylase A	Gmppa	-	-	-	-	-	-	1.5	Up
NM_177331	Gen homolog 1, endonuclease (Drosophila)	Gen1	-	-	-	-	-	-	1.5	Up
NM_0010041	61 gene model 1082, (NCBI)	-	-	-	-	-	-	-	3.7	Up
XM_356476	gene model 1157, (NCBI)	-	-	-	-	-	-	-	1.8	Up
NM_0010041	63 gene model 1553, (NCBI)	-	-	-	-	-	-	-	3.3	Up
XM_196054	gene model 1564, (NCBI)	-	-	-	-	-	-	-	3.5	Up
XM_122407	gene model 1818, (NCBI)	-	-	-	-	-	-	-	2.2	Up
XM_111398	Gene model 22, (NCBI)	Gm22	-	-	1.6	Down	-	-	-	-
XM_137876	gene model 252, (NCBI)	-	-	-	-	-	-	-	2.8	Up
XM_138272	gene model 266, (NCBI)	-	-	-	-	-	-	-	2.3	Up
XM_138671	gene model 274, (NCBI)	-	-	-	-	-	-	-	2.6	Up
NM_0010054	20 Gene model 347, (NCBI)	Gm347	-	-	-	-	-	-	1.7	Up
XM_142049	gene model 378, (NCBI)	-	-	-	-	-	-	-	2.1	Up
XM_144253	Gene model 444, (NCBI)	Gm444	-	-	-	-	-	-	2.4	Up
XM_144338	gene model 447, (NCBI)	-	-	-	-	-	-	-	2.6	Up
XM_146918	gene model 513, (NCBI)	-	-	-	-	-	-	-	3.4	Up
XM_147763	gene model 529, (NCBI)	-	-	-	-	-	-	-	3.4	Up
XM_148894	Gene model 550, (NCBI)	Gm550	-	-	-	-	-	-	2.0	Up
XM_151151	gene model 597, (NCBI)	-	-	-	-	-	-	-	2.3	Up
XM_159329	gene model 614, (NCBI)	-	-	-	-	-	-	-	1.6	Up
XM_286523	gene model 806, (NCBI)	-	-	-	-	-	-	-	2.7	Up
NM_201356	Gene model 839, (NCBI)	Gm839	-	-	-	-	-	-	2.6	Up
XM_354612	gene model 879, (NCBI)	-	-	-	-	-	-	-	2.1	Up
XM_354702	gene model 900, (NCBI)	-	-	-	-	-	-	-	3.0	Up
XM_129009	gene model 94, (NCBI)	-	-	-	-	-	-	-	1.8	Up
XM_355308	gene model 994, (NCBI)	-	-	-	-	-	-	-	3.5	Up
NM_025652	General transcription factor III A	Gtf3a	-	-	-	-	-	-	1.7	Down
NM_198671	Genetic suppressor element 1	Gse1	-	-	-	-	1.8	Up	-	-
NM_025768	GH regulated TBC protein 1	Grtp1	-	-	1.7	Down	-	-	-	-
NM_021488	Ghrelin	Ghrl	-	-	-	-	1.5	Up	1.7	Up
NM_029420	GIY-YIG domain containing 2	Giyd2	-	-	-	-	-	-	1.9	Up
NM_028608	GLI pathogenesis-related 1 (glioma)	Glipr1	-	-	-	-	-	-	1.7	Down
NM_175459	GLIS family zinc finger 3	Glis3	-	-	-	-	-	-	2.2	Up
NM_020273	Glucocorticoid modulatory element binding protein 1	Gmeb1	-	-	-	-	-	-	1.6	Up
NM_028087	Glucosaminyl (N-acetyl) transferase 3, mucin type	Gcnt3	-	-	-	-	-	-	1.7	Up

NM_175935	Glucose 6 phosphatase, catalytic, 3	G6pc3	-	-	-	-	-	-	3.6	Up
XM_135211	Glutamate decarboxylase-like 1	Gad11	-	-	-	-	-	-	1.6	Up
XM_144901	glutamate receptor interacting protein 2	-	-	-	-	-	-	-	1.8	Up
XM_205495	glutamate receptor ionotropic, NMDA3A	-	-	-	-	-	-	-	2.9	Up
NM_008166	Glutamate receptor, ionotropic, delta 1	Grid1	-	-	-	-	-	-	1.6	Up
NM_010349	Glutamate receptor, ionotropic, kainate 2 (beta 2)	Grik2	-	-	-	-	-	-	3.1	Up
NM_008168	Glutamate receptor, ionotropic, kainate 5 (gamma 2)	Grik5	-	-	-	-	-	-	1.8	Up
NM_008169	Glutamate receptor, ionotropic, NMDA1 (zeta 1)	Grin1	-	-	-	-	-	-	2.2	Up
XM_149971	glutamate receptor, metabotropic 5	-	-	-	-	-	-	-	4.3	Up
NM_008174	Glutamate receptor, metabotropic 8	Grm8	-	-	-	-	-	-	3.2	Up
NM_153601	Glutamate-ammonia ligase (glutamine synthetase) domain containing 1	Glud1	-	-	-	-	-	-	1.7	Up
NM_173866	Glutamic pyruvate transaminase (alanine aminotransferase) 2	Gpt2	-	-	-	-	-	-	2.7	Up
XM_125928	glutaminase 2 (liver, mitochondrial)	-	-	-	1.9	Down	-	-	-	-
NM_013529	Glutamine fructose-6-phosphate transaminase 2	Gfpt2	-	-	-	-	-	-	2.3	Up
NM_133794	Glutaminyl-tRNA synthetase	Qars	-	-	-	-	-	-	2.4	Down
NM_023505	Glutaredoxin 2 (thioltransferase)	Glrx2	-	-	-	-	-	-	1.8	Down
NM_010343	Glutathione peroxidase 5	Gpx5	-	-	-	-	-	-	3.2	Up
NM_008182	Glutathione S-transferase, alpha 2 (Yc2)	Gsta2	-	-	-	-	-	-	1.6	Up
NM_010356	Glutathione S-transferase, alpha 3	Gsta3	-	-	-	-	-	-	1.7	Down
NM_010358	Glutathione S-transferase, mu 1	Gstm1	-	-	-	-	1.6	Up	-	-
NM_010360	Glutathione S-transferase, mu 5	Gstm5	-	-	-	-	-	-	1.7	Down
NM_177352	Glycerol kinase 5 (putative)	Gk5	-	-	-	-	-	-	1.9	Up
NM_177696	Glycerophosphodiester phosphodiesterase domain containing 4	Gdpd4	-	-	-	-	-	-	3.5	Up
NM_010298	Glycine receptor, beta subunit	Glrb	-	-	-	-	-	-	1.7	Up
NM_013755	Glycogenin	Gyg	-	-	-	-	-	-	1.5	Down
NM_021610	Glycoprotein A33 (transmembrane)	Gpa33	-	-	-	-	-	-	1.9	Up
NM_175644	Glycoprotein hormone beta 5	Gphb5	-	-	-	-	-	-	2.4	Up
NM_008156	Glycosylphosphatidylinositol specific phospholipase D1	Gpld1	-	-	-	-	-	-	1.9	Up
NM_177005	Glycosyltransferase 1 domain containing 1	Gltd1	-	-	1.8	Down	-	-	-	-
NM_025374	Glyoxalase 1	Glo1	1.6	Up	-	-	-	-	1.5	Down
NM_027227	Glyoxalase domain containing 5	Glod5	-	-	-	-	-	-	2.1	Up
NM_010299	GM2 ganglioside activator protein	Gm2a	-	-	-	-	3.0	Up	-	-
NM_010309	GNAS (guanine nucleotide binding protein, alpha stimulating) complex locus	Gnas	-	-	-	-	-	-	1.6	Up
NM_018748	Golgi autoantigen, golgin subfamily a, 4	Golga4	-	-	-	-	-	-	2.2	Down
NM_178930	Golgi-specific brefeldin A-resistance factor 1	Gbf1	-	-	-	-	-	-	2.3	Down
NM_010331	GPI anchor attachment protein 1	Gpaal	-	-	-	-	3.0	Up	-	-
NM_024216	GPN-loop GTPase 3	Gpn3	-	-	-	-	-	-	1.6	Down
NM_183183	GPRIN family member 3	Gprin3	-	-	-	-	-	-	3.1	Up
NM_010371	Granzyme C	Gzmc	-	-	1.9	Down	-	-	-	-
NM_010375	Granzyme G	Gzmg	-	-	-	-	-	-	2.5	Up

NM_153052	Granzyme N	Gzmn	-	-	-	-	-	-	1.5	Up
NM_010815	GRB2-related adaptor protein 2	Grap2	-	-	-	-	1.9	Up	3.1	Up
NM_019521	Growth arrest specific 6	Gas6	-	-	-	-	-	-	1.6	Up
XM_204668	growth arrest-specific 2 like 2	-	-	-	-	-	-	-	2.8	Up
NM_019506	Growth differentiation factor 2	Gdf2	-	-	-	-	-	-	1.9	Up
NM_021356	Growth factor receptor bound protein 2-associated protein 1	Gab1	-	-	-	-	-	-	1.6	Down
NM_078478	Growth hormone inducible transmembrane protein	Ghitm	-	-	-	-	-	-	2.7	Down
NM_024478	GrpE-like 1, mitochondrial	Grpel1	-	-	-	-	2.1	Up	-	-
NM_053266	GTF2I repeat domain containing 2	Gtf2ird2	-	-	-	-	-	-	1.6	Down
NM_008102	GTP cyclohydrolase 1	Gch1	-	-	-	-	-	-	1.7	Down
NM_146167	GTPase, IMAP family member 7	Gimap7	-	-	-	-	-	-	4.2	Up
NM_022422	Guanine nucleotide binding protein (G protein), gamma 13	Gng13	-	-	-	-	-	-	2.7	Up
NM_010319	Guanine nucleotide binding protein (G protein), gamma 7	Gng7	-	-	-	-	-	-	3.1	Up
XM_144196	guanine nucleotide binding protein, alpha transducing 3	-	-	-	-	-	-	-	1.8	Up
NM_010311	Guanine nucleotide binding protein, alpha z subunit	Gnaz	-	-	-	-	-	-	2.5	Up
NM_010273	Guanosine diphosphate (GDP) dissociation inhibitor 1	Gdi1	-	-	-	-	-	-	1.8	Up
NM_146079	Guanylate cyclase activator 1B	Guca1b	-	-	-	-	-	-	3.9	Up
NM_008191	Guanylate cyclase activator 2b (retina)	Guca2b	-	-	-	-	-	-	1.6	Up
NM_008197	H1 histone family, member 0	H1f0	-	-	-	-	1.8	Up	-	-
NM_198622	H1 histone family, member X	H1fx	-	-	-	-	-	-	3.0	Up
NM_008210	H3 histone, family 3A	H3f3a	-	-	-	-	1.9	Up	-	-
NM_008211	H3 histone, family 3B	H3f3b	-	-	-	-	-	-	3.1	Down
NM_010445	H6 homeo box 1	Hmx1	-	-	-	-	-	-	1.9	Up
XM_133872	H6 homeo box 2	-	-	-	-	-	-	-	3.6	Up
NM_008257	H6 homeo box 3	Hmx3	-	-	-	-	-	-	1.7	Up
NM_008237	Hairy and enhancer of split 3 (Drosophila)	Hes3	-	-	-	-	-	-	2.8	Up
NM_026108	Haloacid dehalogenase-like hydrolase domain containing 1A	Hdhd1a	-	-	-	-	-	-	2.7	Up
NM_019702	Hbs1-like (S. cerevisiae)	Hbs1l	-	-	-	-	-	-	1.8	Down
XM_125542	HD domain containing 2	-	-	-	-	-	-	-	1.9	Down
NM_013558	Heat shock protein 1-like	Hspa1l	-	-	-	-	-	-	1.6	Up
NM_010481	Heat shock protein 9	Hspa9	-	-	-	-	-	-	1.9	Down
NM_030175	hedgehog interacting protein-like 2	-	-	-	-	-	-	-	2.7	Up
NM_198298	Helicase with zinc finger domain	Helz	-	-	-	-	-	-	1.9	Up
XM_132236	helicase, mus308-like (Drosophila)	-	-	-	-	-	-	-	2.6	Up
NM_008258	Hematological and neurological expressed sequence 1	Hn1	-	-	-	-	-	-	1.9	Down
NM_013546	Heme binding protein 1	Hebp1	-	-	-	-	-	-	2.6	Down
NM_010442	Heme oxygenase (decycling) 1	Hmox1	-	-	-	-	-	-	2.5	Down
NM_018805	Heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1	Hs3st3b1	-	-	-	-	-	-	1.6	Up
NM_152803	Heparanase	Hpse	-	-	-	-	-	-	3.4	Up
NM_172563	Hepatic leukemia factor	Hlf	-	-	-	-	-	-	2.1	Up
NM_013920	Hepatocyte nuclear factor 4, gamma	Hnf4g	-	-	-	-	-	-	4.0	Up

NM_016884	Heterogeneous nuclear ribonucleoprotein C	Hnrnpc	-	-	-	-	1.7	Up	-	-
NM_025279	Heterogeneous nuclear ribonucleoprotein K	Hnrnpk	-	-	-	-	1.9	Up	-	-
XM_203501	hexamthylene bis-acetamide inducible 2	-	-	-	-	-	-	-	3.3	Up
NM_010438	Hexokinase 1	Hk1	-	-	-	-	-	-	1.6	Up
NM_025933	HIG1 domain family, member 2A	Higd2a	-	-	-	-	1.6	Up	-	-
NM_008253	High mobility group box 3	Hmgb3	-	-	-	-	2.2	Up	-	-
XM_142098	highly divergent homeobox	-	-	-	-	-	-	-	2.6	Up
NM_016677	Hippocalcin-like 1	Hpcal1	-	-	-	-	2.3	Up	-	-
NM_153087	Histamine receptor H4	Hrh4	-	-	-	-	-	-	1.8	Down
NM_173760	Histidine acid phosphatase domain containing 1	Hisppd1	-	-	-	-	-	-	3.4	Up
NM_008230	Histidine decarboxylase	Hdc	-	-	1.6	Down	-	-	-	-
NM_025798	Histidine triad nucleotide binding protein 3	Hint3	-	-	-	-	-	-	1.8	Down
NM_010378	Histocompatibility 2, class II antigen A, alpha	H2-Aa	-	-	-	-	1.9	Up	-	-
NM_010386	Histocompatibility 2, class II, locus DMa	H2-DMa	-	-	-	-	1.9	Up	-	-
NM_201611	Histocompatibility 2, M region locus 10.6	H2-M10.6	-	-	-	-	-	-	1.9	Up
NM_010390	Histocompatibility 2, Q region locus 1	H2-K1	-	-	-	-	-	-	2.3	Up
NM_010392	Histocompatibility 2, Q region locus 2	H2-Q2	-	-	-	-	-	-	2.7	Up
NM_010394	Histocompatibility 2, Q region locus 7	H2-Q7	-	-	-	-	3.1	Up	-	-
NM_024439	Histocompatibility 47	H47	-	-	-	-	-	-	2.9	Down
NM_175658	Histone cluster 1, H2aa	Hist1h2a	-	-	-	-	-	-	2.6	Up
NM_013550	Histone cluster 1, H3a	Hist1h3a	-	-	-	-	3.0	Up	2.5	Up
NM_178204	Histone cluster 1, H3d	Hist1h3d	-	-	-	-	-	-	2.1	Down
NM_145073	Histone cluster 1, H3g	Hist1h3g	-	-	-	-	-	-	3.3	Up
NM_013549	Histone cluster 2, H2aa1	Hist2h2a	-	-	-	-	1.7	Up	-	-
NM_175666	Histone cluster 2, H2bb	Hist2h2b	-	-	-	-	2.7	Up	3.1	Up
NM_206882	Histone cluster 3, H2bb	Hist3h2b	-	-	-	-	1.8	Up	-	-
NM_010413	Histone deacetylase 6	Hdac6	-	-	-	-	1.5	Up	-	-
NM_020027	HLA-B associated transcript 2	Bat2	-	-	-	-	2.5	Up	1.8	Up
NM_057171	HLA-B-associated transcript 3	Bat3	-	-	1.8	Down	-	-	-	-
NM_023130	HnRNP-associated with lethal yellow	a	-	-	-	-	-	-	1.9	Up
NM_008222	Holocytochrome c synthetase	Hccs	-	-	-	-	-	-	3.6	Up
NM_010454	Homeo box A6	Hoxa6	-	-	-	-	-	-	1.9	Up
NM_013554	Homeo box D10	Hoxd10	-	-	-	-	-	-	2.0	Up
XM_284398	HtrA serine peptidase 4	-	-	-	-	-	-	-	2.4	Up
NM_153072	Hus1 homolog b (S. pombe)	Hus1b	-	-	-	-	-	-	1.9	Up
NM_022031	Hyaluronan and proteoglycan link protein 2	Hapln2	-	-	-	-	-	-	2.2	Up
NM_010489	Hyaluronoglucosaminidase 2	Hyal2	-	-	-	-	-	-	2.4	Up



NM_178020	Hyaluronoglucosaminidase 3	Hyal3	-	-	-	-	-	-	3.8	Up
NM_172916	Hydrocephalus inducing	Hydin	-	-	-	-	-	-	1.7	Up
NM_010403	Hydroxyacid oxidase 1, liver	Hao1	-	-	-	-	-	-	3.8	Up
NM_024284	Hydroxyacyl glutathione hydrolase	Hagh	-	-	-	-	1.6	Up	-	-
NM_178878	Hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha	Hadha	-	-	-	-	-	-	1.6	Down
NM_008289	Hydroxysteroid 11-beta dehydrogenase 2	Hsd11b2	-	-	-	-	-	-	3.5	Up
NM_198959	Hypocretin (orexin) receptor 1	Hcrtr1	-	-	-	-	-	-	1.8	Up
XM_488745	hypothetical gene supported by AK040104	-	-	-	-	-	-	-	2.0	Up
XM_484697	hypothetical gene supported by AK043736	-	-	-	-	-	-	-	1.7	Up
XM_112107	hypothetical LOC194615	-	-	-	-	-	-	-	2.2	Up
NM_177837	hypothetical protein 6530439I21	-	-	-	-	-	-	-	2.3	Up
XM_488999	hypothetical protein A530017F20	-	-	-	-	-	-	-	1.6	Up
NM_011772	IKAROS family zinc finger 4	Ikzf4	-	-	-	-	-	-	2.8	Up
NM_025409	Immediate early response 3 interacting protein 1	Ier3ip1	-	-	-	-	1.7	Up	-	-
NM_008784	Immunoglobulin (CD79A) binding protein 1	Igbp1	-	-	-	-	-	-	1.7	Down
NM_015777	Immunoglobulin (CD79A) binding protein 1b	Igbp1b	-	-	-	-	-	-	2.5	Up
XM_356613	immunoglobulin heavy chain variable region	-	-	-	-	-	-	-	2.3	Up
NM_177193	Immunoglobulin superfamily containing leucine-rich repeat 2	Islr2	-	-	-	-	-	-	2.0	Up
NM_170599	Immunoglobulin superfamily, member 11	Igsf11	-	-	1.7	Down	-	-	-	-
NM_033608	Immunoglobulin superfamily, member 9	Igsf9	-	-	-	-	-	-	3.4	Up
NM_145949	Indoleamine-pyrrole 2,3 dioxygenase-like 1	Indo11	-	-	1.7	Down	-	-	-	-
NM_010565	Inhibin beta-C	Inhbc	-	-	-	-	-	-	1.9	Up
NM_029340	inhibitor of growth family, member 5	-	-	-	1.7	Down	-	-	-	-
NM_010546	Inhibitor of kappaB kinase beta	Ikbkb	-	-	-	-	-	-	1.8	Down
XM_355376	INO80 complex homolog 1 (S. cerevisiae)	-	-	-	-	-	-	-	2.0	Up
NM_011830	Inosine 5-phosphate dehydrogenase 2	Impdh2	-	-	-	-	-	-	1.7	Down
NM_025922	Inosine triphosphatase (nucleoside triphosphate pyrophosphatase)	Itpa	-	-	-	-	-	-	1.6	Up
NM_010585	Inositol 1,4,5-triphosphate receptor 1	Itp1	-	-	-	-	-	-	3.0	Up
XM_205854	inositol 1,4,5-trisphosphate 3-kinase B	-	-	-	-	-	-	-	1.6	Up
XM_134427	inositol polyphosphate-4-phosphatase, type II	-	-	-	-	-	-	-	3.9	Down
NM_173767	Inscuteable homolog (Drosophila)	Insc	-	-	-	-	-	-	2.0	Up
NM_178082	Insulin induced gene 2	Insig2	-	-	-	-	-	-	1.8	Up
NM_009951	Insulin-like growth factor 2 mRNA binding protein 1	Igf2bp1	-	-	-	-	-	-	2.4	Up
NM_183029	Insulin-like growth factor 2 mRNA binding protein 2	Igf2bp2	-	-	-	-	-	-	2.0	Up
NM_008343	Insulin-like growth factor binding protein 3	Igfbp3	-	-	-	-	-	-	2.1	Up
NM_008340	Insulin-like growth factor binding protein, acid labile subunit	Igfals	-	-	-	-	-	-	1.8	Up
NM_020287	Insulinoma-associated 2	Insm2	-	-	-	-	-	-	2.4	Up
NM_027927	Integrator complex subunit 12	Ints12	-	-	-	-	-	-	1.8	Down
NM_153414	Integrator complex subunit 9	Ints9	-	-	-	-	-	-	1.9	Down
NM_028007	Integrin alpha FG-GAP repeat containing 1	Iifg1	-	-	-	-	-	-	1.6	Down

NM_008400	Integrin alpha L	Itgal	-	-	-	-	-	-	-	1.6	Up
NM_001005607	integrin beta 4	-	-	-	-	-	-	2.5	Down	-	-
NM_013566	Integrin beta 7	Itgb7	4.3	Down	-	-	-	-	-	-	-
XM_112192	integrin, alpha 10	-	-	-	-	-	-	-	-	1.6	Up
NM_008406	Inter-alpha trypsin inhibitor, heavy chain 1	Itih1	-	-	-	-	-	-	-	3.0	Up
NM_010509	Interferon (alpha and beta) receptor 2	Ifnar2	1.7	Up	-	-	-	-	-	-	-
NM_008328	Interferon activated gene 203	Ifi203	-	-	-	-	-	-	-	2.2	Down
NM_010504	Interferon alpha 4	Ifna4	-	-	-	-	-	-	-	1.5	Up
NM_206871	Interferon alpha 6	Ifna6	-	-	-	-	-	-	-	2.5	Up
NM_010507	Interferon alpha 9	Ifna9	-	-	1.9	Down	-	-	-	-	-
NM_023065	Interferon gamma inducible protein 30	Ifi30	-	-	-	-	-	1.5	Up	-	-
NM_008338	Interferon gamma receptor 2	Ifngr2	-	-	-	-	-	-	-	3.2	Up
NM_027835	Interferon induced with helicase C domain 1	Ifih1	-	-	-	-	-	-	-	2.0	Down
NM_016851	Interferon regulatory factor 6	Irf6	-	-	1.7	Down	-	-	-	-	-
NM_008394	Interferon regulatory factor 9	Irf9	-	-	-	-	-	-	-	2.5	Down
NM_197889	Interferon zeta	Ifnz	-	-	-	-	-	-	-	1.9	Up
NM_008331	Interferon-induced protein with tetratricopeptide repeats 1	Ifit1	-	-	-	-	-	-	-	2.2	Up
NM_008332	Interferon-induced protein with tetratricopeptide repeats 2	Ifit2	-	-	-	-	-	-	-	2.3	Up
NM_025903	Interferon-related developmental regulator 2	Ifrd2	-	-	-	-	-	2.5	Up	-	-
NM_010743	Interleukin 1 receptor-like 1	Il1rl1	-	-	-	-	-	-	-	2.6	Up
NM_054079	Interleukin 10-related T cell-derived inducible factor beta	Il1fib	-	-	1.5	Down	-	-	-	-	-
NM_010550	Interleukin 11 receptor, alpha chain 2	Il11ra2	-	-	-	-	-	-	-	4.2	Up
NM_145856	Interleukin 17F	Il17f	-	-	-	-	-	-	-	3.3	Up
NM_008360	Interleukin 18	Il18	-	-	-	-	-	-	-	1.9	Down
XM_283649	interleukin 19	-	-	-	1.8	Down	-	-	-	-	-
NM_008367	Interleukin 2 receptor, alpha chain	Il2ra	-	-	-	-	-	-	-	1.9	Up
NM_013563	Interleukin 2 receptor, gamma chain	Il2rg	-	-	-	-	-	1.9	Up	-	-
NM_178257	Interleukin 22 receptor, alpha 1	Il22ra1	-	-	-	-	-	-	-	3.5	Up
NM_174851	Interleukin 28 receptor alpha	Il28ra	-	-	-	-	-	-	-	3.1	Up
NM_133775	Interleukin 33	Il33	-	-	-	-	-	-	-	2.3	Down
NM_008370	Interleukin 5 receptor, alpha	Il5ra	-	-	-	-	-	-	-	1.9	Up
NM_031168	Interleukin 6	Il6	-	-	-	-	-	-	-	2.3	Up
NM_008363	Interleukin-1 receptor-associated kinase 1	Irak1	-	-	1.6	Up	-	-	-	1.6	Down
NM_029926	Interleukin-1 receptor-associated kinase 4	Irak4	-	-	-	-	-	-	-	2.1	Up
XM_134330	intestine specific homeobox	-	-	-	-	-	-	-	-	2.5	Up
NM_031177	Intraflagellar transport 122 homolog (Chlamydomonas)	Ift122	-	-	-	-	-	-	-	1.7	Down
NM_001005475	IQ motif and Sec7 domain 2	Iqsec2	-	-	-	-	-	-	-	2.5	Up
XM_486254	IQ motif containing F1	Iqcf1	-	-	-	-	-	-	-	3.3	Up
NM_026645	IQ motif containing F3	Iqcf3	-	-	-	-	-	-	-	2.7	Up
NM_008393	Iroquois related homeobox 3 (Drosophila)	Irx3	-	-	-	-	-	-	-	2.1	Up

NM_018885	Iroquois related homeobox 4 (Drosophila)	Irxd4	-	-	-	-	-	-	2.4	Up
NM_025526	IscU iron-sulfur cluster scaffold homolog (E. coli)	Iscu	-	-	-	-	-	-	2.6	Down
NM_010491	Islet amyloid polypeptide	Iapp	-	-	-	-	-	-	2.8	Up
NM_130884	Isocitrate dehydrogenase 3 (NAD+) beta	Idh3b	-	-	-	-	1.8	Up	-	-
NM_172015	Isoleucine-tRNA synthetase	Iars	-	-	-	-	1.6	Up	-	-
NM_026365	Jagunal homolog 1 (Drosophila)	Jagn1	-	-	-	-	-	-	1.6	Down
NM_178394	Janus kinase and microtubule interacting protein 1	Jakmip1	-	-	-	-	-	-	2.0	Down
XM_129010	Janus kinase and microtubule interacting protein 2	Jakmip2	-	-	1.5	Down	-	-	-	-
NM_144787	Jumonji domain containing 2C	Jmjd2c	-	-	-	-	1.6	Up	-	-
NM_021310	Junction-mediating and regulatory protein	Jmy	-	-	-	-	1.8	Up	4.1	Up
NM_021566	Junctophilin 2	Jph2	-	-	-	-	-	-	2.4	Up
NM_0010038	Junctophilin 4	Jph4	-	-	-	-	-	-	2.2	Up
NM_010114	Kallikrein 1-related peptidase b22	Klk1b22	-	-	-	-	-	-	3.2	Up
NM_133969	Kallikrein B, plasma 1	Cyp4v3	-	-	-	-	-	-	1.8	Down
NM_133712	Kallikrein related-peptidase 10	Klk10	-	-	-	-	-	-	2.5	Up
NM_174866	Kallikrein related-peptidase 14	Klk14	-	-	-	-	-	-	2.2	Up
NM_011177	Kallikrein related-peptidase 6	Klk6	-	-	-	-	-	-	3.1	Up
NM_011835	Katanin p60 (ATPase-containing) subunit A1	Katna1	-	-	-	-	-	-	3.1	Down
NM_178929	Kazal-type serine peptidase inhibitor domain 1	Kazald1	-	-	-	-	3.6	Down	-	-
NM_133950	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1	Kdelr1	-	-	-	-	-	-	2.1	Down
NM_026167	Kelch-like 13 (Drosophila)	Klhl13	-	-	-	-	-	-	2.3	Up
XM_131360	kelch-like 32 (Drosophila)	-	-	-	-	-	-	-	2.5	Up
NM_008469	Keratin 15	Krt15	-	-	-	-	-	-	1.8	Up
NM_008470	Keratin 16	Krt16	-	-	-	-	-	-	2.6	Up
NM_033373	Keratin 23	Krt23	-	-	-	-	-	-	2.3	Up
XM_109734	keratin 26	-	-	-	-	-	-	-	2.5	Up
NM_010659	Keratin 31	Krt31	-	-	-	-	-	-	2.3	Up
XM_484076	keratin 40	-	-	-	-	-	-	-	2.7	Up
NM_183189	Keratin associated protein 13-1	Krtap13-1	-	-	-	-	-	-	2.8	Up
NM_183296	Keratin associated protein 16-3	Krtap16-10	-	-	-	-	-	-	4.3	Up
NM_027105	Keratin associated protein 26-1	Krtap26-1	-	-	-	-	-	-	2.2	Up
NM_010672	Keratin associated protein 6-1	Krtap6-1	-	-	1.7	Down	-	-	1.9	Up
NM_010676	Keratin associated protein 8-2	Krtap8-2	-	-	1.7	Down	-	-	-	-
NM_025327	Keratinocyte associated protein 2	Krtcap2	-	-	-	-	-	-	1.5	Down
NM_010158	KH domain containing, RNA binding, signal transduction associated 3	Khdrbs3	-	-	-	-	1.5	Up	1.7	Up
NM_029550	Kidney expressed gene 1	Keg1	-	-	-	-	-	-	2.4	Up

NM_010649	Killer cell lectin-like receptor subfamily A, member 22	Klra7	-	-	1.9	Down	-	-	-	-
NM_010651	Killer cell lectin-like receptor subfamily A, member 9	Klra9	-	-	-	-	2.0	Up	2.2	Up
NM_010653	Killer cell lectin-like receptor subfamily C, member 2	Klrc2	-	-	-	-	-	-	1.8	Up
NM_021378	Killer cell lectin-like receptor subfamily C, member 3	Klrc3	1.8	Down	-	-	-	-	2.4	Down
NM_008477	Kinectin 1	Ktn1	-	-	-	-	-	-	2.1	Down
NM_010620	Kinesin family member 15	Kif15	-	-	-	-	-	-	1.9	Up
NM_139303	Kinesin family member 18A	Kif18a	1.8	Up	-	-	-	-	-	-
NM_008443	Kinesin family member 3A	Kif3a	-	-	-	-	-	-	2.7	Up
NM_008447	Kinesin family member 5A	Kif5a	-	-	-	-	-	-	2.0	Up
NM_010630	Kinesin family member C2	Kifc2	-	-	-	-	-	-	1.7	Up
NM_023125	Kininogen 1	Kng1	-	-	-	-	-	-	2.1	Up
NM_053244	KISS1 receptor	Kiss1r	-	-	-	-	-	-	3.2	Up
NM_013823	Klotho	Kl	-	-	-	-	-	-	1.9	Up
NM_010635	Kruppel-like factor 1 (erythroid)	Klf1	-	-	-	-	-	-	1.7	Up
NM_021366	Kruppel-like factor 13	Klf13	-	-	-	-	-	-	2.4	Down
NM_009769	Kruppel-like factor 5	Klf5	-	-	-	-	-	-	1.7	Up
XM_485097	L(3)mbt-like (Drosophila)	-	-	-	-	-	-	-	1.8	Up
NM_145993	L(3)mbt-like 2 (Drosophila)	L3mbtl2	-	-	-	-	1.6	Up	-	-
NM_177278	L(3)mbt-like 4 (Drosophila)	L3mbtl4	-	-	-	-	-	-	2.5	Up
XM_128090	La ribonucleoprotein domain family, member 4	-	-	-	-	-	1.6	Up	-	-
NM_008492	Lactate dehydrogenase B	Ldhb	-	-	-	-	-	-	2.7	Up
NM_133664	Ladinin	Lad1	-	-	-	-	-	-	2.0	Up
XM_203796	laminin, alpha 5	-	-	-	-	-	-	-	1.6	Up
NM_021295	LanC (bacterial lantibiotic synthetase component C)-like 1	Lancl1	-	-	-	-	-	-	2.7	Up
NM_146006	Lanosterol synthase	Lss	-	-	-	-	-	-	2.3	Up
NM_025984	Late cornified envelope 1A1	Lce1a1	-	-	1.7	Down	-	-	-	-
NM_026811	Late cornified envelope 1E	Lce1e	-	-	1.6	Down	-	-	-	-
NM_028628	Late cornified envelope 1L	Lce1l	-	-	-	-	-	-	3.4	Down
XM_131258	latrophilin 2	-	-	-	-	-	-	-	1.9	Up
XM_205556	latrophilin 3	-	-	-	-	-	-	-	1.8	Up
NM_0010014	92	Lca5l	-	-	-	-	-	-	2.0	Up
NM_019516	Leber congenital amaurosis 5-like	Lgals12	-	-	-	-	-	-	2.3	Up
NM_010706	Lectin, galactose binding, soluble 12	Lgals4	-	-	-	-	-	-	4.2	Up
NM_018886	Lectin, galactose binding, soluble 8	Lgals8	-	-	-	-	-	-	2.4	Down
NM_199222	Lectin, mannose-binding 1 like	Lman1l	-	-	1.5	Down	-	-	-	-
NM_177099	Left-right determination factor 2	Lefty2	-	-	-	-	-	-	2.9	Up
NM_011175	Legumain	Lgmn	-	-	-	-	2.6	Up	-	-
XM_132983	leiomodrin 2 (cardiac)	-	-	-	-	-	-	-	2.0	Up
XM_149772	leiomodrin 3 (fetal)	-	-	-	-	-	-	-	2.6	Up
NM_020517	Lens epithelial protein	Lenep	-	-	-	-	2.1	Up	3.0	Up

NM_010704	Leptin receptor	Lepr	-	-	-	-	-	-	3.2	Up
NM_008515	Leucine rich repeat (in FLII) interacting protein 1	Lrrfip1	-	-	-	-	-	-	2.6	Up
NM_146242	Leucine rich repeat containing 10	Lrrc10	-	-	-	-	-	-	2.2	Up
NM_026253	Leucine rich repeat containing 18	Lrrc18	-	-	-	-	-	-	2.3	Up
NM_198119	Leucine rich repeat containing 24	Lrrc24	-	-	-	-	-	-	3.7	Up
XM_133916	leucine rich repeat containing 27	-	-	-	-	-	-	-	2.4	Up
NM_177449	Leucine rich repeat containing 29	Lrrc29	-	-	-	-	-	-	2.0	Up
XM_485967	leucine rich repeat containing 32	-	-	-	-	-	-	-	1.6	Up
XM_137868	Leucine rich repeat containing 37A	Lrrc37a	-	-	-	-	-	-	3.2	Up
NM_029985	Leucine rich repeat containing 42	Lrrc42	-	-	-	-	-	-	2.1	Down
NM_201226	Leucine rich repeat containing 47	Lrrc47	-	-	-	-	2.8	Up	-	-
XM_136373	leucine rich repeat containing 52	-	-	-	-	-	-	-	1.5	Up
NM_133807	Leucine rich repeat containing 59	Lrrc59	-	-	-	-	-	-	1.8	Down
NM_153568	Leucine rich repeat containing 66	Lrrc66	-	-	-	-	-	-	2.0	Up
NM_199149	Leucine rich repeat containing 68	Lrrc68	-	-	2.3	Down	-	-	-	-
NM_022654	Leucine-rich and death domain containing	Lrdd	-	-	-	-	-	-	1.6	Up
NM_145219	Leucine-rich repeat LGI family, member 3	Lgi3	-	-	-	-	-	-	1.9	Up
XM_355385	leucine-rich repeat-containing G protein-coupled receptor 4	-	-	-	-	-	-	-	3.3	Up
NM_153168	leucyl-tRNA synthetase, mitochondrial	-	-	-	4.2	Down	3.0	Down	-	-
NM_172827	Leucyl/cystinyl aminopeptidase	Lnpep	-	-	-	-	-	-	1.5	Down
NM_010701	Leukocyte cell derived chemotaxin 1	Lect1	-	-	-	-	-	-	2.3	Up
NM_011095	Leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3	Lilrb3	-	-	-	-	2.3	Up	2.7	Down
NM_010727	Ligand of numb-protein X 1	Lnx1	-	-	-	-	1.7	Down	2.2	Up
NM_0010019	80									
NM_010698	LIM and calponin homology domains 1	Limch1	-	-	-	-	-	-	1.7	Up
NM_010698	LIM domain binding 2	Ldb2	-	-	-	-	-	-	2.1	Up
NM_010711	LIM homeobox protein 3	-	-	-	-	-	-	-	3.0	Up
NM_008499	LIM homeobox protein 5	Lhx5	-	-	-	-	-	-	2.0	Up
NM_010714	LIM homeobox protein 9	Lhx9	-	-	-	-	-	-	2.3	Up
NM_033652	LIM homeobox transcription factor 1 alpha	Lmx1a	-	-	-	-	-	-	1.8	Up
NM_011698	Lin-7 homolog B (C. elegans)	Lin7b	-	-	-	-	-	-	1.7	Up
NM_010689	Linker for activation of T cells	Lat	-	-	-	-	3.2	Up	2.4	Up
NM_022964	Linker for activation of T cells family, member 2	Lat2	-	-	1.6	Up	-	-	3.6	Up
NM_172837	Lipase, family member K	Lipk	-	-	-	-	-	-	3.4	Up
NM_153558	Lipocalin 13	Lcn13	-	-	-	-	-	-	2.8	Up
NM_017405	Lipolysis stimulated lipoprotein receptor	Lsr	-	-	-	-	-	-	1.7	Up
NM_172767	Loss of heterozygosity, 11, chromosomal region 2, gene A homolog (human)	Loh11cr2a	-	-	-	-	-	-	2.2	Down
NM_026371	Loss of heterozygosity, 12, chromosomal region 1 homolog (human)	Loh12cr1	-	-	-	-	2.8	Up	3.1	Up
XM_487829	low density lipoprotein receptor A domain containing 2	-	-	-	-	-	-	-	2.4	Up
XM_357867	LSM1 homolog, U6 small nuclear RNA associated (S. cerevisiae)	-	-	-	-	-	-	-	1.7	Down

NM_177727	LSM14 homolog B (SCD6, <i>S. cerevisiae</i> )	Lsm14b	-	-	-	-	-	-	2.8	Up
NM_015816	LSM4 homolog, U6 small nuclear RNA associated ( <i>S. cerevisiae</i> )	Lsm4	-	-	-	-	1.7	Up	-	-
NM_138680	LUC7-like 2 ( <i>S. cerevisiae</i> )	Luc7l2	-	-	-	-	-	-	1.8	Down
NM_145100	Ly6/Plaur domain containing 1	Lypd1	-	-	-	-	-	-	3.0	Up
NM_148939	Lymphocyte antigen 6 complex, locus G5B	Ly6g5b	-	-	-	-	-	-	2.0	Up
NM_013825	Lymphocyte antigen 75	Ly75	-	-	-	-	1.9	Up	-	-
NM_010745	Lymphocyte antigen 86	Ly86	-	-	-	-	2.1	Up	-	-
NM_019391	Lymphocyte specific 1	Lsp1	-	-	-	-	-	-	1.6	Down
NM_175215	LysM, putative peptidoglycan-binding, domain containing 4	Lysmd4	-	-	-	-	-	-	2.9	Up
XM_128781	lysocardiolipin acyltransferase	-	-	-	1.6	Down	-	-	-	-
NM_010336	Lysophosphatidic acid receptor 1	Lpar1	-	-	-	-	-	-	1.7	Down
NM_172266	Lysophosphatidylglycerol acyltransferase 1	Lpgat1	-	-	-	-	1.8	Up	-	-
NM_053083	Lysyl oxidase-like 4	Loxl4	-	-	-	-	-	-	2.1	Up
NM_007794, NM_181322	M20000182	-	-	-	-	-	-	-	3.2	Down
M200001020	M200001020	-	-	-	1.6	Up	-	-	-	-
NM_009400, NM_021985	M200001227	-	-	-	-	-	-	-	2.4	Down
M200001365	M200001365	-	-	-	-	-	-	-	1.9	Up
NM_0010022 72,NM_0195 48,NM_2076 79	M200001405	-	-	-	-	-	-	-	1.5	Up
NM_010486, NM_207685, NM_207686	M200001464	-	-	-	-	-	-	-	2.2	Up
NM_008310, XM_489584	M200002110	-	-	-	-	-	-	-	3.2	Up
NM_008941, NM_178855	M200002202	-	-	-	-	-	-	-	3.9	Up
M200002405	M200002405	-	-	-	-	-	3.2	Up	-	-
NM_008107, NM_138647	M200002609	-	-	-	-	-	-	-	1.5	Up
NM_019412, NM_198048	M200002876	-	-	-	-	-	-	-	2.1	Up
M200003051	M200003051	-	-	-	-	-	1.9	Up	-	-
NM_011901, NM_175770	M200003062	-	-	-	-	-	2.2	Up	-	-
NM_016808, NM_198091, NM_198092	M200003187	-	-	-	-	-	-	-	1.8	Up
M200003360	M200003360	-	-	-	-	-	-	-	1.6	Up
XM_110614,	M200003522	-	-	-	-	-	-	-	2.0	Up

XM_132615													
M200003531	M200003531	-	-	-	1.7	Down	-	-	-	-	-	-	-
M200003653	M200003653	-	-	-	-	-	-	-	-	-	2.0	Down	-
NM_019919, NM_206958	M200003756	-	-	-	-	-	-	-	-	-	1.9	Up	-
M200003942	M200003942	-	-	-	-	-	-	-	-	-	2.1	Down	-
NM_018770, NM_207675, NM_207676	M200004005	-	-	-	-	-	-	-	-	-	2.0	Down	-
M200004164	M200004164	-	-	-	-	-	-	-	-	-	2.0	Down	-
M200004221	M200004221	-	-	-	-	-	-	-	-	-	2.7	Down	-
NM_028344, XM_488519	M200004225	-	-	-	-	-	-	-	-	-	1.6	Up	-
M200004257	M200004257	-	-	-	-	-	-	2.3	Up	-	2.7	Up	-
M200004367	M200004367	-	-	-	-	-	-	-	-	-	3.6	Up	-
NM_011225, NM_181070	M200004463	-	-	-	-	-	-	2.6	Up	-	-	-	-
XM_489221	M200004562	-	-	-	-	-	-	-	-	-	1.7	Up	-
M200004625	M200004625	-	-	-	1.7	Down	-	1.5	Down	-	-	-	-
M200004748	M200004748	-	-	-	-	-	-	-	-	-	2.2	Up	-
NM_020011, NM_203280	M200004833	-	-	-	2.0	Up	-	2.8	Up	-	1.9	Up	-
M200005063	M200005063	-	-	-	-	-	-	2.1	Up	-	-	-	-
M200005224	M200005224	-	-	-	-	-	-	-	-	-	1.6	Up	-
M200005295	M200005295	-	-	-	-	-	-	-	-	-	1.9	Down	-
XM_148044, XM_489508	M200005393	-	-	-	-	-	-	1.5	Up	-	-	-	-
M200005467	M200005467	-	-	-	-	-	-	-	-	-	1.5	Up	-
M200005577	M200005577	-	-	-	-	-	-	-	-	-	2.1	Down	-
M200005776	M200005776	-	-	-	-	-	-	2.5	Up	-	-	-	-
XM_207130, XM_289920	M200005809	-	-	-	-	-	-	2.0	Up	-	-	-	-
NM_026638, NM_138754	M200005892	-	-	-	-	-	-	2.2	Up	-	-	-	-
M200006042	M200006042	-	-	-	-	-	-	1.7	Up	-	-	-	-
M200006084	M200006084	-	-	-	1.6	Down	-	-	-	-	-	-	-
M200006146	M200006146	-	-	-	-	-	-	-	-	-	2.0	Down	-
M200006204	M200006204	-	-	-	-	-	-	-	-	-	2.5	Down	-
NM_025702	M200006294	-	-	-	-	-	-	-	-	-	1.6	Down	-
NM_024193, XM_357943	M200006451	-	-	-	-	-	-	-	-	-	1.9	Down	-
XM_485868	M200006572	-	-	-	-	-	-	-	-	-	2.6	Down	-
NM_139295,	M200006923	-	-	-	-	-	-	2.4	Up	-	-	-	-

NM_176808													
M200007275	M200007275	-	-	-	1.8	Down	-	-	-	-	-	-	-
M200007360	M200007360	-	-	-	-	-	-	-	-	-	3.0	Down	-
M200007408	M200007408	-	-	-	-	-	3.1	Up	-	-	-	-	-
M200007432	M200007432	-	-	-	-	-	-	-	-	-	1.6	Up	-
M200007480	M200007480	-	-	-	-	-	-	-	-	-	1.7	Down	-
M200007640	M200007640	-	-	-	-	-	-	-	-	-	1.8	Down	-
M200007646	M200007646	-	-	-	-	-	-	-	-	-	2.8	Up	-
M200007921	M200007921	-	-	-	-	-	-	-	-	-	1.6	Up	-
M200007993	M200007993	-	-	-	-	-	-	-	-	-	2.7	Down	-
M200007999	M200007999	-	-	-	-	-	-	-	-	-	2.2	Up	-
NM_008884, NM_178087 NM_015788,	M200008084	-	-	-	-	-	2.1	Up	-	-	-	-	-
XM_484383 NM_020292,	M200008588	-	-	-	-	-	-	-	-	-	2.8	Up	-
NM_146760 M200008661	M200008614 M200008661	-	-	-	-	-	-	-	-	-	2.1	Up	-
M200008661 XM_484073	M200008661 M200008773	-	-	-	-	-	-	-	-	-	3.1	Up	-
XM_484073 NM_019514, NM_207109	M200008773 M200008808	-	-	-	-	-	-	-	-	-	2.3	Up	-
NM_207109 XM_484572	M200008808 M200009264	-	-	-	-	-	-	-	-	-	2.9	Up	-
XM_484572 M200009299	M200009264 M200009299	-	-	-	-	-	1.7	Up	-	-	3.1	Up	-
M200009299 M200009585	M200009299 M200009585	-	-	-	-	-	-	-	-	-	1.7	Up	-
M200009585 M200009601	M200009585 M200009601	-	-	-	-	-	-	-	-	-	2.8	Up	-
M200009601 XM_485635	M200009601 M200009613	-	-	-	-	-	-	-	-	-	2.1	Up	-
XM_485635 NM_026813, NM_027805	M200009613 M200009770	-	-	-	-	-	1.6	Up	-	-	1.8	Up	-
NM_026813, NM_027805 NM_0010037 19,NM_0199 94	M200009770 M200009789	-	-	-	-	-	-	-	-	-	-	-	-
19,NM_0199 94 M200009797	M200009789 M200009797	-	-	-	-	-	2.1	Down	-	-	1.9	Up	-
M200009797 M200010054	M200009797 M200010054	-	-	-	-	-	-	-	-	-	-	-	-
M200010054 M200010063	M200010054 M200010063	-	-	-	-	-	-	-	-	-	1.8	Up	-
M200010063 M200010088	M200010063 M200010088	-	-	-	-	-	-	-	-	-	2.5	Up	-
M200010088 M200010457	M200010088 M200010457	-	-	-	-	1.7	Down	-	-	-	-	-	-
M200010457 M200010617	M200010457 M200010617	-	-	-	-	-	-	-	-	-	2.1	Up	-
M200010617 M200010674	M200010617 M200010674	-	-	-	-	1.6	Down	-	-	-	-	-	-
M200010674 M200010738	M200010674 M200010738	-	-	-	-	-	-	-	-	-	1.6	Up	-
M200010738 M200010758	M200010738 M200010758	-	-	-	-	-	-	-	-	-	3.1	Up	-
M200010758 M200010887	M200010758 M200010887	-	-	-	-	-	-	-	-	-	3.6	Up	-
M200010887 M200011273	M200010887 M200011273	-	-	-	-	-	-	-	-	-	2.0	Up	-
M200011273	M200011273	-	-	-	-	-	-	-	-	-	2.0	Up	-



M200011387	M200011387	-	-	-	-	-	-	-	-	1.6	Up
M200011458	M200011458	-	-	-	-	-	-	1.8	Up	3.4	Up
M200011465	M200011465	-	-	-	-	-	-	-	-	2.0	Up
M200011511	M200011511	-	-	-	-	-	-	-	-	3.3	Up
M200011617	M200011617	-	-	-	-	-	-	-	-	2.1	Up
M200011681	M200011681	-	-	-	-	-	-	-	-	3.3	Up
M200011822	M200011822	-	-	-	-	-	-	-	-	2.4	Up
NM_152806, NM_199080	M200012005	-	-	-	-	-	-	1.9	Up	-	-
M200012069	M200012069	-	-	-	-	1.5	Up	1.5	Up	-	-
M200012111	M200012111	-	-	-	-	-	-	1.9	Up	-	-
M200012427	M200012427	-	-	-	-	-	-	-	-	2.5	Up
M200012459	M200012459	-	-	-	-	-	-	-	-	2.1	Up
M200012858	M200012858	-	-	-	-	-	-	-	-	2.8	Up
M200012861	M200012861	-	-	-	-	-	-	-	-	2.4	Up
M200013016	M200013016	-	-	-	-	-	-	-	-	1.7	Up
M200013058	M200013058	-	-	-	-	-	-	-	-	4.2	Down
M200013099	M200013099	-	1.6	Down	-	-	-	-	-	-	-
NM_053007, NM_170786	M200013217	-	3.1	Down	-	-	-	-	-	-	-
M200013383	M200013383	-	-	-	-	-	-	-	-	3.4	Up
M200014004	M200014004	-	-	-	-	-	-	-	-	2.1	Down
M200014069	M200014069	-	-	-	-	-	-	-	-	1.8	Up
M200014388	M200014388	-	-	-	-	-	-	-	-	2.4	Up
M200014397	M200014397	-	-	-	-	-	-	-	-	3.9	Up
M200014421	M200014421	-	-	-	-	-	-	-	-	1.7	Up
XM_487682	M200014430	-	-	-	-	-	-	1.6	Up	-	-
M200014540	M200014540	-	-	-	-	-	-	-	-	1.6	Up
M200014558	M200014558	-	-	-	-	-	-	-	-	2.6	Up
M200015099	M200015099	-	-	-	-	-	-	-	-	1.6	Up
M200015129	M200015129	-	-	-	-	-	-	-	-	2.4	Up
M200015131	M200015131	-	-	-	-	-	-	-	-	2.3	Up
M200015132	M200015132	-	-	-	-	-	-	-	-	3.4	Up
NM_023719, XM_485282	M200015455	-	-	-	-	-	-	-	-	3.3	Down
XM_484892, XM_487606	M200015660	-	-	-	-	-	-	2.0	Up	3.6	Up
M200015853	M200015853	-	-	-	-	-	-	-	-	1.7	Up
M200016151	M200016151	-	-	-	-	2.3	Down	-	-	-	-
M200016171	M200016171	-	-	-	-	-	-	-	-	4.0	Down
M200016362	M200016362	-	-	-	-	-	-	-	-	2.5	Up
M2NC00000	M2NC000001	-	-	-	-	2.8	Down	-	-	3.6	Down

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M2NC00000													
2	M2NC000002	-	-	-	-	-	-	-	-	-	-	1.6	Up
M2NC00000													
3	M2NC000003	-	-	-	-	-	-	-	-	-	-	2.0	Up
M2NC00000													
5	M2NC000005	-	-	-	-	-	-	-	-	-	-	3.4	Up
M2NC00000													
6	M2NC000006	-	-	-	-	-	-	3.1	Up			3.4	Up
M2NC00001													
1	M2NC000011	-	-	-	-	-	-	-	-	-	-	2.2	Up
M2NC00001													
2	M2NC000012	-	-	-	-	-	-	-	-	-	-	2.7	Up
M300000195	M300000195	-	-	-	-	-	-	-	-	-	-	2.4	Down
M300000283	M300000283	-	-	-	-	-	-	-	-	-	-	1.8	Up
M300000473	M300000473	-	-	-	-	-	-	1.7	Up	-	-	-	-
M300000599	M300000599	-	-	-	-	-	-	2.7	Up	-	-	-	-
NM_021449, NM_175357	M300000666	-	-	-	-	-	-	2.2	Up	-	-	-	-
M300000830	M300000830	-	-	-	-	-	-	-	-	-	-	1.7	Down
M300000905	M300000905	-	-	-	-	-	-	-	-	-	-	2.4	Up
XM_283318	M300000951	-	-	-	-	-	-	-	-	-	-	1.9	Up
M300001073	M300001073	-	-	-	-	-	-	-	-	-	-	2.3	Down
M300001108	M300001108	-	-	-	-	-	-	-	-	-	-	1.8	Down
M300001255	M300001255	-	-	-	-	-	-	-	-	-	-	2.8	Up
NM_0010052 47,NM_0010 05248,NM_1 78742	M300001296	-	-	-	-	-	-	-	-	-	-	1.6	Up
M300001326	M300001326	-	-	-	-	-	-	-	-	-	-	2.1	Down
M300001350	M300001350	-	-	-	-	-	-	2.3	Up			2.7	Up
XM_140038	M300001431	-	-	-	-	-	-	-	-	-	-	2.4	Up
XM_488525, XM_489912	M300001489	-	-	-	-	-	-	-	-	-	-	1.6	Up
M300001646	M300001646	-	-	-	-	-	-	-	-	-	-	2.4	Up
M300001650	M300001650	-	-	-	-	-	-	-	-	-	-	1.9	Down
M300001663	M300001663	-	-	-	-	-	-	-	-	-	-	1.9	Up
M300001730	M300001730	-	-	-	-	-	-	-	-	-	-	2.6	Up
M300001895	M300001895	-	-	-	-	-	-	-	-	-	-	3.0	Up
M300002028	M300002028	-	-	-	-	-	-	-	-	-	-	2.3	Up
M300002051	M300002051	-	-	-	-	-	-	-	-	-	-	2.0	Up
M300002054	M300002054	-	-	-	-	-	-	-	-	-	-	2.3	Down
NM_0010038	M300002443	-	-	-	-	-	-	-	-	-	-	3.1	Up

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M300002460	M300002460	-	-	-	-	-	-	-	-	1.5	Up
M300002714	M300002714	-	-	-	-	-	-	-	-	3.7	Up
M300002937	M300002937	-	-	-	-	-	-	-	-	2.0	Down
M300002979	M300002979	-	-	-	1.9	Down	-	-	-	2.1	Down
M300003043	M300003043	-	-	-	1.8	Down	-	-	-	-	-
M300003050	M300003050	-	-	-	-	-	-	-	-	2.9	Up
M300003067	M300003067	-	-	-	-	-	-	-	-	2.1	Down
M300003130	M300003130	-	-	-	2.0	Down	-	-	-	-	-
M300003136	M300003136	-	-	-	-	-	-	-	-	1.5	Up
M300003176	M300003176	-	-	-	2.1	Down	-	-	-	-	-
NM_026340, NM_152894	M300003214	-	-	-	-	-	-	-	-	1.6	Up
M300003442	M300003442	-	-	-	-	-	-	-	-	2.5	Down
XM_489634	M300003532	-	-	-	-	-	-	-	-	1.9	Up
M300003585	M300003585	-	-	-	-	-	-	-	-	2.7	Down
XM_354972, XM_489606	M300003594	-	-	-	-	-	-	-	-	1.9	Down
M300003614	M300003614	-	-	-	-	-	-	-	-	2.3	Up
M300003644	M300003644	-	-	-	1.5	Down	-	-	-	-	-
M300003645	M300003645	-	-	-	-	-	-	-	-	1.6	Up
M300003728	M300003728	-	-	-	3.0	Down	-	-	-	-	-
M300003743	M300003743	-	-	-	-	-	-	-	-	2.2	Up
M300003871	M300003871	-	-	-	-	-	1.9	Up	-	-	-
M300003897	M300003897	-	-	-	-	-	1.8	Up	-	-	-
M300003905	M300003905	-	-	-	-	-	-	-	-	1.9	Up
M300004000	M300004000	-	-	-	-	-	1.8	Up	-	-	-
M300004057	M300004057	-	-	-	-	-	-	-	-	2.3	Down
NM_019706, NM_207623	M300004059	-	-	-	-	-	-	-	-	1.5	Down
M300004076	M300004076	-	-	-	-	-	2.6	Up	-	-	-
M300004090	M300004090	-	-	-	-	-	-	-	-	2.5	Up
M300004251	M300004251	-	-	-	-	-	-	-	-	2.4	Down
M300004339	M300004339	-	-	-	-	-	-	-	-	2.2	Down
M300004395	M300004395	-	-	-	-	-	1.6	Up	-	-	-
M300004401	M300004401	-	-	-	-	-	-	-	-	2.6	Up
M300004503	M300004503	-	-	-	-	-	-	-	-	2.1	Down
NM_030716, NM_145703, NM_145704	M300004519	-	-	-	-	-	1.7	Up	-	3.5	Up
NM_008746,	M300004565	-	-	-	-	-	-	-	-	2.4	Up

NM_182809															
M300004585	M300004585	-	-	-	-	-	-	-	-	-	-	-	2.4	Up	
M300004611	M300004611	-	-	-	-	-	-	-	-	-	-	-	2.2	Up	
M300004656	M300004656	-	-	-	-	-	-	-	-	-	-	-	1.9	Down	
M300004888	M300004888	-	-	-	-	-	-	-	-	-	-	-	2.5	Up	
M300004891	M300004891	-	-	-	-	-	-	-	-	-	-	-	2.7	Down	
M300005004	M300005004	-	-	-	-	-	-	-	-	-	-	-	2.1	Down	
M300005031	M300005031	-	-	-	-	-	-	-	-	-	-	-	1.9	Up	
M300005050	M300005050	-	-	-	-	-	-	-	-	-	-	-	1.9	Up	
M300005117	M300005117	-	-	-	-	-	-	-	-	-	-	-	2.2	Up	
M300005119	M300005119	-	-	-	-	-	-	-	-	-	-	-	2.6	Up	
M300005153	M300005153	-	-	-	-	-	-	-	-	-	-	-	2.2	Down	
M300005307	M300005307	-	-	-	-	-	-	-	-	-	-	-	2.2	Up	
M300005376	M300005376	-	-	-	-	-	-	-	-	-	-	-	2.8	Down	
XM_484981	M300005386	-	-	-	-	-	-	-	2.0	Up	-	-	-	-	
M300005636	M300005636	-	-	-	-	2.0	Down	-	-	-	-	-	1.5	Down	
M300005772	M300005772	-	-	-	-	-	-	-	-	-	-	-	1.9	Down	
M300005855	M300005855	-	-	-	-	-	-	-	-	-	-	-	1.6	Up	
XM_485309	M300005907	-	-	-	-	-	-	-	-	-	-	-	2.4	Up	
M300006331	M300006331	-	-	-	-	-	-	-	2.1	Up	-	-	-	-	
M300006384	M300006384	-	-	-	-	-	-	-	2.6	Up	-	-	-	-	
NM_010812,															
NM_199068	M300006746	-	-	-	-	-	-	-	-	-	-	-	2.7	Up	
XM_132483	M300006765	-	-	-	-	-	-	-	-	-	-	-	2.9	Up	
M300006773	M300006773	-	-	-	-	-	-	-	-	-	-	-	2.1	Up	
M300006885	M300006885	-	-	-	-	1.9	Down	-	-	-	-	-	-	-	
NM_020495,															
NM_178235	M300007092	-	-	-	-	-	-	-	-	-	-	-	1.7	Up	
M300007329	M300007329	-	-	-	-	-	-	-	-	-	-	-	4.1	Up	
M300007351	M300007351	-	-	-	-	1.5	Down	-	-	-	-	-	-	-	
M300007519	M300007519	-	-	-	-	-	-	-	-	-	-	-	2.6	Down	
M300007624	M300007624	-	-	-	-	-	-	-	-	-	-	-	3.0	Down	
XM_486739	M300007675	-	-	-	-	-	-	-	-	-	-	-	2.2	Up	
M300007696	M300007696	-	-	-	-	-	-	-	-	-	-	-	1.9	Up	
M300007707	M300007707	-	-	-	-	-	-	-	-	-	-	-	1.8	Up	
M300007732	M300007732	-	-	-	-	-	-	-	-	-	-	-	2.6	Up	
M300007761	M300007761	-	-	-	-	-	-	-	2.0	Up	-	-	-	-	
M300007786	M300007786	-	-	-	-	-	-	-	-	-	-	-	2.1	Up	
XM_486093	M300007807	-	-	-	-	-	-	-	-	-	-	-	2.6	Up	
XM_357975	M300008296	-	-	-	-	-	-	-	-	-	-	-	2.6	Up	
M300008392	M300008392	-	-	-	-	-	-	-	1.6	Up	-	-	-	-	
M300008426	M300008426	-	-	-	-	-	-	-	1.8	Up	-	-	-	-	

M300008459	M300008459	-	-	-	-	-	1.7	Up	3.5	Up
M300008475	M300008475	-	-	-	-	-	-	-	2.5	Up
NM_145140,										
NM_170680	M300008477	-	-	-	-	-	-	-	1.8	Up
M300008482	M300008482	-	-	-	-	-	-	-	1.8	Up
M300008489	M300008489	-	2.5	Down	-	-	-	-	-	-
NM_0010041										
73,XM_3593										
76	M300008504	-	-	-	-	-	-	-	1.6	Up
M300008520	M300008520	-	-	-	-	-	-	-	3.7	Up
M300008570	M300008570	-	-	-	-	-	-	-	1.8	Up
XM_487667	M300008664	-	-	-	-	-	-	-	1.5	Up
XM_488520	M300008696	-	-	-	-	-	-	-	2.2	Up
XM_485800	M300008786	-	-	-	1.7	Down	-	-	-	-
NM_053104,										
NM_175387	M300008835	-	-	-	-	-	-	-	1.7	Up
M300008869	M300008869	-	-	-	-	-	-	-	2.1	Up
M300008988	M300008988	-	-	-	-	-	-	-	2.3	Up
M300009012	M300009012	-	-	-	-	-	-	-	1.7	Up
M300009113	M300009113	-	-	-	-	-	-	-	1.8	Up
M300009122	M300009122	-	-	-	-	-	-	-	1.5	Down
M300009228	M300009228	-	-	-	-	-	-	-	3.5	Up
M300009325	M300009325	-	-	-	-	-	-	-	2.8	Up
M300009430	M300009430	-	-	-	-	-	-	-	3.5	Up
M300009549	M300009549	-	-	-	-	-	-	-	4.1	Up
M300009598	M300009598	-	-	-	-	-	-	-	2.5	Up
M300009610	M300009610	-	1.7	Down	-	-	-	-	1.9	Up
M300009638	M300009638	-	-	-	-	-	-	-	2.6	Up
M300009668	M300009668	-	-	-	-	-	-	-	3.5	Down
NM_177546,										
NM_211138	M300009809	-	-	-	-	-	-	-	2.0	Up
M300009835	M300009835	-	-	-	-	-	-	-	1.9	Up
M300010054	M300010054	-	-	-	-	-	-	-	2.0	Up
M300010223	M300010223	-	-	-	-	-	-	-	1.7	Up
M300010280	M300010280	-	-	-	-	-	2.0	Up	-	-
M300010348	M300010348	-	-	-	-	-	-	-	3.2	Up
M300010355	M300010355	-	-	-	-	-	-	-	2.6	Up
M300010376	M300010376	-	-	-	-	-	-	-	2.5	Up
M300010382	M300010382	-	-	-	-	-	-	-	2.7	Up
M300010409	M300010409	-	-	-	-	-	2.0	Up	1.6	Up
NM_054037,										
NM_170727	M300010504	-	-	-	1.7	Down	-	-	-	-

NM_177819	M300010538	-	-	-	-	-	-	-	-	4.1	Up
M300010551	M300010551	-	-	-	-	-	-	-	-	3.0	Up
M300010635	M300010635	-	-	-	-	-	-	-	-	2.1	Up
M300010679	M300010679	-	-	-	2.7	Down	-	-	-	-	-
M300010682	M300010682	-	-	-	-	-	-	-	-	1.7	Up
M300010789	M300010789	-	-	-	-	-	-	-	-	2.4	Up
M300010838	M300010838	-	1.6	Down	-	-	-	-	-	-	-
M300010970	M300010970	-	-	-	-	-	-	-	-	1.5	Up
M300010981	M300010981	-	-	-	-	-	-	-	-	1.6	Up
NM_010387, NM_010388	M300010992	-	-	-	-	-	2.9	Up	-	-	-
M300011013	M300011013	-	-	-	-	-	-	-	-	1.8	Down
M300011063	M300011063	-	-	-	-	-	-	-	-	1.9	Up
M300011157	M300011157	-	-	-	-	-	-	-	-	1.9	Up
M300011191	M300011191	-	-	-	-	-	-	-	-	3.8	Up
M300011253	M300011253	-	-	-	-	-	-	-	-	2.8	Up
M300011266	M300011266	-	-	-	-	-	-	-	-	1.9	Up
M300011355	M300011355	-	-	-	-	-	-	-	-	2.3	Up
M300011356	M300011356	-	-	-	-	-	-	-	-	4.1	Up
XM_127329, XM_355635	M300011368	-	-	-	-	-	-	-	-	3.6	Up
NM_0010041 57, XM_3587 47	M300011405	-	-	-	-	-	-	-	-	2.1	Up
XM_143418, XM_289760	M300011515	-	-	-	-	-	-	-	-	2.1	Up
XM_488538	M300011522	-	-	-	-	-	-	-	-	2.0	Up
M300011579	M300011579	-	-	-	-	-	-	-	-	1.6	Up
M300011590	M300011590	-	-	-	-	-	-	-	-	3.1	Up
M300011614	M300011614	-	-	-	-	-	-	-	-	2.6	Up
M300011648	M300011648	-	-	-	1.6	Down	-	-	-	-	-
M300011672	M300011672	-	-	-	-	-	-	-	-	2.9	Down
NM_133901, XM_485694	M300011797	-	-	-	1.7	Down	-	-	-	-	-
M300011825	M300011825	-	-	-	-	-	-	-	-	2.5	Up
XM_138939	M300011846	-	-	-	-	-	-	-	-	2.6	Up
M300011947	M300011947	-	-	-	-	-	-	-	-	1.7	Up
M300011959	M300011959	-	-	-	-	-	-	-	-	2.0	Up
M300011986	M300011986	-	-	-	-	-	-	-	-	1.9	Up
NM_133643, NM_175746	M300012093	-	-	-	-	-	-	-	-	2.4	Up
M300012097	M300012097	-	-	-	-	-	-	-	-	2.0	Up

M300012150	M300012150	-	-	-	-	-	-	-	-	2.2	Up
XM_488535	M300012157	-	-	-	-	-	-	1.6	Up	-	-
XM_485692	M300012184	-	-	-	-	-	-	-	-	2.1	Up
M300012553	M300012553	-	-	-	-	-	-	-	-	3.4	Up
M300012625	M300012625	-	-	-	-	-	-	-	-	1.9	Up
M300012640	M300012640	-	-	-	-	-	-	-	-	1.7	Up
M300012665	M300012665	-	-	-	-	-	-	2.2	Up	4.0	Up
M300012719	M300012719	-	-	-	-	-	-	-	-	2.4	Up
M300012724	M300012724	-	-	-	-	1.7	Down	-	-	-	-
NM_008722, XM_486188	M300012771	-	-	-	-	-	-	-	-	3.8	Down
M300012871	M300012871	-	-	-	-	-	-	-	-	2.4	Up
XM_286749, XM_358776, XM_489766	M300013197	-	-	-	-	-	-	-	-	2.3	Up
M300013245	M300013245	-	-	-	-	-	-	-	-	2.8	Up
M300013290	M300013290	-	-	-	-	-	-	-	-	2.4	Up
M300013332	M300013332	-	-	-	-	-	-	-	-	1.7	Up
XM_358380	M300013460	-	-	-	-	-	-	-	-	2.9	Up
M300013462	M300013462	-	-	-	-	-	-	-	-	1.8	Up
M300013623	M300013623	-	-	-	-	2.2	Down	-	-	-	-
M300013691	M300013691	-	-	-	-	-	-	-	-	1.8	Up
M300013788	M300013788	-	-	-	-	-	-	-	-	3.7	Up
M300013801	M300013801	-	-	-	-	-	-	-	-	4.2	Up
M300013932	M300013932	-	-	-	-	-	-	-	-	2.6	Up
M300013976	M300013976	-	-	-	-	-	-	-	-	2.4	Up
M300014087	M300014087	-	-	-	-	-	-	-	-	3.8	Up
XM_486120	M300014177	-	-	-	-	-	-	-	-	2.2	Up
M300014181	M300014181	-	-	-	-	-	-	-	-	3.3	Up
M300014255	M300014255	-	-	-	-	-	-	-	-	2.0	Up
M300014326	M300014326	-	-	-	-	-	-	-	-	2.1	Down
M300014332	M300014332	-	-	-	-	-	-	-	-	2.1	Up
M300014400	M300014400	-	-	-	-	-	-	2.0	Up	3.7	Up
M300014437	M300014437	-	-	-	-	-	-	-	-	3.2	Up
M300014495	M300014495	-	-	-	-	-	-	-	-	2.7	Up
M300014542	M300014542	-	-	-	-	-	-	-	-	2.7	Up
XM_354546, XM_359256	M300014543	-	-	-	-	-	-	-	-	2.6	Up
M300014652	M300014652	-	-	-	-	-	-	-	-	2.4	Up
M300014863	M300014863	-	-	-	-	-	-	-	-	1.5	Up
M300014930	M300014930	-	-	-	-	-	-	-	-	1.9	Up
M300014959	M300014959	-	-	-	-	-	-	-	-	2.8	Up

NM_0010039									
53,NM_0010									
05866	M300015193	-	-	-	-	-	-	1.9	Up
XM_486775	M300015372	-	-	-	-	-	-	3.3	Up
M300015630	M300015630	-	-	-	-	-	-	2.1	Up
M300015637	M300015637	-	-	-	1.6	Down	-	-	
M300015702	M300015702	-	-	-	-	-	-	2.2	Up
NM_008376,									
NM_175860	M300015854	-	-	-	-	-	1.7	Up	-
M300015904	M300015904	-	-	-	-	-	-	2.1	Up
NM_177238	M300015921	-	-	-	-	-	-	2.8	Up
M300015923	M300015923	-	-	-	-	-	-	2.9	Up
XM_148040,									
XM_358825	M300016240	-	-	-	-	-	-	3.1	Up
M300016352	M300016352	-	-	-	-	-	-	1.7	Up
M300016405	M300016405	-	-	-	-	-	-	3.5	Up
M300016455	M300016455	-	-	-	-	-	-	1.8	Up
M300016469	M300016469	-	-	-	2.6	Down	-	-	
M300016604	M300016604	-	-	-	-	-	-	2.6	Up
XM_484980	M300016620	-	-	-	-	-	-	1.7	Up
M300016867	M300016867	-	-	-	-	-	-	2.9	Up
NM_0010047									
61,NM_1757									
06	M300016886	-	-	-	-	-	-	2.0	Up
M300016994	M300016994	-	-	-	-	-	-	3.0	Up
M300017147	M300017147	-	-	-	-	-	1.7	Up	-
XM_487719	M300017275	-	-	-	-	-	-	2.6	Up
M300017518	M300017518	-	-	-	-	-	2.0	Up	2.4
XM_486688	M300017591	-	-	-	-	-	-	2.6	Up
M300017679	M300017679	-	-	-	-	-	-	2.7	Up
NM_175673	M300017708	-	-	-	-	-	-	3.3	Up
M300018330	M300018330	-	-	-	-	-	-	2.0	Up
NM_025782	M300018472	-	-	-	-	-	-	1.6	Up
XM_484763	M300018569	-	-	-	2.8	Up	-	-	
M300019020	M300019020	-	-	-	-	-	-	2.0	Up
XM_484091	M300019107	-	-	-	-	-	-	2.1	Up
M300019133	M300019133	-	-	-	-	-	-	2.8	Up
XM_484644	M300019203	-	-	-	-	-	-	2.8	Up
M300019233	M300019233	-	-	-	-	-	-	2.7	Up
NM_177728	M300019544	-	-	-	-	-	-	2.8	Up
XM_156394,									
XM_358764	M300019576	-	-	-	-	-	-	2.0	Up



M300019577	M300019577	-	-	-	-	-	-	-	-	3.8	Up
M300019603	M300019603	-	-	-	-	-	-	-	-	2.3	Up
NM_026050, NM_133703	M300019683	-	-	-	-	-	-	2.2	Up	-	-
M300019696	M300019696	-	-	-	-	2.0	Down	-	-	-	-
M300019802	M300019802	-	-	-	-	-	-	3.1	Up	3.9	Up
M300019932	M300019932	-	-	-	-	-	-	-	-	3.0	Up
M300020065	M300020065	-	-	-	-	-	-	2.0	Up	2.6	Up
M300020084	M300020084	-	-	-	-	-	-	-	-	1.6	Up
XM_484717	M300020097	-	-	-	-	1.9	Down	-	-	-	-
XM_488518	M300020104	-	-	-	-	-	-	-	-	2.7	Up
M300020187	M300020187	-	-	-	-	-	-	-	-	1.5	Up
NM_176970	M300020288	-	-	-	-	-	-	-	-	2.5	Up
XM_485965	M300020322	-	-	-	-	-	-	-	-	1.8	Up
NM_153090, NM_178165	M300020385	-	-	-	-	-	-	1.5	Up	-	-
M300020484	M300020484	-	-	-	-	-	-	-	-	2.8	Up
M300020537	M300020537	-	-	-	-	-	-	-	-	2.3	Up
M300020584	M300020584	-	-	-	-	-	-	-	-	1.8	Up
M300020643	M300020643	-	-	-	-	-	-	-	-	2.5	Up
M300020690	M300020690	-	-	-	-	-	-	-	-	2.2	Up
NM_0010027 87, XM_4853 75	M300020724	-	-	-	-	-	-	-	-	1.9	Up
M300020794	M300020794	-	-	-	-	-	-	-	-	1.9	Up
M300020799	M300020799	-	-	-	-	-	-	-	-	1.8	Up
M300020882	M300020882	-	-	-	-	-	-	-	-	2.1	Up
M300020890	M300020890	-	-	-	-	-	-	-	-	2.3	Up
M300020990	M300020990	-	-	-	-	-	-	-	-	1.8	Up
M300021235	M300021235	-	-	-	-	-	-	-	-	2.2	Up
M300021311	M300021311	-	-	-	-	-	-	-	-	2.0	Up
M300021348	M300021348	-	-	-	-	-	-	-	-	2.1	Up
M300021412	M300021412	-	-	-	-	-	-	-	-	2.4	Up
XM_111691, XM_139933, XM_290002	M300021420	-	-	-	-	-	-	-	-	2.1	Up
M300021484	M300021484	-	-	-	-	-	-	-	-	2.2	Up
M300021566	M300021566	-	-	-	-	1.6	Down	-	-	-	-
M300021640	M300021640	-	-	-	-	-	-	-	-	1.6	Up
M300021707	M300021707	-	-	-	-	-	-	-	-	2.1	Up
M400000027	M400000027	-	-	-	-	-	-	-	-	2.1	Up
M400000040	M400000040	-	-	-	-	-	-	1.9	Up	-	-

XM_111600	M400000042	-	-	-	-	-	-	-	-	2.0	Up
XM_488021	M400000043	-	-	-	-	-	-	-	-	2.1	Up
M400000111	M400000111	-	-	-	-	-	-	-	-	1.8	Up
NM_153744, NM_153745	M400000132	-	-	-	-	-	-	-	-	1.9	Up
M400000136	M400000136	-	-	-	-	-	-	-	-	2.2	Up
M400000143	M400000143	-	-	-	-	-	-	-	-	2.0	Up
M400000151	M400000151	-	-	-	-	-	-	-	-	2.6	Up
M400000158	M400000158	-	-	-	-	-	-	-	-	3.0	Up
XM_127723, XM_359331	M400000162	-	-	-	-	-	-	-	-	1.6	Up
NM_0010072 23, XM_2861 21	M400000163	-	-	-	-	-	-	-	-	3.9	Up
M400000181	M400000181	-	-	-	-	-	-	-	-	2.2	Up
M400000182	M400000182	-	-	-	-	-	-	-	-	3.0	Up
M400000185	M400000185	-	-	-	-	-	-	-	-	2.5	Up
M400000191	M400000191	-	-	-	-	-	-	-	-	2.1	Up
M400000194	M400000194	-	-	-	-	-	-	-	-	2.8	Up
M400000205	M400000205	-	-	-	-	-	-	-	-	2.3	Up
M400000211	M400000211	-	-	-	-	-	-	2.6	Up	3.9	Up
XM_484594	M400000217	-	-	-	-	-	-	-	-	3.0	Up
M400000222	M400000222	-	-	-	-	-	-	-	-	2.3	Up
M400000257	M400000257	-	-	-	-	-	-	-	-	2.1	Up
M400000265	M400000265	-	-	-	-	-	-	-	-	2.2	Up
XM_126120, XM_489743	M400000271	-	-	-	-	-	-	1.6	Up	-	-
M400000283	M400000283	-	-	-	-	-	-	1.8	Up	2.5	Up
M400000316	M400000316	-	-	-	-	-	-	-	-	2.5	Down
M400000318	M400000318	-	-	-	-	-	-	-	-	1.9	Up
M400000335	M400000335	-	-	-	-	1.9	Down	-	-	-	-
M400000348	M400000348	-	-	-	-	-	-	-	-	2.9	Up
XM_483980	M400000387	-	-	-	-	-	-	-	-	1.7	Up
XM_356572	M400000399	-	-	-	-	-	-	-	-	1.9	Up
M400000401	M400000401	-	-	-	-	-	-	-	-	3.1	Up
M400000408	M400000408	-	-	-	-	-	-	-	-	1.5	Up
M400000412	M400000412	-	-	-	-	2.0	Down	-	-	-	-
M400000414	M400000414	-	-	-	-	-	-	1.5	Down	4.2	Down
M400000418	M400000418	-	-	-	-	-	-	-	-	2.5	Up
M400000420	M400000420	-	-	-	-	-	-	-	-	2.9	Up
M400000424	M400000424	-	-	-	-	-	-	-	-	1.6	Up
M400000425	M400000425	-	-	-	-	-	-	-	-	1.8	Up

XM_487260	M400000455	-	-	-	-	-	-	-	-	1.8	Up
M400000464	M400000464	-	-	-	-	-	-	-	-	2.0	Up
M400000468	M400000468	-	-	-	-	-	-	-	-	2.3	Up
M400000472	M400000472	-	-	-	-	-	-	-	-	1.8	Up
M400000479	M400000479	-	-	-	-	-	-	1.7	Up	2.3	Up
M400000484	M400000484	-	-	-	-	-	-	-	-	1.8	Up
M400000485	M400000485	-	-	-	-	-	-	-	-	2.0	Up
M400000495	M400000495	-	-	-	-	-	-	-	-	2.9	Up
XM_484305	M400000500	-	-	-	-	-	-	-	-	2.2	Down
M400000535	M400000535	-	-	-	-	-	-	-	-	2.7	Up
M400000537	M400000537	-	-	-	-	-	-	-	-	1.8	Up
M400000538	M400000538	-	-	-	-	-	-	-	-	2.2	Up
M400000541	M400000541	-	-	-	-	-	-	-	-	1.6	Up
M400000543	M400000543	-	-	-	-	1.6	Down	-	-	-	-
XM_485289	M400000548	-	-	-	-	-	-	-	-	2.3	Up
M400000567	M400000567	-	-	-	-	-	-	-	-	3.9	Up
M400000573	M400000573	-	-	-	-	-	-	-	-	2.7	Up
XM_358750, XM_489496	M400000579	-	-	-	-	-	-	-	-	2.3	Up
M400000589	M400000589	-	-	-	-	-	-	-	-	1.6	Up
XM_285181, XM_484554	M400000603	-	-	-	-	-	-	-	-	2.2	Up
XM_156106, XM_358794	M400000609	-	-	-	-	-	-	-	-	2.7	Up
M400000615	M400000615	-	-	-	-	-	-	-	-	2.2	Up
M400000618	M400000618	-	-	-	-	-	-	-	-	1.9	Up
M400000628	M400000628	-	-	-	-	-	-	-	-	2.7	Down
M400000641	M400000641	-	-	-	-	1.7	Down	-	-	-	-
M400000656	M400000656	-	-	-	-	-	-	-	-	3.0	Up
M400000697	M400000697	-	-	-	-	-	-	-	-	2.3	Up
M400000703	M400000703	-	-	-	-	-	-	-	-	1.6	Up
NM_016761, NM_053173	M400000734	-	-	-	-	2.6	Down	-	-	-	-
M400000739	M400000739	-	-	-	-	-	-	1.6	Down	-	-
M400000740	M400000740	-	-	-	-	-	-	-	-	2.9	Up
M400000745	M400000745	-	-	-	-	1.6	Down	-	-	-	-
M400000778	M400000778	-	-	-	-	-	-	-	-	3.3	Up
M400000786	M400000786	-	-	-	-	-	-	-	-	1.7	Up
M400000791	M400000791	-	-	-	-	-	-	1.5	Down	-	-
M400000793	M400000793	-	-	-	-	-	-	-	-	2.5	Up
M400000796	M400000796	-	-	-	-	2.0	Down	-	-	-	-
M400000811	M400000811	-	-	-	-	-	-	-	-	3.3	Up

M400000833	M400000833	-	-	-	-	-	-	-	-	1.6	Up
M400000835	M400000835	-	-	-	-	-	-	2.0	Up	2.8	Up
M400000845	M400000845	-	-	-	-	-	-	1.5	Down	-	-
M400000853	M400000853	-	-	-	-	-	-	-	-	3.9	Up
M400000866	M400000866	-	-	-	-	1.7	Down	-	-	-	-
M400000876	M400000876	-	-	-	-	-	-	-	-	2.2	Up
M400000900	M400000900	-	-	-	-	-	-	2.1	Up	3.5	Up
M400000904	M400000904	-	-	-	-	-	-	-	-	1.6	Down
M400000905	M400000905	-	-	-	-	-	-	-	-	3.0	Up
M400000906	M400000906	-	-	-	-	-	-	-	-	4.1	Up
M400000926	M400000926	-	-	-	-	-	-	-	-	1.9	Up
M400000941	M400000941	-	-	-	-	-	-	1.6	Up	-	-
NM_011137, NM_198932, NM_198934	M400000942	-	-	-	-	-	-	-	-	2.7	Up
M400000965	M400000965	-	-	-	-	-	-	-	-	2.0	Down
XM_141275	M400000982	-	-	-	-	-	-	-	-	2.3	Up
M400001013	M400001013	-	-	-	-	-	-	-	-	2.8	Up
M400001015	M400001015	-	-	-	-	-	-	-	-	1.6	Down
M400001016	M400001016	-	-	-	-	-	-	-	-	2.0	Down
M400001019	M400001019	-	-	-	-	-	-	-	-	2.5	Up
NM_009323, NM_011534	M400001034	-	-	-	-	-	-	-	-	1.7	Up
M400001039	M400001039	-	-	-	-	-	-	-	-	1.6	Down
M400001043	M400001043	-	-	-	-	-	-	2.8	Up	-	-
M400001066	M400001066	-	-	-	-	-	-	-	-	1.9	Down
NM_019770, XM_486207	M400001162	-	-	-	-	-	-	-	-	2.5	Down
M400001188	M400001188	-	-	-	-	-	-	-	-	2.1	Up
NM_019792, XM_357525	M400001189	-	-	-	-	-	-	-	-	2.4	Up
M400001197	M400001197	-	-	-	-	-	-	1.6	Up	1.7	Up
M400001215	M400001215	-	-	-	-	-	-	-	-	2.2	Up
M400001221	M400001221	-	-	-	-	-	-	-	-	2.7	Up
M400001233	M400001233	-	-	-	-	-	-	1.7	Up	-	-
XM_488092	M400001262	-	-	-	-	-	-	-	-	2.3	Up
M400001278	M400001278	-	-	-	-	-	-	-	-	1.9	Up
M400001279	M400001279	-	-	-	-	-	-	-	-	2.8	Up
M400001284	M400001284	-	-	-	-	-	-	-	-	3.7	Up
M400001301	M400001301	-	-	-	-	1.8	Down	-	-	-	-
M400001302	M400001302	-	-	-	-	-	-	-	-	1.7	Up
NM_030684,	M400001318	-	-	-	-	-	-	-	-	1.9	Down

XM_485979														
M400001322	M400001322		-	-	-	-	-	-	-	-	-	-	2.2	Up
NM_016870,														
NM_212441,														
NM_212442	M400001324		-	-	-	-	-	-	-	-	-	-	1.7	Up
XM_283292,														
XM_487037	M400001326		-	-	-	-	-	-	-	-	-	-	2.3	Up
M400001328	M400001328		-	-	-	-	-	-	-	-	-	-	-	-
M400001334	M400001334		-	-	-	-	1.8	Down	-	-	-	-	2.4	Up
M400001346	M400001346		-	-	-	-	-	-	-	-	-	-	1.7	Up
M400001351	M400001351		-	-	-	-	-	-	-	-	-	-	3.5	Up
M400001363	M400001363		-	-	-	-	-	-	-	1.9	Up	-	-	-
NM_181851,														
NM_199257,														
NM_199258	M400001375		-	-	-	-	-	-	-	-	-	-	3.0	Up
M400001395	M400001395		-	-	-	-	-	-	-	-	-	-	3.3	Up
NM_028532,														
NM_199455	M400001405		-	-	-	-	-	-	-	-	-	-	2.7	Up
M400001410	M400001410		-	-	-	-	-	-	-	-	-	-	1.5	Up
M400001435	M400001435		-	-	-	-	-	-	-	1.9	Up	-	-	-
M400001441	M400001441		-	-	-	-	-	-	-	-	-	-	1.6	Down
M400001458	M400001458		-	-	-	-	-	-	-	-	-	-	2.1	Up
M400001475	M400001475		-	-	-	-	-	-	-	-	-	-	2.2	Up
M400001511	M400001511		-	-	-	-	-	-	-	-	-	-	1.8	Up
M400001531	M400001531		-	-	-	-	-	-	-	-	-	-	1.5	Up
M400001538	M400001538		-	-	-	-	-	-	-	-	-	-	4.1	Up
M400001539	M400001539		-	-	-	-	-	-	-	-	-	-	2.6	Up
M400001558	M400001558		-	-	-	-	-	-	-	-	-	-	3.0	Up
M400001569	M400001569		-	-	-	-	-	-	-	-	-	-	2.5	Up
M400001571	M400001571		-	-	-	-	-	-	-	-	-	-	1.5	Up
M400001583	M400001583		-	-	-	-	-	-	-	-	-	-	3.1	Up
M400001584	M400001584		-	-	-	-	-	-	-	-	-	-	2.2	Up
M400001586	M400001586		-	-	-	-	-	-	-	-	-	-	1.7	Up
M400001594	M400001594		-	-	-	-	-	-	-	-	-	-	2.2	Up
M400001595	M400001595		-	-	-	-	-	-	-	-	-	-	3.5	Up
M400001598	M400001598		-	-	-	-	-	-	-	-	-	-	1.6	Up
M400001600	M400001600		-	-	-	-	-	-	-	-	-	-	2.2	Up
M400001613	M400001613		-	-	-	-	-	-	-	-	-	-	1.5	Up
M400001614	M400001614		-	-	-	-	-	-	-	-	-	-	2.2	Up
M400001630	M400001630		-	-	-	-	-	-	-	-	-	-	2.6	Up
M400001632	M400001632		-	-	-	-	-	-	-	-	-	-	2.0	Up
NM_054043,	M400001635		-	-	-	-	-	-	-	-	-	-	1.7	Up

XM_283029													
M400001636	M400001636		-	-	-	-	-	-	-	-	-	-	2.7 Up
M400001640	M400001640		-	-	-	-	-	-	-	-	-	-	1.6 Up
M400001650	M400001650		-	-	-	-	-	-	-	-	-	-	2.8 Up
M400001653	M400001653		-	-	-	-	-	-	-	-	-	-	2.0 Up
M400001672	M400001672		-	-	-	-	-	-	-	-	-	-	1.7 Up
M400001696	M400001696		-	-	-	-	-	-	-	-	-	-	2.3 Up
M400001699	M400001699		-	-	-	2.4	Down	-	-	-	-	-	-
M400001704	M400001704		-	-	-	-	-	-	-	-	-	-	2.5 Up
M400001712	M400001712		-	-	-	-	-	-	-	-	-	-	2.0 Up
M400001726	M400001726		-	-	-	-	-	-	-	-	-	-	1.7 Up
M400001727	M400001727		-	-	-	-	-	-	-	-	-	-	1.7 Up
XM_205762	M400001730		-	-	-	-	-	-	-	-	-	-	1.7 Up
XM_125716	M400001740		-	-	-	-	-	-	-	-	-	-	2.1 Up
M400001748	M400001748		-	-	-	-	-	-	-	-	-	-	2.3 Up
M400001752	M400001752		-	-	-	-	-	-	-	-	-	-	1.7 Up
XM_143997,													
XM_355504	M400001767		-	-	-	-	-	-	-	-	-	-	2.5 Up
M400001773	M400001773		-	-	-	-	-	-	-	-	-	-	2.2 Up
XM_145307	M400001785		-	-	-	-	-	-	-	-	-	-	2.4 Up
M400001788	M400001788		-	-	-	-	-	-	-	-	-	-	1.8 Up
M400001790	M400001790		-	-	-	-	-	-	-	-	-	-	2.1 Up
XM_141928	M400001794		-	-	-	-	-	-	-	-	-	-	1.7 Up
M400001809	M400001809		-	-	-	-	-	-	-	-	-	-	2.6 Up
M400001812	M400001812		-	-	-	-	-	-	-	-	-	-	1.7 Up
M400001838	M400001838		-	-	-	-	-	-	-	-	-	-	2.8 Up
M400001844	M400001844		-	-	-	-	-	-	-	-	-	-	2.6 Up
M400001855	M400001855		-	-	-	-	-	-	-	-	-	-	2.7 Up
M400001867	M400001867		-	-	-	1.7	Down	-	-	-	-	-	1.9 Down
M400001886	M400001886		-	-	-	-	-	-	-	-	-	-	2.5 Up
XM_139529	M400001892		-	-	-	-	-	-	-	-	-	-	3.4 Up
XM_359278,													
XM_359291,													
XM_489795	M400001903		-	-	-	-	-	-	-	-	-	-	2.1 Up
M400001916	M400001916		-	-	-	-	-	-	1.8	Up	-	-	3.7 Up
M400001920	M400001920		-	-	-	-	-	-	-	-	-	-	2.1 Up
M400001922	M400001922		-	-	-	-	-	-	-	-	-	-	1.7 Up
M400001932	M400001932		-	-	-	-	-	-	-	-	-	-	2.9 Up
XM_355454	M400001939		-	-	-	-	-	-	-	-	-	-	2.2 Up
M400001963	M400001963		-	-	-	-	-	-	-	-	-	-	2.3 Up
M400001972	M400001972		-	-	-	-	-	-	-	-	-	-	1.9 Up
XM_358202	M400001975		-	-	-	-	-	-	-	-	-	-	3.6 Up



M400002447	M400002447	-	-	-	-	-	1.6	Down	-	-
M400002453	M400002453	-	-	-	-	-	-	-	1.9	Up
M400002455	M400002455	-	-	-	-	-	1.7	Up	-	-
M400002515	M400002515	-	-	-	-	-	2.4	Up	3.5	Up
M400002521	M400002521	-	-	-	-	-	-	-	2.4	Up
M400002545	M400002545	-	-	-	-	-	2.1	Up	2.7	Up
M400002555	M400002555	-	-	-	-	-	-	-	1.6	Up
M400002562	M400002562	-	-	-	1.6	Down	-	-	-	-
M400002585	M400002585	-	-	-	-	-	1.6	Up	-	-
M400002663	M400002663	-	-	-	-	-	-	-	1.5	Up
M400002667	M400002667	-	-	-	2.2	Down	-	-	-	-
M400002673	M400002673	-	-	-	-	-	-	-	2.1	Up
M400002682	M400002682	-	-	-	-	-	-	-	3.3	Up
M400002694	M400002694	-	-	-	2.0	Up	-	-	-	-
XM_145847	M400002699	-	-	-	-	-	-	-	3.4	Up
M400002706	M400002706	-	-	-	-	-	-	-	2.2	Up
M400002710	M400002710	-	-	-	-	-	-	-	1.8	Up
M400002714	M400002714	-	-	-	-	-	-	-	2.0	Down
M400002715	M400002715	-	-	-	-	-	1.8	Down	-	-
XM_488375	M400002717	-	-	-	-	-	1.7	Up	1.6	Up
M400002724	M400002724	-	-	-	-	-	-	-	2.4	Up
M400002734	M400002734	-	-	-	-	-	-	-	2.8	Up
M400002746	M400002746	-	-	-	-	-	-	-	1.9	Up
M400002750	M400002750	-	-	-	-	-	-	-	2.4	Up
XM_484254	M400002775	-	-	-	-	-	-	-	2.0	Up
M400002776	M400002776	-	-	-	-	-	-	-	2.8	Up
M400002797	M400002797	-	-	-	-	-	-	-	2.8	Up
M400002800	M400002800	-	-	-	-	-	-	-	3.6	Up
M400002806	M400002806	-	-	-	-	-	-	-	2.3	Up
M400002811	M400002811	-	-	-	-	-	-	-	3.2	Up
M400002818	M400002818	-	-	-	-	-	-	-	2.2	Up
M400002824	M400002824	-	-	-	-	-	-	-	2.6	Up
M400002830	M400002830	-	-	-	-	-	-	-	3.0	Up
M400002848	M400002848	-	-	-	-	-	-	-	3.0	Up
M400002854	M400002854	-	-	-	-	-	1.5	Up	-	-
M400002865	M400002865	-	-	-	-	-	1.6	Up	-	-
XM_489212	M400002877	-	-	-	-	-	-	-	2.6	Up
NM_175391,										
XM_110146	M400002882	-	-	-	-	-	-	-	2.2	Down
M400002891	M400002891	-	-	-	-	-	1.8	Down	-	-
M400002899	M400002899	-	-	-	-	-	-	-	1.7	Down



M400002913	M400002913	-	-	-	-	-	-	-	-	2.2	Up
M400002918	M400002918	-	-	-	-	-	-	-	-	2.6	Up
M400002928	M400002928	-	-	-	-	-	-	-	-	2.0	Down
M400002942	M400002942	-	-	-	-	1.6	Down	-	-	-	-
M400002989	M400002989	-	-	-	-	-	-	-	-	1.6	Up
M400003037	M400003037	-	-	-	-	-	-	-	-	1.6	Up
XM_488011	M400003056	-	-	-	-	-	-	2.0	Up	3.2	Up
M400003058	M400003058	-	-	-	-	-	-	-	-	1.7	Up
M400003059	M400003059	-	-	-	-	-	-	-	-	4.3	Up
M400003067	M400003067	-	-	-	-	-	-	-	-	3.9	Up
M400003086	M400003086	-	-	-	-	-	-	-	-	2.1	Up
M400003108	M400003108	-	-	-	-	-	-	-	-	3.6	Up
NM_0010058											
63,NM_0010											
05864	M400003109	-	-	-	-	-	-	-	-	2.6	Up
M400003112	M400003112	-	-	-	-	-	-	-	-	2.0	Up
M400003114	M400003114	-	-	-	-	-	-	-	-	2.2	Up
M400003115	M400003115	-	-	-	-	-	-	-	-	2.4	Up
M400003132	M400003132	-	-	-	-	1.5	Down	-	-	-	-
M400003138	M400003138	-	-	-	-	-	-	-	-	1.9	Up
M400003139	M400003139	-	-	-	-	-	-	-	-	4.3	Up
M400003152	M400003152	-	1.5	Up	-	-	-	-	-	-	-
M400003156	M400003156	-	-	-	-	-	-	-	-	3.3	Up
M400003159	M400003159	-	-	-	-	-	-	-	-	1.9	Up
M400003162	M400003162	-	-	-	-	-	-	2.4	Up	-	-
NM_134232,											
XM_485346,											
XM_485347	M400003164	-	-	-	-	1.5	Down	-	-	-	-
M400003168	M400003168	-	-	-	-	-	-	1.8	Up	3.3	Up
M400003182	M400003182	-	-	-	-	-	-	-	-	2.5	Up
M400003188	M400003188	-	-	-	-	1.6	Down	-	-	3.2	Down
M400003224	M400003224	-	-	-	-	-	-	-	-	2.2	Up
M400003226	M400003226	-	-	-	-	-	-	-	-	2.2	Up
XM_356544	M400003232	-	-	-	-	-	-	-	-	2.1	Up
M400003260	M400003260	-	-	-	-	-	-	-	-	1.9	Up
M400003262	M400003262	-	-	-	-	-	-	-	-	2.2	Up
M400003269	M400003269	-	-	-	-	-	-	-	-	2.3	Up
M400003292	M400003292	-	-	-	-	-	-	1.6	Up	-	-
M400003301	M400003301	-	-	-	-	-	-	-	-	1.7	Down
XM_357381	M400003302	-	-	-	-	-	-	-	-	2.2	Up
M400003305	M400003305	-	-	-	-	-	-	-	-	2.4	Up
XM_488192	M400003335	-	-	-	-	-	-	-	-	2.0	Up

XM_484633	M400003341	-	-	-	-	-	-	-	-	2.4	Up
M400003345	M400003345	-	-	-	1.9	Down	-	-	-	-	-
M400003346	M400003346	-	-	-	-	-	-	-	-	1.6	Up
M400003351	M400003351	-	-	-	-	-	-	-	-	1.5	Up
M400003352	M400003352	-	-	-	-	-	-	-	-	1.7	Up
M400003358	M400003358	-	1.7	Down	1.9	Down	-	-	-	-	-
M400003394	M400003394	-	-	-	-	-	-	-	-	3.7	Up
M400003398	M400003398	-	-	-	-	-	-	-	-	1.6	Down
M400003406	M400003406	-	-	-	-	-	-	-	-	2.2	Up
M400003418	M400003418	-	-	-	-	-	-	-	-	2.6	Up
M400003440	M400003440	-	-	-	-	-	-	-	-	2.2	Up
M400003441	M400003441	-	-	-	-	-	-	-	-	3.6	Up
M400003446	M400003446	-	-	-	-	-	-	-	-	2.2	Up
M400003462	M400003462	-	-	-	-	-	-	-	-	2.3	Up
M400003463	M400003463	-	-	-	-	-	-	-	-	2.4	Up
M400003464	M400003464	-	-	-	-	-	-	-	-	1.9	Up
M400003465	M400003465	-	-	-	-	-	-	-	-	2.5	Up
XM_485809	M400003469	-	-	-	-	-	-	-	-	2.5	Up
M400003471	M400003471	-	-	-	-	-	-	-	-	3.6	Up
M400003487	M400003487	-	-	-	-	-	-	-	-	1.7	Up
M400003500	M400003500	-	-	-	2.1	Down	-	-	-	-	-
M400003507	M400003507	-	-	-	-	-	-	-	-	2.8	Up
M400003510	M400003510	-	-	-	-	-	-	-	-	1.5	Up
M400003516	M400003516	-	-	-	2.0	Down	-	-	-	-	-
M400003517	M400003517	-	-	-	-	-	-	-	-	2.7	Up
M400003535	M400003535	-	-	-	-	-	-	-	-	2.7	Up
M400003541	M400003541	-	-	-	-	-	-	-	-	2.0	Up
M400003556	M400003556	-	-	-	-	-	-	-	-	2.4	Up
M400003560	M400003560	-	-	-	-	-	-	-	-	2.9	Up
M400003566	M400003566	-	-	-	-	-	1.6	Up	-	-	-
M400003569	M400003569	-	-	-	-	-	-	-	-	2.1	Up
M400003571	M400003571	-	-	-	-	-	-	-	-	1.8	Up
M400003577	M400003577	-	-	-	-	-	-	-	-	1.7	Up
M400003583	M400003583	-	-	-	-	-	-	-	-	3.0	Up
M400003612	M400003612	-	-	-	-	-	-	-	-	2.2	Up
M400003614	M400003614	-	-	-	-	-	-	-	-	2.1	Up
M400003638	M400003638	-	-	-	-	-	-	-	-	4.0	Up
M400003642	M400003642	-	-	-	-	-	-	-	-	1.9	Up
M400003660	M400003660	-	-	-	-	-	-	-	-	2.0	Up
M400003664	M400003664	-	-	-	-	-	-	-	-	2.2	Up
XM_358214,	M400003685	-	-	-	-	-	-	-	-	2.7	Up

XM_359410												
M400003709	M400003709	-	-	-	-	-	-	2.0	Up	3.0	Up	
M400003743	M400003743	-	-	-	-	-	-	-	-	2.2	Up	
M400003744	M400003744	-	-	-	-	-	-	-	-	2.5	Up	
M400003749	M400003749	-	-	-	-	-	-	-	-	2.9	Up	
M400003753	M400003753	-	-	-	-	-	-	-	-	2.2	Up	
M400003798	M400003798	-	-	-	-	-	-	-	-	2.7	Up	
M400003803	M400003803	-	-	-	-	-	-	-	-	3.0	Up	
M400003821	M400003821	-	-	-	-	-	-	-	-	2.4	Up	
M400003825	M400003825	-	-	-	-	-	-	-	-	2.2	Up	
M400003838	M400003838	-	-	-	-	-	-	-	-	1.5	Up	
M400003840	M400003840	-	2.0	Down	-	-	-	-	-	-	-	
M400003842	M400003842	-	-	-	-	-	-	-	-	2.3	Up	
M400003844	M400003844	-	-	-	-	-	-	-	-	2.5	Up	
M400003851	M400003851	-	-	-	-	-	-	-	-	2.5	Up	
XM_156206, XM_285829	M400003856	-	-	-	-	-	-	-	-	2.4	Up	
M400003866	M400003866	-	-	-	-	-	-	-	-	1.9	Down	
M400003880	M400003880	-	-	-	-	-	-	1.6	Up	2.9	Up	
M400003887	M400003887	-	-	-	-	-	-	-	-	2.5	Up	
M400003899	M400003899	-	-	-	-	-	-	-	-	3.0	Up	
M400003918	M400003918	-	-	-	-	-	-	-	-	1.8	Up	
M400003921	M400003921	-	-	-	-	-	-	-	-	2.4	Up	
M400003922	M400003922	-	-	-	-	-	-	-	-	3.8	Up	
M400003926	M400003926	-	-	-	-	-	-	-	-	1.5	Up	
M400003946	M400003946	-	-	-	-	-	-	-	-	2.3	Up	
M400003952	M400003952	-	-	-	-	-	-	-	-	1.7	Up	
M400003956	M400003956	-	-	-	-	-	-	-	-	1.8	Up	
M400003964	M400003964	-	-	-	-	-	-	1.5	Up	-	-	
XM_485812	M400003981	-	-	-	-	-	-	-	-	2.9	Up	
M400003985	M400003985	-	-	-	-	-	-	-	-	2.1	Up	
M400003987	M400003987	-	-	-	-	-	-	-	-	2.6	Up	
M400003988	M400003988	-	-	-	-	-	-	-	-	3.7	Up	
M400003990	M400003990	-	-	-	-	1.9	Down	-	-	-	-	
NM_144541, NM_181279, NM_181280, NM_181281, NM_181282	M400004011	-	-	-	-	2.3	Up	2.8	Up	-	-	
XM_148600, XM_358823	M400004077	-	-	-	-	-	-	-	-	1.9	Up	
M400004094	M400004094	-	-	-	-	-	-	-	-	2.2	Up	

M400004149	M400004149	-	-	-	-	-	-	-	-	2.2	Up
M400004153	M400004153	-	-	-	-	-	-	-	-	1.9	Up
NM_008783, NM_183355	M400004160	-	-	-	-	-	-	1.6	Up	2.9	Up
M400004206	M400004206	-	-	-	-	-	-	-	-	2.5	Up
M400004213	M400004213	-	-	-	-	-	-	-	-	2.1	Up
M400004219	M400004219	-	-	-	-	-	-	-	-	3.1	Up
M400004224	M400004224	-	-	-	-	1.9	Down	-	-	2.6	Down
M400004237	M400004237	-	-	-	-	-	-	-	-	1.7	Up
M400004242	M400004242	-	-	-	-	-	-	-	-	1.5	Up
M400004243	M400004243	-	-	-	-	-	-	-	-	2.0	Up
M400004267	M400004267	-	-	-	-	-	-	-	-	2.7	Up
M400004268	M400004268	-	-	-	-	-	-	-	-	2.1	Up
M400004274	M400004274	-	-	-	-	-	-	-	-	2.0	Up
M400004278	M400004278	-	-	-	-	-	-	-	-	2.3	Up
M400004301	M400004301	-	-	-	-	-	-	-	-	1.9	Up
M400004316	M400004316	-	-	-	-	-	-	-	-	1.5	Up
NM_011531, NM_177129	M400004317	-	-	-	-	-	-	-	-	1.5	Up
M400004320	M400004320	-	-	-	-	-	-	-	-	2.7	Up
NM_175322	M400004326	-	-	-	-	-	-	1.6	Up	2.6	Up
NM_177745	M400004337	-	-	-	-	1.7	Down	-	-	-	-
M400004343	M400004343	-	-	-	-	-	-	-	-	3.5	Up
M400004348	M400004348	-	-	-	-	-	-	-	-	2.2	Up
M400004349	M400004349	-	-	-	-	-	-	-	-	3.6	Up
M400004366	M400004366	-	-	-	-	-	-	2.2	Up	-	-
NM_0010027 71,XM_4842 52	M400004370	-	-	-	-	-	-	-	-	1.5	Up
M400004374	M400004374	-	-	-	-	-	-	-	-	3.9	Up
M400004387	M400004387	-	-	-	-	-	-	-	-	2.2	Down
M400004391	M400004391	-	-	-	-	-	-	-	-	2.9	Up
M400004396	M400004396	-	-	-	-	-	-	-	-	2.4	Up
XM_358115	M400004397	-	-	-	-	-	-	-	-	3.2	Up
M400004412	M400004412	-	-	-	-	-	-	-	-	2.1	Up
M400004421	M400004421	-	-	-	-	-	-	-	-	2.2	Up
M400004438	M400004438	-	-	-	-	-	-	-	-	2.8	Up
NM_0010027 95,XM_4891 95	M400004444	-	-	-	-	-	-	-	-	2.0	Up
M400004459	M400004459	-	-	-	-	-	-	-	-	3.2	Up
M400004460	M400004460	-	-	-	-	-	-	-	-	1.8	Up

M400004469	M400004469	-	-	-	-	-	-	-	-	3.1	Up
M400004481	M400004481	-	-	-	-	-	-	-	-	1.7	Up
M400004485	M400004485	-	-	-	-	-	-	-	-	1.9	Up
M400004495	M400004495	-	-	-	-	-	-	-	-	2.6	Up
M400004503	M400004503	-	-	-	-	-	-	-	-	2.2	Up
M400004507	M400004507	-	-	-	-	-	-	-	-	1.7	Up
M400004522	M400004522	-	-	-	-	-	-	-	-	1.9	Up
M400004551	M400004551	-	-	-	-	-	-	-	-	2.3	Up
M400004563	M400004563	-	-	-	-	-	-	-	-	2.2	Up
M400004564	M400004564	-	-	-	-	1.8	Down	-	-	-	-
M400004584	M400004584	-	-	-	-	-	-	-	-	1.7	Up
M400004598	M400004598	-	-	-	-	-	-	-	-	2.3	Up
M400004599	M400004599	-	-	-	-	-	-	-	-	3.3	Up
M400004603	M400004603	-	-	-	-	-	-	-	-	2.2	Up
M400004605	M400004605	-	-	-	-	-	-	-	-	2.9	Up
M400004606	M400004606	-	-	-	-	-	-	-	-	1.5	Up
M400004620	M400004620	-	-	-	-	1.8	Down	-	-	-	-
XM_486008	M400004624	-	-	-	-	-	-	-	-	2.5	Up
M400004627	M400004627	-	-	-	-	-	-	-	-	1.7	Up
M400004633	M400004633	-	-	-	-	-	-	-	-	2.1	Up
M400004634	M400004634	-	-	-	-	-	-	-	-	3.0	Up
XM_486665	M400004635	-	-	-	-	-	-	-	-	2.6	Up
M400004644	M400004644	-	-	-	-	2.3	Down	-	-	-	-
M400004651	M400004651	-	-	-	-	-	-	1.5	Down	-	-
M400004652	M400004652	-	-	-	-	-	-	-	-	2.4	Up
XM_488192	M400004659	-	-	-	-	-	-	-	-	3.7	Up
M400004678	M400004678	-	-	-	-	2.1	Down	-	-	-	-
M400004711	M400004711	-	-	-	-	1.8	Down	-	-	-	-
M400004716	M400004716	-	-	-	-	1.7	Down	-	-	-	-
M400004723	M400004723	-	-	-	-	-	-	-	-	1.9	Up
M400004726	M400004726	-	-	-	-	-	-	-	-	2.8	Up
M400004733	M400004733	-	-	-	-	-	-	-	-	1.8	Up
M400004739	M400004739	-	-	-	-	1.8	Down	-	-	-	-
M400004746	M400004746	-	-	-	-	-	-	-	-	1.5	Up
M400004750	M400004750	-	-	-	-	-	-	-	-	3.1	Up
M400004752	M400004752	-	-	-	-	-	-	-	-	2.4	Up
XM_485269	M400004754	-	-	-	-	-	-	-	-	3.8	Up
M400004766	M400004766	-	-	-	-	-	-	1.7	Up	-	-
M400004768	M400004768	-	-	-	-	-	-	-	-	1.5	Up
M400004774	M400004774	-	-	-	-	-	-	-	-	2.0	Up
M400004776	M400004776	-	-	-	-	-	-	-	-	1.5	Up

M400004777	M400004777	-	-	-	-	-	-	-	-	3.5	Up
M400004780	M400004780	-	-	-	-	-	-	-	-	2.0	Up
M400004787	M400004787	-	-	-	-	-	-	-	-	2.4	Up
M400004791	M400004791	-	-	-	-	-	-	-	-	2.4	Up
NM_174990,											
NM_175048	M400004812	-	2.2	Down	-	-	-	-	-	-	-
NM_175365	M400004829	-	-	-	-	-	-	-	-	2.0	Up
XM_289125,											
XM_487113	M400004830	-	-	-	-	-	-	-	-	2.5	Up
M400004853	M400004853	-	-	-	-	-	-	-	-	2.2	Up
M400004854	M400004854	-	-	-	-	-	-	-	-	1.9	Up
M400004858	M400004858	-	-	-	-	-	-	-	-	2.5	Up
XM_147444	M400004864	-	-	-	-	-	-	-	-	2.4	Up
M400004866	M400004866	-	-	-	-	-	-	-	-	2.0	Up
M400004869	M400004869	-	-	-	-	-	-	-	-	2.2	Up
M400004871	M400004871	-	-	-	-	-	-	-	-	2.3	Up
NM_009615,											
XM_488213	M400004884	-	-	-	-	-	-	-	-	3.3	Up
XM_488039	M400004893	-	-	-	1.9	Down	-	-	-	-	-
M400004896	M400004896	-	-	-	-	-	-	-	-	3.5	Up
M400004901	M400004901	-	-	-	-	-	-	-	-	2.4	Up
M400004926	M400004926	-	-	-	-	-	-	-	-	1.5	Up
M400004937	M400004937	-	-	-	-	-	-	-	-	2.7	Up
M400004972	M400004972	-	-	-	-	-	-	-	-	2.4	Up
M400004978	M400004978	-	-	-	-	-	-	-	-	1.5	Up
M400004983	M400004983	-	-	-	-	-	-	-	-	2.7	Up
M400004994	M400004994	-	-	-	-	-	-	-	-	1.7	Down
M400004997	M400004997	-	-	-	-	-	-	-	-	2.6	Up
M400005004	M400005004	-	-	-	-	-	-	-	-	1.8	Up
M400005015	M400005015	-	-	-	-	-	-	-	-	2.2	Up
M400005018	M400005018	-	-	-	-	-	-	-	-	1.9	Up
M400005026	M400005026	-	-	-	-	-	-	-	-	3.8	Up
M400005027	M400005027	-	-	-	-	-	-	-	-	2.9	Up
M400005028	M400005028	-	-	-	-	-	-	-	-	2.0	Up
M400005039	M400005039	-	-	-	-	-	-	-	-	2.9	Up
M400005048	M400005048	-	-	-	-	-	-	-	-	1.8	Up
M400005056	M400005056	-	-	-	-	-	-	-	-	2.5	Up
M400005062	M400005062	-	-	-	-	-	-	1.5	Up	2.9	Up
M400005076	M400005076	-	-	-	-	-	-	-	-	2.2	Up
M400005096	M400005096	-	-	-	-	-	-	-	-	1.5	Up
M400005097	M400005097	-	-	-	-	-	-	-	-	1.8	Up
M400005102	M400005102	-	-	-	-	-	-	-	-	2.4	Up

XM_486010	M400005103	-	-	-	-	-	-	-	-	2.0	Up
M400005104	M400005104	-	-	-	-	-	-	-	-	3.5	Up
XM_489051	M400005110	-	-	-	-	-	-	-	-	3.3	Up
M400005127	M400005127	-	-	-	-	-	-	-	-	3.7	Up
M400005145	M400005145	-	-	-	-	-	-	-	-	2.8	Up
M400005150	M400005150	-	-	-	-	-	-	-	-	2.8	Up
M400005151	M400005151	-	-	-	-	-	-	2.5	Up	3.5	Up
M400005164	M400005164	-	-	-	-	-	-	-	-	1.6	Up
M400005175	M400005175	-	-	-	-	-	-	-	-	3.8	Up
NM_007497, XM_204339	M400005232	-	-	-	-	-	-	-	-	2.3	Down
M400005233	M400005233	-	-	-	-	-	-	-	-	2.9	Up
M400005246	M400005246	-	-	-	-	-	-	-	-	2.5	Up
M400005251	M400005251	-	-	-	-	-	-	-	-	1.8	Up
XM_489523	M400005263	-	-	-	-	-	-	-	-	1.6	Up
M400005269	M400005269	-	-	-	-	1.7	Down	-	-	-	-
M400005276	M400005276	-	-	-	-	-	-	-	-	3.6	Up
M400005289	M400005289	-	-	-	-	-	-	-	-	2.3	Up
M400005300	M400005300	-	-	-	-	-	-	-	-	3.3	Up
M400005316	M400005316	-	-	-	-	-	-	-	-	2.2	Down
M400005318	M400005318	-	-	-	-	-	-	-	-	2.0	Up
M400005324	M400005324	-	-	-	-	-	-	-	-	3.1	Up
M400005340	M400005340	-	-	-	-	-	-	-	-	1.7	Up
M400005345	M400005345	-	-	-	-	-	-	-	-	2.3	Up
M400005347	M400005347	-	-	-	-	-	-	-	-	3.3	Up
M400005353	M400005353	-	-	-	-	-	-	-	-	1.7	Up
M400005358	M400005358	-	-	-	-	-	-	-	-	1.8	Up
M400005359	M400005359	-	-	-	-	-	-	-	-	3.7	Up
M400005371	M400005371	-	-	-	-	-	-	-	-	2.8	Up
M400005377	M400005377	-	-	-	-	-	-	-	-	2.8	Up
M400005389	M400005389	-	-	-	-	-	-	-	-	2.1	Up
M400005400	M400005400	-	-	-	-	-	-	-	-	1.5	Up
M400005413	M400005413	-	-	-	-	-	-	-	-	3.1	Up
M400005419	M400005419	-	-	-	-	-	-	-	-	4.3	Up
M400005424	M400005424	-	-	-	-	-	-	-	-	2.4	Up
M400005436	M400005436	-	-	-	-	-	-	-	-	3.9	Up
M400005439	M400005439	-	-	-	-	-	-	-	-	2.1	Up
M400005442	M400005442	-	-	-	-	-	-	-	-	3.9	Up
M400005447	M400005447	-	-	-	-	-	-	-	-	1.9	Up
XM_484239	M400005450	-	-	-	-	-	-	-	-	2.1	Up
M400005454	M400005454	-	-	-	-	-	-	1.6	Up	2.9	Up

M400005478	M400005478	-	-	-	-	-	-	-	-	2.3	Up
M400005501	M400005501	-	-	-	-	-	-	-	-	1.6	Down
M400005519	M400005519	-	-	-	-	1.6	Down	-	-	1.6	Up
M400005548	M400005548	-	-	-	-	-	-	-	-	2.6	Up
M400005555	M400005555	-	-	-	-	-	-	-	-	2.5	Up
M400005584	M400005584	-	-	-	-	-	-	-	-	2.9	Up
M400005597	M400005597	-	-	-	-	-	-	1.9	Up	-	-
NM_207256	M400005606	-	-	-	-	-	-	-	-	1.8	Up
M400005609	M400005609	-	-	-	-	-	-	-	-	3.5	Up
M400005615	M400005615	-	-	-	-	-	-	-	-	3.4	Up
M400005616	M400005616	-	-	-	-	-	-	-	-	2.6	Up
M400005648	M400005648	-	-	-	-	-	-	-	-	1.7	Down
XM_356979	M400005654	-	-	-	-	-	-	-	-	1.6	Down
M400005665	M400005665	-	-	-	-	-	-	-	-	3.2	Up
M400005668	M400005668	-	-	-	-	-	-	-	-	2.9	Up
M400005697	M400005697	-	-	-	-	1.7	Down	-	-	-	-
M400005707	M400005707	-	-	-	-	-	-	-	-	2.1	Up
M400005719	M400005719	-	-	-	-	-	-	-	-	2.2	Up
XM_356386	M400005720	-	-	-	-	-	-	-	-	1.6	Up
M400005725	M400005725	-	-	-	-	-	-	-	-	2.4	Up
M400005726	M400005726	-	-	-	-	-	-	-	-	1.9	Up
M400005742	M400005742	-	-	-	-	-	-	-	-	3.2	Up
M400005743	M400005743	-	-	-	-	-	-	-	-	3.2	Up
M400005745	M400005745	-	-	-	-	-	-	-	-	2.5	Up
M400005756	M400005756	-	-	-	-	-	-	-	-	2.9	Up
M400005769	M400005769	-	-	-	-	-	-	-	-	3.6	Up
M400005773	M400005773	-	-	-	-	-	-	-	-	1.9	Up
XM_486806,											
XM_486833	M400005774	-	-	-	-	-	-	-	-	2.7	Up
M400005775	M400005775	-	-	-	-	-	-	-	-	2.9	Up
M400005781	M400005781	-	-	-	-	-	-	-	-	1.6	Up
M400005784	M400005784	-	-	-	-	1.8	Down	1.6	Down	-	-
M400005787	M400005787	-	-	-	-	-	-	-	-	2.5	Up
M400005792	M400005792	-	-	-	-	-	-	-	-	3.1	Up
M400005805	M400005805	-	-	-	-	-	-	-	-	3.1	Up
M400005815	M400005815	-	-	-	-	-	-	-	-	3.2	Up
M400005819	M400005819	-	-	-	-	-	-	-	-	2.0	Up
M400005827	M400005827	-	-	-	-	-	-	-	-	2.1	Up
M400005831	M400005831	-	-	-	-	1.6	Down	-	-	-	-
M400005833	M400005833	-	-	-	-	-	-	-	-	1.6	Up
NM_146673,											
NM_146674	M400005839	-	-	-	-	-	-	-	-	2.4	Up



M400005842	M400005842	-	-	-	-	-	-	2.9	Up	
M400005857	M400005857	-	-	-	-	-	-	2.0	Down	
M400005864	M400005864	-	-	-	-	-	-	3.9	Up	
M400005868	M400005868	-	-	-	-	-	4.0	Up	2.1	Up
M400005870	M400005870	-	-	-	-	-	-	-	4.3	Up
XM_487099	M400005876	-	-	-	-	-	-	-	2.9	Up
XM_356738	M400005887	-	-	-	-	-	-	-	2.4	Up
M400005893	M400005893	-	2.5	Down	-	-	-	-	-	-
M400005898	M400005898	-	-	-	-	-	1.5	Up	-	-
M400005921	M400005921	-	-	-	-	-	-	-	1.9	Up
M400005922	M400005922	-	-	-	-	-	-	-	1.9	Up
M400005928	M400005928	-	-	-	-	-	-	-	3.5	Up
M400005932	M400005932	-	-	-	-	-	-	-	1.5	Up
M400005941	M400005941	-	-	-	-	-	2.7	Up	-	-
M400005962	M400005962	-	-	-	-	-	-	-	2.2	Down
M400005965	M400005965	-	-	-	-	-	-	-	3.0	Up
M400005968	M400005968	-	-	-	-	-	-	-	1.9	Up
M400005970	M400005970	-	-	-	-	-	-	-	1.7	Up
M400005976	M400005976	-	-	-	-	-	1.9	Up	-	-
M400006001	M400006001	-	-	-	-	-	-	-	2.4	Up
M400006036	M400006036	-	-	-	-	-	-	-	1.9	Up
XM_356849	M400006047	-	-	-	-	-	-	-	1.6	Down
M400006048	M400006048	-	-	-	-	-	-	-	1.9	Up
M400006060	M400006060	-	-	-	-	-	1.9	Up	-	-
M400006069	M400006069	-	-	-	-	-	-	-	1.5	Down
M400006084	M400006084	-	-	-	2.0	Down	-	-	-	-
XM_489874	M400006106	-	-	-	-	-	-	-	2.5	Up
M400006118	M400006118	-	-	-	-	-	1.6	Up	-	-
M400006125	M400006125	-	-	-	-	-	-	-	3.4	Up
M400006128	M400006128	-	-	-	-	-	-	-	2.2	Up
M400006149	M400006149	-	-	-	-	-	-	-	2.0	Up
M400006161	M400006161	-	-	-	-	-	-	-	2.0	Up
M400006167	M400006167	-	-	-	-	-	-	-	3.8	Up
M400006179	M400006179	-	-	-	-	-	-	-	3.0	Up
M400006198	M400006198	-	-	-	-	-	-	-	1.7	Up
M400006200	M400006200	-	-	-	-	-	-	-	2.9	Down
M400006201	M400006201	-	-	-	-	-	-	-	2.0	Up
M400006208	M400006208	-	-	-	-	-	-	-	2.1	Up
M400006213	M400006213	-	-	-	-	-	-	-	2.2	Up
XM_135569, XM_358048, XM_488241	M400006214	-	-	-	-	-	-	-	2.8	Up

M400006220	M400006220	-	-	-	-	-	3.6	Up	-	-
XM_356419	M400006225	-	-	-	-	-	-	-	2.4	Up
XM_123311	M400006238	-	-	-	-	-	-	-	2.8	Up
XM_485802	M400006244	-	-	-	-	-	-	-	3.1	Up
XM_136071, XM_486832	M400006261	-	-	-	-	-	-	-	2.5	Up
M400006264	M400006264	-	2.9	Up	-	-	-	-	-	-
M400006286	M400006286	-	-	-	-	-	1.9	Up	-	-
M400006317	M400006317	-	-	-	1.6	Down	-	-	-	-
M400006318	M400006318	-	-	-	-	-	-	-	1.9	Up
M400006330	M400006330	-	1.6	Down	-	-	-	-	-	-
M400006333	M400006333	-	-	-	-	-	2.4	Up	4.2	Up
M400006339	M400006339	-	-	-	-	-	2.2	Up	3.3	Up
M400006342	M400006342	-	-	-	-	-	-	-	1.9	Up
M400006345	M400006345	-	-	-	-	-	-	-	2.0	Up
XM_143853, XM_485398, XM_485399, XM_485400	M400006350	-	-	-	-	-	-	-	2.9	Up
M400006351	M400006351	-	-	-	-	-	-	-	1.8	Up
M400006357	M400006357	-	-	-	-	-	-	-	3.7	Up
M400006363	M400006363	-	-	-	-	-	2.1	Up	1.9	Up
M400006370	M400006370	-	-	-	3.7	Down	-	-	-	-
M400006439	M400006439	-	-	-	-	-	-	-	1.9	Down
XM_488111	M400006455	-	-	-	-	-	-	-	1.5	Down
XM_285682, XM_487255	M400006493	-	-	-	-	-	-	-	1.9	Up
M400006499	M400006499	-	-	-	-	-	-	-	2.1	Up
M400006505	M400006505	-	-	-	-	-	-	-	2.2	Up
XM_484273	M400006535	-	-	-	-	-	-	-	1.7	Up
XM_484475	M400006559	-	-	-	-	-	1.7	Up	1.9	Up
M400006582	M400006582	-	-	-	-	-	-	-	1.7	Up
M400006600	M400006600	-	-	-	-	-	1.7	Up	2.9	Up
M400006642	M400006642	-	-	-	-	-	-	-	1.7	Up
M400006666	M400006666	-	-	-	-	-	-	-	2.2	Up
M400006707	M400006707	-	-	-	-	-	1.9	Up	-	-
M400006755	M400006755	-	-	-	-	-	-	-	2.7	Up
M400006764	M400006764	-	-	-	3.5	Up	-	-	-	-
M400006812	M400006812	-	-	-	3.4	Up	-	-	-	-
M400006856	M400006856	-	-	-	-	-	-	-	3.3	Up
M400006879	M400006879	-	-	-	-	-	-	-	3.5	Up
M400006903	M400006903	-	-	-	-	-	-	-	2.2	Up

M400006909	M400006909	-	-	-	-	-	-	-	-	1.9	Up
M400006937	M400006937	-	-	-	-	-	-	-	-	1.7	Up
M400006956	M400006956	-	-	-	-	-	-	-	-	3.9	Up
M400006979	M400006979	-	-	-	-	-	-	-	-	1.7	Up
XM_486116	M400007003	-	-	-	-	-	-	-	-	1.6	Up
XM_485820	M400007009	-	-	-	-	-	-	-	-	1.8	Up
M400007028	M400007028	-	-	-	-	-	-	-	-	3.9	Up
XM_485292	M400007033	-	-	-	-	-	-	-	-	2.5	Up
M400007034	M400007034	-	-	-	-	-	-	-	-	3.7	Up
M400007075	M400007075	-	-	-	-	-	-	-	-	2.0	Up
M400007105	M400007105	-	-	-	-	-	-	-	-	2.3	Up
M400007110	M400007110	-	-	-	-	-	-	-	-	1.8	Up
XM_487920	M400007117	-	-	-	-	-	-	-	-	2.1	Up
M400007133	M400007133	-	-	-	-	-	-	-	-	1.5	Up
M400007146	M400007146	-	-	-	-	-	-	-	-	2.0	Up
M400007182	M400007182	-	-	-	-	-	-	-	-	1.9	Up
M400007224	M400007224	-	-	-	-	-	-	-	-	2.3	Up
M400007246	M400007246	-	-	-	-	-	-	-	-	3.1	Up
XM_485738	M400007259	-	-	-	-	-	-	-	-	2.2	Up
M400007295	M400007295	-	-	-	-	-	-	-	-	2.8	Up
M400007325	M400007325	-	-	-	-	-	-	-	-	2.3	Up
M400007346	M400007346	-	1.7	Down	-	-	-	-	-	1.8	Down
M400007348	M400007348	-	-	-	-	-	-	-	-	2.8	Up
NM_146297, NM_207565 NM_010447, XM_486780	M400007388	-	-	-	-	-	-	-	-	2.0	Up
M400007395	M400007395	-	-	-	-	-	-	-	-	1.6	Down
M400007396	M400007396	-	-	-	-	-	-	-	-	1.7	Up
M400007396	M400007396	-	-	-	-	-	-	-	-	3.0	Up
M400007412	M400007412	-	-	-	-	-	-	-	-	1.5	Up
M400007413	M400007413	-	-	-	-	-	-	-	-	2.4	Up
M400007414	M400007414	-	-	-	-	-	-	-	-	4.1	Up
M400007426	M400007426	-	-	-	-	-	-	-	-	1.6	Up
XM_486386	M400007467	-	-	-	-	-	2.0	Up	-	-	-
M400007468	M400007468	-	-	-	-	-	-	-	-	2.0	Down
M400007473	M400007473	-	-	-	-	-	-	-	-	2.1	Up
XM_355961, XM_485879, XM_485885, XM_487992	M400007503	-	-	-	-	-	-	-	-	2.5	Up
M400007556	M400007556	-	-	-	-	-	-	-	-	2.0	Up
XM_122526	M400007734	-	-	-	-	-	2.2	Up	-	2.4	Up

M400007752	M400007752	-	-	-	-	-	-	-	-	2.5	Up
M400007763	M400007763	-	-	-	-	-	-	-	-	1.5	Up
XM_128332,											
XM_358877	M400007764	-	-	-	-	-	-	-	-	2.8	Up
M400007770	M400007770	-	-	-	-	-	-	1.9	Up	3.0	Up
M400007781	M400007781	-	-	-	-	-	-	-	-	1.5	Up
M400007811	M400007811	-	-	-	-	-	-	-	-	2.4	Up
M400007817	M400007817	-	-	-	-	-	-	-	-	3.0	Up
M400007823	M400007823	-	-	-	-	-	-	-	-	1.9	Up
M400007853	M400007853	-	-	-	-	-	-	-	-	1.6	Up
M400007863	M400007863	-	-	-	-	1.7	Down	-	-	-	-
M400007865	M400007865	-	-	-	-	-	-	1.8	Up	-	-
M400007866	M400007866	-	-	-	-	-	-	-	-	2.5	Up
XM_488016	M400007877	-	-	-	-	-	-	-	-	1.9	Up
M400007883	M400007883	-	-	-	-	-	-	-	-	2.7	Up
XM_485950	M400007895	-	-	-	-	-	-	2.2	Up	-	-
M400007960	M400007960	-	-	-	-	2.7	Down	-	-	-	-
M400008000	M400008000	-	-	-	-	1.7	Down	-	-	-	-
M400008001	M400008001	-	-	-	-	-	-	-	-	3.6	Up
M400008025	M400008025	-	-	-	-	-	-	2.3	Up	2.7	Up
M400008054	M400008054	-	-	-	-	-	-	-	-	2.1	Up
M400008073	M400008073	-	-	-	-	-	-	-	-	2.6	Up
M400008074	M400008074	-	-	-	-	-	-	-	-	2.0	Up
XM_487989	M400008079	-	-	-	-	-	-	-	-	1.5	Up
M400008096	M400008096	-	-	-	-	-	-	-	-	3.7	Up
M400008101	M400008101	-	-	-	-	-	-	-	-	2.3	Up
M400008119	M400008119	-	-	-	-	-	-	-	-	2.4	Up
M400008142	M400008142	-	-	-	-	-	-	-	-	2.3	Up
M400008144	M400008144	-	-	-	-	-	-	-	-	2.8	Up
M400008149	M400008149	-	-	-	-	-	-	-	-	1.7	Up
M400008168	M400008168	-	-	-	-	-	-	-	-	2.0	Up
M400008180	M400008180	-	-	-	-	-	-	1.6	Up	-	-
M400008185	M400008185	-	-	-	-	-	-	-	-	1.6	Down
M400008191	M400008191	-	-	-	-	-	-	-	-	3.0	Up
M400008202	M400008202	-	-	-	-	-	-	-	-	1.5	Up
XM_486155	M400008203	-	-	-	-	-	-	-	-	2.7	Up
M400008206	M400008206	-	-	-	-	-	-	-	-	2.0	Up
M400008209	M400008209	-	-	-	-	-	-	2.8	Up	2.8	Up
M400008214	M400008214	-	-	-	-	-	-	-	-	1.6	Up
M400008242	M400008242	-	-	-	-	-	-	-	-	2.8	Down
M400008245	M400008245	-	-	-	-	-	-	3.7	Up	3.7	Up

M400008274	M400008274	-	-	-	-	-	-	-	-	1.8	Up
M400008275	M400008275	-	-	-	-	-	-	2.7	Up	3.6	Up
M400008292	M400008292	-	-	-	-	-	-	-	-	1.6	Up
M400008298	M400008298	-	-	-	-	-	-	-	-	1.8	Up
M400008308	M400008308	-	-	-	-	-	-	-	-	2.3	Down
M400008349	M400008349	-	-	-	-	-	-	-	-	1.6	Up
M400008355	M400008355	-	-	-	-	-	-	-	-	1.6	Down
M400008358	M400008358	-	-	-	-	-	-	-	-	1.6	Up
NM_001004175	M400008363	-	-	-	-	1.8	Down	-	-	-	-
M400008369	M400008369	-	-	-	-	-	-	-	-	2.4	Down
M400008370	M400008370	-	-	-	-	-	-	-	-	2.4	Up
XM_487628	M400008387	-	-	-	-	-	-	-	-	2.5	Up
M400008397	M400008397	-	-	-	-	-	-	2.1	Down	-	-
M400008410	M400008410	-	-	-	-	-	-	-	-	2.9	Up
M400008414	M400008414	-	-	-	-	-	-	-	-	2.1	Up
M400008433	M400008433	-	-	-	-	-	-	2.5	Up	-	-
M400008458	M400008458	-	-	-	-	-	-	-	-	1.9	Up
M400008476	M400008476	-	-	-	-	-	-	-	-	2.8	Up
M400008496	M400008496	-	-	-	-	-	-	-	-	1.5	Up
M400008502	M400008502	-	-	-	-	-	-	-	-	1.6	Up
M400008518	M400008518	-	-	-	-	-	-	-	-	1.5	Up
M400008523	M400008523	-	-	-	-	-	-	-	-	2.6	Up
M400008529	M400008529	-	-	-	-	-	-	-	-	2.6	Up
M400008530	M400008530	-	-	-	-	-	-	2.0	Up	-	-
NM_146462,											
NM_146463	M400008545	-	-	-	-	-	-	-	-	1.8	Up
XM_122818	M400008559	-	-	-	-	-	-	3.8	Up	2.0	Up
M400008560	M400008560	-	-	-	-	2.3	Up	-	-	-	-
M400008562	M400008562	-	-	-	-	-	-	1.5	Down	-	-
M400008589	M400008589	-	-	-	-	-	-	1.7	Up	-	-
M400008595	M400008595	-	-	-	-	-	-	2.0	Up	-	-
M400008643	M400008643	-	-	-	-	-	-	-	-	1.9	Up
M400008645	M400008645	-	-	-	-	-	-	-	-	3.6	Up
M400008648	M400008648	-	-	-	-	-	-	-	-	1.7	Up
M400008675	M400008675	-	-	-	-	2.0	Up	-	-	-	-
M400008689	M400008689	-	-	-	-	-	-	-	-	3.4	Up
M400008723	M400008723	-	-	-	-	-	-	-	-	1.9	Down
M400008743	M400008743	-	-	-	-	1.6	Down	-	-	-	-
M400008765	M400008765	-	-	-	-	-	-	-	-	1.8	Up
M400008766	M400008766	-	-	-	-	-	-	-	-	1.6	Up
M400008767	M400008767	-	-	-	-	-	-	1.5	Up	1.9	Up

M400008779	M400008779	-	-	-	-	-	-	-	-	2.5	Up
M400008783	M400008783	-	-	-	-	-	-	-	-	1.8	Down
M400008790	M400008790	-	-	-	-	-	-	-	-	1.8	Up
M400008791	M400008791	-	-	-	-	-	-	-	-	2.8	Up
M400008797	M400008797	-	-	-	-	-	-	-	-	1.5	Up
M400008804	M400008804	-	-	-	-	1.6	Down	-	-	-	-
M400008856	M400008856	-	-	-	-	-	-	-	-	4.0	Up
M400008879	M400008879	-	-	-	-	-	-	-	-	2.4	Up
M400008880	M400008880	-	-	-	-	-	-	2.2	Up	2.2	Up
M400008883	M400008883	-	-	-	-	-	-	-	-	2.5	Up
M400008898	M400008898	-	-	-	-	-	-	-	-	1.6	Up
M400008900	M400008900	-	-	-	-	-	-	-	-	1.7	Up
M400008909	M400008909	-	-	-	-	-	-	-	-	2.0	Up
XM_484343	M400008918	-	-	-	-	1.5	Down	-	-	-	-
M400008946	M400008946	-	-	-	-	-	-	-	-	1.7	Up
M400008951	M400008951	-	-	-	-	-	-	-	-	2.4	Up
M400008957	M400008957	-	-	-	-	-	-	-	-	2.8	Up
M400008974	M400008974	-	-	-	-	-	-	-	-	1.8	Up
M400008975	M400008975	-	-	-	-	-	-	-	-	2.2	Up
M400008980	M400008980	-	-	-	-	-	-	-	-	2.5	Up
M400008981	M400008981	-	-	-	-	-	-	-	-	2.9	Up
M400009001	M400009001	-	-	-	-	-	-	-	-	2.0	Up
M400009005	M400009005	-	-	-	-	-	-	2.1	Up	3.7	Up
XM_484614,											
XM_489778	M400009029	-	-	-	-	-	-	1.7	Up	2.6	Up
M400009082	M400009082	-	-	-	-	-	-	-	-	1.8	Up
M400009094	M400009094	-	-	-	-	-	-	-	-	2.6	Up
M400009100	M400009100	-	-	-	-	-	-	-	-	1.9	Up
XM_111780	M400009112	-	-	-	-	-	-	-	-	1.9	Up
M400009128	M400009128	-	-	-	-	-	-	-	-	4.2	Up
NM_010004,											
XM_135557	M400009135	-	-	-	-	-	-	-	-	2.4	Up
M400009136	M400009136	-	-	-	-	-	-	-	-	2.3	Up
M400009147	M400009147	-	-	-	-	-	-	2.2	Up	-	-
M400009159	M400009159	-	-	-	-	-	-	-	-	2.7	Up
M400009168	M400009168	-	-	-	-	-	-	-	-	2.1	Down
M400009182	M400009182	-	-	-	-	-	-	-	-	1.7	Up
M400009187	M400009187	-	-	-	-	-	-	-	-	1.6	Up
M400009189	M400009189	-	-	-	-	-	-	-	-	1.7	Up
M400009195	M400009195	-	-	-	-	-	-	-	-	1.6	Up
M400009200	M400009200	-	-	-	-	-	-	-	-	1.6	Up
M400009219	M400009219	-	-	-	-	-	-	-	-	1.9	Up

M400009220	M400009220	-	-	-	-	-	-	-	-	1.6	Up
M400009225	M400009225	-	-	-	-	-	-	1.9	Up	-	-
M400009235	M400009235	-	-	-	-	-	-	-	-	2.0	Up
M400009236	M400009236	-	-	-	-	-	-	-	-	2.9	Up
M400009260	M400009260	-	-	-	-	-	-	-	-	2.7	Up
M400009290	M400009290	-	-	-	-	-	-	-	-	2.2	Up
M400009331	M400009331	-	-	-	-	-	-	-	-	2.6	Up
M400009342	M400009342	-	-	-	-	-	-	-	-	1.9	Up
M400009347	M400009347	-	-	-	-	-	-	-	-	3.8	Up
M400009403	M400009403	-	-	-	-	-	-	-	-	1.7	Up
M400009420	M400009420	-	-	-	-	-	-	-	-	1.9	Up
M400009443	M400009443	-	-	-	-	-	-	-	-	2.0	Up
M400009444	M400009444	-	-	-	-	-	-	-	-	1.7	Up
M400009510	M400009510	-	-	-	-	-	-	-	-	2.5	Up
M400009533	M400009533	-	-	-	-	-	-	-	-	1.5	Up
M400009593	M400009593	-	-	-	-	-	-	-	-	2.8	Up
M400009594	M400009594	-	-	-	-	-	-	-	-	4.0	Up
M400009628	M400009628	-	-	-	-	-	-	-	-	2.6	Up
M400009658	M400009658	-	-	-	-	-	-	-	-	2.6	Up
M400009693	M400009693	-	-	-	-	-	-	-	-	3.1	Up
M400009727	M400009727	-	-	-	-	-	-	1.8	Up	-	-
M400009728	M400009728	-	-	-	-	-	-	-	-	1.6	Up
M400009741	M400009741	-	-	-	-	-	-	-	-	3.1	Up
M400009771	M400009771	-	-	-	-	-	-	-	-	1.9	Up
M400009775	M400009775	-	-	-	-	-	-	-	-	1.7	Up
M400009788	M400009788	-	-	-	-	1.6	Down	-	-	-	-
M400009801	M400009801	-	-	-	-	-	-	1.9	Up	-	-
M400009806	M400009806	-	-	-	-	-	-	-	-	2.2	Up
M400009818	M400009818	-	-	-	-	-	-	-	-	1.8	Up
M400009828	M400009828	-	-	-	-	1.5	Down	-	-	-	-
M400009836	M400009836	-	-	-	-	-	-	1.5	Up	2.6	Up
M400009866	M400009866	-	-	-	-	-	-	-	-	1.7	Up
M400009870	M400009870	-	-	-	-	-	-	-	-	1.7	Up
M400009890	M400009890	-	-	-	-	-	-	-	-	1.6	Up
M400009901	M400009901	-	-	-	-	-	-	-	-	3.1	Up
M400009902	M400009902	-	-	-	-	-	-	-	-	1.8	Up
M400009910	M400009910	-	-	-	-	-	-	-	-	2.9	Up
M400009911	M400009911	-	-	-	-	-	-	-	-	2.1	Up
M400009919	M400009919	-	-	-	-	-	-	-	-	3.4	Up
M400009920	M400009920	-	-	-	-	-	-	-	-	2.3	Up
M400009930	M400009930	-	-	-	-	-	-	-	-	1.8	Up

M400009931	M400009931	-	-	-	-	-	-	-	-	3.1	Up
M400009937	M400009937	-	-	-	-	-	-	-	-	1.7	Up
M400009943	M400009943	-	-	-	-	-	-	-	-	2.8	Up
M400009946	M400009946	-	-	-	-	-	-	-	-	1.6	Up
M400009948	M400009948	-	-	-	-	-	-	-	-	2.2	Up
M400009949	M400009949	-	-	-	-	-	-	-	-	2.3	Up
M400009952	M400009952	-	-	-	-	-	-	-	-	1.5	Up
M400009954	M400009954	-	-	-	-	-	-	-	-	2.5	Up
M400009967	M400009967	-	-	-	-	-	-	-	-	2.4	Up
M400009970	M400009970	-	-	-	-	-	-	-	-	2.4	Up
XM_487283	M400009971	-	-	-	-	-	-	-	-	2.4	Up
M400009973	M400009973	-	-	-	-	-	-	-	-	3.4	Up
M400009978	M400009978	-	-	-	-	-	-	-	-	2.0	Up
M400009979	M400009979	-	-	-	-	-	-	-	-	3.4	Up
M400009985	M400009985	-	-	-	-	-	-	-	-	2.3	Up
M400009995	M400009995	-	-	-	-	-	-	1.6	Up	-	-
M400009996	M400009996	-	-	-	-	-	-	-	-	3.0	Up
M400010002	M400010002	-	-	-	-	-	-	1.6	Up	2.5	Up
M400010007	M400010007	-	-	-	-	1.6	Down	-	-	-	-
M400010010	M400010010	-	-	-	-	-	-	-	-	1.9	Up
M400010019	M400010019	-	-	-	-	-	-	-	-	1.9	Up
M400010023	M400010023	-	-	-	-	-	-	-	-	1.6	Up
M400010025	M400010025	-	-	-	-	2.3	Down	-	-	-	-
M400010026	M400010026	-	-	-	-	-	-	-	-	3.7	Up
M400010038	M400010038	-	-	-	-	2.2	Up	2.0	Up	2.1	Up
M400010050	M400010050	-	-	-	-	-	-	-	-	3.8	Up
M400010055	M400010055	-	-	-	-	-	-	-	-	1.7	Up
XM_489523	M400010061	-	-	-	-	-	-	-	-	2.0	Up
XM_489768	M400010062	-	-	-	-	-	-	-	-	2.5	Up
M400010064	M400010064	-	-	-	-	-	-	-	-	1.7	Up
XM_148692, XM_148700	M400010068	-	-	-	-	-	-	-	-	3.1	Up
M400010070	M400010070	-	-	-	-	-	-	-	-	2.2	Up
XM_156060, XM_358801	M400010073	-	-	-	-	-	-	-	-	2.6	Up
XM_489563	M400010077	-	-	-	-	-	-	-	-	1.9	Up
M400010084	M400010084	-	-	-	-	-	-	-	-	2.2	Down
M400010088	M400010088	-	-	-	-	-	-	-	-	2.1	Up
M400010103	M400010103	-	-	-	-	-	-	2.1	Up	-	-
M400010108	M400010108	-	-	-	-	-	-	-	-	1.6	Up
M400010109	M400010109	-	-	-	-	-	-	-	-	2.0	Up
M400010114	M400010114	-	-	-	-	-	-	-	-	2.9	Up



M400010115	M400010115	-	-	-	-	-	-	-	-	3.3	Up
M400010119	M400010119	-	-	-	-	1.6	Down	-	-	-	-
M400010127	M400010127	-	-	-	-	-	-	-	-	2.1	Up
M400010145	M400010145	-	-	-	-	-	-	1.8	Up	3.0	Up
M400010150	M400010150	-	-	-	-	-	-	-	-	2.1	Up
M400010162	M400010162	-	-	-	-	-	-	-	-	1.6	Up
M400010165	M400010165	-	-	-	-	1.5	Down	-	-	-	-
M400010186	M400010186	-	-	-	-	-	-	-	-	2.1	Up
M400010192	M400010192	-	-	-	-	-	-	-	-	1.7	Up
M400010198	M400010198	-	-	-	-	-	-	-	-	1.8	Up
M400010203	M400010203	-	-	-	-	-	-	-	-	1.5	Up
M400010209	M400010209	-	-	-	-	-	-	-	-	1.6	Up
M400010216	M400010216	-	-	-	-	-	-	-	-	1.9	Up
M400010235	M400010235	-	-	-	-	1.8	Down	-	-	-	-
M400010240	M400010240	-	-	-	-	-	-	-	-	2.5	Up
M400010246	M400010246	-	-	-	-	-	-	-	-	2.5	Up
M400010264	M400010264	-	-	-	-	-	-	-	-	1.9	Up
M400010270	M400010270	-	-	-	-	-	-	-	-	2.2	Up
M400010273	M400010273	-	-	-	-	-	-	-	-	3.3	Up
M400010281	M400010281	-	-	-	-	-	-	-	-	2.6	Up
M400010287	M400010287	-	-	-	-	-	-	-	-	2.4	Up
M400010288	M400010288	-	-	-	-	-	-	-	-	1.6	Up
M400010293	M400010293	-	-	-	-	-	-	-	-	3.7	Up
M400010299	M400010299	-	-	-	-	-	-	-	-	3.0	Up
M400010306	M400010306	-	-	-	-	-	-	-	-	1.6	Up
M400010311	M400010311	-	-	-	-	-	-	-	-	3.6	Up
M400010316	M400010316	-	-	-	-	-	-	-	-	2.4	Up
M400010317	M400010317	-	-	-	-	-	-	-	-	2.3	Up
M400010323	M400010323	-	-	-	-	-	-	-	-	2.1	Up
XM_143801	M400010324	-	-	-	-	-	-	-	-	2.7	Up
M400010329	M400010329	-	-	-	-	-	-	-	-	2.9	Up
M400010332	M400010332	-	-	-	-	-	-	-	-	1.6	Up
M400010347	M400010347	-	-	-	-	-	-	-	-	3.1	Up
M400010357	M400010357	-	-	-	-	-	-	-	-	2.1	Up
M400010365	M400010365	-	-	-	-	-	-	-	-	2.3	Up
M400010380	M400010380	-	-	-	-	1.6	Down	-	-	-	-
M400010387	M400010387	-	-	-	-	-	-	-	-	1.8	Up
M400010393	M400010393	-	-	-	-	-	-	-	-	2.2	Up
M400010394	M400010394	-	-	-	-	-	-	-	-	3.8	Up
M400010399	M400010399	-	-	-	-	-	-	-	-	3.6	Up
M400010400	M400010400	-	-	-	-	-	-	-	-	2.7	Up

M400010403	M400010403	-	-	-	-	-	-	-	-	1.9	Up
M400010409	M400010409	-	-	-	-	-	-	-	-	1.7	Up
M400010412	M400010412	-	-	-	-	-	-	-	-	2.6	Up
M400010416	M400010416	-	-	-	-	-	-	-	-	2.0	Up
M400010421	M400010421	-	-	-	-	-	-	-	-	1.9	Up
M400010423	M400010423	-	-	-	-	-	-	-	-	1.9	Up
M400010424	M400010424	-	-	-	-	-	-	-	-	3.5	Up
M400010426	M400010426	-	-	-	-	-	-	-	-	2.1	Up
M400010436	M400010436	-	-	-	-	-	-	-	-	2.6	Up
M400010438	M400010438	-	-	-	-	-	-	-	-	1.9	Up
M400010440	M400010440	-	-	-	-	-	-	-	-	2.1	Up
M400010442	M400010442	-	-	-	-	-	-	1.6	Up	-	-
M400010447	M400010447	-	-	-	-	-	-	-	-	2.0	Up
M400010453	M400010453	-	-	-	-	-	-	-	-	2.3	Up
M400010457	M400010457	-	1.8	Down	-	-	-	-	-	-	-
M400010458	M400010458	-	-	-	-	-	-	-	-	2.2	Up
M400010459	M400010459	-	-	-	-	-	-	-	-	2.1	Up
M400010462	M400010462	-	-	-	-	-	-	-	-	1.9	Up
M400010465	M400010465	-	-	-	-	-	-	-	-	2.4	Up
M400010476	M400010476	-	-	-	-	-	-	-	-	1.6	Up
M400010482	M400010482	-	-	-	-	-	-	-	-	2.0	Up
M400010489	M400010489	-	-	-	-	-	-	-	-	3.4	Up
M400010494	M400010494	-	-	-	-	-	-	-	-	2.2	Up
M400010495	M400010495	-	-	-	-	-	-	1.6	Up	2.7	Up
M400010513	M400010513	-	-	-	-	-	-	3.1	Up	2.5	Up
M400010515	M400010515	-	-	-	2.0	Down	-	-	-	-	-
M400010518	M400010518	-	-	-	-	-	-	-	-	2.3	Up
M400010525	M400010525	-	-	-	-	-	-	-	-	3.2	Up
M400010536	M400010536	-	-	-	-	-	-	1.7	Up	1.8	Up
M400010537	M400010537	-	-	-	-	-	-	1.8	Up	-	-
M400010555	M400010555	-	-	-	-	-	-	-	-	2.0	Up
M400010565	M400010565	-	-	-	-	-	-	-	-	2.3	Up
M400010566	M400010566	-	-	-	-	-	-	-	-	2.0	Up
M400010572	M400010572	-	-	-	2.0	Down	-	-	-	-	-
M400010575	M400010575	-	-	-	-	-	-	-	-	1.9	Up
M400010578	M400010578	-	-	-	-	-	-	-	-	1.8	Up
M400010585	M400010585	-	-	-	-	-	-	-	-	3.8	Up
M400010589	M400010589	-	-	-	-	-	-	-	-	2.6	Up
XM_486201	M400010590	-	-	-	-	-	-	-	-	2.4	Up
M400010593	M400010593	-	-	-	-	-	-	-	-	2.8	Up
M400010601	M400010601	-	-	-	-	-	-	-	-	2.1	Up

M400010608	M400010608	-	-	-	-	-	-	-	-	2.0	Up
M400010619	M400010619	-	-	-	-	-	-	-	-	1.8	Up
M400010626	M400010626	-	-	-	-	-	-	-	-	3.3	Up
M400010637	M400010637	-	-	-	-	-	-	-	-	2.1	Up
M400010638	M400010638	-	-	-	-	-	-	-	-	3.0	Up
M400010639	M400010639	-	-	-	-	-	-	-	-	1.5	Up
M400010649	M400010649	-	-	-	-	-	-	-	-	2.3	Up
M400010655	M400010655	-	-	-	-	-	-	-	-	2.0	Up
M400010656	M400010656	-	-	-	-	-	-	-	-	2.6	Up
M400010660	M400010660	-	-	-	-	-	-	-	-	2.9	Up
M400010661	M400010661	-	-	-	-	-	-	-	-	3.1	Up
M400010667	M400010667	-	-	-	-	-	-	-	-	1.7	Up
XM_358268, XM_358269	M400010673	-	-	-	-	-	-	-	-	3.5	Up
NM_0010015 58	M400010683	-	-	-	-	-	-	-	-	2.1	Up
NM_0010027 79	M400010696	-	-	-	-	-	-	-	-	2.3	Up
NM_0010027 81, XM_4849 75	M400010697	-	-	-	-	-	-	-	-	3.1	Up
NM_008111	M400010798	-	-	-	-	-	-	-	-	1.6	Up
NM_008194, NM_212444	M400010803	-	-	-	-	-	-	-	-	1.8	Up
NM_011423	M400011135	-	-	-	-	-	-	2.1	Up	-	-
M400011230	M400011230	-	-	-	-	-	-	-	-	2.2	Down
NM_013893, XM_485843	M400011231	-	-	-	-	-	-	-	-	3.1	Up
NM_025640	M400011505	-	-	-	-	-	-	-	-	2.1	Up
M400011585	M400011585	-	-	-	-	-	-	-	-	3.1	Down
NM_030264	M400011701	-	-	-	-	-	-	-	-	2.5	Up
NM_053189	M400011769	-	-	-	-	-	-	-	-	2.5	Up
NM_146130, XM_485356	M400011932	-	-	-	-	-	-	1.6	Up	-	-
NM_146585	M400012009	-	-	-	-	-	-	-	-	1.5	Up
NM_172423	M400012223	-	-	-	-	-	-	-	-	1.8	Up
NM_172432	M400012226	-	-	-	-	-	-	-	-	2.3	Up
NM_172542	M400012233	-	-	-	-	-	-	-	-	2.1	Up
NM_175426	M400012312	-	-	-	-	-	-	-	-	2.8	Up
M400012318	M400012318	-	-	-	-	-	-	2.0	Up	3.4	Up
NM_175662, NM_178213	M400012323	-	-	-	-	-	-	-	-	1.5	Up
NM_177206	M400012388	-	-	-	-	-	-	-	-	2.0	Up

NM_177276	M400012401	-	-	-	-	-	1.9	Up	2.2	Up
NM_177891	M400012440	-	-	-	-	-	-	-	2.6	Up
NM_183101	M400012537	-	-	-	-	-	-	-	2.6	Up
NM_183120	M400012538	-	-	-	-	-	-	-	2.0	Up
NM_201234	M400012603	-	-	-	-	-	-	-	1.8	Up
NM_207257	M400012637	-	-	-	-	-	-	-	2.7	Up
NR_000042	M400012673	-	-	-	2.0	Down	-	-	-	-
M400012691	M400012691	-	-	-	-	-	-	-	2.6	Down
XM_486649, XM_486656, XM_486659	M400012698	-	-	-	-	-	-	-	1.6	Up
M400012700	M400012700	-	-	-	-	-	-	-	2.7	Up
M400012702	M400012702	-	-	-	-	-	-	-	4.2	Up
M400012703	M400012703	-	-	-	-	-	-	-	2.5	Up
NM_146130, XM_485356, XM_486721, XM_489746	M400012710	-	-	-	-	-	1.5	Up	-	-
M400012713	M400012713	-	-	-	-	-	-	-	1.5	Up
M400012716	M400012716	-	-	-	-	-	-	-	3.5	Up
M400012727	M400012727	-	-	-	-	-	-	-	2.9	Up
M400012728	M400012728	-	-	-	-	-	-	-	3.2	Up
M400012733	M400012733	-	-	-	-	-	-	-	3.4	Up
M400012734	M400012734	-	-	-	-	-	2.3	Up	3.3	Up
M400012739	M400012739	-	-	-	2.5	Down	-	-	-	-
M400012740	M400012740	-	-	-	-	-	2.1	Up	4.1	Up
M400012746	M400012746	-	-	-	-	-	-	-	2.6	Up
M400012754	M400012754	-	-	-	-	-	-	-	1.9	Up
M400012760	M400012760	-	-	-	-	-	-	-	1.5	Up
M400012762	M400012762	-	-	-	-	-	-	-	2.5	Up
M400012766	M400012766	-	-	-	-	-	-	-	1.7	Up
M400012768	M400012768	-	-	-	-	-	-	-	2.6	Up
M400012777	M400012777	-	-	-	-	-	-	-	2.6	Up
M400012784	M400012784	-	-	-	-	-	-	-	1.9	Up
M400012786	M400012786	-	-	-	-	-	-	-	2.0	Up
M400012796	M400012796	-	-	-	-	-	-	-	2.6	Up
M400012825	M400012825	-	1.8	Down	-	-	-	-	-	-
M400012827	M400012827	-	-	-	-	-	-	-	2.3	Up
XM_488610	M400012828	-	-	-	-	-	-	-	3.5	Up
XM_488640	M400012832	-	1.8	Down	-	-	-	-	1.7	Up
M400012835	M400012835	-	-	-	-	-	-	-	2.3	Up
M400012839	M400012839	-	-	-	-	-	-	-	1.5	Up

M400012845	M400012845	-	-	-	-	-	-	-	-	3.6	Up
M400012851	M400012851	-	-	-	-	-	-	-	-	2.7	Up
M400012852	M400012852	-	-	-	-	-	-	-	-	3.3	Up
M400012858	M400012858	-	-	-	-	-	-	-	-	1.8	Up
M400012870	M400012870	-	-	-	-	-	-	-	-	2.4	Up
M400012876	M400012876	-	-	-	-	-	-	-	-	1.5	Up
M400012894	M400012894	-	-	-	-	-	-	1.8	Up	3.3	Up
M400012900	M400012900	-	-	-	-	-	-	-	-	1.6	Up
M400012906	M400012906	-	-	-	-	-	-	-	-	2.9	Up
M400012912	M400012912	-	-	-	-	-	-	-	-	2.4	Up
XM_489320	M400012922	-	-	-	-	2.4	Down	-	-	-	-
M400012924	M400012924	-	-	-	-	-	-	-	-	2.7	Up
M400012930	M400012930	-	-	-	-	-	-	-	-	1.8	Down
M400012938	M400012938	-	-	-	-	1.9	Down	-	-	1.6	Up
M400012942	M400012942	-	-	-	-	-	-	-	-	1.7	Up
M400012945	M400012945	-	-	-	-	-	-	-	-	1.5	Down
M400012965	M400012965	-	-	-	-	-	-	-	-	3.6	Up
M400012971	M400012971	-	-	-	-	-	-	-	-	2.1	Up
M400012976	M400012976	-	-	-	-	-	-	-	-	1.9	Up
M400012995	M400012995	-	-	-	-	-	-	-	-	2.4	Up
M400013008	M400013008	-	-	-	-	-	-	-	-	2.3	Up
M400013016	M400013016	-	-	-	-	1.7	Down	-	-	-	-
M400013017	M400013017	-	-	-	-	2.1	Down	-	-	1.8	Up
M400013029	M400013029	-	-	-	-	-	-	-	-	2.6	Down
M400013030	M400013030	-	-	-	-	-	-	-	-	1.9	Up
M400013031	M400013031	-	-	-	-	-	-	-	-	1.7	Up
M400013032	M400013032	-	-	-	-	2.6	Down	-	-	3.5	Down
M400013038	M400013038	-	-	-	-	-	-	-	-	2.6	Up
M400013042	M400013042	-	-	-	-	-	-	-	-	3.8	Up
M400013053	M400013053	-	-	-	-	-	-	-	-	1.7	Down
M400013056	M400013056	-	-	-	-	1.7	Down	-	-	2.6	Down
M400013065	M400013065	-	-	-	-	-	-	-	-	2.4	Up
M400013070	M400013070	-	-	-	-	1.6	Down	-	-	-	-
M400013090	M400013090	-	-	-	-	-	-	-	-	2.0	Up
M400013096	M400013096	-	-	-	-	-	-	1.6	Up	-	-
M400013118	M400013118	-	-	-	-	-	-	-	-	2.1	Up
M400013123	M400013123	-	-	-	-	-	-	1.6	Down	-	-
M400013124	M400013124	-	-	-	-	-	-	-	-	2.5	Up
M400013135	M400013135	-	-	-	-	-	-	-	-	1.5	Up
M400013137	M400013137	-	-	-	-	-	-	2.1	Up	-	-
M400013138	M400013138	-	-	-	-	-	-	-	-	2.0	Up

M400013139	M400013139	-	-	-	-	-	-	-	-	2.4	Up
M400013141	M400013141	-	-	-	-	-	-	-	-	2.2	Up
M400013142	M400013142	-	-	-	-	-	-	-	-	2.9	Up
M400013143	M400013143	-	-	-	-	-	-	-	-	2.3	Up
M400013147	M400013147	-	-	-	-	-	-	-	-	1.6	Up
M400013148	M400013148	-	-	-	-	-	-	-	-	2.7	Up
M400013151	M400013151	-	-	-	-	-	-	-	-	3.5	Up
M400013152	M400013152	-	-	-	-	-	-	-	-	2.4	Up
M400013155	M400013155	-	-	-	-	-	-	-	-	3.5	Up
M400013160	M400013160	-	-	-	-	-	-	-	-	2.9	Up
M400013164	M400013164	-	-	-	-	-	-	-	-	1.7	Up
M400013166	M400013166	-	-	-	-	-	-	-	-	3.3	Up
M400013177	M400013177	-	-	-	-	-	-	-	-	1.6	Up
M400013181	M400013181	-	-	-	-	2.9	Down	-	-	-	-
M400013187	M400013187	-	-	-	-	-	-	-	-	3.1	Up
M400013193	M400013193	-	-	-	-	-	-	-	-	1.8	Up
M400013211	M400013211	-	-	-	-	-	-	-	-	2.2	Up
M400013215	M400013215	-	-	-	-	1.6	Up	-	-	-	-
M400013220	M400013220	-	-	-	-	-	-	-	-	2.0	Up
M400013223	M400013223	-	-	-	-	-	-	-	-	1.9	Up
M400013226	M400013226	-	-	-	-	-	-	-	-	3.8	Up
M400013242	M400013242	-	-	-	-	-	-	-	-	2.0	Down
M400013250	M400013250	-	-	-	-	-	-	-	-	2.9	Up
M400013256	M400013256	-	-	-	-	-	-	-	-	3.9	Up
M400013261	M400013261	-	-	-	-	-	-	-	-	1.6	Up
M400013274	M400013274	-	-	-	-	-	-	-	-	1.5	Up
M400013280	M400013280	-	-	-	-	-	-	1.8	Up	-	-
M400013304	M400013304	-	-	-	-	-	-	-	-	1.7	Up
M400013310	M400013310	-	-	-	-	-	-	-	-	1.5	Up
M400013316	M400013316	-	-	-	-	-	-	-	-	2.2	Up
M400013332	M400013332	-	-	-	-	-	-	-	-	2.0	Up
M400013340	M400013340	-	-	-	-	-	-	-	-	3.4	Up
M400013345	M400013345	-	-	-	-	-	-	-	-	2.3	Up
M400013351	M400013351	-	-	-	-	-	-	2.4	Up	-	-
M400013363	M400013363	-	-	-	-	-	-	-	-	2.6	Up
M400013364	M400013364	-	-	-	-	-	-	-	-	2.2	Up
M400013375	M400013375	-	-	-	-	-	-	-	-	2.4	Up
M400013381	M400013381	-	-	-	-	-	-	-	-	1.7	Up
M400013387	M400013387	-	-	-	-	-	-	-	-	2.4	Up
M400013388	M400013388	-	-	-	-	-	-	-	-	2.2	Up
M400013393	M400013393	-	-	-	-	-	-	-	-	2.0	Up

M400013399	M400013399	-	-	-	-	-	-	-	-	2.8	Up
M400013405	M400013405	-	-	-	-	-	-	-	-	1.8	Up
M400013411	M400013411	-	-	-	-	-	-	-	-	2.8	Up
M400013419	M400013419	-	-	-	-	-	-	-	-	1.9	Up
M400013420	M400013420	-	-	-	-	1.8	Down	-	-	-	-
M400013426	M400013426	-	-	-	-	-	-	-	-	1.7	Up
M400013432	M400013432	-	-	-	-	-	-	-	-	2.7	Up
M400013434	M400013434	-	-	-	-	-	-	1.8	Up	-	-
M400013436	M400013436	-	-	-	-	-	-	-	-	1.5	Up
M400013439	M400013439	-	-	-	-	-	-	1.5	Up	-	-
M400013442	M400013442	-	-	-	-	-	-	-	-	1.7	Up
M400013443	M400013443	-	-	-	-	-	-	-	-	1.7	Up
M400013445	M400013445	-	-	-	-	-	-	-	-	2.9	Up
M400013446	M400013446	-	-	-	-	-	-	-	-	3.1	Up
M400013450	M400013450	-	-	-	-	-	-	-	-	2.4	Up
M400013464	M400013464	-	-	-	-	-	-	-	-	3.7	Up
M400013470	M400013470	-	-	-	-	-	-	-	-	3.6	Up
M400013474	M400013474	-	-	-	-	-	-	-	-	2.2	Up
M400013482	M400013482	-	-	-	-	-	-	-	-	2.5	Up
M400013484	M400013484	-	-	-	-	-	-	-	-	1.7	Up
M400013485	M400013485	-	-	-	-	-	-	-	-	2.4	Up
M400013487	M400013487	-	-	-	-	-	-	-	-	3.4	Up
M400013488	M400013488	-	-	-	-	-	-	-	-	3.7	Up
M400013493	M400013493	-	-	-	-	-	-	-	-	1.5	Up
M400013494	M400013494	-	-	-	-	-	-	-	-	3.6	Up
M400013499	M400013499	-	-	-	-	1.7	Down	-	-	-	-
M400013500	M400013500	-	-	-	-	-	-	1.8	Up	-	-
M400013506	M400013506	-	-	-	-	-	-	2.0	Up	3.0	Up
M400013510	M400013510	-	-	-	-	-	-	-	-	1.9	Up
M400013511	M400013511	-	-	-	-	-	-	-	-	2.3	Up
XM_489243	M400013521	-	-	-	-	-	-	-	-	1.6	Up
M400013522	M400013522	-	-	-	-	-	-	-	-	2.6	Up
M400013526	M400013526	-	-	-	-	-	-	-	-	1.9	Up
M400013534	M400013534	-	-	-	-	-	-	-	-	1.8	Up
M400013535	M400013535	-	-	-	-	-	-	-	-	3.5	Up
M400013541	M400013541	-	-	-	-	-	-	-	-	3.5	Up
M400013546	M400013546	-	-	-	-	-	-	-	-	1.7	Up
M400013552	M400013552	-	-	-	-	-	-	-	-	1.9	Up
M400013558	M400013558	-	-	-	-	-	-	-	-	3.0	Up
M400013559	M400013559	-	-	-	-	-	-	-	-	2.8	Up
M400013564	M400013564	-	-	-	-	-	-	-	-	2.6	Up

M400013565	M400013565	-	-	-	-	-	-	-	-	3.3	Up
M400013568	M400013568	-	-	-	-	-	-	-	-	1.7	Up
M400013570	M400013570	-	-	-	-	-	-	-	-	2.3	Up
M400013574	M400013574	-	-	-	-	1.8	Down	-	-	-	-
M400013579	M400013579	-	-	-	-	-	-	-	-	1.5	Up
M400013585	M400013585	-	-	-	-	-	-	-	-	1.5	Down
M400013586	M400013586	-	-	-	-	-	-	-	-	3.1	Down
M400013588	M400013588	-	-	-	-	-	-	1.6	Up	-	-
M400013589	M400013589	-	-	-	-	-	-	-	-	4.1	Up
M400013595	M400013595	-	-	-	-	-	-	-	-	1.9	Up
M400013612	M400013612	-	-	-	-	-	-	-	-	3.8	Up
M400013623	M400013623	-	-	-	-	-	-	-	-	2.0	Up
XM_355454	M400013635	-	-	-	-	-	-	-	-	1.8	Up
M400013645	M400013645	-	-	-	-	-	-	-	-	2.3	Down
M400013646	M400013646	-	-	-	-	-	-	-	-	1.6	Down
M400013657	M400013657	-	-	-	-	1.9	Down	1.6	Down	-	-
M400013663	M400013663	-	-	-	-	-	-	-	-	1.5	Up
M400013669	M400013669	-	-	-	-	-	-	-	-	2.1	Up
M400013678	M400013678	-	-	-	-	-	-	-	-	2.2	Up
M400013684	M400013684	-	-	-	-	1.5	Down	-	-	1.6	Up
M400013696	M400013696	-	-	-	-	-	-	-	-	1.7	Up
M400013701	M400013701	-	-	-	-	-	-	-	-	2.6	Up
M400013702	M400013702	-	-	-	-	-	-	-	-	2.3	Up
M400013707	M400013707	-	-	-	-	-	-	-	-	3.7	Up
M400013719	M400013719	-	-	-	-	-	-	-	-	2.5	Up
M400013722	M400013722	-	-	-	-	-	-	-	-	3.0	Up
M400013723	M400013723	-	-	-	-	-	-	-	-	1.7	Up
M400013724	M400013724	-	-	-	-	-	-	-	-	1.7	Up
M400013725	M400013725	-	-	-	-	-	-	-	-	3.3	Up
M400013728	M400013728	-	-	-	-	-	-	-	-	2.3	Up
M400013730	M400013730	-	-	-	-	-	-	-	-	2.6	Up
M400013737	M400013737	-	-	-	-	-	-	-	-	2.2	Up
M400013743	M400013743	-	-	-	-	-	-	-	-	3.5	Up
M400013744	M400013744	-	-	-	-	-	-	-	-	1.7	Up
M400013747	M400013747	-	-	-	-	-	-	-	-	1.8	Up
M400013749	M400013749	-	-	-	-	-	-	-	-	1.6	Up
M400013753	M400013753	-	-	-	-	-	-	-	-	2.2	Up
M400013754	M400013754	-	-	-	-	-	-	-	-	2.6	Up
M400013755	M400013755	-	-	-	-	-	-	-	-	2.2	Up
M400013767	M400013767	-	-	-	-	-	-	-	-	2.3	Up
M400013773	M400013773	-	-	-	-	-	-	-	-	3.6	Up



M400013776	M400013776	-	-	-	-	-	-	-	-	1.9	Up
M400013782	M400013782	-	-	-	-	-	-	-	-	2.3	Down
M400013785	M400013785	-	-	-	-	-	-	-	-	4.0	Up
M400013790	M400013790	-	-	-	-	-	-	-	-	2.1	Up
M400013798	M400013798	-	-	-	-	-	-	-	-	1.8	Up
M400013799	M400013799	-	-	-	-	-	-	-	-	1.8	Up
M400013808	M400013808	-	-	-	-	-	-	2.2	Up	3.1	Up
M400013811	M400013811	-	-	-	-	-	-	1.7	Down	-	-
M400013812	M400013812	-	-	-	-	-	-	-	-	1.8	Up
M400013813	M400013813	-	-	-	-	-	-	-	-	1.5	Up
M400013814	M400013814	-	-	-	-	-	-	-	-	2.5	Up
XM_110264,											
XM_128555	M400013816	-	-	-	-	-	-	-	-	1.5	Up
M400013823	M400013823	-	-	-	-	-	-	-	-	1.7	Up
XM_484853	M400013830	-	-	-	-	-	-	-	-	1.5	Up
M400013835	M400013835	-	-	-	-	2.9	Down	-	-	-	-
M400013838	M400013838	-	-	-	-	-	-	-	-	2.4	Up
M400013842	M400013842	-	-	-	-	-	-	-	-	1.7	Down
M400013843	M400013843	-	-	-	-	-	-	-	-	3.9	Up
M400013844	M400013844	-	-	-	-	-	-	-	-	2.6	Up
M400013854	M400013854	-	-	-	-	-	-	-	-	1.6	Up
M400013861	M400013861	-	-	-	-	-	-	-	-	2.1	Down
M400013862	M400013862	-	-	-	-	-	-	2.4	Up	3.3	Up
M400013864	M400013864	-	-	-	-	-	-	-	-	2.0	Up
M400013865	M400013865	-	-	-	-	-	-	-	-	1.9	Up
M400013866	M400013866	-	-	-	-	-	-	-	-	2.2	Up
M400013867	M400013867	-	-	-	-	-	-	-	-	3.0	Up
M400013868	M400013868	-	-	-	-	-	-	-	-	2.4	Up
M400013870	M400013870	-	-	-	-	-	-	-	-	2.1	Up
M400013872	M400013872	-	-	-	-	-	-	-	-	1.7	Up
M400013874	M400013874	-	-	-	-	-	-	-	-	3.8	Up
M400013880	M400013880	-	-	-	-	-	-	-	-	2.9	Up
M400013883	M400013883	-	-	-	-	-	-	-	-	3.1	Down
M400013884	M400013884	-	-	-	-	-	-	1.7	Down	-	-
M400013886	M400013886	-	-	-	-	-	-	-	-	3.0	Up
M400013889	M400013889	-	-	-	-	-	-	-	-	1.9	Down
M400013893	M400013893	-	-	-	-	-	-	-	-	2.0	Down
M400013896	M400013896	-	-	-	-	-	-	-	-	2.5	Up
M400013897	M400013897	-	-	-	-	-	-	1.8	Up	-	-
M400013901	M400013901	-	-	-	-	-	-	-	-	1.8	Down
M400013907	M400013907	-	-	-	-	-	-	-	-	3.4	Up

M400013908	M400013908	-	-	-	-	-	-	-	-	3.5	Up
M400013920	M400013920	-	-	-	-	-	-	-	-	2.6	Up
M400013926	M400013926	-	-	-	-	-	-	-	-	2.5	Up
M400013933	M400013933	-	-	-	-	-	-	-	-	2.1	Up
M400013947	M400013947	-	-	-	-	-	-	-	-	2.2	Up
M400013951	M400013951	-	-	-	-	-	-	2.8	Up	1.5	Up
M400013959	M400013959	-	-	-	-	-	-	-	-	1.6	Down
M400013962	M400013962	-	-	-	-	-	-	-	-	2.3	Up
M400013968	M400013968	-	-	-	-	-	-	-	-	1.9	Up
M400013969	M400013969	-	-	-	-	-	-	-	-	2.9	Up
M400013973	M400013973	-	-	-	-	-	-	-	-	1.5	Up
M400013980	M400013980	-	-	-	-	-	-	-	-	2.3	Up
M400013981	M400013981	-	-	-	-	-	-	-	-	2.1	Up
M400013983	M400013983	-	-	-	-	-	-	-	-	2.1	Up
M400013986	M400013986	-	-	-	-	-	-	-	-	3.0	Up
M400013987	M400013987	-	-	-	-	-	-	-	-	1.8	Up
M400013989	M400013989	-	-	-	-	-	-	-	-	2.0	Up
M400013992	M400013992	-	-	-	-	-	-	-	-	2.4	Up
M400013996	M400013996	-	-	-	-	-	-	-	-	1.6	Up
M400014009	M400014009	-	-	-	-	-	-	-	-	1.8	Up
M400014013	M400014013	-	-	-	-	1.6	Down	-	-	-	-
M400014014	M400014014	-	-	-	-	1.6	Down	-	-	-	-
M400014016	M400014016	-	-	-	-	-	-	-	-	2.6	Up
M400014028	M400014028	-	-	-	-	-	-	-	-	2.5	Up
M400014037	M400014037	-	-	-	-	-	-	-	-	2.0	Up
M400014038	M400014038	-	-	-	-	1.5	Down	-	-	-	-
M400014039	M400014039	-	-	-	-	1.9	Down	-	-	-	-
M400014040	M400014040	-	-	-	-	-	-	-	-	2.5	Up
M400014045	M400014045	-	-	-	-	-	-	-	-	2.2	Up
M400014046	M400014046	-	-	-	-	-	-	-	-	2.3	Up
M400014049	M400014049	-	-	-	-	-	-	-	-	1.7	Up
M400014050	M400014050	-	-	-	-	-	-	-	-	1.8	Up
M400014058	M400014058	-	-	-	-	-	-	-	-	3.6	Up
M400014059	M400014059	-	-	-	-	-	-	-	-	1.5	Up
M400014061	M400014061	-	-	-	-	-	-	-	-	1.7	Up
M400014067	M400014067	-	-	-	-	-	-	-	-	1.8	Up
M400014069	M400014069	-	-	-	-	-	-	-	-	1.7	Up
M400014074	M400014074	-	-	-	-	-	-	-	-	2.2	Down
M400014078	M400014078	-	-	-	-	-	-	-	-	2.4	Up
M400014080	M400014080	-	-	-	-	-	-	-	-	3.5	Up
M400014081	M400014081	-	-	-	-	-	-	-	-	3.5	Up

M400014082	M400014082	-	-	-	-	-	-	-	-	2.6	Up
M400014084	M400014084	-	-	-	-	-	-	-	-	3.3	Up
M400014085	M400014085	-	-	-	-	-	-	-	-	2.7	Up
M400014086	M400014086	-	-	-	-	-	-	-	-	2.7	Up
M400014096	M400014096	-	-	-	-	-	-	-	-	2.7	Up
M400014099	M400014099	-	-	-	-	-	-	-	-	2.4	Up
M400014100	M400014100	-	-	-	-	-	-	-	-	2.0	Up
M400014102	M400014102	-	-	-	-	-	-	-	-	2.6	Up
M400014103	M400014103	-	-	-	-	-	-	-	-	1.8	Up
M400014104	M400014104	-	-	-	-	-	-	-	-	2.7	Up
M400014105	M400014105	-	-	-	-	-	-	-	-	4.3	Up
M400014106	M400014106	-	-	-	-	-	-	-	-	2.5	Up
M400014108	M400014108	-	-	-	-	-	-	-	-	3.0	Up
M400014109	M400014109	-	-	-	-	-	-	-	-	2.8	Up
M400014111	M400014111	-	-	-	-	-	-	1.5	Up	2.6	Up
M400014122	M400014122	-	-	-	-	-	-	-	-	2.4	Up
M400014127	M400014127	-	-	-	-	2.0	Down	-	-	-	-
M400014134	M400014134	-	-	-	-	-	-	-	-	3.1	Up
M400014135	M400014135	-	-	-	-	-	-	-	-	3.9	Up
M400014140	M400014140	-	-	-	-	-	-	-	-	2.7	Up
M400014146	M400014146	-	-	-	-	-	-	-	-	2.2	Up
M400014156	M400014156	-	-	-	-	-	-	1.7	Down	-	-
M400014158	M400014158	-	-	-	-	-	-	-	-	1.5	Up
M400014164	M400014164	-	-	-	-	1.7	Down	-	-	1.8	Up
M400014165	M400014165	-	-	-	-	-	-	-	-	3.1	Up
M400014170	M400014170	-	-	-	-	-	-	-	-	2.8	Up
M400014171	M400014171	-	-	-	-	-	-	-	-	3.6	Up
M400014172	M400014172	-	-	-	-	-	-	-	-	2.0	Up
M400014174	M400014174	-	-	-	-	-	-	-	-	3.7	Up
M400014175	M400014175	-	-	-	-	-	-	-	-	3.7	Up
M400014176	M400014176	-	-	-	-	-	-	1.9	Up	3.3	Up
M400014179	M400014179	-	-	-	-	-	-	-	-	1.8	Up
M400014181	M400014181	-	-	-	-	-	-	-	-	3.1	Up
M400014188	M400014188	-	-	-	-	-	-	-	-	3.2	Up
M400014194	M400014194	-	-	-	-	-	-	-	-	2.8	Up
M400014196	M400014196	-	-	-	-	-	-	-	-	3.3	Up
M400014197	M400014197	-	-	-	-	-	-	-	-	3.0	Up
M400014199	M400014199	-	-	-	-	-	-	-	-	4.3	Up
M400014204	M400014204	-	-	-	-	-	-	-	-	2.2	Up
M400014205	M400014205	-	-	-	-	-	-	-	-	2.8	Up
M400014206	M400014206	-	-	-	-	-	-	-	-	3.8	Up

M400014209	M400014209	-	-	-	-	-	-	-	-	2.4	Up
M400014212	M400014212	-	-	-	-	-	-	-	-	3.8	Up
M400014215	M400014215	-	-	-	-	2.1	Down	-	-	-	-
M400014217	M400014217	-	-	-	-	1.5	Down	-	-	-	-
M400014218	M400014218	-	-	-	-	-	-	-	-	3.9	Up
M400014220	M400014220	-	-	-	-	-	-	-	-	2.3	Up
M400014221	M400014221	-	-	-	-	-	-	-	-	2.0	Up
M400014224	M400014224	-	-	-	-	-	-	-	-	3.6	Up
M400014226	M400014226	-	-	-	-	-	-	-	-	3.2	Up
M400014230	M400014230	-	-	-	-	-	-	-	-	3.9	Up
M400014234	M400014234	-	-	-	-	-	-	-	-	2.2	Up
M400014239	M400014239	-	-	-	-	-	-	2.4	Down	-	-
XM_489291,											
XM_489300	M400014240	-	-	-	-	-	-	-	-	2.3	Up
M400014245	M400014245	-	-	-	-	-	-	-	-	1.6	Up
M400014247	M400014247	-	-	-	-	-	-	1.9	Down	-	-
M400014248	M400014248	-	-	-	-	-	-	2.8	Up	-	-
M400014260	M400014260	-	-	-	-	-	-	-	-	2.5	Up
M400014265	M400014265	-	-	-	-	2.5	Down	-	-	-	-
M400014269	M400014269	-	-	-	-	-	-	-	-	1.9	Up
M400014273	M400014273	-	-	-	-	-	-	-	-	1.6	Up
M400014274	M400014274	-	-	-	-	-	-	-	-	1.8	Up
M400014276	M400014276	-	-	-	-	-	-	-	-	2.3	Up
M400014282	M400014282	-	-	-	-	-	-	-	-	3.5	Up
M400014285	M400014285	-	-	-	-	-	-	-	-	2.9	Up
M400014288	M400014288	-	-	-	-	-	-	-	-	2.3	Up
M400014295	M400014295	-	-	-	-	-	-	-	-	3.5	Up
M400014298	M400014298	-	-	-	-	-	-	-	-	2.0	Up
M400014300	M400014300	-	-	-	-	-	-	-	-	3.5	Up
M400014306	M400014306	-	-	-	-	-	-	-	-	1.9	Up
M400014311	M400014311	-	-	-	-	-	-	-	-	1.5	Up
M400014312	M400014312	-	-	-	-	-	-	-	-	2.4	Up
M400014316	M400014316	-	-	-	-	-	-	-	-	3.1	Up
M400014317	M400014317	-	-	-	-	2.1	Down	-	-	-	-
M400014318	M400014318	-	-	-	-	-	-	-	-	2.8	Up
M400014321	M400014321	-	-	-	-	2.0	Down	-	-	-	-
M400014324	M400014324	-	-	-	-	-	-	-	-	3.9	Up
XM_489282	M400014325	-	-	-	-	-	-	-	-	2.5	Up
M400014336	M400014336	-	-	-	-	-	-	-	-	2.7	Up
M400014341	M400014341	-	-	-	-	-	-	-	-	2.2	Up
M400014342	M400014342	-	-	-	-	-	-	-	-	3.1	Up

M400014345	M400014345	-	-	-	-	-	-	-	-	1.9	Up
M400014347	M400014347	-	-	-	-	-	-	-	-	2.0	Up
M400014348	M400014348	-	-	-	-	-	-	-	-	3.0	Up
M400014349	M400014349	-	-	-	-	-	-	-	-	3.0	Up
M400014361	M400014361	-	-	-	-	-	-	-	-	2.5	Up
M400014366	M400014366	-	-	-	-	-	-	-	-	3.9	Up
M400014370	M400014370	-	-	-	-	-	-	-	-	3.9	Up
M400014372	M400014372	-	-	-	-	-	-	-	-	3.2	Up
M400014387	M400014387	-	-	-	-	-	-	-	-	2.0	Up
M400014391	M400014391	-	-	-	-	-	-	-	-	2.1	Up
M400014395	M400014395	-	-	-	-	1.7	Down	-	-	-	-
M400014401	M400014401	-	-	-	-	-	-	-	-	4.0	Up
M400014407	M400014407	-	-	-	-	-	-	-	-	2.1	Up
M400014408	M400014408	-	-	-	-	1.5	Down	-	-	-	-
M400014425	M400014425	-	-	-	-	-	-	-	-	1.8	Up
M400014426	M400014426	-	-	-	-	-	-	-	-	2.5	Up
M400014435	M400014435	-	-	-	-	-	-	-	-	1.6	Up
XM_194140	M400014438	-	-	-	-	-	-	-	-	1.6	Up
M400014450	M400014450	-	-	-	-	-	-	-	-	2.1	Up
M400014460	M400014460	-	-	-	-	-	-	-	-	3.3	Up
M400014461	M400014461	-	-	-	-	-	-	-	-	3.2	Up
M400014462	M400014462	-	-	-	-	-	-	-	-	2.2	Up
M400014467	M400014467	-	-	-	-	-	-	-	-	3.8	Up
M400014473	M400014473	-	-	-	-	1.5	Down	-	-	2.4	Up
M400014480	M400014480	-	-	-	-	-	-	-	-	2.0	Up
M400014482	M400014482	-	-	-	-	-	-	-	-	2.6	Up
M400014485	M400014485	-	-	-	-	-	-	-	-	3.9	Up
M400014489	M400014489	-	-	-	-	-	-	-	-	2.5	Up
M400014491	M400014491	-	-	-	-	-	-	-	-	2.2	Up
M400014496	M400014496	-	-	-	-	-	-	-	-	1.5	Up
M400014497	M400014497	-	-	-	-	-	-	-	-	3.1	Up
M400014506	M400014506	-	-	-	-	-	-	1.9	Down	-	-
M400014507	M400014507	-	-	-	-	-	-	1.9	Down	2.6	Up
M400014508	M400014508	-	-	-	-	1.6	Down	-	-	1.9	Up
M400014509	M400014509	-	-	-	-	-	-	-	-	3.3	Up
M400014512	M400014512	-	2.0	Down	-	-	-	-	-	-	-
M400014513	M400014513	-	-	-	-	-	-	-	-	2.9	Up
M400014515	M400014515	-	-	-	-	-	-	-	-	2.6	Up
M400014533	M400014533	-	-	-	-	-	-	1.5	Up	-	-
M400014536	M400014536	-	-	-	-	2.0	Down	-	-	1.8	Up
M400014537	M400014537	-	-	-	-	-	-	-	-	3.5	Up

XM_489130	M400014544	-	-	-	-	-	-	-	-	2.4	Up
M400014550	M400014550	-	-	-	-	-	-	-	-	3.2	Up
M400014551	M400014551	-	-	-	-	-	-	-	-	3.0	Up
M400014554	M400014554	-	-	-	-	-	-	-	-	2.6	Up
M400014555	M400014555	-	-	-	-	-	-	-	-	2.6	Up
M400014559	M400014559	-	-	-	-	-	-	-	-	2.9	Up
M400014560	M400014560	-	-	-	1.8	Down	1.6	Down	-	-	-
M400014568	M400014568	-	-	-	-	-	2.4	Up	-	-	-
M400014572	M400014572	-	-	-	2.6	Down	-	-	2.9	Down	-
M400014577	M400014577	-	-	-	-	-	-	-	1.6	Up	-
M400014578	M400014578	-	-	-	-	-	-	-	2.4	Up	-
M400014579	M400014579	-	-	-	-	-	-	-	3.1	Up	-
M400014580	M400014580	-	-	-	-	-	-	-	3.3	Up	-
M400014586	M400014586	-	-	-	-	-	1.8	Up	3.6	Up	-
M400014590	M400014590	-	-	-	-	-	-	-	2.0	Up	-
M400014600	M400014600	-	-	-	-	-	-	-	1.6	Up	-
M400014603	M400014603	-	-	-	-	-	-	-	2.8	Up	-
M400014606	M400014606	-	-	-	-	-	-	-	1.9	Up	-
M400014607	M400014607	-	-	-	-	-	-	-	2.2	Up	-
M400014609	M400014609	-	-	-	-	-	-	-	3.9	Up	-
M400014615	M400014615	-	-	-	1.5	Down	-	-	-	-	-
M400014619	M400014619	-	-	-	-	-	-	-	2.5	Up	-
M400014624	M400014624	-	-	-	-	-	-	-	2.3	Up	-
M400014631	M400014631	-	-	-	-	-	-	-	3.0	Up	-
M400014634	M400014634	-	-	-	2.1	Down	-	-	-	-	-
M400014640	M400014640	-	-	-	-	-	2.1	Up	4.0	Up	-
M400014645	M400014645	-	-	-	-	-	-	-	2.1	Up	-
M400014646	M400014646	-	-	-	-	-	-	-	2.6	Up	-
M400014650	M400014650	-	-	-	-	-	-	-	2.9	Up	-
M400014651	M400014651	-	-	-	-	-	1.5	Up	3.8	Up	-
M400014653	M400014653	-	-	-	1.8	Down	-	-	-	-	-
M400014655	M400014655	-	-	-	-	-	-	-	2.7	Up	-
M400014663	M400014663	-	-	-	-	-	-	-	2.1	Up	-
M400014665	M400014665	-	-	-	-	-	-	-	3.5	Up	-
M400014671	M400014671	-	-	-	1.9	Down	-	-	-	-	-
M400014677	M400014677	-	-	-	1.8	Down	-	-	-	-	-
M400014680	M400014680	-	-	-	-	-	-	-	3.5	Up	-
M400014689	M400014689	-	-	-	-	-	-	-	1.5	Up	-
M400014697	M400014697	-	-	-	-	-	-	-	2.1	Up	-
M400014705	M400014705	-	-	-	-	-	-	-	3.4	Up	-
M400014708	M400014708	-	-	-	-	-	-	-	2.4	Down	-

M400014710	M400014710	-	-	-	-	-	-	-	-	1.7	Up
M400014711	M400014711	-	-	-	-	-	-	-	-	2.2	Up
M400014725	M400014725	-	-	-	-	-	-	-	-	2.9	Up
M400014727	M400014727	-	-	-	-	-	-	-	-	1.9	Up
M400014728	M400014728	-	-	-	-	-	-	-	-	2.7	Up
M400014731	M400014731	-	-	-	-	1.8	Down	-	-	-	-
M400014734	M400014734	-	-	-	-	-	-	-	-	1.5	Up
M400014737	M400014737	-	-	-	-	-	-	-	-	1.6	Up
M400014740	M400014740	-	-	-	-	-	-	-	-	2.2	Up
M400014746	M400014746	-	-	-	-	-	-	1.7	Up	-	-
M400014764	M400014764	-	-	-	-	-	-	-	-	2.8	Up
M400014774	M400014774	-	-	-	-	2.2	Down	-	-	-	-
M400014793	M400014793	-	-	-	-	-	-	-	-	2.5	Up
M400014794	M400014794	-	-	-	-	-	-	-	-	2.9	Up
M400014800	M400014800	-	-	-	-	-	-	-	-	2.8	Up
M400014811	M400014811	-	-	-	-	-	-	-	-	2.5	Up
M400014818	M400014818	-	-	-	-	-	-	1.8	Up	-	-
M400014824	M400014824	-	-	-	-	-	-	-	-	3.2	Up
M400014841	M400014841	-	-	-	-	-	-	-	-	3.9	Up
M400014844	M400014844	-	-	-	-	-	-	-	-	2.7	Up
M400014850	M400014850	-	-	-	-	-	-	-	-	2.2	Up
M400014852	M400014852	-	-	-	-	1.5	Down	-	-	-	-
M400014853	M400014853	-	-	-	-	-	-	1.6	Up	-	-
M400014862	M400014862	-	-	-	-	-	-	-	-	1.7	Up
M400014863	M400014863	-	-	-	-	-	-	-	-	2.5	Up
M400014865	M400014865	-	-	-	-	-	-	-	-	3.4	Up
M400014869	M400014869	-	-	-	-	-	-	-	-	1.8	Up
M400014870	M400014870	-	-	-	-	-	-	-	-	2.7	Up
M400014877	M400014877	-	-	-	-	-	-	-	-	2.3	Up
M400014889	M400014889	-	-	-	-	-	-	-	-	2.6	Up
M400014890	M400014890	-	-	-	-	-	-	-	-	1.5	Up
M400014892	M400014892	-	-	-	-	-	-	-	-	2.2	Up
M400014894	M400014894	-	-	-	-	-	-	-	-	3.3	Up
M400014895	M400014895	-	-	-	-	-	-	-	-	2.2	Up
M400014900	M400014900	-	-	-	-	-	-	-	-	2.6	Up
M400014901	M400014901	-	-	-	-	-	-	-	-	3.8	Up
M400014906	M400014906	-	-	-	-	-	-	-	-	2.1	Up
M400014907	M400014907	-	-	-	-	-	-	-	-	3.6	Up
M400014911	M400014911	-	-	-	-	-	-	-	-	2.5	Up
M400014913	M400014913	-	-	-	-	-	-	-	-	3.1	Up
M400014916	M400014916	-	-	-	-	-	-	-	-	3.2	Up

M400014917	M400014917	-	-	-	-	-	-	-	-	1.8	Up	
M400014918	M400014918	-	-	-	-	-	-	-	-	3.2	Up	
M400014930	M400014930	-	-	-	-	2.2	Down	-	1.9	Down	-	
M400014934	M400014934	-	-	-	-	-	-	-	-	1.7	Up	
M400014938	M400014938	-	-	-	-	-	-	-	-	2.2	Up	
M400014939	M400014939	-	-	-	-	-	-	-	-	2.7	Up	
M400014940	M400014940	-	-	-	-	-	-	-	-	2.3	Up	
M400014942	M400014942	-	-	-	-	-	-	-	1.7	Up	2.8	Up
M400014946	M400014946	-	-	-	-	-	-	-	-	2.5	Up	
M400014947	M400014947	-	-	-	-	-	-	-	-	2.7	Up	
M400014953	M400014953	-	-	-	-	-	-	-	-	2.0	Up	
M400014962	M400014962	-	-	-	-	-	-	-	-	2.6	Up	
M400014963	M400014963	-	-	-	-	-	-	-	-	2.9	Up	
M400014966	M400014966	-	-	-	-	-	-	-	-	3.6	Up	
M400014977	M400014977	-	-	-	-	-	-	-	-	1.5	Up	
M400014980	M400014980	-	-	-	-	-	-	-	-	2.1	Up	
M400014982	M400014982	-	-	-	-	-	-	-	-	2.6	Up	
M400014983	M400014983	-	-	-	-	-	-	-	-	2.8	Up	
M400014984	M400014984	-	-	-	-	-	-	-	-	3.5	Up	
M400014986	M400014986	-	-	-	-	-	-	-	-	3.3	Up	
M400014988	M400014988	-	-	-	-	-	-	-	-	3.5	Up	
M400014989	M400014989	-	-	-	-	-	-	-	-	3.5	Up	
M400014995	M400014995	-	-	-	-	-	-	-	-	3.1	Up	
M400015002	M400015002	-	-	-	-	-	-	-	-	3.4	Up	
M400015004	M400015004	-	-	-	-	-	-	-	-	2.7	Up	
M400015008	M400015008	-	-	-	-	-	-	-	-	4.2	Up	
M400015010	M400015010	-	-	-	-	-	-	-	-	2.3	Up	
M400015011	M400015011	-	-	-	-	-	-	-	-	2.9	Up	
M400015013	M400015013	-	-	-	-	-	-	-	-	3.0	Up	
M400015014	M400015014	-	-	-	-	-	-	-	-	3.7	Up	
M400015017	M400015017	-	-	-	-	-	-	-	-	2.0	Up	
M400015019	M400015019	-	-	-	-	-	-	-	-	3.0	Up	
M400015020	M400015020	-	-	-	-	-	-	-	-	3.5	Up	
M400015025	M400015025	-	-	-	-	-	-	-	-	3.6	Up	
M400015026	M400015026	-	-	-	-	-	-	-	1.8	Up	3.8	Up
M400015027	M400015027	-	-	-	-	-	-	-	-	1.5	Up	
M400015029	M400015029	-	-	-	-	-	-	-	-	2.0	Up	
M400015030	M400015030	-	-	-	-	-	-	-	-	2.6	Up	
M400015031	M400015031	-	-	-	-	-	-	-	-	3.6	Up	
M400015033	M400015033	-	-	-	-	1.8	Down	-	-	-	-	
M400015035	M400015035	-	-	-	-	2.2	Down	-	-	-	-	



M400015036	M400015036	-	-	-	-	-	-	-	-	1.9	Up
M400015049	M400015049	-	-	-	-	-	-	-	-	2.1	Up
M400015051	M400015051	-	-	-	-	-	-	-	-	1.7	Up
M400015066	M400015066	-	-	-	-	-	-	-	-	1.8	Up
M400015071	M400015071	-	-	-	-	-	-	-	-	1.9	Up
M400015073	M400015073	-	-	-	-	-	-	-	-	2.4	Up
M400015084	M400015084	-	-	-	-	-	-	2.0	Up	2.8	Up
M400015090	M400015090	-	-	-	-	-	-	-	-	3.0	Up
M400015097	M400015097	-	-	-	-	-	-	-	-	2.6	Up
M400015105	M400015105	-	-	-	-	-	-	-	-	2.4	Up
M400015123	M400015123	-	-	-	-	-	-	-	-	1.7	Up
M400015126	M400015126	-	-	-	-	-	-	-	-	2.9	Up
M400015127	M400015127	-	-	-	-	-	-	-	-	1.7	Up
M400015129	M400015129	-	-	-	-	-	-	-	-	2.2	Up
M400015130	M400015130	-	-	-	-	1.6	Down	-	-	3.6	Down
M400015131	M400015131	-	-	-	-	-	-	-	-	2.0	Up
M400015135	M400015135	-	-	-	-	-	-	-	-	2.7	Up
M400015150	M400015150	-	-	-	-	-	-	-	-	2.3	Up
M400015153	M400015153	-	-	-	-	2.1	Down	1.5	Down	-	-
M400015154	M400015154	-	-	-	-	-	-	-	-	2.2	Down
M400015156	M400015156	-	-	-	-	-	-	-	-	2.1	Up
M400015159	M400015159	-	-	-	-	-	-	-	-	3.0	Up
M400015161	M400015161	-	-	-	-	-	-	-	-	1.8	Up
M400015165	M400015165	-	-	-	-	-	-	-	-	1.5	Up
M400015167	M400015167	-	-	-	-	-	-	-	-	2.3	Up
M400015168	M400015168	-	-	-	-	-	-	-	-	4.0	Up
M400015169	M400015169	-	-	-	-	-	-	-	-	1.9	Up
M400015191	M400015191	-	-	-	-	-	-	-	-	1.7	Up
M400015197	M400015197	-	-	-	-	-	-	-	-	1.5	Up
M400015209	M400015209	-	-	-	-	-	-	-	-	2.5	Up
M400015218	M400015218	-	-	-	-	-	-	-	-	2.6	Up
M400015219	M400015219	-	-	-	-	-	-	-	-	2.1	Up
M400015221	M400015221	-	-	-	-	-	-	-	-	1.8	Up
M400015224	M400015224	-	-	-	-	-	-	-	-	1.7	Up
M400015226	M400015226	-	-	-	-	-	-	-	-	2.4	Up
M400015230	M400015230	-	-	-	-	-	-	-	-	1.8	Up
M400015231	M400015231	-	-	-	-	-	-	-	-	3.0	Up
M400015232	M400015232	-	-	-	-	-	-	-	-	2.3	Up
M400015239	M400015239	-	-	-	-	-	-	-	-	3.7	Up
M400015242	M400015242	-	-	-	-	-	-	-	-	3.2	Up
M400015243	M400015243	-	-	-	-	-	-	-	-	3.4	Up

M400015244	M400015244	-	-	-	-	-	-	-	-	1.9	Up
M400015245	M400015245	-	-	-	-	-	-	-	-	2.6	Up
M400015248	M400015248	-	-	-	-	-	-	-	-	2.0	Up
M400015249	M400015249	-	-	-	-	-	-	-	-	3.3	Up
M400015256	M400015256	-	-	-	-	-	-	-	-	1.6	Up
M400015258	M400015258	-	-	-	-	-	-	-	-	2.6	Up
M400015261	M400015261	-	-	-	-	1.5	Down	-	-	-	-
M400015266	M400015266	-	-	-	-	-	-	-	-	1.7	Up
M400015267	M400015267	-	-	-	-	-	-	-	-	3.2	Up
M400015269	M400015269	-	-	-	-	-	-	-	-	3.3	Up
M400015275	M400015275	-	-	-	-	2.0	Down	-	-	-	-
M400015284	M400015284	-	-	-	-	-	-	-	-	2.6	Down
M400015287	M400015287	-	-	-	-	-	-	-	-	2.1	Up
M400015288	M400015288	-	-	-	-	-	-	-	-	2.5	Up
M400015290	M400015290	-	-	-	-	-	-	-	-	3.0	Up
M400015291	M400015291	-	-	-	-	-	-	-	-	2.5	Up
M400015292	M400015292	-	-	-	-	-	-	-	-	2.4	Up
M400015293	M400015293	-	-	-	-	-	-	-	-	3.8	Up
M400015297	M400015297	-	-	-	-	-	-	-	-	3.6	Up
M400015298	M400015298	-	-	-	-	-	-	-	-	2.9	Up
M400015299	M400015299	-	-	-	-	-	-	-	-	4.1	Up
M400015302	M400015302	-	-	-	-	-	-	-	-	2.3	Up
M400015305	M400015305	-	-	-	-	-	-	1.6	Up	3.4	Up
M400015308	M400015308	-	-	-	-	-	-	-	-	1.9	Up
M400015310	M400015310	-	-	-	-	-	-	-	-	3.1	Up
M400015313	M400015313	-	-	-	-	-	-	-	-	1.8	Up
M400015314	M400015314	-	-	-	-	2.6	Down	-	-	-	-
M400015315	M400015315	-	-	-	-	-	-	-	-	1.9	Up
M400015316	M400015316	-	-	-	-	-	-	-	-	3.7	Up
M400015320	M400015320	-	-	-	-	1.9	Down	1.7	Down	1.9	Up
M400015321	M400015321	-	-	-	-	-	-	-	-	3.4	Up
M400015322	M400015322	-	-	-	-	-	-	-	-	4.0	Up
M400015333	M400015333	-	-	-	-	-	-	-	-	2.9	Up
M400015334	M400015334	-	-	-	-	-	-	1.6	Up	3.0	Up
M400015336	M400015336	-	-	-	-	-	-	-	-	3.1	Up
M400015338	M400015338	-	-	-	-	-	-	-	-	2.5	Up
M400015339	M400015339	-	-	-	-	-	-	-	-	2.6	Up
M400015340	M400015340	-	-	-	-	-	-	-	-	2.0	Up
M400015342	M400015342	-	-	-	-	-	-	-	-	2.5	Up
M400015345	M400015345	-	-	-	-	-	-	-	-	1.7	Up
M400015346	M400015346	-	-	-	-	-	-	-	-	4.1	Up

M400015352	M400015352	-	-	-	-	-	-	-	-	2.6	Up
M400015361	M400015361	-	-	-	-	-	-	-	-	3.0	Up
M400015362	M400015362	-	-	-	-	-	-	-	-	3.7	Up
M400015363	M400015363	-	-	-	-	-	-	-	-	2.7	Up
M400015364	M400015364	-	-	-	-	-	-	-	-	3.9	Up
M400015368	M400015368	-	-	-	-	-	-	-	-	1.6	Up
M400015369	M400015369	-	-	-	-	-	-	-	-	3.2	Up
M400015370	M400015370	-	-	-	-	-	-	-	-	3.7	Up
M400015376	M400015376	-	-	-	-	-	-	-	-	3.0	Up
M400015381	M400015381	-	-	-	-	-	-	-	-	3.5	Up
M400015384	M400015384	-	-	-	-	-	-	-	-	3.6	Up
M400015385	M400015385	-	-	-	-	-	-	-	-	2.3	Up
M400015386	M400015386	-	-	-	1.6	Down	-	-	-	2.2	Up
M400015387	M400015387	-	-	-	-	-	-	-	-	3.7	Up
M400015388	M400015388	-	-	-	-	-	2.0	Up	-	-	-
M400015390	M400015390	-	-	-	-	-	-	-	-	2.2	Up
M400015391	M400015391	-	-	-	-	-	-	-	-	1.9	Up
M400015392	M400015392	-	-	-	-	-	-	-	-	1.7	Up
M400015393	M400015393	-	-	-	-	-	-	-	-	2.9	Up
M400015400	M400015400	-	-	-	-	-	2.1	Up	-	4.3	Up
M400015405	M400015405	-	-	-	-	-	-	-	-	2.7	Up
M400015407	M400015407	-	-	-	-	-	-	-	-	2.0	Up
M400015408	M400015408	-	-	-	1.7	Down	-	-	-	-	-
M400015417	M400015417	-	-	-	-	-	-	-	-	2.9	Up
M400015421	M400015421	-	-	-	-	-	-	-	-	2.7	Up
M400015428	M400015428	-	-	-	-	-	-	-	-	2.5	Up
M400015431	M400015431	-	-	-	-	-	-	-	-	2.5	Up
M400015434	M400015434	-	-	-	-	-	-	-	-	2.5	Up
M400015440	M400015440	-	-	-	-	-	-	-	-	2.1	Up
M400015444	M400015444	-	-	-	-	-	1.5	Down	-	-	-
M400015447	M400015447	-	-	-	-	-	-	-	-	3.9	Up
M400015449	M400015449	-	2.3	Down	1.9	Down	1.8	Down	-	-	-
M400015452	M400015452	-	-	-	-	-	-	-	-	2.5	Up
M400015453	M400015453	-	-	-	-	-	-	-	-	2.6	Up
M400015458	M400015458	-	-	-	-	-	-	-	-	3.0	Up
M400015459	M400015459	-	-	-	-	-	-	-	-	3.2	Up
M400015461	M400015461	-	-	-	-	-	-	-	-	3.2	Up
M400015462	M400015462	-	-	-	-	-	-	-	-	3.0	Up
M400015463	M400015463	-	-	-	2.6	Down	-	-	-	-	-
M400015465	M400015465	-	-	-	-	-	-	-	-	3.6	Up
M400015468	M400015468	-	-	-	-	-	-	-	-	2.7	Up

M400015470	M400015470	-	-	-	-	-	-	-	-	1.9	Up
M400015474	M400015474	-	-	-	-	-	-	-	-	1.9	Up
M400015476	M400015476	-	-	-	-	-	-	-	-	3.3	Up
M400015477	M400015477	-	-	-	-	-	-	-	-	3.1	Up
M400015481	M400015481	-	-	-	-	2.0	Down	-	-	-	-
M400015482	M400015482	-	-	-	-	-	-	-	-	1.6	Up
M400015483	M400015483	-	-	-	-	-	-	-	-	3.6	Up
M400015487	M400015487	-	-	-	-	2.3	Down	1.7	Down	-	-
M400015488	M400015488	-	-	-	-	-	-	-	-	2.4	Up
M400015489	M400015489	-	-	-	-	-	-	-	-	4.0	Up
M400015498	M400015498	-	-	-	-	1.5	Down	-	-	-	-
M400015503	M400015503	-	-	-	-	1.8	Down	-	-	-	-
M400015505	M400015505	-	-	-	-	-	-	-	-	1.5	Up
M400015509	M400015509	-	-	-	-	-	-	-	-	3.8	Up
M400015510	M400015510	-	-	-	-	1.6	Down	-	-	-	-
M400015516	M400015516	-	-	-	-	-	-	-	-	1.7	Up
M400015517	M400015517	-	-	-	-	-	-	-	-	3.5	Up
M400015524	M400015524	-	-	-	-	-	-	1.8	Up	2.5	Up
M400015525	M400015525	-	-	-	-	-	-	-	-	2.3	Up
M400015527	M400015527	-	-	-	-	-	-	-	-	2.0	Up
M400015529	M400015529	-	-	-	-	-	-	-	-	3.0	Up
M400015536	M400015536	-	-	-	-	-	-	-	-	4.0	Up
M400015539	M400015539	-	-	-	-	-	-	-	-	1.6	Up
M400015540	M400015540	-	-	-	-	-	-	-	-	2.2	Up
M400015541	M400015541	-	-	-	-	-	-	-	-	2.8	Up
M400015542	M400015542	-	-	-	-	-	-	-	-	2.8	Up
M400015546	M400015546	-	-	-	-	-	-	-	-	1.8	Up
M400015547	M400015547	-	-	-	-	-	-	-	-	3.4	Up
M400015552	M400015552	-	-	-	-	-	-	-	-	2.0	Up
M400015553	M400015553	-	-	-	-	1.7	Down	-	-	-	-
M400015554	M400015554	-	-	-	-	-	-	-	-	1.6	Up
M400015560	M400015560	-	-	-	-	-	-	1.6	Up	4.1	Up
M400015566	M400015566	-	-	-	-	-	-	-	-	2.8	Up
M400015569	M400015569	-	-	-	-	-	-	-	-	2.2	Up
M400015570	M400015570	-	-	-	-	-	-	-	-	2.0	Up
M400015572	M400015572	-	-	-	-	-	-	1.6	Up	4.2	Up
M400015576	M400015576	-	-	-	-	1.5	Down	-	-	-	-
M400015579	M400015579	-	-	-	-	-	-	-	-	1.6	Up
M400015590	M400015590	-	-	-	-	-	-	-	-	2.7	Up
M400015598	M400015598	-	-	-	-	-	-	-	-	2.3	Up
M400015601	M400015601	-	-	-	-	-	-	-	-	2.5	Up

M400015606	M400015606	-	-	-	-	-	-	-	-	2.8	Up
M400015608	M400015608	-	-	-	-	-	-	1.7	Down	-	-
M400015613	M400015613	-	-	-	-	-	-	-	-	3.8	Up
M400015617	M400015617	-	-	-	-	-	-	-	-	1.5	Up
M400015618	M400015618	-	-	-	-	-	-	-	-	1.7	Up
M400015619	M400015619	-	-	-	-	-	-	-	-	1.9	Up
M400015623	M400015623	-	-	-	-	-	-	2.0	Down	-	-
M400015629	M400015629	-	-	-	-	-	-	-	-	2.5	Up
M400015634	M400015634	-	-	-	-	-	-	-	-	1.6	Up
M400015637	M400015637	-	-	-	-	-	-	-	-	2.2	Up
M400015642	M400015642	-	-	-	-	-	-	-	-	2.4	Up
M400015643	M400015643	-	-	-	-	-	-	-	-	2.7	Up
M400015644	M400015644	-	-	-	-	-	-	-	-	1.9	Up
XM_489249	M400015647	-	-	-	-	-	-	-	-	2.4	Up
M400015649	M400015649	-	-	-	-	-	-	-	-	4.2	Up
M400015650	M400015650	-	-	-	-	-	-	-	-	1.9	Up
M400015652	M400015652	-	-	-	-	-	-	-	-	1.6	Up
M400015653	M400015653	-	-	-	-	-	-	-	-	2.4	Up
M400015654	M400015654	-	-	-	-	-	-	-	-	3.0	Up
M400015655	M400015655	-	-	-	-	-	-	-	-	1.5	Up
M400015661	M400015661	-	-	-	-	-	-	-	-	1.8	Up
M400015667	M400015667	-	-	-	-	-	-	-	-	2.1	Up
M400015676	M400015676	-	1.9	Down	-	1.8	Down	-	2.0	Down	-
M400015677	M400015677	-	-	-	-	-	-	-	-	2.9	Up
M400015679	M400015679	-	-	-	-	-	-	-	-	3.8	Up
M400015691	M400015691	-	-	-	-	-	-	-	-	2.3	Up
M400015693	M400015693	-	-	-	-	-	-	-	-	2.3	Up
M400015696	M400015696	-	-	-	-	-	-	-	-	3.9	Up
M400015701	M400015701	-	-	-	-	-	-	-	-	2.8	Up
M400015702	M400015702	-	-	-	-	-	-	-	-	3.8	Up
M400015705	M400015705	-	-	-	-	-	-	-	-	1.8	Up
M400015706	M400015706	-	-	-	-	-	-	-	-	1.6	Up
M400015712	M400015712	-	-	-	-	-	-	-	-	2.9	Up
M400015714	M400015714	-	-	-	-	-	-	-	-	2.5	Up
M400015717	M400015717	-	-	-	-	-	-	-	-	1.9	Up
M400015719	M400015719	-	-	-	-	-	-	-	-	3.4	Up
M400015723	M400015723	-	-	-	-	-	-	-	-	1.9	Up
M400015725	M400015725	-	-	-	-	-	-	-	-	3.6	Up
M400015726	M400015726	-	-	-	-	-	-	-	-	3.6	Up
M400015729	M400015729	-	-	-	-	-	-	-	-	3.0	Up
M400015732	M400015732	-	-	-	-	-	-	-	-	2.6	Up

M400015736	M400015736	-	-	-	-	-	-	-	-	2.5	Up
M400015737	M400015737	-	-	-	-	-	-	-	-	3.4	Up
M400015740	M400015740	-	-	-	-	-	-	-	-	1.7	Up
M400015741	M400015741	-	-	-	-	-	-	-	-	2.5	Up
M400015744	M400015744	-	-	-	-	-	-	-	-	3.7	Up
M400015746	M400015746	-	1.5	Down	-	-	-	-	-	-	-
M400015747	M400015747	-	-	-	-	-	-	-	-	2.3	Up
M400015749	M400015749	-	-	-	-	-	-	-	-	2.2	Up
M400015750	M400015750	-	-	-	-	-	-	2.5	Up	-	-
M400015755	M400015755	-	2.2	Down	2.3	Down	-	-	-	-	-
M400015768	M400015768	-	-	-	-	-	-	-	-	4.0	Up
M400015770	M400015770	-	-	-	1.7	Down	-	-	-	-	-
M400015771	M400015771	-	-	-	-	-	-	-	-	2.2	Up
M400015772	M400015772	-	-	-	-	-	-	-	-	2.8	Up
M400015774	M400015774	-	-	-	-	-	-	-	-	3.8	Up
M400015777	M400015777	-	-	-	-	-	-	-	-	1.7	Up
M400015780	M400015780	-	-	-	-	-	-	-	-	3.0	Up
M400015797	M400015797	-	-	-	-	-	-	-	-	4.0	Up
M400015803	M400015803	-	-	-	-	-	-	-	-	2.8	Up
M400015805	M400015805	-	-	-	-	-	-	-	-	1.5	Up
M400015808	M400015808	-	-	-	-	-	-	-	-	1.9	Up
M400015812	M400015812	-	-	-	-	-	-	-	-	1.7	Up
M400015814	M400015814	-	-	-	-	-	-	-	-	3.1	Up
M400015815	M400015815	-	-	-	-	-	-	-	-	1.9	Up
M400015821	M400015821	-	-	-	-	-	-	-	-	3.9	Up
M400015825	M400015825	-	-	-	-	-	-	-	-	2.5	Up
M400015836	M400015836	-	-	-	-	-	-	-	-	1.6	Up
M400015837	M400015837	-	-	-	-	-	-	-	-	1.7	Up
M400015845	M400015845	-	-	-	-	-	-	-	-	3.6	Up
M400015850	M400015850	-	-	-	-	-	-	-	-	2.6	Up
M400015853	M400015853	-	-	-	-	-	-	-	-	1.9	Up
M400015854	M400015854	-	-	-	-	-	-	1.5	Down	-	-
M400015857	M400015857	-	-	-	-	-	-	-	-	3.4	Up
M400015859	M400015859	-	-	-	-	-	-	-	-	3.0	Up
M400015860	M400015860	-	-	-	-	-	-	-	-	2.8	Up
M400015863	M400015863	-	-	-	-	-	-	-	-	4.2	Up
M400015865	M400015865	-	-	-	1.5	Down	-	-	-	1.7	Up
M400015869	M400015869	-	-	-	-	-	-	2.1	Up	3.6	Up
M400015875	M400015875	-	-	-	-	-	-	-	-	2.6	Up
M400015880	M400015880	-	-	-	-	-	-	-	-	2.0	Up
XM_489349,	M400015885	-	-	-	-	-	-	-	-	2.0	Up

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M400015886	M400015886	-	-	-	-	-	-	-	-	2.4	Up
M400015898	M400015898	-	-	-	-	-	-	-	-	1.9	Up
M400015902	M400015902	-	-	-	-	-	-	-	-	3.2	Down
M400015910	M400015910	-	-	-	-	-	-	-	-	2.5	Up
M400015915	M400015915	-	-	-	-	-	-	-	-	2.2	Down
M400015916	M400015916	-	-	-	-	-	-	-	-	1.8	Up
M400015934	M400015934	-	-	-	-	-	-	-	-	2.0	Up
M400015938	M400015938	-	-	-	-	1.5	Down	-	-	-	-
M400015940	M400015940	-	-	-	-	1.6	Down	-	-	-	-
M400015946	M400015946	-	-	-	-	-	-	-	-	2.0	Up
M400015952	M400015952	-	-	-	-	-	-	-	-	2.4	Up
M400015953	M400015953	-	-	-	-	-	-	-	-	1.9	Up
M400015958	M400015958	-	-	-	-	-	-	-	-	1.6	Up
M400015963	M400015963	-	-	-	-	1.5	Down	-	-	-	-
M400015964	M400015964	-	-	-	-	-	-	1.8	Up	3.2	Up
M400015969	M400015969	-	-	-	-	-	-	-	-	1.9	Up
M400015981	M400015981	-	-	-	-	-	-	-	-	3.3	Up
M400015985	M400015985	-	-	-	-	-	-	-	-	2.0	Up
M400015987	M400015987	-	-	-	-	-	-	-	-	3.2	Up
M400015991	M400015991	-	-	-	-	-	-	-	-	1.6	Up
M400015993	M400015993	-	-	-	-	-	-	1.8	Up	3.2	Up
M400015998	M400015998	-	-	-	-	-	-	-	-	2.5	Up
M400016005	M400016005	-	-	-	-	-	-	-	-	3.3	Up
M400016008	M400016008	-	-	-	-	-	-	-	-	3.0	Up
M400016011	M400016011	-	-	-	-	2.1	Down	-	-	2.5	Up
M400016016	M400016016	-	-	-	-	-	-	-	-	2.1	Up
M400016020	M400016020	-	-	-	-	-	-	-	-	1.5	Up
M400016023	M400016023	-	-	-	-	-	-	-	-	2.7	Up
M400016026	M400016026	-	-	-	-	-	-	-	-	2.7	Up
M400016027	M400016027	-	1.8	Down	-	-	-	-	-	-	-
M400016032	M400016032	-	-	-	-	-	-	-	-	2.6	Up
M400016034	M400016034	-	-	-	-	-	-	-	-	2.2	Up
M400016035	M400016035	-	-	-	-	-	-	-	-	3.4	Up
M400016040	M400016040	-	-	-	-	-	-	-	-	2.0	Up
M400016048	M400016048	-	-	-	-	-	-	-	-	3.1	Up
M400016052	M400016052	-	-	-	-	-	-	-	-	3.5	Up
M400016053	M400016053	-	-	-	-	-	-	-	-	2.6	Up
M400016054	M400016054	-	-	-	-	-	-	2.5	Down	-	-
M400016074	M400016074	-	-	-	-	-	-	-	-	2.0	Up
M400016087	M400016087	-	-	-	-	-	-	-	-	1.8	Up

M400016088	M400016088	-	-	-	-	-	-	-	-	3.0	Up
M400016091	M400016091	-	-	-	1.9	Down	-	-	-	-	-
M400016092	M400016092	-	-	-	-	-	-	-	-	2.5	Up
M400016093	M400016093	-	-	-	2.2	Down	-	-	-	-	-
M400016096	M400016096	-	-	-	-	-	-	-	-	2.8	Up
M400016102	M400016102	-	-	-	-	-	-	-	-	1.9	Up
M400016105	M400016105	-	-	-	-	-	-	-	-	3.1	Up
M400016108	M400016108	-	-	-	-	-	-	-	-	1.7	Up
M400016110	M400016110	-	-	-	-	-	-	-	-	2.9	Up
M400016112	M400016112	-	-	-	-	-	-	-	-	2.7	Up
M400016116	M400016116	-	-	-	-	-	-	-	-	2.6	Up
M400016117	M400016117	-	-	-	2.2	Down	-	-	-	-	-
M400016118	M400016118	-	-	-	-	-	2.0	Up	-	3.1	Up
M400016126	M400016126	-	-	-	-	-	-	-	-	1.6	Up
M400016127	M400016127	-	-	-	-	-	1.8	Down	-	3.2	Up
M400016130	M400016130	-	-	-	-	-	-	-	-	4.1	Up
M400016134	M400016134	-	-	-	-	-	-	-	-	2.5	Up
M400016141	M400016141	-	-	-	-	-	-	-	-	2.1	Up
M400016142	M400016142	-	-	-	-	-	-	-	-	3.0	Up
M400016144	M400016144	-	-	-	-	-	-	-	-	2.0	Up
M400016145	M400016145	-	-	-	-	-	-	-	-	1.5	Up
M400016147	M400016147	-	-	-	-	-	-	-	-	1.9	Up
M400016150	M400016150	-	-	-	-	-	-	-	-	2.4	Up
M400016154	M400016154	-	-	-	-	-	-	-	-	3.8	Up
M400016162	M400016162	-	-	-	-	-	-	-	-	2.1	Up
M400016164	M400016164	-	-	-	-	-	-	-	-	2.6	Up
M400016165	M400016165	-	-	-	-	-	-	-	-	2.5	Up
M400016167	M400016167	-	-	-	-	-	-	-	-	2.0	Up
M400016170	M400016170	-	-	-	-	-	-	-	-	3.4	Up
M400016171	M400016171	-	-	-	-	-	2.0	Up	-	3.9	Up
M400016173	M400016173	-	-	-	1.6	Down	-	-	-	-	-
M400016175	M400016175	-	-	-	1.9	Down	-	-	-	-	-
M400016177	M400016177	-	-	-	-	-	2.4	Up	-	3.3	Up
M400016179	M400016179	-	-	-	-	-	-	-	-	1.8	Up
M400016183	M400016183	-	-	-	-	-	2.3	Up	-	2.9	Up
M400016191	M400016191	-	-	-	2.5	Down	-	-	-	-	-
M400016194	M400016194	-	-	-	-	-	-	-	-	3.4	Up
M400016195	M400016195	-	-	-	-	-	-	-	-	4.0	Up
XM_489086	M400016200	-	-	-	-	-	-	-	-	3.2	Up
M400016201	M400016201	-	-	-	-	-	-	-	-	3.2	Up
M400016205	M400016205	-	-	-	-	-	-	-	-	2.5	Up



M400016207	M400016207	-	-	-	-	-	-	-	-	2.9	Up
M400016209	M400016209	-	-	-	-	-	-	-	-	2.4	Up
M400016212	M400016212	-	-	-	-	-	-	-	-	1.9	Up
M400016213	M400016213	-	-	-	-	-	-	-	-	2.7	Up
M400016229	M400016229	-	-	-	-	-	-	-	-	1.6	Up
M400016243	M400016243	-	-	-	-	-	-	-	-	4.0	Up
XM_488558	M400016245	-	-	-	2.3	Down	-	-	-	1.7	Up
M400016248	M400016248	-	-	-	-	-	-	-	-	3.2	Up
M400016254	M400016254	-	-	-	-	-	-	-	-	2.6	Up
M400016264	M400016264	-	-	-	-	-	-	-	-	1.6	Up
M400016266	M400016266	-	-	-	-	-	-	-	-	3.6	Up
M400016275	M400016275	-	-	-	-	-	-	-	-	2.6	Up
M400016278	M400016278	-	-	-	-	-	-	-	-	3.3	Up
M400016289	M400016289	-	-	-	-	-	-	-	-	2.0	Up
M400016296	M400016296	-	-	-	-	-	-	-	-	2.7	Up
M400016312	M400016312	-	-	-	3.3	Down	-	-	-	-	-
M400016314	M400016314	-	-	-	-	-	-	-	-	3.3	Up
M400016319	M400016319	-	-	-	1.7	Down	-	-	-	-	-
M400016320	M400016320	-	-	-	-	-	-	-	-	2.7	Up
M400016326	M400016326	-	-	-	-	-	-	-	-	2.1	Up
M400016329	M400016329	-	-	-	-	-	-	-	-	2.2	Up
M400016332	M400016332	-	-	-	-	-	-	-	-	1.7	Up
M400016335	M400016335	-	-	-	-	-	-	-	-	2.5	Up
M400016336	M400016336	-	-	-	-	-	-	-	-	1.7	Up
M400016337	M400016337	-	-	-	-	-	-	-	-	2.9	Up
M400016338	M400016338	-	-	-	-	-	-	-	-	2.4	Up
M400016342	M400016342	-	-	-	2.1	Down	-	-	-	-	-
M400016344	M400016344	-	-	-	-	-	-	-	-	2.9	Up
M400016350	M400016350	-	-	-	-	-	-	-	-	1.9	Up
M400016353	M400016353	-	-	-	-	-	-	-	-	3.2	Up
M400016358	M400016358	-	-	-	-	-	-	-	-	2.6	Up
M400016361	M400016361	-	-	-	-	-	-	-	-	4.0	Up
M400016362	M400016362	-	-	-	1.7	Down	-	-	-	-	-
M400016364	M400016364	-	-	-	-	-	-	-	-	3.1	Up
M400016365	M400016365	-	-	-	-	-	-	-	-	2.9	Up
M400016367	M400016367	-	-	-	-	-	1.7	Up	-	3.6	Up
M400016370	M400016370	-	-	-	-	-	-	-	-	1.6	Up
M400016372	M400016372	-	-	-	-	-	2.0	Up	-	2.6	Up
M400016378	M400016378	-	-	-	-	-	-	-	-	3.3	Up
M400016383	M400016383	-	-	-	-	-	-	-	-	2.4	Up
M400016384	M400016384	-	-	-	-	-	-	-	-	3.8	Up

M400016385	M400016385	-	-	-	-	-	1.5	Up	4.1	Up
M400016388	M400016388	-	-	-	-	-	-	-	2.6	Up
M400016390	M400016390	-	-	-	-	-	-	-	3.1	Up
M400016391	M400016391	-	-	-	-	-	-	-	2.5	Up
M400016396	M400016396	-	-	-	-	-	-	-	2.9	Up
M400016400	M400016400	-	-	-	-	-	-	-	2.4	Up
M400016402	M400016402	-	-	-	-	-	-	-	2.4	Up
M400016403	M400016403	-	-	-	-	-	-	-	3.0	Up
M400016404	M400016404	-	-	-	2.0	Down	-	-	-	-
M400016406	M400016406	-	-	-	-	-	-	-	2.1	Up
M400016407	M400016407	-	-	-	-	-	-	-	2.7	Up
M400016409	M400016409	-	-	-	-	-	-	-	4.1	Up
M400016412	M400016412	-	-	-	-	-	-	-	1.9	Up
M400016413	M400016413	-	-	-	-	-	1.7	Down	2.1	Up
M400016414	M400016414	-	-	-	-	-	-	-	2.7	Up
M400016415	M400016415	-	-	-	-	-	-	-	3.8	Up
M400016418	M400016418	-	-	-	-	-	-	-	2.8	Up
M400016420	M400016420	-	-	-	1.7	Down	-	-	-	-
M400016422	M400016422	-	-	-	-	-	-	-	1.7	Up
M400016426	M400016426	-	-	-	-	-	-	-	1.7	Up
XM_488879	M400016427	-	-	-	-	-	-	-	3.7	Up
M400016430	M400016430	-	-	-	-	-	-	-	2.3	Up
M400016431	M400016431	-	-	-	-	-	-	-	2.7	Up
M400016432	M400016432	-	-	-	-	-	-	-	2.7	Up
M400016434	M400016434	-	-	-	-	-	-	-	2.4	Up
M400016436	M400016436	-	-	-	-	-	-	-	3.1	Up
M400016437	M400016437	-	-	-	-	-	-	-	4.1	Up
M400016438	M400016438	-	-	-	-	-	-	-	1.9	Up
M400016439	M400016439	-	-	-	-	-	-	-	3.1	Up
M400016444	M400016444	-	-	-	-	-	-	-	3.3	Up
M400016445	M400016445	-	-	-	-	-	-	-	2.7	Up
M400016450	M400016450	-	-	-	-	-	-	-	2.3	Up
M400016451	M400016451	-	-	-	-	-	-	-	3.8	Up
M400016452	M400016452	-	-	-	-	-	-	-	2.6	Up
M400016453	M400016453	-	-	-	-	-	-	-	2.1	Up
M400016454	M400016454	-	-	-	-	-	-	-	2.4	Up
M400016455	M400016455	-	-	-	-	-	1.5	Up	-	-
XM_483888	M400016456	-	-	-	-	-	-	-	4.1	Up
M400016458	M400016458	-	-	-	-	-	-	-	1.9	Up
M400016459	M400016459	-	-	-	-	-	-	-	2.9	Up
M400016474	M400016474	-	-	-	-	-	2.2	Up	3.2	Up

M400016476	M400016476	-	-	-	-	-	-	-	-	3.4	Up
M400016479	M400016479	-	-	-	-	-	-	-	-	2.6	Up
M400016480	M400016480	-	-	-	-	-	-	-	-	4.3	Up
M400016482	M400016482	-	-	-	-	-	-	-	-	3.3	Up
XM_489189	M400016483	-	-	-	-	-	-	-	-	2.5	Up
M400016486	M400016486	-	-	-	-	-	-	-	-	3.5	Up
M400016491	M400016491	-	-	-	-	-	-	-	-	2.8	Up
M400016492	M400016492	-	-	-	-	-	-	2.4	Up	4.3	Up
M400016497	M400016497	-	-	-	-	-	-	-	-	2.1	Up
M400016498	M400016498	-	-	-	-	-	-	2.5	Up	3.2	Up
M400016500	M400016500	-	-	-	-	-	-	-	-	3.6	Up
M400016502	M400016502	-	-	-	-	-	-	-	-	2.4	Up
M400016503	M400016503	-	-	-	-	-	-	-	-	4.1	Up
M400016504	M400016504	-	-	-	-	-	-	-	-	4.3	Up
M400016509	M400016509	-	-	-	-	-	-	-	-	3.2	Up
M400016510	M400016510	-	-	-	-	-	-	-	-	3.6	Up
M400016515	M400016515	-	-	-	-	-	-	-	-	1.7	Down
M400016516	M400016516	-	-	-	-	-	-	2.5	Up	4.1	Up
M400016519	M400016519	-	-	-	-	-	-	-	-	1.6	Down
M400016521	M400016521	-	-	-	-	-	-	-	-	2.2	Up
M400016522	M400016522	-	-	-	-	-	-	1.7	Up	3.6	Up
XM_489154	M400016524	-	-	-	-	-	-	-	-	1.9	Up
M400016525	M400016525	-	-	-	-	-	-	-	-	3.2	Up
M400016526	M400016526	-	-	-	-	-	-	-	-	1.9	Up
M400016527	M400016527	-	-	-	-	-	-	-	-	3.3	Up
M400016528	M400016528	-	-	-	-	-	-	-	-	1.6	Up
M400016530	M400016530	-	-	-	-	-	-	-	-	3.0	Up
XM_488952	M400016531	-	-	-	-	-	-	-	-	3.4	Up
M400016532	M400016532	-	-	-	-	-	-	-	-	3.1	Up
M400016533	M400016533	-	-	-	-	-	-	-	-	3.8	Up
M400016536	M400016536	-	-	-	-	1.9	Down	-	-	-	-
M400016539	M400016539	-	-	-	-	-	-	-	-	2.1	Up
M400016540	M400016540	-	-	-	-	-	-	-	-	3.4	Up
M400016545	M400016545	-	-	-	-	-	-	-	-	3.1	Up
M400016549	M400016549	-	-	-	-	-	-	-	-	2.5	Up
M400016550	M400016550	-	-	-	-	-	-	-	-	3.6	Up
M400016556	M400016556	-	-	-	-	-	-	-	-	3.0	Up
M400016557	M400016557	-	-	-	-	-	-	2.1	Up	-	-
M400016559	M400016559	-	-	-	-	-	-	1.8	Down	-	-
M400016562	M400016562	-	-	-	-	-	-	-	-	3.7	Up
XM_488856	M400016566	-	-	-	-	-	-	-	-	1.9	Up

M400016568	M400016568	-	-	-	-	-	-	-	-	2.5	Up
M400016572	M400016572	-	-	-	-	-	-	-	-	2.6	Up
M400016574	M400016574	-	-	-	-	-	-	-	-	2.9	Up
M400016580	M400016580	-	-	-	-	-	-	-	-	3.8	Up
M400016581	M400016581	-	-	-	-	-	-	3.3	Up	2.6	Up
M400016584	M400016584	-	-	-	-	-	-	-	-	2.0	Up
M400016586	M400016586	-	-	-	-	-	-	-	-	1.8	Up
M400016587	M400016587	-	-	-	-	-	-	-	-	2.9	Up
M400016592	M400016592	-	-	-	-	-	-	-	-	4.1	Up
M400016595	M400016595	-	-	-	-	-	-	-	-	1.6	Up
M400016596	M400016596	-	-	-	-	-	-	-	-	2.6	Up
M400016598	M400016598	-	-	-	-	-	-	-	-	3.1	Up
M400016601	M400016601	-	1.7	Down	2.3	Down	2.0	Down	-	-	-
M400016607	M400016607	-	-	-	-	-	2.0	Down	-	-	-
M400016609	M400016609	-	-	-	-	-	-	-	-	2.6	Up
M400016610	M400016610	-	-	-	-	-	-	-	-	3.5	Up
M400016614	M400016614	-	-	-	-	-	-	-	-	1.6	Up
M400016622	M400016622	-	-	-	-	-	-	-	-	1.9	Up
M400016625	M400016625	-	-	-	-	-	-	-	-	3.0	Up
M400016629	M400016629	-	-	-	-	-	-	-	-	2.9	Up
M400016634	M400016634	-	-	-	-	-	-	-	-	2.3	Up
M400016635	M400016635	-	-	-	-	-	-	-	-	2.0	Up
M400016640	M400016640	-	-	-	-	-	-	-	-	3.5	Up
M400016646	M400016646	-	-	-	-	-	-	-	-	2.6	Up
M400016650	M400016650	-	-	-	1.6	Down	-	-	-	-	-
XM_489032	M400016655	-	-	-	-	-	-	-	-	2.3	Up
M400016658	M400016658	-	-	-	-	-	-	-	-	2.7	Up
M400016668	M400016668	-	-	-	-	-	-	-	-	1.6	Up
M400016669	M400016669	-	-	-	-	-	-	-	-	2.4	Up
M400016670	M400016670	-	-	-	-	-	-	-	-	2.2	Up
M400016673	M400016673	-	-	-	-	-	-	-	-	2.1	Up
M400016674	M400016674	-	-	-	-	-	-	-	-	2.0	Up
M400016675	M400016675	-	-	-	-	-	-	-	-	3.7	Up
M400016676	M400016676	-	-	-	-	-	-	-	-	3.6	Up
M400016685	M400016685	-	-	-	-	-	-	-	-	2.8	Up
M400016694	M400016694	-	-	-	-	-	-	-	-	3.0	Up
M400016697	M400016697	-	-	-	-	-	-	-	-	2.0	Up
M400016699	M400016699	-	-	-	-	-	-	-	-	1.6	Up
M400016700	M400016700	-	-	-	-	-	-	-	-	3.4	Up
M400016705	M400016705	-	-	-	-	-	-	-	-	2.8	Up
M400016706	M400016706	-	-	-	-	-	-	-	-	2.8	Up

M400016710	M400016710	-	-	-	-	-	-	-	-	1.9	Up
XM_488629	M400016712	-	-	-	-	-	-	-	-	2.1	Up
M400016718	M400016718	-	-	-	-	-	-	-	-	2.5	Up
M400016719	M400016719	-	-	-	-	-	-	-	-	1.6	Up
M400016723	M400016723	-	-	-	-	-	-	-	-	1.6	Up
M400016727	M400016727	-	-	-	-	-	-	-	-	2.3	Up
M400016730	M400016730	-	-	-	-	-	-	-	-	2.4	Up
M400016736	M400016736	-	-	-	-	-	-	-	-	1.8	Up
M400016739	M400016739	-	-	-	-	-	-	-	-	2.5	Up
M400016742	M400016742	-	-	-	-	-	-	-	-	1.7	Up
M400016744	M400016744	-	-	-	-	-	-	-	-	2.3	Up
M400016745	M400016745	-	-	-	-	-	-	-	-	2.9	Up
M400016746	M400016746	-	-	-	-	-	-	-	-	2.8	Up
M400016747	M400016747	-	-	-	-	-	-	-	-	3.5	Up
M400016756	M400016756	-	-	-	-	-	-	-	-	2.7	Up
M400016759	M400016759	-	-	-	-	-	-	-	-	3.1	Up
M400016762	M400016762	-	-	-	-	-	-	-	-	4.1	Up
M400016763	M400016763	-	-	-	-	-	-	-	-	3.6	Up
M400016764	M400016764	-	-	-	-	-	-	-	-	2.4	Up
M400016765	M400016765	-	-	-	-	-	-	-	-	3.8	Up
M400016768	M400016768	-	-	-	-	-	-	-	-	1.8	Up
M400016769	M400016769	-	-	-	-	-	-	-	-	3.6	Up
M400016771	M400016771	-	-	-	-	-	-	-	-	3.7	Up
M400016772	M400016772	-	-	-	-	-	-	-	-	1.6	Up
M400016774	M400016774	-	-	-	-	-	-	-	-	2.2	Up
M400016777	M400016777	-	-	-	-	-	-	-	-	3.2	Up
M400016781	M400016781	-	-	-	-	-	-	-	-	2.4	Up
M400016782	M400016782	-	-	-	-	-	-	-	-	3.0	Up
M400016783	M400016783	-	-	-	-	-	-	-	-	1.9	Up
M400016784	M400016784	-	-	-	-	-	-	-	-	1.9	Up
M400016786	M400016786	-	-	-	-	-	-	-	-	2.0	Up
M400016787	M400016787	-	-	-	-	-	-	-	-	2.4	Up
M400016789	M400016789	-	-	-	-	-	-	-	-	3.9	Up
M400016794	M400016794	-	-	-	-	2.9	Down	-	-	-	-
M400016795	M400016795	-	-	-	-	-	-	-	-	3.8	Up
M400016806	M400016806	-	-	-	-	-	-	-	-	2.1	Up
M400016807	M400016807	-	-	-	-	-	-	-	-	1.9	Up
M400016808	M400016808	-	-	-	-	2.0	Down	-	-	-	-
M400016810	M400016810	-	-	-	-	-	-	-	-	3.2	Up
M400016811	M400016811	-	-	-	-	-	-	-	-	3.5	Up
M400016812	M400016812	-	-	-	-	-	-	-	-	3.7	Up

M400016816	M400016816	-	-	-	-	-	-	-	-	2.5	Up
M400016817	M400016817	-	-	-	-	-	-	-	-	2.4	Up
M400016819	M400016819	-	-	-	-	-	-	-	-	3.2	Up
M400016824	M400016824	-	-	-	-	-	-	-	-	2.6	Up
M400016829	M400016829	-	-	-	-	-	-	-	-	1.9	Up
M400016832	M400016832	-	-	-	-	-	-	-	-	2.5	Up
M400016834	M400016834	-	-	-	-	-	-	-	-	2.3	Up
M400016835	M400016835	-	-	-	-	-	-	-	-	4.3	Up
M400016836	M400016836	-	-	-	-	-	-	-	-	3.9	Up
M400016839	M400016839	-	-	-	-	-	-	-	-	3.0	Up
M400016840	M400016840	-	-	-	-	-	-	-	-	3.1	Up
M400016841	M400016841	-	-	-	-	-	-	-	-	3.7	Up
M400016842	M400016842	-	-	-	-	-	-	-	-	3.9	Up
M400016845	M400016845	-	-	-	-	-	-	-	-	3.0	Up
M400016847	M400016847	-	-	-	-	-	-	-	-	2.9	Up
M400016851	M400016851	-	-	-	-	-	-	-	-	2.0	Up
M400016853	M400016853	-	-	-	-	-	-	-	-	1.9	Up
M400016856	M400016856	-	-	-	-	-	-	-	-	3.2	Up
M400016857	M400016857	-	-	-	-	-	-	-	-	2.6	Up
M400016862	M400016862	-	-	-	-	-	-	-	-	3.0	Up
M400016863	M400016863	-	-	-	-	-	-	-	-	3.3	Up
M400016864	M400016864	-	-	-	-	-	-	-	-	2.4	Up
M400016865	M400016865	-	-	-	-	-	-	-	-	3.8	Up
M400016866	M400016866	-	-	-	-	-	-	-	-	4.0	Up
M400016871	M400016871	-	1.8	Down	2.6	Down	-	-	-	-	-
M400016872	M400016872	-	-	-	-	-	-	-	-	4.0	Up
M400016875	M400016875	-	-	-	-	-	-	-	-	1.9	Up
M400016877	M400016877	-	-	-	-	-	-	-	-	1.7	Up
M400016878	M400016878	-	-	-	-	-	-	-	-	3.9	Up
M400016881	M400016881	-	-	-	-	-	-	-	-	2.0	Up
M400016883	M400016883	-	-	-	-	-	-	-	-	3.7	Up
M400016884	M400016884	-	-	-	-	-	-	-	-	4.0	Up
M400016887	M400016887	-	-	-	-	-	-	-	-	1.9	Up
M400016889	M400016889	-	-	-	-	-	-	-	-	1.7	Up
M400016890	M400016890	-	-	-	-	-	-	-	-	3.5	Up
M400016893	M400016893	-	-	-	-	-	-	-	-	3.4	Up
M400016894	M400016894	-	-	-	-	-	-	-	-	2.3	Up
M400016899	M400016899	-	-	-	-	-	-	-	-	2.1	Up
M400016900	M400016900	-	-	-	-	-	-	-	-	2.0	Up
M400016902	M400016902	-	-	-	-	-	-	-	-	3.2	Up
M400016904	M400016904	-	-	-	-	-	-	-	-	2.0	Up

M400016905	M400016905	-	-	-	-	-	-	-	-	3.3	Up
XM_488675	M400016908	-	-	-	-	-	-	-	-	4.2	Up
M400016911	M400016911	-	-	-	-	-	-	-	-	2.4	Up
M400016912	M400016912	-	-	-	-	2.0	Down	-	-	-	-
M400016913	M400016913	-	-	-	-	-	-	-	-	3.5	Up
M400016914	M400016914	-	-	-	-	-	-	-	-	3.6	Up
M400016918	M400016918	-	-	-	-	-	-	-	-	2.9	Up
M400016919	M400016919	-	-	-	-	-	-	-	-	1.7	Up
M400016920	M400016920	-	-	-	-	-	-	-	-	2.8	Up
M400016924	M400016924	-	-	-	-	-	-	-	-	2.5	Up
M400016925	M400016925	-	-	-	-	-	-	-	-	3.3	Up
M400016929	M400016929	-	-	-	-	2.8	Down	-	-	-	-
M400016930	M400016930	-	-	-	-	-	-	-	-	2.3	Up
XM_488869	M400016931	-	-	-	-	-	-	-	-	3.9	Up
M400016933	M400016933	-	-	-	-	2.0	Down	-	-	-	-
M400016936	M400016936	-	-	-	-	-	-	-	-	2.6	Up
M400016937	M400016937	-	-	-	-	-	-	-	-	4.0	Up
M400016946	M400016946	-	-	-	-	-	-	-	-	3.2	Up
M400016947	M400016947	-	-	-	-	-	-	-	-	2.2	Up
M400016949	M400016949	-	-	-	-	-	-	2.4	Up	-	-
M400016953	M400016953	-	-	-	-	-	-	-	-	2.3	Up
M400016955	M400016955	-	-	-	-	-	-	-	-	3.7	Up
M400016957	M400016957	-	-	-	-	-	-	-	-	2.2	Up
M400016958	M400016958	-	-	-	-	-	-	-	-	1.7	Up
M400016959	M400016959	-	-	-	-	3.2	Down	-	-	-	-
M400016965	M400016965	-	-	-	-	-	-	-	-	2.6	Up
M400016966	M400016966	-	-	-	-	-	-	-	-	2.6	Up
M400016971	M400016971	-	-	-	-	-	-	-	-	2.4	Up
M400016972	M400016972	-	-	-	-	-	-	-	-	3.2	Up
M400016977	M400016977	-	-	-	-	2.0	Down	-	-	-	-
M400016982	M400016982	-	-	-	-	1.8	Down	-	-	-	-
M400016984	M400016984	-	-	-	-	1.8	Down	-	-	-	-
M400016987	M400016987	-	-	-	-	-	-	-	-	3.3	Up
M400016988	M400016988	-	-	-	-	-	-	-	-	4.3	Up
M400016989	M400016989	-	-	-	-	-	-	-	-	1.7	Up
M400016990	M400016990	-	-	-	-	-	-	-	-	3.3	Up
M400016991	M400016991	-	-	-	-	-	-	-	-	2.9	Up
M400016996	M400016996	-	-	-	-	-	-	-	-	3.1	Up
M400017000	M400017000	-	-	-	-	-	-	-	-	2.2	Up
M400017003	M400017003	-	-	-	-	-	-	1.9	Up	4.1	Up
M400017008	M400017008	-	-	-	-	-	-	-	-	2.6	Up

M400017014	M400017014	-	-	-	-	-	-	-	-	2.4	Up
M400017015	M400017015	-	-	-	-	-	-	1.7	Up	3.2	Up
M400017020	M400017020	-	-	-	-	-	-	-	-	2.6	Down
M400017023	M400017023	-	-	-	-	2.2	Down	2.0	Down	-	-
M400017024	M400017024	-	-	-	-	-	-	-	-	2.2	Up
M400017025	M400017025	-	-	-	-	1.6	Down	-	-	-	-
M400017026	M400017026	-	-	-	-	-	-	-	-	1.9	Up
M400017027	M400017027	-	-	-	-	-	-	-	-	1.9	Up
M400017029	M400017029	-	-	-	-	-	-	-	-	2.2	Up
M400017030	M400017030	-	-	-	-	1.7	Down	-	-	-	-
M400017035	M400017035	-	-	-	-	-	-	-	-	2.0	Up
XM_489183	M400017037	-	-	-	-	-	-	-	-	2.6	Up
M400017038	M400017038	-	-	-	-	-	-	-	-	3.3	Up
M400017041	M400017041	-	-	-	-	-	-	-	-	2.0	Up
M400017043	M400017043	-	-	-	-	-	-	-	-	1.7	Up
M400017044	M400017044	-	-	-	-	-	-	-	-	4.0	Up
M400017049	M400017049	-	-	-	-	-	-	-	-	2.4	Up
M400017050	M400017050	-	-	-	-	-	-	-	-	2.1	Up
M400017051	M400017051	-	-	-	-	-	-	-	-	4.2	Up
M400017053	M400017053	-	-	-	-	-	-	-	-	2.8	Up
M400017054	M400017054	-	-	-	-	-	-	-	-	2.5	Up
M400017055	M400017055	-	-	-	-	2.1	Down	-	-	-	-
M400017056	M400017056	-	-	-	-	-	-	-	-	3.5	Up
M400017059	M400017059	-	-	-	-	-	-	-	-	2.2	Up
M400017060	M400017060	-	-	-	-	-	-	-	-	1.7	Up
M400017062	M400017062	-	-	-	-	-	-	-	-	1.8	Up
M400017073	M400017073	-	-	-	-	-	-	-	-	3.0	Up
M400017078	M400017078	-	-	-	-	-	-	-	-	2.4	Up
M400017080	M400017080	-	-	-	-	-	-	-	-	2.1	Up
M400017086	M400017086	-	-	-	-	-	-	1.6	Up	4.3	Up
M400017089	M400017089	-	-	-	-	-	-	-	-	2.5	Up
M400017091	M400017091	-	-	-	-	-	-	-	-	2.3	Up
M400017098	M400017098	-	-	-	-	-	-	-	-	2.6	Up
M400017103	M400017103	-	-	-	-	-	-	-	-	2.8	Up
M400017104	M400017104	-	-	-	-	-	-	-	-	3.1	Up
M400017118	M400017118	-	-	-	-	-	-	-	-	1.6	Up
M400017119	M400017119	-	-	-	-	-	-	-	-	2.9	Up
M400017121	M400017121	-	-	-	-	-	-	-	-	3.2	Up
M400017124	M400017124	-	-	-	-	-	-	-	-	3.3	Up
M400017127	M400017127	-	-	-	-	-	-	-	-	2.6	Up
M400017128	M400017128	-	-	-	-	-	-	-	-	1.9	Up



M400017132	M400017132	-	-	-	-	-	-	-	-	2.4	Up
M400017133	M400017133	-	-	-	-	-	-	-	-	1.6	Down
M400017140	M400017140	-	-	-	-	-	-	-	-	3.0	Up
M400017144	M400017144	-	-	-	-	-	-	-	-	1.6	Up
M400017145	M400017145	-	-	-	-	-	-	-	-	3.0	Up
M400017150	M400017150	-	-	-	-	-	-	-	-	1.6	Up
M400017156	M400017156	-	-	-	-	-	-	-	-	2.3	Up
M400017157	M400017157	-	-	-	-	1.5	Down	-	-	-	-
M400017162	M400017162	-	-	-	-	-	-	-	-	1.9	Up
M400017163	M400017163	-	-	-	-	-	-	-	-	1.8	Up
M400017167	M400017167	-	-	-	-	-	-	-	-	2.3	Up
M400017169	M400017169	-	-	-	-	-	-	-	-	3.3	Up
M400017172	M400017172	-	-	-	-	-	-	1.9	Down	-	-
M400017173	M400017173	-	-	-	-	-	-	-	-	2.5	Up
M400017174	M400017174	-	-	-	-	-	-	-	-	3.2	Up
M400017175	M400017175	-	-	-	-	-	-	-	-	3.7	Up
M400017185	M400017185	-	-	-	-	-	-	-	-	1.8	Up
M400017186	M400017186	-	-	-	-	-	-	-	-	2.9	Up
M400017188	M400017188	-	-	-	-	-	-	-	-	1.6	Up
M400017192	M400017192	-	-	-	-	-	-	-	-	3.5	Up
M400017193	M400017193	-	-	-	-	-	-	-	-	3.0	Up
M400017196	M400017196	-	-	-	-	1.9	Down	-	-	-	-
M400017197	M400017197	-	-	-	-	-	-	-	-	3.2	Up
M400017198	M400017198	-	-	-	-	-	-	-	-	3.7	Up
M400017199	M400017199	-	-	-	-	-	-	-	-	3.6	Up
M400017205	M400017205	-	-	-	-	-	-	-	-	3.0	Up
M400017210	M400017210	-	-	-	-	1.7	Down	-	-	-	-
M400017211	M400017211	-	-	-	-	-	-	-	-	3.4	Up
M400017212	M400017212	-	-	-	-	-	-	-	-	2.6	Up
M400017213	M400017213	-	-	-	-	-	-	-	-	2.8	Up
M400017215	M400017215	-	-	-	-	-	-	-	-	1.6	Up
M400017219	M400017219	-	-	-	-	-	-	-	-	4.2	Up
M400017220	M400017220	-	-	-	-	-	-	-	-	2.1	Up
M400017222	M400017222	-	-	-	-	-	-	-	-	3.6	Up
M400017227	M400017227	-	-	-	-	-	-	-	-	4.1	Up
M400017237	M400017237	-	-	-	-	-	-	-	-	1.8	Up
M400017239	M400017239	-	-	-	-	-	-	-	-	3.1	Up
M400017243	M400017243	-	-	-	-	-	-	-	-	3.8	Up
M400017246	M400017246	-	-	-	-	1.5	Down	-	-	-	-
M400017249	M400017249	-	-	-	-	1.9	Down	-	-	-	-
XM_489351	M400017251	-	-	-	-	-	-	-	-	2.8	Up

M400017255	M400017255	-	-	-	1.7	Down	-	-	1.5	Up
M400017256	M400017256	-	-	-	-	-	-	-	2.0	Up
M400017257	M400017257	-	-	-	-	-	-	-	3.2	Up
M400017258	M400017258	-	-	-	-	-	-	-	2.7	Up
M400017263	M400017263	-	-	-	-	-	-	-	3.3	Up
M400017266	M400017266	-	-	-	-	-	-	-	1.9	Up
M400017270	M400017270	-	-	-	-	-	-	-	3.8	Up
M400017275	M400017275	-	-	-	-	-	-	-	2.6	Up
M400017276	M400017276	-	-	-	-	-	-	-	2.4	Up
M400017279	M400017279	-	-	-	-	-	-	-	2.1	Up
M400017280	M400017280	-	-	-	-	-	-	-	3.2	Up
M400017281	M400017281	-	-	-	-	-	-	-	3.0	Up
M400017287	M400017287	-	-	-	-	-	-	-	2.3	Up
M400017288	M400017288	-	-	-	-	-	-	-	3.9	Up
M400017291	M400017291	-	-	-	-	-	-	-	1.7	Up
M400017292	M400017292	-	-	-	-	-	-	-	2.5	Up
M400017293	M400017293	-	-	-	-	-	-	-	3.5	Up
M400017294	M400017294	-	-	-	-	-	-	-	3.8	Up
M400017297	M400017297	-	-	-	-	-	-	-	1.8	Up
M400017298	M400017298	-	-	-	-	-	-	-	2.1	Up
M400017299	M400017299	-	-	-	-	-	-	-	3.1	Up
M400017300	M400017300	-	-	-	-	-	-	-	3.0	Up
M400017304	M400017304	-	-	-	-	-	-	-	2.4	Up
M400017305	M400017305	-	-	-	-	-	-	-	3.5	Up
XM_488809	M400017307	-	-	-	-	-	-	-	2.7	Up
M400017311	M400017311	-	-	-	-	-	-	-	4.0	Up
M400017313	M400017313	-	-	-	-	-	-	-	2.7	Up
M400017317	M400017317	-	-	-	-	-	1.6	Up	3.5	Up
M400017325	M400017325	-	-	-	1.5	Up	-	-	2.1	Up
M400017332	M400017332	-	-	-	-	-	-	-	2.3	Up
M400017335	M400017335	-	-	-	-	-	-	-	3.2	Up
M400017341	M400017341	-	-	-	-	-	-	-	2.7	Up
M400017346	M400017346	-	-	-	-	-	-	-	2.1	Up
M400017352	M400017352	-	-	-	-	-	-	-	1.7	Up
M400017353	M400017353	-	-	-	-	-	-	-	1.8	Up
M400017364	M400017364	-	-	-	-	-	-	-	3.1	Up
XM_488657	M400017365	-	-	-	-	-	-	-	3.9	Up
XM_488651	M400017367	-	-	-	-	-	-	-	2.8	Up
M400017371	M400017371	-	-	-	-	-	-	-	3.3	Up
M400017375	M400017375	-	-	-	-	-	-	-	2.1	Up
M400017383	M400017383	-	-	-	-	-	-	-	3.6	Up

M400017389	M400017389	-	-	-	-	-	2.0	Up	3.8	Up
M400017405	M400017405	-	-	-	-	-	-	-	3.4	Up
M400017406	M400017406	-	-	-	-	-	-	-	3.0	Up
M400017412	M400017412	-	-	-	-	-	-	-	2.2	Up
M400017418	M400017418	-	-	-	-	-	-	-	2.3	Up
M400017421	M400017421	-	-	-	-	-	-	-	2.2	Up
M400017430	M400017430	-	-	-	-	-	-	-	3.4	Up
M400017436	M400017436	-	-	-	-	-	-	-	2.5	Up
M400017447	M400017447	-	-	-	-	-	-	-	2.0	Up
M400017452	M400017452	-	-	-	-	-	-	-	1.9	Up
M400017454	M400017454	-	-	-	1.5	Down	-	-	-	-
M400017457	M400017457	-	-	-	-	-	-	-	2.3	Up
M400017459	M400017459	-	-	-	-	-	-	-	1.5	Up
M400017460	M400017460	-	-	-	-	-	-	-	2.6	Up
M400017466	M400017466	-	-	-	-	-	-	-	1.8	Up
M400017469	M400017469	-	-	-	-	-	-	-	4.2	Up
M400017472	M400017472	-	-	-	-	-	-	-	1.7	Up
M400017483	M400017483	-	1.7	Down	-	-	-	-	-	-
M400017484	M400017484	-	-	-	-	-	1.6	Up	3.0	Up
M400017499	M400017499	-	-	-	-	-	-	-	2.3	Up
M400017501	M400017501	-	-	-	-	-	2.6	Up	-	-
M400017504	M400017504	-	-	-	-	-	-	-	2.3	Up
M400017505	M400017505	-	-	-	-	-	-	-	2.5	Up
M400017506	M400017506	-	-	-	-	-	-	-	3.6	Up
M400017513	M400017513	-	-	-	-	-	1.7	Up	3.1	Up
M400017518	M400017518	-	-	-	-	-	-	-	3.1	Up
M400017519	M400017519	-	-	-	-	-	-	-	3.8	Up
M400017522	M400017522	-	-	-	-	-	-	-	3.2	Up
M400017524	M400017524	-	-	-	-	-	-	-	3.5	Up
M400017525	M400017525	-	-	-	-	-	-	-	3.0	Up
M400017526	M400017526	-	-	-	-	-	-	-	3.6	Up
M400017531	M400017531	-	-	-	-	-	-	-	2.1	Up
M400017534	M400017534	-	-	-	-	-	1.8	Down	-	-
M400017535	M400017535	-	-	-	-	-	-	-	1.6	Up
M400017543	M400017543	-	-	-	-	-	-	-	2.9	Up
M400017548	M400017548	-	-	-	-	-	-	-	2.9	Up
M400017552	M400017552	-	-	-	-	-	-	-	1.6	Up
M400017553	M400017553	-	-	-	-	-	-	-	1.8	Up
M400017554	M400017554	-	-	-	1.6	Down	-	-	-	-
M400017555	M400017555	-	-	-	-	-	-	-	4.3	Up
M400017556	M400017556	-	-	-	-	-	-	-	1.8	Up

M400017560	M400017560	-	-	-	-	-	-	-	-	2.1	Up
M400017564	M400017564	-	-	-	-	1.6	Down	-	-	-	-
M400017566	M400017566	-	-	-	-	-	-	-	-	3.2	Up
XM_488787, XM_489688	M400017567	-	-	-	-	-	-	-	-	2.9	Up
M400017568	M400017568	-	-	-	-	1.5	Down	-	-	-	-
M400017571	M400017571	-	-	-	-	-	-	-	-	3.3	Up
M400017572	M400017572	-	-	-	-	-	-	-	-	3.4	Up
M400017577	M400017577	-	-	-	-	-	-	-	-	1.8	Up
M400017578	M400017578	-	-	-	-	-	-	-	-	3.8	Up
M400017579	M400017579	-	-	-	-	-	-	-	-	4.3	Up
M400017584	M400017584	-	-	-	-	-	-	-	-	2.7	Up
M400017585	M400017585	-	-	-	-	-	-	-	-	3.6	Up
M400017591	M400017591	-	-	-	-	-	-	-	-	3.8	Up
M400017593	M400017593	-	-	-	-	-	-	-	-	2.6	Up
M400017594	M400017594	-	-	-	-	-	-	-	-	3.5	Up
XM_488771, XM_489674	M400017595	-	-	-	-	2.0	Down	-	-	2.5	Up
M400017596	M400017596	-	-	-	-	-	-	-	-	3.7	Up
M400017599	M400017599	-	-	-	-	-	-	-	-	2.4	Up
M400017601	M400017601	-	-	-	-	-	-	-	-	3.2	Up
M400017606	M400017606	-	1.9	Down	-	1.8	Down	-	-	-	-
M400017607	M400017607	-	-	-	-	-	-	-	-	2.0	Up
M400017608	M400017608	-	-	-	-	-	-	-	-	2.5	Up
M400017610	M400017610	-	-	-	-	-	-	-	-	2.0	Up
M400017612	M400017612	-	-	-	-	-	-	-	-	1.9	Up
M400017617	M400017617	-	1.9	Down	-	-	-	-	-	2.5	Up
M400017619	M400017619	-	-	-	-	-	-	-	-	3.5	Up
M400017623	M400017623	-	-	-	-	-	-	-	-	2.8	Up
M400017624	M400017624	-	-	-	-	-	-	-	-	2.2	Up
M400017625	M400017625	-	-	-	-	-	-	-	-	4.3	Up
M400017628	M400017628	-	-	-	-	-	-	-	-	1.9	Up
M400017629	M400017629	-	-	-	-	-	-	-	-	3.1	Up
M400017630	M400017630	-	-	-	-	-	-	-	-	2.3	Up
M400017632	M400017632	-	-	-	-	-	-	-	-	3.4	Up
M400017635	M400017635	-	-	-	-	-	-	-	-	2.8	Up
M400017636	M400017636	-	-	-	-	-	-	-	-	2.3	Up
M400017640	M400017640	-	-	-	-	-	-	-	-	1.9	Up
M400017641	M400017641	-	-	-	-	1.6	Down	-	-	-	-
M400017644	M400017644	-	-	-	-	-	-	1.9	Up	2.3	Up
M400017653	M400017653	-	-	-	-	-	-	-	-	2.6	Up
M400017661	M400017661	-	-	-	-	-	-	-	-	2.3	Up

M400017662	M400017662	-	-	-	-	-	2.2	Up	3.4	Up
M400017665	M400017665	-	-	-	-	-	-	-	2.4	Up
M400017666	M400017666	-	-	-	-	-	-	-	2.1	Up
M400017667	M400017667	-	-	-	-	-	-	-	2.6	Up
M400017668	M400017668	-	-	-	-	-	-	-	3.4	Up
M400017671	M400017671	-	-	-	-	-	-	-	1.7	Up
M400017672	M400017672	-	-	-	-	-	-	-	2.8	Up
M400017673	M400017673	-	-	-	-	-	-	-	3.9	Up
M400017674	M400017674	-	-	-	-	-	-	-	4.2	Up
M400017676	M400017676	-	-	-	-	-	-	-	2.3	Up
M400017679	M400017679	-	-	-	-	-	-	-	2.1	Up
M400017680	M400017680	-	-	-	-	-	-	-	3.1	Up
M400017684	M400017684	-	-	-	-	-	-	-	1.7	Up
M400017685	M400017685	-	-	-	-	-	-	-	3.5	Up
M400017686	M400017686	-	-	-	-	-	2.3	Up	3.9	Up
M400017695	M400017695	-	-	-	-	-	-	-	2.5	Up
M400017700	M400017700	-	-	-	-	-	-	-	2.3	Up
M400017702	M400017702	-	-	-	-	-	-	-	2.2	Up
M400017703	M400017703	-	-	-	-	-	-	-	2.0	Up
M400017705	M400017705	-	-	-	-	-	-	-	2.5	Up
M400017707	M400017707	-	-	-	-	-	-	-	1.8	Up
M400017708	M400017708	-	-	-	-	-	-	-	2.7	Up
M400017712	M400017712	-	-	-	-	-	1.9	Down	-	-
M400017713	M400017713	-	-	-	-	-	-	-	2.5	Up
M400017714	M400017714	-	-	-	-	-	-	-	2.8	Up
M400017715	M400017715	-	-	-	-	-	-	-	3.7	Up
M400017720	M400017720	-	-	-	-	-	-	-	4.2	Up
M400017724	M400017724	-	-	-	-	-	-	-	2.2	Up
M400017725	M400017725	-	-	-	-	-	-	-	1.7	Up
M400017733	M400017733	-	-	-	-	-	-	-	2.5	Up
M400017735	M400017735	-	-	-	-	-	-	-	2.6	Up
M400017738	M400017738	-	-	-	-	-	-	-	3.8	Up
M400017742	M400017742	-	-	-	-	2.3	Down	-	-	-
M400017744	M400017744	-	-	-	-	-	-	-	3.7	Up
M400017748	M400017748	-	-	-	-	-	-	-	1.9	Up
M400017756	M400017756	-	-	-	-	-	-	-	2.5	Up
M400017760	M400017760	-	-	-	-	-	-	-	3.7	Up
M400017766	M400017766	-	-	-	-	-	-	-	2.6	Up
M400017769	M400017769	-	-	-	-	-	2.5	Up	-	-
M400017772	M400017772	-	-	-	-	-	-	-	3.1	Up
M400017773	M400017773	-	-	-	-	-	-	-	1.6	Up

M400017774	M400017774	-	-	-	-	-	-	-	-	2.4	Up
M400017775	M400017775	-	-	-	-	-	-	-	-	2.4	Up
M400017779	M400017779	-	-	-	-	-	-	-	-	2.5	Up
M400017780	M400017780	-	-	-	-	-	-	-	-	3.2	Up
M400017781	M400017781	-	-	-	-	-	-	-	-	2.6	Up
M400017786	M400017786	-	-	-	-	-	-	-	-	3.8	Up
M400017789	M400017789	-	-	-	-	-	-	-	-	2.6	Up
M400017790	M400017790	-	-	-	-	1.5	Down	-	-	1.9	Up
M400017791	M400017791	-	-	-	-	-	-	-	-	1.7	Up
M400017792	M400017792	-	-	-	-	-	-	1.6	Up	3.2	Up
M400017795	M400017795	-	-	-	-	-	-	-	-	2.0	Up
M400017796	M400017796	-	-	-	-	-	-	-	-	2.1	Up
M400017798	M400017798	-	-	-	-	-	-	-	-	3.0	Up
M400017801	M400017801	-	-	-	-	-	-	-	-	2.5	Up
M400017803	M400017803	-	-	-	-	-	-	-	-	3.5	Up
M400017807	M400017807	-	-	-	-	2.0	Down	-	-	-	-
M400017809	M400017809	-	-	-	-	-	-	-	-	2.0	Up
M400017810	M400017810	-	-	-	-	-	-	-	-	2.5	Up
M400017816	M400017816	-	-	-	-	-	-	-	-	4.1	Up
M400017820	M400017820	-	-	-	-	-	-	-	-	1.8	Up
M400017821	M400017821	-	-	-	-	-	-	-	-	1.6	Up
M400017822	M400017822	-	-	-	-	-	-	-	-	2.9	Up
M400017827	M400017827	-	-	-	-	-	-	-	-	3.5	Up
M400017828	M400017828	-	-	-	-	-	-	-	-	2.5	Up
M400017831	M400017831	-	-	-	-	-	-	-	-	1.8	Up
M400017840	M400017840	-	-	-	-	-	-	-	-	2.8	Up
M400017843	M400017843	-	-	-	-	-	-	-	-	1.6	Up
M400017844	M400017844	-	-	-	-	-	-	-	-	1.6	Up
M400017849	M400017849	-	-	-	-	-	-	-	-	1.8	Up
M400017850	M400017850	-	-	-	-	-	-	-	-	2.3	Up
M400017851	M400017851	-	-	-	-	-	-	-	-	2.4	Up
M400017852	M400017852	-	-	-	-	-	-	-	-	1.9	Up
M400017857	M400017857	-	-	-	-	2.0	Down	-	-	-	-
M400017858	M400017858	-	-	-	-	-	-	-	-	2.6	Up
M400017861	M400017861	-	-	-	-	-	-	-	-	3.3	Up
M400017869	M400017869	-	-	-	-	-	-	-	-	1.7	Up
M400017870	M400017870	-	-	-	-	-	-	-	-	2.0	Up
M400017875	M400017875	-	-	-	-	-	-	-	-	3.4	Up
M400017876	M400017876	-	-	-	-	-	-	-	-	3.3	Up
M400017878	M400017878	-	-	-	-	-	-	-	-	1.7	Up
M400017880	M400017880	-	-	-	-	-	-	-	-	3.7	Up

M400017881	M400017881	-	-	-	-	-	-	-	-	2.9	Up
M400017885	M400017885	-	-	-	-	-	-	-	-	2.1	Up
M400017886	M400017886	-	-	-	-	-	-	-	-	3.6	Up
M400017887	M400017887	-	-	-	-	1.5	Down	-	-	-	-
M400017888	M400017888	-	-	-	-	-	-	-	-	1.5	Up
M400017893	M400017893	-	-	-	-	-	-	-	-	2.5	Up
M400017898	M400017898	-	-	-	-	-	-	-	-	2.7	Up
M400017905	M400017905	-	-	-	-	-	-	-	-	3.0	Up
M400017910	M400017910	-	-	-	-	-	-	-	-	3.5	Up
M400017912	M400017912	-	-	-	-	2.2	Down	-	-	-	-
M400017916	M400017916	-	-	-	-	1.9	Down	-	-	-	-
M400017920	M400017920	-	-	-	-	-	-	1.8	Down	-	-
M400017923	M400017923	-	-	-	-	-	-	-	-	3.2	Up
M400017927	M400017927	-	-	-	-	-	-	-	-	3.4	Up
M400017928	M400017928	-	-	-	-	-	-	-	-	2.8	Up
M400017929	M400017929	-	-	-	-	-	-	-	-	3.8	Up
M400017933	M400017933	-	-	-	-	-	-	-	-	2.5	Up
M400017934	M400017934	-	-	-	-	-	-	-	-	1.8	Up
M400017935	M400017935	-	-	-	-	-	-	-	-	2.9	Up
M400017941	M400017941	-	-	-	-	-	-	1.7	Up	2.8	Up
M400017951	M400017951	-	-	-	-	-	-	-	-	3.3	Up
M400017952	M400017952	-	-	-	-	-	-	-	-	2.9	Up
M400017953	M400017953	-	-	-	-	-	-	-	-	4.0	Up
XM_489069	M400017956	-	-	-	-	-	-	-	-	2.1	Up
M400017957	M400017957	-	-	-	-	-	-	-	-	2.4	Up
M400017958	M400017958	-	-	-	-	-	-	-	-	3.2	Up
M400017959	M400017959	-	-	-	-	-	-	-	-	4.3	Up
M400017968	M400017968	-	-	-	-	-	-	-	-	1.8	Up
M400017970	M400017970	-	-	-	-	-	-	-	-	2.5	Up
XM_489100	M400017972	-	-	-	-	-	-	-	-	2.2	Up
M400017973	M400017973	-	-	-	-	-	-	-	-	3.6	Up
M400017974	M400017974	-	-	-	-	-	-	-	-	2.1	Up
M400017975	M400017975	-	-	-	-	-	-	-	-	3.5	Up
M400017978	M400017978	-	-	-	-	-	-	-	-	3.9	Up
M400017981	M400017981	-	-	-	-	-	-	-	-	2.9	Up
M400017987	M400017987	-	-	-	-	-	-	-	-	2.9	Up
M400017988	M400017988	-	-	-	-	-	-	2.4	Up	-	-
M400017994	M400017994	-	-	-	-	-	-	2.4	Up	3.2	Up
M400017997	M400017997	-	-	-	-	-	-	1.6	Down	-	-
M400018000	M400018000	-	-	-	-	-	-	-	-	4.0	Up
M400018005	M400018005	-	-	-	-	-	-	-	-	3.8	Up

M400018011	M400018011	-	-	-	-	-	-	-	-	2.0	Up
M400018012	M400018012	-	-	-	-	-	-	-	-	3.2	Up
M400018017	M400018017	-	-	-	-	-	-	-	-	2.2	Up
M400018018	M400018018	-	-	-	-	-	-	-	-	3.7	Up
M400018020	M400018020	-	-	-	-	-	-	-	-	2.4	Up
M400018021	M400018021	-	-	-	-	-	-	-	-	2.4	Up
M400018023	M400018023	-	-	-	-	-	-	-	-	1.6	Up
M400018024	M400018024	-	-	-	-	-	-	-	-	3.2	Up
M400018026	M400018026	-	-	-	-	-	-	-	-	3.5	Up
M400018027	M400018027	-	-	-	-	1.5	Down	-	-	-	-
M400018029	M400018029	-	-	-	-	-	-	-	-	2.7	Up
M400018034	M400018034	-	-	-	-	2.1	Down	-	-	-	-
M400018036	M400018036	-	-	-	-	-	-	-	-	3.9	Up
M400018041	M400018041	-	-	-	-	-	-	-	-	2.5	Up
M400018042	M400018042	-	-	-	-	-	-	-	-	3.0	Up
M400018045	M400018045	-	-	-	-	-	-	-	-	2.3	Up
M400018047	M400018047	-	-	-	-	-	-	-	-	3.1	Up
M400018050	M400018050	-	-	-	-	-	-	-	-	3.0	Up
M400018051	M400018051	-	-	-	-	-	-	-	-	2.2	Up
M400018053	M400018053	-	-	-	-	-	-	-	-	3.3	Up
M400018054	M400018054	-	-	-	-	-	-	-	-	4.3	Up
M400018057	M400018057	-	-	-	-	-	-	-	-	3.3	Up
M400018060	M400018060	-	-	-	-	-	-	-	-	3.2	Up
M400018066	M400018066	-	-	-	-	-	-	-	-	3.8	Up
M400018068	M400018068	-	-	-	-	-	-	-	-	2.7	Up
M400018074	M400018074	-	1.8	Down	-	-	-	-	-	-	-
M400018076	M400018076	-	-	-	-	-	-	-	-	2.7	Up
M400018081	M400018081	-	-	-	-	-	-	-	-	3.3	Up
M400018086	M400018086	-	-	-	-	-	-	-	-	2.1	Up
M400018087	M400018087	-	-	-	-	-	-	-	-	3.8	Up
M400018088	M400018088	-	-	-	-	-	-	-	-	2.2	Up
M400018091	M400018091	-	-	-	-	-	-	-	-	2.0	Up
M400018106	M400018106	-	-	-	-	-	-	-	-	2.1	Up
M400018111	M400018111	-	-	-	-	-	-	-	-	2.4	Up
M400018112	M400018112	-	-	-	-	-	-	-	-	2.5	Up
M400018117	M400018117	-	-	-	-	2.3	Down	-	-	-	-
M400018121	M400018121	-	-	-	-	-	-	2.4	Down	-	-
M400018123	M400018123	-	-	-	-	-	-	-	-	2.2	Up
M400018141	M400018141	-	-	-	-	1.8	Down	-	-	-	-
M400018143	M400018143	-	-	-	-	-	-	-	-	4.2	Up
M400018146	M400018146	-	1.8	Down	-	2.2	Down	1.6	Down	-	-



M400018154	M400018154	-	-	-	-	-	-	-	-	2.9	Up
M400018158	M400018158	-	-	-	-	-	-	-	-	2.0	Up
M400018159	M400018159	-	-	-	-	-	-	-	-	2.1	Up
M400018160	M400018160	-	-	-	-	-	-	-	-	3.5	Up
M400018163	M400018163	-	-	-	-	1.6	Down	-	-	-	-
M400018164	M400018164	-	-	-	-	-	-	-	-	2.6	Up
M400018169	M400018169	-	-	-	-	-	-	-	-	2.0	Up
M400018170	M400018170	-	-	-	-	1.7	Down	-	-	-	-
M400018172	M400018172	-	-	-	-	-	-	-	-	2.6	Up
M400018175	M400018175	-	-	-	-	-	-	-	-	1.9	Up
M400018178	M400018178	-	-	-	-	-	-	-	-	3.0	Up
M400018185	M400018185	-	-	-	-	-	-	-	-	1.7	Up
M400018190	M400018190	-	-	-	-	-	-	-	-	2.4	Up
M400018195	M400018195	-	-	-	-	-	-	-	-	2.1	Up
M400018200	M400018200	-	-	-	-	-	-	-	-	3.6	Up
M400018206	M400018206	-	-	-	-	-	-	-	-	1.8	Up
M400018208	M400018208	-	-	-	-	-	-	-	-	3.9	Up
M400018214	M400018214	-	-	-	-	-	-	-	-	3.3	Up
M400018215	M400018215	-	-	-	-	1.5	Down	-	-	-	-
M400018218	M400018218	-	-	-	-	-	-	-	-	2.2	Up
M400018220	M400018220	-	-	-	-	-	-	-	-	2.1	Up
M400018224	M400018224	-	-	-	-	-	-	1.6	Down	-	-
XM_489054	M400018233	-	-	-	-	-	-	-	-	2.0	Up
M400018241	M400018241	-	-	-	-	-	-	-	-	1.9	Up
M400018244	M400018244	-	-	-	-	-	-	-	-	2.3	Up
M400018250	M400018250	-	-	-	-	-	-	-	-	3.0	Up
M400018253	M400018253	-	-	-	-	-	-	-	-	2.9	Up
M400018255	M400018255	-	-	-	-	-	-	-	-	1.7	Up
M400018256	M400018256	-	-	-	-	-	-	-	-	3.0	Up
M400018258	M400018258	-	-	-	-	-	-	-	-	1.9	Up
M400018259	M400018259	-	-	-	-	-	-	-	-	3.1	Up
M400018261	M400018261	-	-	-	-	1.5	Down	-	-	1.6	Up
M400018266	M400018266	-	-	-	-	-	-	-	-	2.5	Up
M400018267	M400018267	-	-	-	-	-	-	-	-	3.2	Up
M400018270	M400018270	-	-	-	-	-	-	-	-	1.7	Up
M400018272	M400018272	-	-	-	-	-	-	-	-	2.5	Up
M400018276	M400018276	-	-	-	-	-	-	-	-	2.3	Up
M400018278	M400018278	-	-	-	-	-	-	-	-	3.7	Up
M400018279	M400018279	-	-	-	-	-	-	-	-	2.9	Up
M400018280	M400018280	-	-	-	-	-	-	-	-	2.2	Up
M400018282	M400018282	-	-	-	-	1.7	Down	-	-	-	-

M400018283	M400018283	-	-	-	-	-	-	-	-	3.5	Up
M400018284	M400018284	-	-	-	-	1.6	Down	-	-	1.7	Up
M400018285	M400018285	-	-	-	-	-	-	-	-	2.5	Up
M400018289	M400018289	-	-	-	-	-	-	-	-	3.6	Up
M400018291	M400018291	-	-	-	-	-	-	-	-	3.6	Up
M400018296	M400018296	-	-	-	-	-	-	-	-	2.0	Up
M400018302	M400018302	-	-	-	-	-	-	-	-	3.8	Up
M400018306	M400018306	-	-	-	-	-	-	-	-	2.0	Up
M400018308	M400018308	-	-	-	-	-	-	-	-	3.6	Up
M400018315	M400018315	-	-	-	-	-	-	1.7	Up	3.5	Up
M400018320	M400018320	-	-	-	-	-	-	-	-	3.0	Up
M400018326	M400018326	-	-	-	-	-	-	-	-	3.4	Up
M400018331	M400018331	-	-	-	-	-	-	-	-	2.3	Up
M400018336	M400018336	-	-	-	-	-	-	-	-	2.3	Up
M400018344	M400018344	-	-	-	-	-	-	-	-	3.0	Up
M400018349	M400018349	-	-	-	-	-	-	-	-	1.8	Up
M400018351	M400018351	-	-	-	-	-	-	-	-	2.1	Up
M400018352	M400018352	-	-	-	-	-	-	-	-	1.8	Up
M400018353	M400018353	-	-	-	-	-	-	-	-	1.6	Up
M400018355	M400018355	-	-	-	-	-	-	-	-	3.4	Up
M400018356	M400018356	-	-	-	-	-	-	-	-	4.3	Up
M400018358	M400018358	-	-	-	-	-	-	-	-	2.4	Up
M400018360	M400018360	-	-	-	-	2.1	Down	-	-	-	-
M400018361	M400018361	-	-	-	-	-	-	-	-	3.4	Up
M400018362	M400018362	-	-	-	-	-	-	-	-	4.0	Up
M400018365	M400018365	-	-	-	-	-	-	-	-	2.6	Up
M400018366	M400018366	-	-	-	-	-	-	-	-	1.9	Up
M400018367	M400018367	-	-	-	-	-	-	-	-	2.0	Up
M400018368	M400018368	-	-	-	-	-	-	-	-	2.7	Up
M400018373	M400018373	-	-	-	-	-	-	-	-	3.4	Up
M400018376	M400018376	-	-	-	-	-	-	-	-	1.7	Up
M400018379	M400018379	-	-	-	-	-	-	-	-	2.9	Up
M400018380	M400018380	-	-	-	-	-	-	-	-	4.3	Up
M400018382	M400018382	-	-	-	-	-	-	-	-	2.0	Up
M400018383	M400018383	-	-	-	-	1.7	Down	-	-	-	-
M400018385	M400018385	-	-	-	-	-	-	-	-	2.7	Up
M400018396	M400018396	-	-	-	-	-	-	-	-	2.5	Up
M400018400	M400018400	-	-	-	-	-	-	-	-	1.7	Up
M400018406	M400018406	-	-	-	-	-	-	-	-	1.9	Up
XM_283202	M400018407	-	-	-	-	-	-	-	-	2.0	Up
M400018410	M400018410	-	-	-	-	-	-	-	-	4.1	Up

M400018420	M400018420	-	-	-	-	-	-	-	-	2.5	Up
M400018424	M400018424	-	-	-	-	-	-	-	-	4.1	Up
M400018427	M400018427	-	-	-	-	-	-	-	-	3.3	Up
M400018430	M400018430	-	-	-	-	-	-	-	-	1.5	Up
M400018433	M400018433	-	-	-	-	-	-	-	-	2.6	Up
M400018437	M400018437	-	-	-	-	-	-	-	-	2.1	Up
M400018438	M400018438	-	-	-	-	-	-	-	-	2.5	Up
M400018440	M400018440	-	-	-	-	-	-	-	-	2.3	Up
XM_488995	M400018444	-	-	-	-	-	-	-	-	2.5	Up
M400018445	M400018445	-	-	-	-	1.6	Down	-	-	-	-
M400018456	M400018456	-	-	-	-	-	-	-	-	2.4	Up
M400018461	M400018461	-	-	-	-	-	-	-	-	2.0	Up
M400018462	M400018462	-	-	-	-	-	-	-	-	1.8	Up
M400018466	M400018466	-	-	-	-	-	-	-	-	1.6	Up
M400018468	M400018468	-	-	-	-	-	-	-	-	1.9	Up
M400018471	M400018471	-	-	-	-	-	-	-	-	1.9	Up
M400018474	M400018474	-	-	-	-	-	-	-	-	4.0	Up
M400018478	M400018478	-	-	-	-	-	-	-	-	1.9	Up
M400018481	M400018481	-	-	-	-	2.2	Up	-	-	3.9	Up
M400018495	M400018495	-	-	-	-	-	-	-	-	2.7	Up
M400018503	M400018503	-	-	-	-	-	-	-	-	2.9	Up
M400018507	M400018507	-	-	-	-	-	-	-	-	1.5	Up
M400018515	M400018515	-	-	-	-	-	-	-	-	2.2	Up
M400018519	M400018519	-	-	-	-	-	-	-	-	1.5	Up
M400018520	M400018520	-	-	-	-	-	-	-	-	2.7	Up
M400018525	M400018525	-	-	-	-	-	-	-	-	2.4	Up
M400018527	M400018527	-	-	-	-	-	-	-	-	1.9	Up
M400018538	M400018538	-	-	-	-	-	-	-	-	1.5	Up
M400018539	M400018539	-	-	-	-	-	-	-	-	1.6	Up
M400018540	M400018540	-	2.2	Down	-	-	-	-	-	-	-
M400018546	M400018546	-	-	-	-	-	-	-	-	2.6	Up
M400018551	M400018551	-	-	-	-	-	-	1.6	Up	-	-
M400018555	M400018555	-	-	-	-	-	-	-	-	2.2	Up
M400018562	M400018562	-	-	-	-	-	-	-	-	3.0	Up
M400018564	M400018564	-	-	-	-	-	-	-	-	1.7	Up
M400018575	M400018575	-	-	-	-	-	-	-	-	2.7	Up
M400018576	M400018576	-	-	-	-	-	-	-	-	3.2	Up
M400018582	M400018582	-	-	-	-	-	-	-	-	3.3	Up
M400018588	M400018588	-	-	-	-	-	-	-	-	2.3	Up
M400018594	M400018594	-	-	-	-	-	-	-	-	3.3	Up
M400018600	M400018600	-	-	-	-	-	-	-	-	2.6	Up

M400018603	M400018603	-	-	-	-	-	-	-	-	2.1	Up
M400018606	M400018606	-	-	-	-	-	-	-	-	3.2	Up
M400018611	M400018611	-	-	-	-	-	-	-	-	1.6	Up
M400018617	M400018617	-	-	-	-	-	-	-	-	3.7	Up
M400018618	M400018618	-	-	-	-	-	-	1.8	Up	4.1	Up
M400018623	M400018623	-	-	-	-	-	-	-	-	2.8	Up
M400018635	M400018635	-	-	-	-	-	-	-	-	2.2	Up
M400018636	M400018636	-	-	-	-	-	-	-	-	3.1	Up
M400018638	M400018638	-	-	-	-	-	-	-	-	3.3	Up
M400018645	M400018645	-	-	-	-	1.8	Down	-	-	-	-
M400018647	M400018647	-	-	-	-	-	-	-	-	2.6	Up
M400018652	M400018652	-	-	-	-	-	-	-	-	2.8	Up
M400018653	M400018653	-	-	-	-	-	-	-	-	2.3	Up
M400018657	M400018657	-	-	-	-	-	-	-	-	1.5	Up
M400018658	M400018658	-	-	-	-	-	-	-	-	2.9	Up
M400018659	M400018659	-	-	-	-	-	-	-	-	3.2	Up
M400018660	M400018660	-	-	-	-	-	-	-	-	3.0	Up
M400018671	M400018671	-	-	-	-	-	-	-	-	3.8	Up
M400018675	M400018675	-	-	-	-	-	-	-	-	2.2	Up
M400018682	M400018682	-	-	-	-	-	-	-	-	2.4	Up
M400018683	M400018683	-	-	-	-	-	-	-	-	3.3	Up
M400018687	M400018687	-	-	-	-	-	-	-	-	3.5	Up
M400018689	M400018689	-	-	-	-	1.9	Down	-	-	-	-
M400018695	M400018695	-	-	-	-	-	-	-	-	1.5	Up
M400018696	M400018696	-	-	-	-	2.2	Down	-	-	-	-
M400018701	M400018701	-	-	-	-	-	-	1.8	Up	2.5	Up
M400018706	M400018706	-	-	-	-	-	-	-	-	2.6	Up
M400018707	M400018707	-	-	-	-	-	-	-	-	2.8	Up
M400018713	M400018713	-	-	-	-	-	-	-	-	2.5	Up
M400018717	M400018717	-	-	-	-	-	-	2.4	Down	-	-
M400018730	M400018730	-	-	-	-	-	-	-	-	2.5	Up
M400018731	M400018731	-	-	-	-	-	-	-	-	1.7	Up
M400018732	M400018732	-	-	-	-	-	-	-	-	2.2	Up
M400018733	M400018733	-	-	-	-	-	-	-	-	2.8	Up
M400018736	M400018736	-	-	-	-	-	-	-	-	3.6	Up
M400018738	M400018738	-	-	-	-	-	-	-	-	1.9	Up
M400018740	M400018740	-	-	-	-	-	-	-	-	1.9	Up
M400018741	M400018741	-	-	-	-	-	-	-	-	3.3	Up
M400018745	M400018745	-	-	-	-	2.1	Down	-	-	-	-
M400018746	M400018746	-	-	-	-	-	-	-	-	2.6	Up
M400018757	M400018757	-	-	-	-	-	-	-	-	2.5	Up

M400018763	M400018763	-	-	-	-	-	-	-	-	2.3	Up
M400018764	M400018764	-	-	-	-	-	-	-	-	4.0	Up
M400018765	M400018765	-	-	-	-	-	-	-	-	2.7	Up
M400018766	M400018766	-	-	-	-	-	-	-	-	2.8	Up
M400018770	M400018770	-	-	-	-	-	-	-	-	1.6	Up
M400018771	M400018771	-	-	-	-	-	-	-	-	2.0	Up
M400018778	M400018778	-	-	-	-	-	-	1.6	Up	-	-
M400018780	M400018780	-	-	-	-	-	-	-	-	2.4	Up
M400018781	M400018781	-	-	-	-	-	-	-	-	2.3	Up
M400018782	M400018782	-	-	-	-	1.7	Down	-	-	-	-
M400018786	M400018786	-	-	-	-	-	-	-	-	1.9	Up
M400018794	M400018794	-	-	-	-	-	-	-	-	1.7	Up
M400018796	M400018796	-	-	-	-	-	-	-	-	3.7	Up
M400018805	M400018805	-	-	-	-	-	-	-	-	1.7	Up
M400018812	M400018812	-	-	-	-	-	-	-	-	2.6	Up
M400018813	M400018813	-	-	-	-	-	-	-	-	2.5	Up
M400018818	M400018818	-	-	-	-	-	-	-	-	1.8	Up
M400018820	M400018820	-	-	-	-	-	-	-	-	3.5	Up
M400018825	M400018825	-	-	-	-	-	-	-	-	1.7	Up
M400018831	M400018831	-	-	-	-	1.7	Up	2.7	Up	3.3	Up
M400018835	M400018835	-	-	-	-	-	-	-	-	3.3	Up
M400018841	M400018841	-	-	-	-	-	-	-	-	3.4	Up
M400018848	M400018848	-	-	-	-	-	-	-	-	2.8	Up
M400018854	M400018854	-	-	-	-	-	-	-	-	2.1	Up
M400018855	M400018855	-	-	-	-	-	-	2.1	Up	-	-
M400018861	M400018861	-	-	-	-	-	-	2.2	Up	-	-
M400018871	M400018871	-	-	-	-	-	-	-	-	3.2	Up
M400018878	M400018878	-	-	-	-	-	-	-	-	2.9	Up
M400018884	M400018884	-	-	-	-	-	-	-	-	3.4	Up
M400018885	M400018885	-	-	-	-	-	-	1.7	Up	3.2	Up
M400018887	M400018887	-	-	-	-	-	-	-	-	2.0	Up
M400018888	M400018888	-	-	-	-	-	-	-	-	1.6	Up
M400018889	M400018889	-	-	-	-	-	-	-	-	1.5	Up
M400018891	M400018891	-	-	-	-	-	-	-	-	2.9	Up
M400018900	M400018900	-	-	-	-	-	-	-	-	2.6	Up
M400018902	M400018902	-	-	-	-	-	-	-	-	1.8	Up
M400018918	M400018918	-	-	-	-	-	-	-	-	2.0	Up
M400018920	M400018920	-	-	-	-	-	-	-	-	2.9	Up
M400018926	M400018926	-	-	-	-	-	-	-	-	3.8	Up
M400018929	M400018929	-	-	-	-	2.0	Down	-	-	-	-
M400018931	M400018931	-	-	-	-	-	-	-	-	2.7	Up

M400018932	M400018932	-	-	-	-	-	-	-	-	3.8	Up
M400018935	M400018935	-	-	-	-	-	-	-	-	2.2	Up
M400018944	M400018944	-	-	-	-	-	-	-	-	3.0	Up
M400018951	M400018951	-	-	-	-	-	-	-	-	2.0	Up
M400018956	M400018956	-	-	-	-	-	-	-	-	4.1	Up
M400018961	M400018961	-	2.0	Down	-	-	-	-	-	-	-
M400018962	M400018962	-	-	-	-	-	1.8	Up	-	-	-
M400018986	M400018986	-	-	-	-	-	-	-	-	3.1	Up
M400018996	M400018996	-	-	-	-	-	-	-	-	1.7	Up
M400018998	M400018998	-	-	-	-	-	-	-	-	2.0	Up
M400019009	M400019009	-	-	-	1.9	Down	-	-	-	3.3	Down
M400019013	M400019013	-	-	-	-	-	-	-	-	1.6	Up
M400019014	M400019014	-	-	-	-	-	-	-	-	2.0	Up
M400019020	M400019020	-	-	-	-	-	-	-	-	3.1	Up
M400019021	M400019021	-	-	-	-	-	-	-	-	4.0	Up
M400019024	M400019024	-	-	-	-	-	-	-	-	1.9	Down
M400019026	M400019026	-	-	-	-	-	-	-	-	4.3	Up
M400019027	M400019027	-	-	-	-	-	-	-	-	2.3	Up
M400019032	M400019032	-	-	-	-	-	-	-	-	2.1	Up
M400019033	M400019033	-	-	-	-	-	-	-	-	2.0	Up
M400019040	M400019040	-	-	-	-	-	-	-	-	3.5	Down
M400019043	M400019043	-	-	-	-	-	-	-	-	1.9	Up
M400019046	M400019046	-	-	-	-	-	-	-	-	1.9	Down
M400019049	M400019049	-	-	-	-	-	-	-	-	2.2	Up
M400019050	M400019050	-	-	-	-	-	-	-	-	2.9	Up
M400019051	M400019051	-	-	-	-	-	-	-	-	3.5	Up
M400019055	M400019055	-	-	-	-	-	-	-	-	1.8	Up
M400019061	M400019061	-	-	-	-	-	-	-	-	1.5	Up
M400019063	M400019063	-	-	-	-	-	2.0	Up	-	2.5	Up
M400019067	M400019067	-	-	-	-	-	-	-	-	3.3	Up
M400019068	M400019068	-	-	-	-	-	-	-	-	3.7	Up
M400019069	M400019069	-	-	-	-	-	-	-	-	3.8	Up
M400019070	M400019070	-	-	-	-	-	-	-	-	1.6	Down
M400019073	M400019073	-	-	-	-	-	-	-	-	3.5	Up
M400019074	M400019074	-	-	-	-	-	-	-	-	2.5	Up
M400019075	M400019075	-	-	-	-	-	-	-	-	2.3	Up
M400019080	M400019080	-	-	-	-	-	-	-	-	1.9	Up
M400019087	M400019087	-	-	-	-	-	1.7	Up	-	2.7	Up
M400019091	M400019091	-	-	-	-	-	-	-	-	2.4	Up
M400019092	M400019092	-	-	-	-	-	-	-	-	2.6	Up
M400019097	M400019097	-	-	-	-	-	-	-	-	2.4	Up

M400019099	M400019099	-	-	-	-	-	-	-	-	3.4	Up
M400019104	M400019104	-	-	-	-	-	-	-	-	2.7	Up
M400019110	M400019110	-	-	-	-	-	-	-	-	2.8	Up
M400019113	M400019113	-	-	-	-	-	-	-	-	2.4	Up
M400019115	M400019115	-	-	-	-	-	-	-	-	3.3	Up
M400019118	M400019118	-	-	-	-	-	-	-	-	1.5	Up
M400019120	M400019120	-	-	-	-	-	-	-	-	2.4	Up
M400019122	M400019122	-	-	-	-	-	-	-	-	4.0	Up
M400019126	M400019126	-	-	-	-	-	-	-	-	1.9	Up
M400019128	M400019128	-	-	-	-	-	-	-	-	3.7	Up
M400019134	M400019134	-	-	-	-	-	-	2.8	Up	-	-
M400019136	M400019136	-	-	-	-	-	-	-	-	2.5	Up
M400019139	M400019139	-	-	-	-	-	-	-	-	3.4	Up
M400019142	M400019142	-	-	-	-	-	-	-	-	2.8	Up
M400019145	M400019145	-	-	-	-	-	-	-	-	2.3	Up
M400019152	M400019152	-	-	-	-	-	-	-	-	3.1	Up
M400019155	M400019155	-	-	-	-	1.6	Down	1.8	Down	-	-
M400019158	M400019158	-	-	-	-	-	-	2.7	Up	3.8	Up
M400019160	M400019160	-	-	-	-	-	-	-	-	3.0	Up
M400019161	M400019161	-	-	-	-	-	-	-	-	2.1	Up
M400019164	M400019164	-	-	-	-	-	-	1.8	Up	-	-
M400019167	M400019167	-	-	-	-	-	-	-	-	3.2	Up
M400019169	M400019169	-	-	-	-	-	-	-	-	3.5	Up
M400019178	M400019178	-	-	-	-	-	-	1.6	Down	-	-
M400019181	M400019181	-	-	-	-	-	-	-	-	3.6	Up
M400019187	M400019187	-	-	-	-	-	-	-	-	3.8	Up
M400019190	M400019190	-	-	-	-	-	-	-	-	1.6	Up
M400019191	M400019191	-	-	-	-	-	-	-	-	2.1	Up
M400019193	M400019193	-	-	-	-	-	-	-	-	3.9	Up
M400019194	M400019194	-	-	-	-	-	-	-	-	3.8	Up
M400019197	M400019197	-	-	-	-	-	-	-	-	2.1	Up
M400019199	M400019199	-	-	-	-	-	-	-	-	2.1	Up
M400019200	M400019200	-	-	-	-	-	-	-	-	3.4	Up
M400019203	M400019203	-	-	-	-	-	-	-	-	1.7	Up
M400019205	M400019205	-	-	-	-	-	-	-	-	3.0	Up
M400019208	M400019208	-	-	-	-	-	-	-	-	2.0	Up
M400019211	M400019211	-	-	-	-	-	-	1.9	Up	-	-
M400019213	M400019213	-	-	-	-	-	-	-	-	1.6	Up
M400019239	M400019239	-	-	2.8	Down	-	-	-	-	-	-
M400019241	M400019241	-	-	-	-	-	-	2.9	Up	-	-
M400019246	M400019246	-	-	-	-	-	-	-	-	3.0	Up

M400019252	M400019252	-	-	-	-	-	-	-	-	1.9	Up
M400019257	M400019257	-	-	-	-	-	-	-	-	1.6	Up
M400019259	M400019259	-	-	-	-	-	-	1.7	Up	3.0	Up
M400019264	M400019264	-	-	-	-	-	-	-	-	2.4	Up
M400019265	M400019265	-	-	-	-	-	-	-	-	3.3	Up
M400019270	M400019270	-	-	-	-	-	-	-	-	2.6	Up
M400019276	M400019276	-	-	-	-	-	-	-	-	3.6	Up
M400019279	M400019279	-	-	-	-	-	-	-	-	1.6	Down
M400019280	M400019280	-	-	-	-	-	-	-	-	2.7	Up
M400019282	M400019282	-	-	-	-	-	-	-	-	2.8	Up
M400019294	M400019294	-	-	-	-	-	-	-	-	2.5	Up
M400019295	M400019295	-	-	-	-	-	-	-	-	2.4	Up
M400019312	M400019312	-	-	-	-	-	-	-	-	3.7	Up
M400019317	M400019317	-	-	-	-	-	-	-	-	3.5	Up
M400019321	M400019321	-	-	-	-	2.1	Down	-	-	-	-
M400019324	M400019324	-	-	-	-	-	-	-	-	2.8	Up
M400019330	M400019330	-	-	-	-	-	-	-	-	3.5	Up
XM_489153	M400019336	-	-	-	-	-	-	-	-	2.6	Up
M400019357	M400019357	-	-	-	-	-	-	-	-	1.9	Up
M400019358	M400019358	-	-	-	-	-	-	-	-	2.1	Up
M400019371	M400019371	-	-	-	-	-	-	-	-	2.5	Up
M400019372	M400019372	-	-	-	-	-	-	-	-	3.5	Up
M400019375	M400019375	-	-	-	-	-	-	-	-	2.1	Up
M400019376	M400019376	-	-	-	-	-	-	-	-	2.4	Up
M400019378	M400019378	-	-	-	-	-	-	1.6	Up	3.4	Up
M400019379	M400019379	-	-	-	-	-	-	-	-	2.7	Up
M400019381	M400019381	-	-	-	-	-	-	-	-	1.6	Up
M400019398	M400019398	-	-	-	-	-	-	-	-	2.0	Up
M400019400	M400019400	-	-	-	-	-	-	-	-	2.4	Up
M400019401	M400019401	-	-	-	-	-	-	-	-	3.8	Up
M400019404	M400019404	-	-	-	-	-	-	-	-	3.1	Up
M400019406	M400019406	-	-	-	-	-	-	-	-	3.2	Up
M400019407	M400019407	-	-	-	-	-	-	-	-	4.0	Up
M400019416	M400019416	-	-	-	-	-	-	-	-	1.9	Up
M400019419	M400019419	-	-	-	-	-	-	-	-	2.3	Up
M400019422	M400019422	-	-	-	-	-	-	-	-	2.5	Up
M400019423	M400019423	-	-	-	-	-	-	-	-	2.1	Up
M400019425	M400019425	-	-	-	-	-	-	-	-	3.7	Up
NM_177015	M400019428	-	-	-	-	-	-	-	-	3.0	Up
M400019429	M400019429	-	-	-	-	-	-	-	-	3.0	Up
M400019430	M400019430	-	-	-	-	-	-	-	-	4.0	Up



M400019436	M400019436	-	-	-	-	-	-	-	-	3.5	Up
M400019437	M400019437	-	-	-	-	-	-	-	-	3.2	Up
M400019444	M400019444	-	-	-	-	2.2	Down	-	-	-	-
M400019446	M400019446	-	-	-	-	1.8	Down	-	-	-	-
M400019447	M400019447	-	-	-	-	-	-	-	-	2.1	Up
M400019448	M400019448	-	-	-	-	-	-	-	-	3.6	Up
M400019449	M400019449	-	-	-	-	-	-	-	-	3.5	Up
M400019453	M400019453	-	-	-	-	1.8	Down	-	-	1.9	Up
M400019454	M400019454	-	-	-	-	-	-	-	-	2.3	Up
M400019460	M400019460	-	-	-	-	-	-	-	-	3.4	Up
M400019464	M400019464	-	-	-	-	-	-	-	-	1.9	Up
M400019467	M400019467	-	-	-	-	-	-	-	-	3.3	Up
M400019468	M400019468	-	-	-	-	-	-	-	-	2.5	Up
M400019471	M400019471	-	-	-	-	2.0	Down	-	-	-	-
M400019472	M400019472	-	-	-	-	-	-	-	-	1.5	Up
M400019473	M400019473	-	-	-	-	-	-	-	-	3.3	Up
M400019477	M400019477	-	-	-	-	-	-	-	-	2.6	Up
M400019478	M400019478	-	-	-	-	-	-	-	-	3.0	Up
M400019486	M400019486	-	-	-	-	-	-	-	-	1.8	Up
M400019488	M400019488	-	-	-	-	-	-	-	-	1.6	Up
M400019492	M400019492	-	-	-	-	-	-	-	-	2.4	Up
M400019493	M400019493	-	-	-	-	-	-	-	-	2.6	Up
M400019494	M400019494	-	-	-	-	-	-	-	-	2.6	Up
M400019496	M400019496	-	-	-	-	-	-	-	-	4.3	Up
M400019500	M400019500	-	-	-	-	-	-	-	-	2.9	Up
M400019501	M400019501	-	-	-	-	-	-	-	-	3.0	Up
M400019502	M400019502	-	-	-	-	-	-	-	-	4.0	Up
M400019507	M400019507	-	-	-	-	-	-	-	-	2.8	Up
M400019508	M400019508	-	-	-	-	-	-	-	-	3.0	Up
M400019518	M400019518	-	-	-	-	-	-	-	-	2.2	Up
M400019522	M400019522	-	-	-	-	-	-	1.5	Down	-	-
M400019524	M400019524	-	-	-	-	-	-	-	-	2.8	Up
XM_488997	M400019526	-	-	-	-	-	-	-	-	4.1	Up
NM_010750	Mab-21-like 1 (C. elegans)	Mab2111	-	-	-	-	-	-	-	2.1	Up
NM_021500	Macrophage erythroblast attacher	Maea	-	-	-	-	-	2.2	Up	-	-
NM_010796	Macrophage galactose N-acetyl-galactosamine specific lectin 1	Mgl1	-	-	-	-	-	-	-	2.0	Down
NM_008243	Macrophage stimulating 1 (hepatocyte growth factor-like)	Mst1	-	-	-	-	-	-	-	1.9	Up
NM_010754	MAD homolog 2 (Drosophila)	Smad2	-	-	-	-	-	-	-	1.7	Down
NM_016769	MAD homolog 3 (Drosophila)	Smad3	-	-	-	-	-	-	-	1.6	Up
NM_026859	MAF1 homolog (S. cerevisiae)	Maf1	-	-	-	3.3	Up	-	3.2	Up	-
NM_010760	Mago-nashi homolog, proliferation-associated (Drosophila)	MagoH	-	-	-	-	-	-	1.7	Up	-

NM_029657	Mahogunin, ring finger 1	Mgrn1	-	-	-	-	2.6	Up	-	-
NM_026660	Major facilitator superfamily domain containing 10	Mfsd10	-	-	-	-	-	-	1.8	Down
NM_008209	Major histocompatibility complex, class I-related	Mr1	-	-	-	-	-	-	1.9	Up
NM_008648	Major urinary protein 4	Mup4	-	-	2.0	Down	-	-	-	-
NM_008617	Malate dehydrogenase 2, NAD (mitochondrial)	Mdh2	-	-	-	-	-	-	1.9	Down
NM_008547	Male germ cell-associated kinase	Mak	-	-	-	-	2.1	Up	3.7	Up
NM_207010	MAM domain containing glycosylphosphatidylinositol anchor 2	Mdga2	-	-	-	-	-	-	4.0	Up
NM_010749	Mannose-6-phosphate receptor, cation dependent	M6pr	-	-	-	-	-	-	2.3	Down
NM_028636	Mannosidase, alpha, class 2C, member 1	Man2c1	-	-	-	-	-	-	3.5	Up
XM_130628	mannosidase, beta A, lysosomal-like	-	-	-	-	-	1.6	Up	-	-
NM_010795	Mannoside acetylglucosaminyltransferase 3	Mgat3	-	-	3.2	Down	-	-	-	-
NM_178369	MAP-kinase activating death domain	-	-	-	-	-	-	-	2.8	Up
NM_145442	MAP3K12 binding inhibitory protein 1	Mbip	-	-	-	-	-	-	1.6	Down
XM_136135	MAP7 domain containing 2	-	-	-	-	-	-	-	3.3	Up
NM_205821	MAS-related GPR, member A6	Mrgpra6	-	-	-	-	-	-	2.0	Up
NM_010771	Matrin 3	Matr3	-	-	-	-	-	-	2.4	Down
NM_008597	Matrix Gla protein	Mgp	-	-	-	-	-	-	1.7	Down
NM_011846	Matrix metalloproteinase 17	Mmp17	-	-	-	-	-	-	2.5	Up
NM_032006	Matrix metalloproteinase 1a (interstitial collagenase)	Mmp1a	-	-	-	-	-	-	2.5	Up
NM_032007	Matrix metalloproteinase 1b (interstitial collagenase)	Mmp1b	-	-	-	-	-	-	2.4	Up
NM_010839	Mature T-cell proliferation 1	Mtcp1	-	-	-	-	-	-	1.6	Down
NM_010847	Max interacting protein 1	Mxi1	-	-	-	-	-	-	2.3	Down
NM_133197	Mcf.2 transforming sequence	Mcf2	-	-	-	-	-	-	1.7	Up
NM_021527	McKusick-Kaufman syndrome protein	Mkks	-	-	-	-	-	-	2.4	Up
XM_354636	Meckel syndrome, type 1	-	-	-	-	-	-	-	1.7	Up
XM_109726	mediator complex subunit 13	-	-	-	-	-	-	-	3.5	Up
NM_144933	Mediator complex subunit 17	Med17	-	-	-	-	-	-	2.9	Up
NM_027485	Mediator complex subunit 26	Med26	-	-	-	-	-	-	2.2	Up
NM_025895	Mediator of RNA polymerase II transcription, subunit 28 homolog (yeast)	Med28	-	-	-	-	1.5	Up	-	-
NM_026068	Mediator of RNA polymerase II transcription, subunit 31 homolog (yeast)	Med31	-	-	-	-	-	-	2.0	Down
NM_008613	Meiosis-specific nuclear structural protein 1	Mns1	-	-	-	-	-	-	3.3	Up
NM_010789	Meis homeobox 1	Meis1	-	-	-	-	-	-	2.0	Up
NM_010825	Meis homeobox 2	Meis2	-	-	-	-	-	-	1.6	Up
NM_008559	Melanocortin 1 receptor	Mc1r	-	-	-	-	-	-	1.6	Up
NM_008560	Melanocortin 2 receptor	Mc2r	-	-	-	-	-	-	2.8	Up
NM_173783	Melanoma antigen family B, 18	Mageb18	-	-	-	-	-	-	2.2	Up
NM_175541	Melanoma associated antigen (mutated) 1-like 1	Mum111	-	-	-	-	-	-	2.9	Up
NM_177389	Melanoma inhibitory activity 3	Mia3	-	-	-	-	1.5	Down	2.1	Up
NM_010367	Membrane associated guanylate kinase, WW and PDZ domain containing 1	Magi1	-	-	-	-	-	-	2.2	Up

NM_015823	Membrane associated guanylate kinase, WW and PDZ domain containing 2	Magi2	-	-	1.7	Down	-	-	-	-
NM_008621	Membrane protein, palmitoylated	Mpp1	-	-	-	-	1.9	Up	-	-
NM_007863	Membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3)	Mpp3	-	-	-	-	-	-	2.0	Up
NM_145486	Membrane-associated ring finger (C3HC4) 2	3-Mar	-	-	-	-	2.7	Up	-	-
NM_177115	Membrane-associated ring finger (C3HC4) 3	4-Mar	-	-	-	-	-	-	2.8	Up
NM_010791	Mesenchyme homeobox 1	Meox1	-	-	1.8	Down	-	-	-	-
NM_008590	Mesoderm specific transcript	Mest	-	-	-	-	-	-	3.2	Up
NM_026002	Metadherin	Mtdh	-	-	-	-	-	-	2.6	Down
NM_172610	Metallophosphoesterase domain containing 1	Mpped1	-	-	-	-	-	-	1.6	Up
NM_016664	metastasis associated gene 2	-	-	-	-	-	-	-	1.6	Up
NM_144797	Meteorin, glial cell differentiation regulator-like	Metrn1	-	-	-	-	-	-	2.3	Down
NM_134017	Methionine adenosyltransferase II, beta	Mat2b	-	-	-	-	-	-	1.7	Down
NM_177092	Methionine sulfoxide reductase B3	Msrb3	-	-	-	-	-	-	2.8	Up
NM_175439	Methionine-tRNA synthetase 2 (mitochondrial)	Mars2	-	-	-	-	-	-	1.7	Up
NM_010773	Methyl-CpG binding domain protein 2	Mbd2	-	-	-	-	-	-	1.5	Down
XM_283719	methyl-CpG binding domain protein 5	-	-	-	-	-	-	-	1.8	Up
NM_144913	Methylphosphate capping enzyme	Mepce	-	-	-	-	2.0	Up	-	-
NM_176917	Methyltransferase like 4	Mettl4	-	-	-	-	-	-	1.5	Up
NM_027853	Methyltransferase like 7B	Mettl7b	-	-	-	-	1.8	Up	-	-
NM_023556	Mevalonate kinase	Mvk	-	-	-	-	2.4	Up	-	-
NM_008601	Microphthalmia-associated transcription factor	Mitf	-	-	-	-	-	-	1.6	Up
NM_010816	Microorchidia 1	Morc1	-	-	-	-	2.6	Down	-	-
NM_177719	Microorchidia 2B	Morc2b	-	-	-	-	-	-	1.6	Up
NM_025735	Microtubule-associated protein 1 light chain 3 alpha	Map1lc3a	-	-	-	-	-	-	2.1	Down
NM_173013	Microtubule-associated protein 1S	Mtap1s	-	-	-	-	-	-	2.2	Down
NM_008633	Microtubule-associated protein 4	Mtap4	-	-	-	-	-	-	2.6	Down
NM_026524	Mid1 interacting protein 1 (gastrulation specific G12-like (zebrafish))	Mid1ip1	-	-	-	-	-	-	1.9	Down
NM_010797	Midline 1	Mid1	-	-	-	-	-	-	2.9	Up
NM_144860	Mindbomb homolog 1 (Drosophila)	Mib1	-	-	1.6	Down	-	-	-	-
NM_027290	Minichromosome maintenance deficient 10 (S. cerevisiae)	Mcm10	-	-	-	-	-	-	1.8	Up
NM_025571	Mitochondria-associated protein involved in granulocyte-macrophage colony-stimulating factor signal transduction	Magmas	-	-	-	-	-	-	2.7	Down
NM_026732	Mitochondrial ribosomal protein L14	Mrpl14	-	-	-	-	-	-	1.7	Down
NM_026310	Mitochondrial ribosomal protein L18	Mrpl18	-	-	-	-	3.3	Up	-	-
NM_026490	Mitochondrial ribosomal protein L19	Mrpl19	-	-	-	-	-	-	1.6	Down
NM_053162	Mitochondrial ribosomal protein L34	Mrpl34	-	-	-	-	2.1	Up	-	-
NM_025500	Mitochondrial ribosomal protein L37	Mrpl37	-	-	-	-	-	-	1.5	Down
NM_025927	mitochondrial ribosomal protein L45	-	-	-	-	-	-	-	1.6	Down
NM_025450	Mitochondrial ribosomal protein S17	Mrps17	-	-	-	-	-	-	1.6	Down

XM_194230	mitochondrial ribosomal protein S18C	-	-	-	-	-	-	1.9	Up	
NM_078479	Mitochondrial ribosomal protein S21	Mrps21	-	-	-	-	2.0	Up	-	
NM_029963	Mitochondrial ribosomal protein S5	Mrps5	-	-	-	-	-	-	2.4	
		Mapk1ip1l	-	-	-	-	-	-	2.3	Up
NM_178684	Mitogen-activated protein kinase 1 interacting protein 1-like	Mapk3	-	-	-	-	1.8	Up	-	
NM_011952	Mitogen-activated protein kinase 3	Mapk8ip2	-	-	1.7	Down	-	-	-	
NM_021921	Mitogen-activated protein kinase 8 interacting protein 2	Map2k7	-	-	-	-	-	-	2.9	Up
NM_011944	Mitogen-activated protein kinase kinase 7	-	-	-	-	-	-	-	2.1	Up
XM_194344	mitogen-activated protein kinase kinase kinase 10	-	-	-	-	-	-	-	2.1	Up
NM_011947	Mitogen-activated protein kinase kinase kinase 3	Map3k3	-	-	-	-	-	-	1.7	Down
NM_024275	mitogen-activated protein kinase kinase kinase kinase 5	-	-	-	-	-	-	-	2.0	Down
NM_201519	Mitogen-activated protein kinase kinase kinase kinase 5	Map4k5	-	-	-	-	-	-	3.4	Up
		Mapkapk3	-	-	-	-	1.6	Up	-	
NM_178907	Mitogen-activated protein kinase-activated protein kinase 3	Mixl1	-	-	-	-	-	-	3.2	Up
NM_013729	Mix1 homeobox-like 1 ( <i>Xenopus laevis</i> )	Mlxip	-	-	-	-	-	-	3.4	Up
NM_177582	MLX interacting protein	Mms19	-	-	-	-	-	-	2.0	Up
NM_028152	MMS19 ( <i>MET18 S. cerevisiae</i> )	Mobkl3	-	-	-	-	-	-	2.9	Down
NM_025283	MOB1, Mps One Binder kinase activator-like 3 (yeast)	Mkx	-	-	-	-	-	-	3.2	Up
NM_177595	Mohawk	Mocs1	-	-	-	-	-	-	2.1	Up
NM_020042	Molybdenum cofactor synthesis 1	Moxd1	-	-	-	-	-	-	1.6	Up
NM_021509	Monooxygenase, DBH-like 1	Mospd3	-	-	-	-	1.6	Up	-	
NM_030037	Motile sperm domain containing 3	Mpnd	-	-	-	-	2.0	Up	-	
NM_026530	MPN domain containing	Muc10	-	-	-	-	-	-	2.8	Up
NM_008644	Mucin 10, submandibular gland salivary mucin	Muc13	-	-	-	-	-	-	2.0	Up
NM_010739	Mucin 13, epithelial transmembrane	Mupcdh	-	-	-	-	-	-	1.8	Up
NM_028069	Mucin-like protocadherin	Men1	-	-	-	-	-	-	1.7	Up
NM_008583	Multiple endocrine neoplasia 1	Minpp1	-	-	-	-	-	-	2.6	Up
NM_010799	Multiple inositol polyphosphate histidine phosphatase 1	Mug1	-	-	-	-	-	-	2.9	Up
NM_008645	Murinoglobulin 1	Pygm	-	-	-	-	-	-	1.6	Up
NM_011224	Muscle glycogen phosphorylase	-	-	-	-	-	-	-	2.9	Up
XM_484162	mutL homolog 3 ( <i>E coli</i> )	Mycbp2	-	-	-	-	-	-	1.7	Down
NM_207215	MYC binding protein 2	Mog	-	-	1.8	Down	-	-	-	
NM_010814	Myelin oligodendrocyte glycoprotein	Mobp	-	-	-	-	-	-	1.5	Up
NM_008614	Myelin-associated oligodendrocytic basic protein	Mybl1	-	-	-	-	-	-	1.5	Up
NM_008651	Myeloblastosis oncogene-like 1	Mlf1	-	-	-	-	-	-	2.1	Up
NM_010801	Myeloid leukemia factor 1	Myadm	-	-	-	-	-	-	2.2	Down
NM_016969	Myeloid-associated differentiation marker	-	-	-	-	-	1.9	Up	1.9	Up
XM_110671	myeloid/lymphoid or mixed-lineage leukemia 1	Mpo	1.6	Up	-	-	-	-	-	
NM_010824	Myeloperoxidase	Isyna1	-	-	1.5	Up	-	-	-	
NM_023627	Myo-inositol 1-phosphate synthase A1	Mdf1	-	-	-	-	-	-	1.7	Up
NM_010783	MyoD family inhibitor	-	-	-	-	-	-	-	-	

NM_146163	myosin 1H	-	-	-	-	-	-	2.7	Up
XM_483962	myosin IA	-	-	-	-	-	-	2.8	Up
NM_010863	Myosin IB	Myo1b	-	-	-	-	-	1.6	Up
NM_177390	Myosin ID	Myo1d	-	-	-	-	-	1.7	Up
NM_015742	Myosin IXb	Myo9b	-	-	-	-	-	1.6	Up
NM_025414	myosin XIX	-	-	-	-	1.5	Up	2.4	Up
XM_203357	myosin XVB	-	-	-	-	-	-	1.5	Up
XM_356059	myosin XVI	-	-	-	-	-	-	3.7	Up
NM_013607	Myosin, heavy polypeptide 11, smooth muscle	Myh11	-	-	-	-	-	2.7	Up
NM_010861	Myosin, light polypeptide 2, regulatory, cardiac, slow	Myl2	-	-	-	-	-	2.6	Up
NM_139300	Myosin, light polypeptide kinase	Mylk	-	-	-	-	-	3.2	Up
NM_026849	Myotubularin related protein 14	Mttr14	-	-	-	-	1.7	Up	-
NM_177893	myotubularin related protein 15	-	-	-	-	-	-	1.6	Up
NM_133215	Myotubularin related protein 4	Mttr4	-	-	-	-	1.7	Up	-
XM_355137	N-acetylated alpha-linked acidic dipeptidase-like 1	-	-	-	-	-	-	1.8	Up
NM_008674	N-acetyltransferase 3	Nat3	-	-	-	-	-	1.8	Up
NM_175731	N-acylsphingosine amidohydrolase (alkaline ceramidase) 3	Asah3	-	-	-	-	-	2.8	Up
NM_010811	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2	Ndst2	-	-	-	-	2.1	Up	2.4
NM_178877	Na <sup>+</sup> /H <sup>+</sup> exchanger domain containing 2	Nhedc2	-	-	-	-	-	2.0	Up
AF198054	NAC1 (Arabidopsis NAC domain containing protein 21, Arabidopsis NAC domain containing protein 22); transcription factor	NAC1	-	-	2.6	Up	2.9	Up	3.4
NM_176940	NACHT and WD repeat domain containing 1	Nwd1	-	-	-	-	-	2.1	Up
NM_025348	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3	Ndufa3	-	-	-	-	1.9	Up	-
NM_023202	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a)	Ndufa7	-	-	-	-	1.9	Up	-
XM_128594	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10	-	-	-	-	-	-	1.6	Down
XM_131359	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6	-	-	-	-	-	2.3	Up	-
NM_025523	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1	Ndufc1	-	-	-	-	1.5	Up	-
XM_130347	NADH dehydrogenase (ubiquinone) Fe-S protein 3	-	-	-	-	-	1.9	Up	-
NM_029272	NADH dehydrogenase (ubiquinone) Fe-S protein 7	Ndufs7	-	-	-	-	1.8	Up	-
NM_030729	NCK interacting protein with SH3 domain	Nckipsd	-	-	1.6	Up	-	-	-
NM_016965	NCK-associated protein 1	Nckap1	-	-	-	-	-	1.6	Down
NM_198059	Nebulin-related anchoring protein	Nrap	-	-	-	-	-	2.7	Up
XM_128893	Nedd4 family interacting protein 1	-	-	-	-	-	-	1.6	Down
NM_029561	Nedd4 family interacting protein 2	Ndfip2	-	-	-	-	2.0	Up	1.6
NM_177413	NEL-like 1 (chicken)	-	-	-	-	-	-	2.1	Up
NM_033525	Nephronectin	Npnt	-	-	-	-	-	2.7	Up
NM_021320	Netrin 4	Ntn4	-	-	-	-	-	2.1	Up
NM_008721	Neural proliferation, differentiation and control gene 1	Npdc1	-	-	-	-	-	2.1	Up
NM_009513	Neurensin 1	Nrsn1	-	-	-	-	-	1.9	Up
NM_020252	Neurexin I	Nrxn1	-	-	-	-	-	3.1	Up
NM_172544	Neurexin III	Nrxn3	-	-	-	-	-	1.5	Up

NM_008752	Neurexophilin 2	Nxph2	-	-	-	-	-	-	3.5	Up
XM_150243	neurobeachin-like 2	-	-	-	-	-	-	-	2.4	Up
NM_007789	Neurocan	Ncan	-	-	2.6	Down	-	-	-	-
NM_172932	Neuroigin 3	Nlgn3	-	-	-	-	-	-	2.2	Up
NM_173437	Neuron navigator 1	Nav1	-	-	-	-	-	-	2.7	Down
NM_176930	Neuron-glia-CAM-related cell adhesion molecule	Nrcam	-	-	-	-	-	-	2.3	Up
NM_019867	Neuronal guanine nucleotide exchange factor	Ngef	-	-	-	-	-	-	2.3	Up
NM_010923	Neuronatin	Nnat	-	-	-	-	-	-	2.8	Up
XM_137119	Neuropeptide FF receptor 1	Npffr1	-	-	-	-	-	-	3.2	Up
NM_023456	Neuropeptide Y	Npy	-	-	-	-	-	-	4.0	Up
NM_144946	Neuropilin (NRP) and tolloid (TLL)-like 1	Neto1	-	-	-	-	-	-	1.5	Up
XM_134498	neuropilin (NRP) and tolloid (TLL)-like 2	-	-	-	2.0	Down	-	-	-	-
NM_008747	Neurotensin receptor 2	Ntsr2	-	-	-	-	-	-	3.3	Up
NM_026012	Neurotrophin receptor associated death domain	Nradd	-	-	-	-	-	-	2.6	Up
NM_008677	Neutrophil cytosolic factor 4	Ncf4	-	-	-	-	2.2	Up	-	-
NM_175340	NHL repeat containing 1	Nhlrc1	-	-	-	-	-	-	2.4	Up
NM_011482	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)	Nhp211	-	-	-	-	3.4	Up	-	-
NM_175460	Nicotinamide nucleotide adenylyltransferase 2	Nmnat2	-	-	-	-	-	-	1.9	Up
XM_138906	NIMA (never in mitosis gene a)- related kinase 10	-	-	-	1.5	Down	-	-	-	-
NM_177898	NIMA (never in mitosis gene a)-related expressed kinase 5	Nek5	-	-	-	-	-	-	1.6	Up
NM_013610	Ninjurin 1	Ninj1	-	-	-	-	2.4	Up	-	-
NM_022656	Nischarin	Nisch	-	-	-	-	-	-	2.2	Down
XM_129577	nitric oxide synthase 1 (neuronal) adaptor protein	-	-	-	-	-	-	-	1.7	Up
NM_009385	NK2 homeobox 1	Nkx2-1	-	-	2.0	Down	-	-	-	-
NM_023504	NK2 transcription factor related, locus 4 (Drosophila)	Nkx2-4	-	-	-	-	-	-	2.6	Up
XM_486147	NLR family, CARD domain containing 5	-	-	-	-	-	-	-	2.6	Up
NM_0010041	NLR family, pyrin domain containing 1A	Nlrp1a	-	-	-	-	1.5	Down	2.2	Up
NM_031389	NLR family, pyrin domain containing 4C	Nlrp4c	-	-	-	-	-	-	3.9	Up
NM_194056	NLR family, pyrin domain containing 9A	-	-	-	-	-	-	-	3.6	Up
NM_133787	NMD3 homolog (S. cerevisiae)	Nmd3	-	-	-	-	2.6	Up	-	-
NM_053089	NMDA receptor-regulated gene 1	Narg1	-	-	-	-	-	-	2.5	Down
NM_178925	NOL1/NOP2/Sun domain family 3	Nsun3	-	-	-	-	-	-	2.9	Up
NM_027602	NOL1/NOP2/Sun domain family, member 7	Nsun7	-	-	-	-	-	-	3.0	Up
NM_023144	Non-POU-domain-containing, octamer binding protein	Nono	-	-	-	-	2.2	Up	-	-
NM_026330	Non-SMC element 1 homolog (S. cerevisiae)	Nsmce1	-	-	-	-	-	-	2.7	Down
NM_010928	Notch gene homolog 2 (Drosophila)	Notch2	-	-	-	-	-	-	1.9	Up
NM_008743	Nth (endonuclease III)-like 1 (E.coli)	Nthl1	-	-	-	-	-	-	1.6	Up
NM_023317	Nuclear distribution gene E homolog 1 (A nidulans)	Nde1	-	-	-	-	-	-	1.7	Down
NM_008688	Nuclear factor I/C	Nfic	-	-	-	-	-	-	1.8	Up
NM_016791	Nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1	Nfatc1	-	-	-	-	2.3	Up	-	-

NM_023699	Nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4	Nfatc4	-	-	2.0	Down	-	-	-	-
NM_008689	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1, p105	Nfkb1	-	-	-	-	2.5	Up	-	-
NM_010907	Nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	Nfkbia	-	-	-	-	-	-	2.2	Down
NM_008690	Nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon	Nfkbie	-	-	-	-	-	-	2.0	Down
NM_025391	Nuclear import 7 homolog (S. cerevisiae)	Nip7	-	-	-	-	-	-	2.0	Down
NM_008679	Nuclear receptor coactivator 3	Ncoa3	-	-	-	-	-	-	2.4	Up
NM_019825	Nuclear receptor coactivator 6	Ncoa6	-	-	-	-	1.9	Up	-	-
NM_009803	Nuclear receptor subfamily 1, group I, member 3	Nr1i3	-	-	-	-	-	-	1.5	Up
NM_011629	Nuclear receptor subfamily 2, group C, member 1	Nr2c1	-	-	-	-	-	-	2.1	Up
XM_356093	nuclear receptor subfamily 3, group C, member 2	-	-	-	-	-	-	-	2.2	Up
NM_013613	Nuclear receptor subfamily 4, group A, member 2	Nr4a2	-	-	-	-	2.2	Up	-	-
NM_130888	Nuclear RNA export factor 7	Nxf7	-	-	-	-	-	-	3.5	Up
NM_053086	Nucleolar and coiled-body phosphoprotein 1	Nolc1	-	-	-	-	-	-	1.7	Up
NM_138747	Nucleolar protein 1	Nol1	-	-	-	-	1.9	Up	2.7	Up
NM_199024	Nucleolar protein 4	Nol4	-	-	-	-	-	-	2.6	Up
NM_139236	Nucleolar protein family 6 (RNA-associated)	Nol6	-	-	-	-	-	-	3.6	Up
NM_008750	Nucleoredoxin	Nxn	-	-	-	-	-	-	1.8	Up
NM_008671	Nucleosome assembly protein 1-like 2	Nap112	-	-	-	-	-	-	3.5	Up
NM_021432	Nucleosome assembly protein 1-like 5	Nap115	-	-	-	-	-	-	1.9	Up
NM_025839	Nudix (nucleoside diphosphate linked moiety X)-type motif 16-like 1	Nudt1611	-	-	-	-	2.1	Up	-	-
NM_153136	Nudix (nucleoside diphosphate linked moiety X)-type motif 18	Nudt18	-	-	-	-	1.9	Up	-	-
NM_033080	Nudix (nucleoside diphosphate linked moiety X)-type motif 19	Nudt19	-	-	-	-	-	-	1.8	Down
NM_028794	Nudix (nucleoside diphosphate linked moiety X)-type motif 9	Nudt9	-	-	-	-	-	-	1.5	Down
NM_139144	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	Ogt	-	-	-	-	-	-	2.5	Up
NM_145517	O-sialoglycoprotein endopeptidase-like 1	Ormdl1	-	-	-	-	-	-	2.4	Down
NM_025942	Obg-like ATPase 1	Ola1	-	-	-	-	-	-	2.0	Down
NM_0010039	14	-	-	-	-	-	-	-	2.9	Up
NM_023429	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF	-	-	-	-	-	-	-	3.2	Down
NM_011855	OCIA domain containing 1	Ociad1	-	-	-	-	-	-	2.6	Up
XM_132137	Odd Oz/ten-m homolog 1 (Drosophila)	Odz1	-	-	-	-	-	-	2.2	Up
NM_172907	odontogenic, ameloblast associated	-	-	-	-	-	-	-	2.7	Up
NM_206822	Olfactomedin-like 1	Olfml1	-	-	-	-	-	-	2.9	Up
NM_146866	Olfactory receptor 10	Olf10	-	-	-	-	-	-	2.6	Up
NM_146572	Olfactory receptor 1008	Olf1008	-	-	-	-	-	-	1.6	Up
NM_146834	Olfactory receptor 1009	Olf1009	-	-	-	-	-	-	2.2	Up
NM_207149	Olfactory receptor 101	Olf101	-	-	-	-	-	-	2.2	Up
	Olfactory receptor 1010	Olf1010	-	-	-	-	-	-	2.2	Up

NM_146762	Olfactory receptor 1013	Olfr1013	-	-	-	-	-	-	2.9	Up
NM_146580	Olfactory receptor 1020	Olfr1020	-	-	-	-	-	-	2.7	Up
NM_0010052 30	Olfactory receptor 1024	Olfr1024	-	-	-	-	-	-	2.5	Up
NM_146577	Olfactory receptor 1043	Olfr1043	-	-	-	-	-	-	2.1	Up
NM_147017	Olfactory receptor 1045	Olfr1045	-	-	-	-	-	-	1.6	Up
NM_207562	Olfactory receptor 1051	Olfr1051	-	-	-	-	-	-	2.5	Up
NM_147021	Olfactory receptor 1055	Olfr1055	-	-	-	-	-	-	2.4	Up
NM_207563	Olfactory receptor 1057	Olfr1057	-	-	-	-	-	-	4.1	Up
NM_146409	Olfactory receptor 1080	Olfr1080	-	-	-	-	-	-	2.7	Up
NM_146835	Olfactory receptor 109	Olfr109	-	-	1.7	Down	-	-	-	-
NM_146767	Olfactory receptor 1104	Olfr1104	-	-	-	-	-	-	2.6	Up
NM_147031	Olfactory receptor 1122	Olfr1122	-	-	-	-	1.5	Up	-	-
NM_146350	Olfactory receptor 1123	Olfr1123	-	-	-	-	-	-	3.6	Up
NM_146838	Olfactory receptor 1130	Olfr1130	-	-	-	-	-	-	3.0	Up
NM_146659	Olfactory receptor 1136	Olfr1136	-	-	-	-	-	-	2.3	Up
NM_146639	Olfactory receptor 1138	Olfr1138	-	-	-	-	-	-	2.9	Up
NM_146642	Olfactory receptor 1140	Olfr1140	-	-	-	-	-	-	1.7	Up
NM_146320	Olfactory receptor 1145	Olfr1145	-	-	-	-	-	-	2.8	Up
NM_146848	Olfactory receptor 1161	Olfr1161	-	-	-	-	-	-	3.6	Up
NM_146641	Olfactory receptor 1164	Olfr1164	-	-	-	-	1.8	Up	2.9	Up
NM_146650	Olfactory receptor 1166	Olfr1166	-	-	-	-	-	-	1.9	Up
NM_146917	Olfactory receptor 1179	Olfr1179	-	-	-	-	-	-	2.6	Up
NM_213721	Olfactory receptor 118	Olfr118	-	-	-	-	-	-	2.9	Up
NM_146823	Olfactory receptor 1184	Olfr1184	-	-	1.9	Down	-	-	-	-
NM_146461	Olfactory receptor 1209	Olfr1209	-	-	-	-	-	-	2.3	Up
NM_146629	Olfactory receptor 121	Olfr121	-	-	-	-	-	-	1.6	Up
NM_146899	Olfactory receptor 1219	Olfr1219	-	-	-	-	-	-	2.7	Up
NM_146288	Olfactory receptor 122	Olfr122	-	-	-	-	-	-	2.4	Up
NM_146630	Olfactory receptor 123	Olfr123	-	-	-	-	-	-	1.5	Up
NM_146972	Olfactory receptor 1233	Olfr1233	-	-	-	-	-	-	1.8	Up
NM_146969	Olfactory receptor 1243	Olfr1243	-	-	-	-	-	-	2.7	Up
NM_146983	Olfactory receptor 1256	Olfr1256	-	-	1.9	Down	-	-	-	-
NM_146982	Olfactory receptor 1257	Olfr1257	-	-	-	-	1.8	Up	3.8	Up
NM_146978	Olfactory receptor 1258	Olfr1258	-	-	1.7	Down	-	-	-	-
NM_146981	Olfactory receptor 1260	Olfr1260	-	-	-	-	-	-	2.4	Up
NM_146980	Olfactory receptor 1272	Olfr1272	-	-	-	-	-	-	2.4	Up
NM_146975	Olfactory receptor 1273	Olfr1273	-	-	-	-	-	-	2.4	Up
NM_146393	Olfactory receptor 1279	Olfr1279	-	-	-	-	3.0	Up	3.4	Up
NM_146888	Olfactory receptor 1297	Olfr1297	-	-	-	-	-	-	2.0	Up
NM_146886	Olfactory receptor 1298	Olfr1298	-	-	-	-	-	-	2.3	Up



NM_146334	Olfactory receptor 1330	Olfr1330	-	-	-	-	-	-	2.3	Up
NM_146915	Olfactory receptor 1336	Olfr1336	-	-	-	-	-	-	3.8	Up
NM_146713	Olfactory receptor 1342	Olfr1342	-	-	-	-	-	-	2.8	Up
NM_177061	Olfactory receptor 1344	Olfr1344	-	-	-	-	-	-	2.5	Up
NM_147071	Olfactory receptor 1352	Olfr1352	-	-	-	-	-	-	2.4	Up
NM_147042	Olfactory receptor 1353	Olfr1353	-	-	-	-	-	-	1.6	Up
NM_146534	Olfactory receptor 1368	Olfr1368	-	-	-	-	-	-	2.4	Up
NM_146488	Olfactory receptor 137	Olfr137	-	-	-	-	-	-	2.2	Up
NM_146535	Olfactory receptor 1370	Olfr1370	-	-	-	-	-	-	2.7	Up
NM_146910	Olfactory receptor 1378	Olfr1378	-	-	-	-	-	-	2.0	Up
NM_147066	Olfactory receptor 1389	Olfr1389	-	-	-	-	-	-	1.7	Up
NM_146470	Olfactory receptor 1392	Olfr1392	-	-	2.7	Down	-	-	-	-
NM_146881	Olfactory receptor 1404	Olfr1404	-	-	-	-	-	-	2.0	Up
NM_146936	Olfactory receptor 1417	Olfr1417	-	-	-	-	-	-	2.2	Up
NM_146681	Olfactory receptor 1424	Olfr1424	-	-	-	-	-	-	3.0	Up
NM_146702	Olfactory receptor 1444	Olfr1444	-	-	-	-	-	-	2.0	Up
NM_146371	Olfactory receptor 1450	Olfr1450	-	-	-	-	-	-	1.6	Up
NM_146689	Olfactory receptor 1459	Olfr1459	-	-	-	-	-	-	1.6	Up
NM_146302	Olfactory receptor 1461	Olfr1461	-	-	-	-	-	-	1.9	Up
NM_146505	Olfactory receptor 148	Olfr148	-	-	1.9	Down	-	-	-	-
NM_146990	Olfactory receptor 1494	Olfr1494	-	-	-	-	-	-	1.7	Up
NM_146989	Olfactory receptor 1496	Olfr1496	-	-	-	-	-	-	1.6	Up
NM_146634	Olfactory receptor 1504	Olfr1504	-	-	2.2	Up	-	-	-	-
NM_020512	Olfactory receptor 1507	Olfr1507	-	-	-	-	-	-	2.6	Up
NM_0010018	Olfactory receptor 1514	Olfr221	-	-	-	-	-	-	2.0	Up
NM_206823	Olfactory receptor 153	Olfr153	-	-	-	-	3.2	Down	-	-
NM_146997	Olfactory receptor 178	Olfr178	-	-	-	-	-	-	3.0	Up
NM_146397	Olfactory receptor 190	Olfr190	-	-	-	-	-	-	2.2	Up
NM_207549	Olfactory receptor 192	Olfr192	-	-	-	-	-	-	1.9	Up
NM_146484	Olfactory receptor 197	Olfr197	-	-	-	-	-	-	2.7	Up
NM_146991	Olfactory receptor 206	Olfr206	-	-	-	-	-	-	2.6	Up
NM_146446	Olfactory receptor 215	Olfr215	-	-	-	-	1.7	Up	1.6	Up
NM_146870	Olfactory receptor 25	Olfr25	2.0	Up	-	-	-	-	-	-
NM_146920	Olfactory receptor 267	Olfr267	-	-	-	-	-	-	2.3	Up
NM_010974	Olfactory receptor 27	Olfr27	-	-	-	-	-	-	4.0	Up
NM_146280	Olfactory receptor 281	Olfr281	-	-	-	-	-	-	2.0	Up
NM_146416	Olfactory receptor 290	Olfr290	-	-	-	-	2.3	Up	2.4	Up
NM_146619	Olfactory receptor 303	Olfr303	-	-	1.6	Down	-	-	-	-
NM_146617	Olfactory receptor 307	Olfr307	-	-	-	-	-	-	1.8	Up
NM_207230	Olfactory receptor 318	Olfr318	-	-	-	-	-	-	2.2	Up

NM_146502	Olfactory receptor 328	Olf328	-	-	1.7	Down	-	-	-	-
NM_146628	Olfactory receptor 344	Olf344	-	-	-	-	2.2	Up	2.1	Up
NM_146943	Olfactory receptor 347	Olf347	-	-	-	-	-	-	2.6	Up
NM_146944	Olfactory receptor 348	Olf348	-	-	-	-	-	-	2.4	Up
NM_146939	Olfactory receptor 354	Olf354	-	-	-	-	-	-	2.1	Up
NM_146624	Olfactory receptor 356	Olf356	-	-	-	-	-	-	1.8	Up
NM_146623	Olfactory receptor 357	Olf357	-	-	-	-	-	-	2.2	Up
NM_146622	Olfactory receptor 360	Olf360	-	-	-	-	1.9	Up	-	-
NM_146270	Olfactory receptor 370	Olf370	-	-	-	-	-	-	1.7	Up
NM_147024	Olfactory receptor 378	Olf378	-	-	1.6	Down	-	-	-	-
NM_147022	Olfactory receptor 381	Olf381	-	-	-	-	-	-	1.9	Up
NM_147007	Olfactory receptor 394	Olf394	-	-	-	-	1.9	Up	3.4	Up
NM_207158	Olfactory receptor 427	Olf427	-	-	-	-	1.7	Up	3.1	Up
NM_146711	Olfactory receptor 43	Olf43	-	-	-	-	-	-	2.0	Up
NM_146718	Olfactory receptor 430	Olf430	-	-	-	-	-	-	2.6	Up
NM_146716	Olfactory receptor 432	Olf432	-	-	-	-	-	-	2.8	Up
NM_146445	Olfactory receptor 450	Olf450	-	-	1.5	Down	-	-	-	-
NM_146444	Olfactory receptor 458	Olf458	-	-	-	-	-	-	2.5	Up
NM_146383	Olfactory receptor 460	Olf460	-	-	-	-	-	-	2.8	Up
NM_146413	Olfactory receptor 463	Olf463	-	-	-	-	-	-	2.0	Up
NM_146774	Olfactory receptor 472	Olf472	-	-	1.8	Down	-	-	-	-
NM_146925	Olfactory receptor 481	Olf481	-	-	-	-	-	-	4.2	Up
NM_146914	Olfactory receptor 5	Olf5	-	-	-	-	-	-	1.5	Up
NM_146726	Olfactory receptor 514	Olf514	-	-	-	-	-	-	1.9	Up
NM_146583	Olfactory receptor 52	Olf52	-	-	-	-	-	-	2.5	Up
NM_147063	Olfactory receptor 520	Olf520	-	-	-	-	-	-	1.6	Up
NM_010997	Olfactory receptor 54	Olf54	-	-	3.0	Up	-	-	-	-
NM_147101	Olfactory receptor 549	Olf549	-	-	-	-	1.7	Up	2.8	Up
NM_146359	Olfactory receptor 564	Olf564	-	-	-	-	-	-	1.5	Up
NM_146360	Olfactory receptor 574	Olf574	-	-	-	-	2.6	Up	3.8	Up
NM_147114	Olfactory receptor 575	Olf575	-	-	-	-	-	-	1.8	Up
NM_0010018										
05	Olfactory receptor 576	Olf576	-	-	1.8	Down	-	-	-	-
NM_147115	Olfactory receptor 578	Olf578	-	-	-	-	-	-	2.7	Up
NM_147087	Olfactory receptor 585	Olf585	-	-	-	-	-	-	2.5	Up
NM_207556	Olfactory receptor 592	Olf592	-	-	-	-	-	-	2.3	Up
NM_146380	Olfactory receptor 593	Olf593	-	-	-	-	1.7	Up	-	-
NM_146314	Olfactory receptor 601	Olf601	-	-	-	-	1.6	Up	2.4	Up
NM_146756	Olfactory receptor 608	Olf608	-	-	-	-	-	-	2.8	Up
NM_146964	Olfactory receptor 61	Olf61	-	-	-	-	2.1	Up	2.3	Up
NM_147084	Olfactory receptor 639	Olf639	-	-	-	-	-	-	2.2	Up

NM_013617	Olfactory receptor 64	Olfr64	-	-	-	-	-	-	2.2	Up
NM_146312	Olfactory receptor 657	Olfr657	-	-	-	-	-	-	1.9	Up
NM_207146	Olfactory receptor 670	Olfr670	-	-	-	-	-	-	2.2	Up
NM_146358	Olfactory receptor 677	Olfr677	-	-	-	-	-	-	3.2	Up
NM_147045	Olfactory receptor 683	Olfr683	-	-	-	-	-	-	3.9	Up
NM_147061	Olfactory receptor 691	Olfr691	-	-	-	-	-	-	3.4	Up
NM_146453	Olfactory receptor 693	Olfr693	-	-	-	-	-	-	1.8	Up
NM_146598	Olfactory receptor 695	Olfr695	-	-	-	-	-	-	4.2	Up
NM_147035	Olfactory receptor 711	Olfr711	-	-	1.8	Down	-	-	2.2	Up
NM_147033	Olfactory receptor 714	Olfr714	-	-	-	-	-	-	2.3	Up
NM_146317	Olfactory receptor 725	Olfr725	-	-	-	-	-	-	1.7	Up
NM_146664	Olfactory receptor 734	Olfr734	-	-	-	-	-	-	2.5	Up
NM_207558	Olfactory receptor 750	Olfr750	-	-	-	-	-	-	2.5	Up
NM_146682	Olfactory receptor 76	Olfr76	-	-	-	-	-	-	2.8	Up
NM_146862	Olfactory receptor 763	Olfr763	-	-	-	-	1.6	Up	4.1	Up
NM_146339	Olfactory receptor 77	Olfr77	-	-	-	-	-	-	2.4	Up
NM_146544	Olfactory receptor 777	Olfr777	-	-	-	-	2.3	Up	2.7	Up
NM_130866	Olfactory receptor 78	Olfr78	-	-	-	-	-	-	1.7	Up
NM_146931	Olfactory receptor 796	Olfr796	-	-	-	-	-	-	3.5	Up
NM_146548	Olfactory receptor 800	Olfr800	-	-	-	-	-	-	1.8	Up
NM_146553	Olfactory receptor 806	Olfr806	-	-	-	-	-	-	2.5	Up
NM_146929	Olfactory receptor 807	Olfr807	-	-	-	-	-	-	2.5	Up
NM_146324	Olfactory receptor 809	Olfr809	-	-	-	-	-	-	3.3	Up
NM_146795	Olfactory receptor 812	Olfr812	-	-	-	-	-	-	2.2	Up
NM_146675	Olfactory receptor 820	Olfr820	-	-	-	-	-	-	1.9	Up
NM_146565	Olfactory receptor 837	Olfr837	-	-	-	-	-	-	2.0	Up
NM_146567	Olfactory receptor 843	Olfr843	-	-	-	-	-	-	3.1	Up
NM_146905	Olfactory receptor 851	Olfr851	-	-	-	-	-	-	1.5	Up
NM_146417	Olfactory receptor 877	Olfr877	-	-	-	-	-	-	3.0	Up
NM_146798	Olfactory receptor 878	Olfr878	-	-	-	-	-	-	1.7	Up
NM_146871	Olfactory receptor 898	Olfr898	-	-	-	-	-	-	1.7	Up
NM_207552	Olfactory receptor 899	Olfr899	-	-	-	-	-	-	2.3	Up
NM_146802	Olfactory receptor 902	Olfr902	-	-	-	-	-	-	1.6	Up
NM_146801	Olfactory receptor 904	Olfr904	-	-	1.7	Down	-	-	-	-
NM_146375	Olfactory receptor 918	Olfr918	-	-	-	-	-	-	2.2	Up
NM_146816	Olfactory receptor 923	Olfr923	-	-	-	-	-	-	1.7	Up
NM_146815	Olfactory receptor 926	Olfr926	-	-	-	-	2.3	Up	2.8	Up
NM_146439	Olfactory receptor 937	Olfr937	-	-	-	-	-	-	1.7	Up
NM_146507	Olfactory receptor 944	Olfr944	-	-	-	-	-	-	1.7	Up
NM_146503	Olfactory receptor 952	Olfr952	-	-	-	-	-	-	2.1	Up
NM_146435	Olfactory receptor 993	Olfr993	-	-	-	-	-	-	2.1	Up

NM_019409	Oligodendrocyte myelin glycoprotein	Omg	-	-	-	-	-	-	2.9	Up
NM_016967	Oligodendrocyte transcription factor 2	Olig2	-	-	-	-	-	-	1.5	Up
NM_153520	Oligodendrocytic myelin paranodal and inner loop protein	Opalin	-	-	-	-	-	-	2.7	Up
NM_052976	Oligophrenin 1	Ophn1	-	-	-	-	-	-	2.2	Up
XM_137493	oncostatin M	-	-	-	-	-	-	-	2.0	Up
NM_201258	Oogenesis 3	Oog3	-	-	-	-	-	-	2.9	Up
NM_0010039	49	ORF61	-	-	-	-	-	-	2.6	Down
NM_020622	Open reading frame 9	ORF9	-	-	-	-	-	-	2.6	Up
NM_011013	opioid receptor, mu 1	-	-	-	-	-	-	-	3.2	Up
NM_013887	Opsin 4 (melanopsin)	Opn4	-	-	-	-	-	-	3.6	Up
NM_011016	Orosomuroid 2	Orm2	-	-	-	-	-	-	1.9	Up
NM_172416	Osteopetrosis associated transmembrane protein 1	Ostm1	-	-	-	-	-	-	3.3	Up
NM_010953	Otoconin 90	Oc90	-	-	-	-	-	-	2.7	Up
NM_031875	Otoferlin	Otof	-	-	2.0	Down	-	-	-	-
NM_172801	Otopettrin 2	Otop2	-	-	-	-	1.9	Up	3.5	Up
NM_198673	Outer dense fiber of sperm tails 3-like 1	Odf3l1	-	-	-	-	-	-	2.1	Up
NM_011022	Ovary testis transcribed	Ott	-	-	-	-	-	-	2.3	Up
XM_355880	OVO homolog-like 3 (Drosophila)	Ovol3	-	-	-	-	-	-	3.4	Up
NM_145950	Oxidative stress induced growth inhibitor family member 2	Osgin2	-	-	-	-	-	-	1.6	Down
XM_138959	oxoglutarate dehydrogenase-like	-	-	-	-	-	-	-	2.3	Up
NM_148958	Oxysterol binding protein-like 10	Osbp10	-	-	-	-	-	-	2.5	Up
NM_008778	P21 (CDKN1A)-activated kinase 3	Pak3	-	-	-	-	-	-	1.7	Up
NM_020005	P300/CBP-associated factor	Pcaf	-	-	-	-	-	-	1.8	Up
NM_008781	Paired box gene 3	Pax3	-	-	-	-	-	-	1.7	Up
NM_0010017	96	Prrxl1	-	-	-	-	-	-	2.2	Up
NM_011090	Paired-Ig-like receptor A3	Pira3	-	-	-	-	-	-	2.7	Up
NM_008888	Paired-like homeobox 2b	Phox2b	-	-	-	-	-	-	2.5	Up
NM_019441	Palmitoyl-protein thioesterase 2	Ppt2	-	-	2.1	Up	2.6	Up	-	-
NM_008918	Pancreatic polypeptide	Ppy	-	-	-	-	-	-	3.3	Up
NM_008919	Pancreatic polypeptide receptor 1	Ppyr1	-	-	-	-	-	-	1.5	Up
NM_153501	Pantothenate kinase 2 (Hallervorden-Spatz syndrome)	Pank2	-	-	-	-	1.5	Up	-	-
NM_026157	PAP associated domain containing 1	Papd1	-	-	-	-	2.1	Up	-	-
NM_033573	Papillary renal cell carcinoma (translocation-associated)	Prcc	-	-	-	-	-	-	2.1	Up
NM_023128	Paralemmin	Palm	-	-	1.7	Down	-	-	1.7	Up
NM_183308	Paraoxonase 2	Pon2	-	-	-	-	1.7	Up	1.5	Up
NM_053256	Parathyroid hormone 2	Pth2	-	-	-	-	-	-	2.2	Up
NM_139270	Parathyroid hormone 2 receptor	Pth2r	-	-	-	-	-	-	2.4	Up
NM_008953	Parotid secretory protein	Psp	-	-	-	-	-	-	1.8	Up
NM_025580	Paroxysmal nonkinesigenic dyskinesia	Pnkd	-	-	-	-	2.1	Up	-	-
NM_013645	Parvalbumin	Pvalb	-	-	2.1	Down	-	-	-	-

NM_022321	Parvin, gamma	Parvg	-	-	-	-	2.1	Up	-	-
XM_484618	patatin-like phospholipase domain containing 1	-	-	-	-	-	-	-	3.3	Up
NM_054088	Patatin-like phospholipase domain containing 3	Pnpla3	-	-	-	-	-	-	1.6	Up
NM_008958	Patched homolog 2	Ptch2	-	-	-	-	-	-	2.8	Up
NM_133915	Paxillin	Pxn	-	-	-	-	-	-	2.8	Up
NM_011049	PCTAIRE-motif protein kinase 1	Pctk1	-	-	-	-	1.8	Up	1.5	Up
NM_008795	PCTAIRE-motif protein kinase 3	Pctk3	-	-	-	-	-	-	3.0	Up
NM_016861	PDZ and LIM domain 1 (elfin)	Pdlim1	-	-	-	-	-	-	2.7	Down
NM_145978	PDZ and LIM domain 2	Pdlim2	-	-	-	-	1.5	Up	-	-
NM_019417	PDZ and LIM domain 4	Pdlim4	-	-	1.6	Up	-	-	-	-
NM_023324	Pellino 1	Peli1	-	-	-	-	-	-	2.0	Down
NM_030015	pellino 1	-	-	-	-	-	-	-	2.2	Up
NM_033602	Pellino 2	Peli2	-	-	-	-	-	-	2.3	Up
NM_172835	Pellino 3	Peli3	-	-	-	-	-	-	1.6	Up
XM_131914	peptidase (mitochondrial processing) beta	-	-	-	-	-	-	-	2.1	Down
NM_021319	Peptidoglycan recognition protein 2	Pglyrp2	-	-	-	-	1.5	Up	2.4	Up
NM_207263	Peptidoglycan recognition protein 4	Pglyrp4	-	-	-	-	-	-	2.7	Up
NM_011059	Peptidyl arginine deiminase, type I	Padi1	-	-	-	-	-	-	1.9	Up
NM_013626	Peptidylglycine alpha-amidating monooxygenase	Pam	-	-	-	-	-	-	1.6	Up
NM_144954	Peptidylprolyl isomerase (cyclophilin)-like 2	Ppil2	-	-	-	-	3.1	Up	-	-
NM_011149	Peptidylprolyl isomerase B	Ppib	-	-	-	-	-	-	2.1	Up
NM_008833	per-hexamer repeat gene 2	-	-	-	-	-	-	-	1.9	Up
NM_023662	Pericentriolar material 1	Pcm1	-	-	-	-	1.6	Up	-	-
NM_011065	Period homolog 1 (Drosophila)	Per1	-	-	-	-	-	-	1.8	Up
NM_175363	Periphilin 1	Pphn1	-	-	-	-	-	-	1.6	Up
NM_011034	peroxiredoxin 1	-	-	-	-	-	-	-	1.9	Down
NM_007452	Peroxiredoxin 3	Prdx3	-	-	-	-	-	-	1.5	Down
XM_357368	Peroxiredoxin 6, related sequence 2	Prdx6-rs2	-	-	-	-	-	-	1.8	Up
NM_021483	Peroxisomal biogenesis factor 5-like	Pex5l	-	-	-	-	-	-	1.5	Up
NM_153390	Peroxisomal, testis specific 1	Pxt1	-	-	-	-	-	-	1.9	Up
NM_008994	Peroxisome biogenesis factor 2	Pex2	-	-	-	-	-	-	1.6	Up
NM_022032	PERP, TP53 apoptosis effector	Perp	-	-	-	-	-	-	3.5	Up
XM_194683	PFTAIRE protein kinase 2	-	-	-	-	-	-	-	4.3	Up
XM_129968	PH domain and leucine rich repeat protein phosphatase	Phlpp	-	-	-	-	-	-	1.9	Down
NM_174852	PHD finger protein 12	Phf12	-	-	-	-	-	-	3.0	Up
NM_028716	PHD finger protein 19	Phf19	-	-	-	-	-	-	3.1	Up
NM_011078	PHD finger protein 2	Phf2	-	-	-	-	-	-	1.8	Up
NM_026737	PHD finger protein 5A	Phf5a	-	-	-	-	-	-	2.6	Down
NM_026701	Phenazine biosynthesis-like protein domain containing	Pbld	-	-	-	-	-	-	1.7	Up
NM_025648	Phenylalanyl-tRNA synthetase, alpha subunit	Farsa	-	-	-	-	-	-	2.9	Up

NM_007898	Phenylalkylamine Ca2+ antagonist (emopamil) binding protein	Ebp	-	-	-	-	-	-	1.8	Down
NM_024458	Phosducin	Pdc	-	-	-	-	-	-	2.6	Up
NM_026176	Phosducin-like	Pdcl	-	-	-	-	-	-	3.2	Up
NM_026850	Phosducin-like 3	Pdcl3	-	-	-	-	-	-	2.8	Down
NM_175306	Phosphatase and actin regulator 4	Phactr4	-	-	-	-	2.3	Up	-	-
NM_009981	Phosphate cytidyltransferase 1, choline, alpha isoform	Pcyt1a	-	-	-	-	-	-	2.2	Up
NM_011077	Phosphate regulating gene with homologies to endopeptidases on the X chromosome (hypophosphatemia, vitamin D resistant ricket	Phex	-	-	-	-	-	-	2.7	Up
NM_011083	Phosphatidylinositol 3-kinase, C2 domain containing, alpha polypeptide	Pik3c2a	-	-	-	-	-	-	1.7	Up
NM_008841	Phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 2 (p85 beta)	Pik3r2	-	-	-	-	-	-	2.4	Up
NM_178016	Phosphatidylinositol glycan anchor biosynthesis, class K	Pigk	-	-	-	-	-	-	2.7	Up
NM_025457	phosphatidylinositol glycan anchor biosynthesis, class Y-like	-	-	-	-	-	2.3	Up	-	-
NM_019640	Phosphatidylinositol transfer protein, beta	Pitpnb	-	-	-	-	1.8	Up	-	-
NM_198191	Phosphatidylinositol-4-phosphate 5-kinase-like 1	Pip5k11	-	-	-	-	-	-	2.0	Up
NM_0010041	46	-	-	-	-	-	-	-	2.9	Up
XM_133606	phosphatidylserine decarboxylase pseudogene	-	-	-	-	-	-	-	1.6	Down
NM_018779	phosphodiesterase 2A, cGMP-stimulated	-	-	-	-	-	-	-	2.2	Up
NM_031401	Phosphodiesterase 3A, cGMP inhibited	Pde3a	-	-	-	-	-	-	1.5	Up
NM_153422	phosphodiesterase 4D interacting protein (myomegalin)	-	-	-	-	-	-	-	3.0	Up
NM_033614	Phosphodiesterase 5A, cGMP-specific	Pde5a	-	-	-	-	-	-	2.5	Up
NM_008801	Phosphodiesterase 6C, cGMP specific, cone, alpha prime	Pde6c	-	-	-	-	-	-	1.7	Up
NM_019703	Phosphodiesterase 6D, cGMP-specific, rod, delta	Pde6d	-	-	-	-	1.7	Up	-	-
XM_355378	Phosphofructokinase, platelet	Pfkp	-	-	-	-	-	-	1.9	Down
NM_013737	phospholipase A2, group IVB (cytosolic)	-	-	-	-	-	-	-	2.2	Up
NM_008874	Phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)	Pla2g7	-	-	-	-	-	-	1.7	Down
NM_054066	Phospholipase C, beta 3	Plcb3	-	-	-	-	-	-	1.6	Up
NM_011116	Phospholipase C, zeta 1	Plcz1	-	-	-	-	-	-	1.9	Up
NM_053182	Phospholipase D family, member 3	Pld3	-	-	-	-	2.7	Up	-	-
NM_199446	Phosphoprotein associated with glycosphingolipid microdomains 1	Pag1	-	-	1.7	Down	-	-	-	-
NM_011079	Phosphorylase kinase beta	Phkb	-	-	-	-	-	-	3.5	Up
NM_010726	Phosphorylase kinase gamma 1	Phkg1	-	-	-	-	-	-	2.8	Up
NM_021308	Phytanoyl-CoA hydroxylase	Phyh	-	-	-	-	-	-	1.9	Down
NM_008827	Pituitary tumor-transforming 1	Pttg1	-	-	-	-	1.5	Up	-	-
NM_019645	Piwi-like homolog 2 (Drosophila)	Piwil2	-	-	-	-	-	-	2.1	Up
NM_019762	Placental growth factor	Pgf	-	-	-	-	1.7	Up	2.0	Up
NM_008877	Plakophilin 1	Pkp1	-	-	-	-	-	-	1.7	Up
NM_008809	Plakophilin 3	Pkp3	-	-	-	-	-	-	1.8	Up
	Plasminogen	Plg	-	-	-	-	-	-	2.0	Up
	Platelet derived growth factor receptor, beta polypeptide	Pdgfrb	-	-	-	-	-	-	1.7	Down

NM_008808	Platelet derived growth factor, alpha	Pdgfa	-	-	-	-	-	-	1.8	Down
NM_027924	Platelet-derived growth factor, D polypeptide	Pdgfd	-	-	-	-	-	-	2.2	Up
NM_030263	Pleckstrin and Sec7 domain containing 3	Psd3	-	-	-	-	-	-	1.9	Up
NM_177611	Pleckstrin and Sec7 domain containing 4	Psd4	-	-	-	-	-	-	1.6	Up
NM_144920	Pleckstrin homology domain containing, family A member 5	Plekha5	-	-	-	-	-	-	2.4	Up
NM_182930	Pleckstrin homology domain containing, family A member 6	Plekha6	-	-	-	-	-	-	4.0	Up
NM_009434	Pleckstrin homology-like domain, family A, member 2	Phlda2	1.5	Up	-	-	-	-	2.0	Up
NM_153537	Pleckstrin homology-like domain, family B, member 1	Phldb1	-	-	-	-	-	-	2.0	Up
NM_139200	Pleckstrin homology, Sec7 and coiled-coil domains, binding protein	Pscdbp	-	-	-	-	-	-	2.6	Down
NM_028195	Pleckstrin homology, Sec7 and coiled/coil domains 4	Pscd4	-	-	-	-	2.0	Up	-	-
NM_201393	Plectin 1	Plec1	-	-	-	-	1.7	Down	-	-
NM_018807	Pleiomorphic adenoma gene-like 2	Plagl2	-	-	-	-	-	-	1.6	Up
NM_0010028										
42	PML-RAR alpha-regulated adaptor molecule 1	Pram1	-	-	-	-	-	-	3.7	Up
XM_194334	PNMA-like 1	-	-	-	-	-	-	-	3.9	Up
NM_172874	Podocan	Podn	-	-	-	-	-	-	2.9	Up
NM_010329	Podoplanin	Pdpn	-	-	-	-	-	-	3.5	Up
NM_008990	Poliovirus receptor-related 2	Pvrl2	-	-	-	-	-	-	2.4	Up
XM_203738	poliovirus receptor-related 4	-	-	-	1.6	Down	-	-	-	-
NM_008774	Poly A binding protein, cytoplasmic 1	Pabpc1	-	-	-	-	-	-	2.3	Down
NM_133691	Poly-U binding splicing factor 60	Puf60	-	-	2.4	Up	-	-	-	-
XM_143201	poly(A) binding protein, cytoplasmic 4-like	-	-	-	-	-	-	-	2.3	Up
NM_026420	Polyadenylate-binding protein-interacting protein 2	Paip2	-	-	-	-	-	-	2.6	Down
NM_025847	polybromo 1	-	-	-	-	-	-	-	1.6	Up
NM_009545	Polycomb group ring finger 2	Pcgf2	-	-	-	-	1.9	Up	3.3	Up
NM_153179	Polycystic kidney and hepatic disease 1	Pkhd1	-	-	-	-	-	-	1.6	Up
NM_138674	Polycystic kidney and hepatic disease 1-like 1	Pkhd11	-	-	-	-	-	-	1.8	Up
NM_181544	Polycystic kidney disease 1 like 3	Pkd1l3	-	-	-	-	-	-	3.6	Up
NM_181422	Polycystic kidney disease 2-like 1	Pkd2l1	-	-	-	-	-	-	2.1	Up
NM_029977	Polymerase (DNA directed), theta	Polq	-	-	-	-	-	-	2.0	Up
NM_025945	Polymerase (RNA) III (DNA directed) polypeptide D	Polr3d	-	-	-	-	-	-	1.5	Up
NM_027241	Polymerase (RNA) III (DNA directed) polypeptide G like	Polr3gl	-	-	-	-	-	-	2.1	Down
NM_008986	Polymerase I and transcript release factor	Ptrf	-	-	-	-	-	-	1.9	Up
NM_024286	Popeye domain containing 3	Popdc3	-	-	-	-	-	-	1.5	Up
NM_026145	Potassium channel tetramerisation domain containing 10	Kctd10	-	-	-	-	-	-	1.7	Down
NM_153143	Potassium channel tetramerisation domain containing 11	Kctd11	-	-	-	-	-	-	3.2	Up
NM_172747	Potassium channel tetramerisation domain containing 13	Kctd13	-	-	-	-	1.8	Up	-	-
NM_021542	Potassium channel, subfamily K, member 5	Kcnk5	-	-	-	-	-	-	2.1	Up
NM_010609	Potassium channel, subfamily K, member 7	Kcnk7	-	-	1.7	Down	-	-	-	-
XM_139425	potassium channel, subfamily K, member 9	-	-	-	-	-	-	-	3.0	Up
NM_032397	Potassium intermediate/small conductance calcium-activated channel, subfamily N, member 1	Kcnn1	-	-	-	-	-	-	1.6	Up

NM_010603	Potassium inwardly-rectifying channel, subfamily J, member 12	Kcnj12	-	-	-	-	-	-	-	3.6	Up
NM_010604	Potassium inwardly-rectifying channel, subfamily J, member 16	Kcnj16	-	-	-	-	-	-	-	3.3	Down
NM_008425	Potassium inwardly-rectifying channel, subfamily J, member 2	Kcnj2	-	-	-	-	-	-	-	2.5	Up
NM_010610	Potassium large conductance calcium-activated channel, subfamily M, alpha member 1	Kcnma1	-	-	-	-	-	-	-	3.9	Up
XM_136482	potassium voltage gated channel, Shab-related subfamily, member 2	-	-	-	-	-	-	-	-	3.1	Up
NM_173417	Potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3	Kcns3	-	-	-	-	-	-	-	2.2	Up
NM_010596	Potassium voltage-gated channel, shaker-related subfamily, member 7	Kcna7	-	-	-	-	-	-	-	3.4	Up
XM_354643	potassium voltage-gated channel, subfamily H (eag-related), member 4	-	-	-	-	-	-	-	-	2.8	Up
NM_011139	POU domain, class 2, transcription factor 3	Pou2f3	-	-	-	-	-	-	-	2.7	Up
NM_011141	POU domain, class 3, transcription factor 1	Pou3f1	-	-	-	-	-	-	-	1.6	Up
NM_138945	POU domain, class 4, transcription factor 3	Pou4f3	-	-	-	-	-	-	-	2.1	Up
NM_010127	POU domain, class 6, transcription factor 1	Pou6f1	-	-	-	-	-	-	-	1.5	Up
XM_131309	PR domain containing 13	-	-	-	-	-	-	-	-	2.8	Up
NM_008853	Praja1, RING-H2 motif containing	Pja1	-	-	-	-	-	-	-	1.6	Down
NM_183355	Pre B-cell leukemia transcription factor 1	Pbx1	-	-	-	-	-	-	-	4.2	Up
NM_138659	Pre-mRNA processing factor 8	Prpf8	-	-	-	-	3.0	Up	-	-	-
XM_145287	predicted gene, 232745	-	-	-	-	-	-	-	-	1.5	Up
NM_0010019	predicted gene, 380687	-	-	-	-	-	-	-	-	2.1	Up
XM_358483	predicted gene, 381002	-	-	-	-	-	-	-	-	1.8	Up
NM_177596	Predicted gene, EG210853	EG210853	-	-	-	-	-	-	-	3.1	Up
XM_136015	Predicted gene, EG212753	EG212753	-	-	1.9	Down	-	-	-	-	-
XM_142027	predicted gene, EG213474	-	-	-	-	-	-	-	-	2.7	Up
XM_136585	predicted gene, EG227054	-	-	-	-	-	-	-	-	1.5	Down
NM_177665	Predicted gene, EG229862	EG229862	-	-	-	-	-	-	-	1.6	Up
XM_486062	predicted gene, EG232801	-	-	-	-	-	1.9	Up	-	3.4	Up
XM_133608	predicted gene, EG233637	-	-	-	-	-	-	-	-	1.8	Up
XM_135370	predicted gene, EG235855	-	-	-	-	-	-	-	-	3.1	Up
XM_125372	predicted gene, EG236622	-	-	-	-	-	-	-	-	2.1	Up
NM_177706	Predicted gene, EG237300	EG237300	-	-	-	-	-	-	-	2.3	Up
XM_138115	predicted gene, EG238199	-	-	-	-	-	-	-	-	2.1	Up
XM_140634	predicted gene, EG240549	-	-	-	-	-	-	-	-	1.6	Up
XM_144783	predicted gene, EG243433	-	-	-	-	-	-	-	-	2.3	Up
XM_141952	predicted gene, EG245516	-	-	-	-	-	-	-	-	2.6	Up
XM_142195	predicted gene, EG245651	-	-	-	-	-	-	-	-	1.7	Up



NM_177825	predicted gene, EG328839	-	-	-	-	-	-	4.1	Up	
NM_207259	predicted gene, EG330776	-	-	-	-	-	-	2.8	Up	
NM_198657	Predicted gene, EG381438	EG381438	-	-	-	-	-	2.7	Up	
NM_001004160	predicted gene, EG381818	-	-	-	-	-	-	1.6	Up	
XM_355864	predicted gene, EG381852	-	-	-	-	-	-	2.0	Up	
NM_198674	Predicted gene, EG382109	EG382109	-	-	-	-	-	2.5	Up	
XM_356392	predicted gene, EG382275	-	-	-	-	-	-	2.2	Up	
XM_356911	predicted gene, EG383189	-	-	-	-	-	1.9	Up	2.2	Up
XM_357052	predicted gene, EG383436	-	-	-	-	-	2.1	Up	-	-
XM_357902	predicted gene, EG384862	-	-	-	-	-	1.8	Up	-	-
NM_001004162	predicted gene, EG432436	-	-	-	-	-	-	1.6	Up	
XM_484651	predicted gene, EG433128	-	-	-	-	-	-	2.6	Down	
XM_485807	predicted gene, EG434067	-	-	-	-	-	3.1	Up	-	-
XM_485863	predicted gene, EG434121	-	-	-	-	-	-	2.5	Up	
XM_485918	predicted gene, EG434172	-	-	-	-	-	-	1.8	Up	
XM_486210	predicted gene, EG434396	-	-	-	-	-	-	2.1	Up	
XM_486618	predicted gene, EG434728	-	-	-	-	-	-	1.8	Up	
XM_486708	predicted gene, EG434797	-	-	-	-	-	-	2.1	Up	
XM_486780	predicted gene, EG434858	-	-	-	-	-	-	2.8	Down	
XM_487244	predicted gene, EG435328	-	-	-	-	-	-	1.9	Up	
XM_487627	predicted gene, EG435651	-	-	-	-	-	-	2.7	Up	
XM_488314	Predicted gene, EG436188	EG436188	-	-	-	-	-	1.7	Up	
XM_354754	Predicted gene, EG627648	EG627648	-	-	-	-	1.5	Up	2.5	Up
NM_173782	predicted gene, EG70793	-	-	-	-	-	-	3.5	Up	
NM_206870	Predicted gene, OTTMUSG00000007655	OTTMUSG00000007655	-	-	-	-	-	1.5	Up	
XM_204040	predicted gene, OTTMUSG00000010332	-	-	-	-	-	-	1.8	Up	
NM_177571	Predicted gene, OTTMUSG00000010433	OTTMUSG00000010433	-	-	-	-	-	3.6	Up	
NM_177848	predicted gene, OTTMUSG00000015529	-	-	-	-	-	-	2.4	Up	
NM_007376	Pregnancy zone protein	Pzp	-	-	-	-	-	1.6	Up	
NM_001004152	Pregnancy-specific glycoprotein 22	Psg22	-	-	-	-	-	1.5	Up	
NM_001002927	Preproenkephalin 1	Penk1	-	-	-	-	2.0	Up	2.6	Up

XM_144905	prickle-like 2 ( <i>Drosophila</i> )	-	-	-	-	-	-	1.9	Up
NM_026398	Processing of precursor 5, ribonuclease P/MRP family ( <i>S. cerevisiae</i> )	Pop5	-	-	-	-	-	1.5	Up
NM_018863	Prodynorphin	Pdyn	-	-	-	-	-	2.7	Up
NM_008829	Progesterone receptor	Pgr	-	-	-	-	-	3.9	Up
NM_019746	Programmed cell death 5	Pdcd5	-	-	-	-	2.4	Up	-
NM_016688	Programmed cell death protein 7	Pdcd7	-	-	-	-	1.6	Up	-
NM_011164	Prolactin	Prl	-	-	-	-	-	1.9	Up
NM_013766	Prolactin family 3, subfamily c, member 1	Prl3c1	-	-	-	-	-	1.6	Up
NM_028447	Proline-rich coiled-coil 1	Prrc1	-	-	-	-	-	2.1	Down
NM_019976	Proline/serine-rich coiled-coil 1	Psrc1	-	-	-	-	-	2.4	Up
NM_028243	Prolylcarboxypeptidase (angiotensinase C)	Prpc	-	-	-	-	-	1.7	Down
NM_013628	Proprotein convertase subtilisin/kexin type 1	Pcsk1	-	-	-	-	-	2.6	Up
NM_008962	Prostaglandin D receptor	Ptgdr	-	-	-	-	-	2.2	Up
NM_008963	Prostaglandin D2 synthase (brain)	Ptgds	-	-	-	-	-	1.5	Up
NM_008967	Prostaglandin I receptor (IP)	Ptgir	-	-	1.8	Down	-	-	-
NM_013637	Protamine 1	Prm1	-	-	1.7	Down	-	-	-
NM_013638	Protamine 3	Prm3	-	-	-	-	-	1.7	Up
NM_008947	Protease (prosome, macropain) 26S subunit, ATPase 1	Psmc1	-	-	-	-	-	1.9	Down
XM_128466	protease, serine, 32	-	-	-	-	-	-	1.5	Up
NM_178372	Protease, serine, 34	Prss34	-	-	-	-	-	2.0	Up
NM_008948	Proteasome (prosome, macropain) 26S subunit, ATPase 3	Psmc3	-	-	-	-	-	1.8	Down
NM_178616	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	Psmc11	-	-	-	-	-	3.4	Down
NM_011875	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 13	Psmc13	-	-	-	-	1.8	Up	-
NM_021526	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	Psmc14	-	-	-	-	-	1.8	Down
NM_008951	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 4	Psmc4	-	-	-	-	2.4	Up	-
NM_025604	Proteasome (prosome, macropain) assembly chaperone 3	Psmg3	-	-	-	-	2.0	Up	-
NM_011966	Proteasome (prosome, macropain) subunit, alpha type 4	Psmc4	-	-	-	-	1.7	Up	-
NM_011968	Proteasome (prosome, macropain) subunit, alpha type 6	Psmc6	-	-	-	-	-	2.5	Down
XM_357002	Proteasome (prosome, macropain) subunit, alpha type, 8	Psmc8	-	-	1.6	Down	-	-	-
NM_011185	Proteasome (prosome, macropain) subunit, beta type 1	Psmc1	-	-	-	-	-	1.5	Down
NM_010724	Proteasome (prosome, macropain) subunit, beta type 8 (large multifunctional peptidase 7)	Psmc8	-	-	-	-	1.9	Up	-
NM_019830	Protein arginine N-methyltransferase 1	Prmt1	-	-	-	-	2.4	Up	-
NM_028295	Protein disulfide isomerase associated 5	Pdia5	-	-	-	-	-	2.1	Up
NM_011862	Protein kinase C and casein kinase substrate in neurons 2	Pacsin2	-	-	-	-	-	2.6	Down
NM_008856	Protein kinase C, eta	Prkch	-	-	-	-	1.7	Up	1.8
NM_008862	Protein kinase inhibitor, alpha	Pkia	-	-	-	-	-	2.5	Up
XM_139298	protein kinase, AMP-activated, alpha 1 catalytic subunit	-	-	-	-	-	-	2.1	Up
NM_178143	Protein kinase, AMP-activated, alpha 2 catalytic subunit	Prkaa2	-	-	-	-	-	2.5	Up
NM_011100	Protein kinase, cAMP dependent, catalytic, beta	Prkacb	-	-	-	-	-	1.9	Up
NM_011160	Protein kinase, cGMP-dependent, type I	Prkg1	-	-	-	-	-	1.6	Up

NM_178726	Protein phosphatase 1 (formerly 2C)-like	Ppm11	-	-	-	-	-	-	2.1	Up
NM_031868	Protein phosphatase 1, catalytic subunit, alpha isoform	Ppp1ca	-	-	-	-	-	-	1.6	Down
NM_153089	Protein phosphatase 1, regulatory (inhibitor) subunit 16B	Ppp1r16b	-	-	-	-	-	-	2.0	Up
NM_144828	Protein phosphatase 1, regulatory (inhibitor) subunit 1B	Ppp1r1b	-	-	-	-	-	-	2.8	Up
NM_146154	Protein phosphatase 1, regulatory (inhibitor) subunit 8	Ppp1r8	-	-	-	-	1.8	Up	-	-
NM_011151	Protein phosphatase 1B, magnesium dependent, beta isoform	Ppm1b	-	-	-	-	-	-	2.4	Down
NM_017374	Protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	Ppp2cb	-	-	-	-	-	-	1.6	Down
NM_144880	Protein phosphatase 2, regulatory subunit B (B56), alpha isoform	Ppp2r5a	-	-	-	-	-	-	2.1	Down
NM_146081	Protein phosphatase 4, regulatory subunit 1	Ppp4r1	-	-	-	-	-	-	2.1	Down
NM_145150	Protein regulator of cytokinesis 1	Prc1	-	-	-	-	-	-	1.9	Up
NM_021345	Protein tyrosine phosphatase-like A domain containing 1	Ptplad1	-	-	-	-	-	-	2.0	Down
NM_025576	Protein tyrosine phosphatase, mitochondrial 1	Ptpmt1	-	-	-	-	-	-	1.6	Down
XM_137234	protein tyrosine phosphatase, receptor type, Q	-	-	-	-	-	-	-	3.2	Up
NM_028410	Protein-kinase, interferon-inducible double stranded RNA dependent inhibitor, repressor of (P58 repressor)	Prkrir	-	-	-	-	1.9	Up	-	-
NM_153415	Protein-O-mannosyltransferase 2	Pomt2	-	-	-	-	-	-	1.6	Up
NM_011123	Proteolipid protein (myelin) 1	Plp1	-	-	-	-	-	-	1.8	Up
NM_017378	Protocadherin 12	Pcdh12	-	-	-	-	-	-	3.3	Up
NM_023115	Protocadherin 15	Pcdh15	-	-	-	-	-	-	2.7	Up
NM_130448	Protocadherin 18	Pcdh18	-	-	-	-	-	-	2.7	Up
NM_178685	Protocadherin 20	Pcdh20	-	-	-	-	-	-	2.4	Up
NM_053135	Protocadherin beta 10	Pcdhb10	-	-	-	-	-	-	2.2	Up
NM_053127	Protocadherin beta 2	Pcdhb2	-	-	-	-	-	-	2.1	Up
NM_053146	Protocadherin beta 21	Pcdhb21	-	-	-	-	-	-	2.9	Up
NM_053130	Protocadherin beta 5	Pcdhb5	-	-	-	-	-	-	2.1	Up
NM_053133	Protocadherin beta 8	Pcdhb8	-	-	-	-	-	-	2.7	Up
NM_033584	Protocadherin gamma subfamily A, 1	Pcdhga1	-	-	-	-	-	-	2.2	Up
NM_033591	Protocadherin gamma subfamily A, 10	Pcdhga12	-	-	-	-	-	-	1.7	Up
NM_033593	Protocadherin gamma subfamily A, 10	Pcdhga12	-	-	-	-	-	-	2.3	Up
NM_033587	Protocadherin gamma subfamily A, 10	Pcdhga12	-	-	-	-	-	-	2.6	Up
NM_033576	Protocadherin gamma subfamily A, 10	Pcdhga12	-	-	-	-	-	-	2.9	Up
NM_134129	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae)	Prpf19	-	-	2.2	Up	1.9	Up	-	-
NM_027328	PRP31 pre-mRNA processing factor 31 homolog (yeast)	Prpf31	-	-	-	-	1.7	Up	-	-
NM_025845	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	Prpf38b	-	-	-	-	-	-	1.6	Down
NM_173347	Prune homolog (Drosophila)	Prune	-	-	-	-	-	-	2.6	Up
NM_019700	Pseudouridine synthase 1	Pus1	-	-	-	-	2.1	Up	-	-

NM_009184	PTK6 protein tyrosine kinase 6	Ptk6	-	-	-	-	-	-	2.3	Up
NM_008773	Purinergic receptor P2Y, G-protein coupled 2	P2ry2	-	-	-	-	-	-	2.0	Up
NM_013629	Putative homeodomain transcription factor 1	Phtf1	-	-	-	-	1.8	Up	-	-
NM_133993	PWP1 homolog (S. cerevisiae)	Pwp1	-	-	-	-	3.1	Up	3.6	Down
NM_023217	Pyroglutamyl-peptidase I	Pgpep1	-	-	-	-	1.8	Up	-	-
NM_008797	Pyruvate carboxylase	Pcx	-	-	-	-	-	-	2.0	Up
NM_008810	Pyruvate dehydrogenase E1 alpha 1	Pdha1	-	-	-	-	-	-	1.6	Down
NM_008811	Pyruvate dehydrogenase E1 alpha 2	Pdha2	-	-	-	-	-	-	1.8	Up
NM_021881	Quaking	Qk	-	-	-	-	2.8	Up	-	-
NM_023268	Quiescin Q6 sulfhydryl oxidase 1	Qsox1	-	-	-	-	-	-	3.2	Up
NM_010261	Rab acceptor 1 (prenylated)	Rabac1	-	-	-	-	1.8	Up	1.9	Down
NM_146121	RAB GTPase activating protein 1	Rabgap1	-	-	-	-	-	-	2.1	Down
NM_021430	Rab interacting lysosomal protein-like 1	Rilpl1	-	-	-	-	-	-	1.7	Down
NM_008996	RAB1, member RAS oncogene family	Rab1	-	-	-	-	3.0	Up	-	-
XM_129331	RAB11 family interacting protein 2 (class I)	-	-	-	-	-	-	-	1.7	Up
NM_026405	RAB32, member RAS oncogene family	Rab32	-	-	-	-	1.9	Up	-	-
NM_033475	RAB34, member of RAS oncogene family	Rab34	-	-	-	-	-	-	2.6	Up
NM_021411	RAB37, member of RAS oncogene family	Rab37	-	-	-	-	-	-	2.2	Down
NM_009003	RAB4A, member RAS oncogene family	Rab4a	-	-	-	-	-	-	1.6	Up
NM_024456	RAB5C, member RAS oncogene family	Rab5c	-	-	-	-	-	-	1.7	Down
NM_023126	RAB8A, member RAS oncogene family	Rab8a	-	-	-	-	1.8	Up	-	-
NM_019773	RAB9, member RAS oncogene family	Rab9	-	-	-	-	-	-	2.9	Down
NM_176971	RAB9B, member RAS oncogene family	Rab9b	-	-	-	-	-	-	1.8	Up
NM_025654	RAD52 motif 1	Rdm1	-	-	-	-	1.8	Up	-	-
NM_025789	Radial spokehead-like 2A	Rshl2a	-	-	-	-	-	-	1.9	Down
XM_137041	Radial spokehead-like 3	Rshl3	-	-	-	-	-	-	2.0	Up
NM_181397	Raftlin lipid raft linker 1	Rftn1	-	-	-	-	-	-	2.2	Up
NM_178631	RALY RNA binding protein-like	Ralyl	-	-	-	-	-	-	2.4	Up
XM_128698	RAN binding protein 3	-	-	-	-	-	2.6	Up	-	-
NM_019930	RAN binding protein 9	Ranbp9	-	-	-	-	-	-	1.7	Up
NM_054050	Rap guanine nucleotide exchange factor (GEF) 1	Rapgef1	-	-	-	-	-	-	2.2	Up
XM_484075	Rap guanine nucleotide exchange factor (GEF)-like 1	-	-	-	-	-	-	-	2.4	Up
NM_011281	RAR-related orphan receptor gamma	Rorc	-	-	-	-	-	-	2.4	Up
NM_177620	Ras and Rab interactor 3	Rin3	-	-	-	-	2.4	Up	-	-
XM_355205	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	-	-	-	-	-	-	-	2.8	Up
NM_027760	Ras association (RalGDS/AF-6) domain family (N-terminal) member 8	Rassf8	-	-	-	-	-	-	2.0	Up
NM_146240	Ras association (RalGDS/AF-6) domain family (N-terminal) member 9	Rassf9	-	-	-	-	-	-	2.5	Up
NM_019713	Ras association (RalGDS/AF-6) domain family member 1	Rassf1	-	-	-	-	1.7	Up	-	-
NM_138956	Ras association (RalGDS/AF-6) domain family member 3	Rassf3	-	-	-	-	-	-	2.6	Down
NM_016802	Ras homolog gene family, member A	Rhoa	-	-	-	-	-	-	2.3	Down

NM_145999	Ras homolog gene family, member T2	Rhot2	-	-	-	-	-	-	1.6	Down
XM_355650	RAS p21 protein activator 4	-	-	-	-	-	-	-	1.5	Down
NM_024457	RAS related protein 1b	Rap1b	-	-	-	-	2.2	Up	-	-
NM_053075	RAS-homolog enriched in brain	Rheb	-	-	-	-	-	-	1.7	Down
NM_181988	RAS-like, estrogen-regulated, growth-inhibitor	Rerg	-	-	-	-	-	-	2.5	Up
XM_134870	RAS-like, family 12	-	-	-	-	-	-	-	3.3	Up
NM_019662	Ras-related associated with diabetes	Rrad	-	-	-	-	2.6	Up	-	-
NM_0010041										
54	Ras-related GTP binding B	Rragb	-	-	-	-	-	-	1.9	Up
NM_017475	Ras-related GTP binding C	Rragc	-	-	-	-	-	-	3.0	Down
NM_207246	RAS, guanyl releasing protein 3	Rasgrp3	-	-	-	-	-	-	2.0	Up
NM_021383	Rcd1 (required for cell differentiation) homolog 1 (S. pombe)	Rqcd1	-	-	-	-	-	-	1.6	Down
XM_355515	rearranged L-myc fusion sequence	-	-	-	-	-	-	-	1.9	Up
NM_172516	Receptor interacting protein kinase 5	Ripk5	-	-	-	-	-	-	1.7	Up
NM_019955	Receptor-interacting serine-threonine kinase 3	Ripk3	-	-	-	-	2.8	Up	-	-
NM_023663	Receptor-interacting serine-threonine kinase 4	Ripk4	-	-	-	-	-	-	1.9	Up
NM_009057	Recombination activating gene 1 activating protein 1	Rag1ap1	-	-	-	-	-	-	2.3	Down
NM_009036	Recombination signal binding protein for immunoglobulin kappa J region-like	Rbpjl	-	-	1.7	Down	-	-	-	-
NM_023042	RecQ protein-like	Recql	-	-	-	-	1.9	Up	-	-
NM_009051	Reduced expression 2	Rex2	-	-	-	-	-	-	3.5	Up
NM_009060	Regucalcin	Rgn	-	-	-	-	-	-	2.3	Up
NM_015811	Regulator of G-protein signaling 1	Rgs1	-	-	-	-	-	-	1.9	Down
NM_016758	Regulator of G-protein signaling 14	Rgs14	-	-	-	-	1.7	Up	-	-
NM_145840	Regulator of G-protein signalling 9 binding protein	Rgs9bp	-	-	-	-	-	-	2.2	Up
NM_0010018										
82	Regulator of telomere elongation helicase 1	Rtel1	-	-	-	-	-	-	2.7	Up
NM_177306	Regulatory factor X domain containing 1	Rfxdc1	-	-	-	-	-	-	2.0	Up
NM_011265	Regulatory factor X, 3 (influences HLA class II expression)	Rfx3	-	-	-	-	-	-	2.4	Up
NM_025846	Related RAS viral (r-ras) oncogene homolog 2	Rras2	-	-	-	-	-	-	2.5	Down
NM_173184	Relaxin 3	Rln3	-	-	-	-	-	-	3.4	Up
NM_031192	Renin 2 tandem duplication of Ren1	Ren1	-	-	-	-	-	-	1.6	Up
NM_023132	Renin binding protein	Renbp	-	-	-	-	1.8	Up	-	-
NM_011284	Replication protein A2	Rpa2	-	-	-	-	1.8	Up	3.0	Up
XM_356401	Reproductive homeobox 13	-	-	-	-	-	-	-	3.5	Up
NM_194063	Reproductive homeobox 3H	Rhox3a	-	-	-	-	-	-	2.3	Up
NM_025346	Required for meiotic nuclear division 5 homolog B (S. cerevisiae)	Rmnd5b	-	-	-	-	1.7	Up	-	-
NM_026395	RER1 retention in endoplasmic reticulum 1 homolog (S. cerevisiae)	Rer1	-	-	-	-	-	-	1.7	Down
NM_053194	Resistance to inhibitors of cholinesterase 8 homolog (C. elegans)	Ric8	-	-	-	-	-	-	1.5	Down
NM_138954	Ret finger protein-like 4	Rfpl4	-	-	1.5	Down	-	-	-	-
NM_009050	Ret proto-oncogene	Ret	-	-	-	-	-	-	2.0	Up
NM_144929	Retbindin	Rtbdn	-	-	-	-	-	-	1.8	Up

NM_199223	Reticulon 4 receptor-like 2	Rtn4r2	-	-	-	-	2.1	Up	2.7	Up
NM_021340	Retinal G protein coupled receptor	Rgr	-	-	-	-	-	-	2.1	Up
NM_009118	Retinal S-antigen	Sag	-	-	-	-	-	-	2.6	Up
NM_011283	Retinitis pigmentosa 1 homolog (human)	Rp1h	-	-	-	-	-	-	1.5	Up
XM_484387	retinitis pigmentosa 1 homolog (human)-like 1	-	-	-	-	-	1.5	Down	1.9	Up
NM_009030	Retinoblastoma binding protein 4	Rbbp4	-	-	-	-	-	-	1.8	Down
NM_011250	Retinoblastoma-like 2	Rbl2	-	-	-	-	-	-	3.6	Up
NM_018740	Retinoic acid induced 12	Rai12	-	-	-	-	2.0	Up	-	-
XM_130987	retinoic acid receptor responder (tazarotene induced) 1	-	-	-	-	-	-	-	2.3	Up
NM_133832	Retinol dehydrogenase 10 (all-trans)	Rdh10	-	-	-	-	-	-	1.7	Up
NM_199313	retinol dehydrogenase 18	-	-	-	-	-	-	-	2.6	Up
NM_027301	Retinol dehydrogenase 20	Rdh20	-	-	-	-	-	-	3.7	Up
XM_134689	retinol dehydrogenase 8	-	-	-	-	-	-	-	2.0	Up
NM_183318	Retrotransposon gag domain containing 4	Rgag4	-	-	-	-	-	-	2.6	Up
NM_184109	Retrotransposon-like 1	Rtl1	-	-	-	-	2.0	Up	3.4	Up
NM_025852	REX1, RNA exonuclease 1 homolog (S. cerevisiae)	Rexo1	-	-	1.9	Down	-	-	-	-
NM_024233	REX2, RNA exonuclease 2 homolog (S. cerevisiae)	Rexo2	-	-	-	-	1.6	Up	-	-
NM_177815	RFT1 homolog (S. cerevisiae)	Rft1	-	-	-	-	-	-	1.6	Up
NM_011269	Rhesus blood group-associated A glycoprotein	Rhag	-	-	-	-	-	-	2.3	Up
NM_030113	Rho GTPase activating protein 10	Arhgap10	-	-	1.8	Down	-	-	-	-
NM_029277	Rho GTPase activating protein 12	Arhgap12	-	-	-	-	-	-	2.8	Up
NM_153820	Rho GTPase activating protein 15	Arhgap15	-	-	-	-	-	-	1.8	Down
NM_017402	Rho guanine nucleotide exchange factor (GEF7)	Arhgef7	-	-	-	-	-	-	1.5	Up
NM_012026	Rho-guanine nucleotide exchange factor	Rgnef	-	-	-	-	-	-	2.5	Up
NM_183163	Rhomboid, veinlet-like 2 (Drosophila)	Rhbdl2	-	-	-	-	-	-	2.2	Up
XM_127683	ribonuclease, RNase A family, 10 (non-active)	-	-	-	-	-	-	-	3.1	Up
NM_183032	Ribonuclease, RNase A family, 9 (non-active)	Rnase9	-	-	-	-	-	-	2.3	Up
NM_145135	Ribonuclease/angiogenin inhibitor 1	Rnh1	-	-	2.6	Up	-	-	2.1	Up
NM_025919	Ribosomal protein L11	Rpl11	-	-	-	-	-	-	3.0	Up
NM_172086	Ribosomal protein L32	Rpl32	-	-	-	-	-	-	1.9	Down
NM_011290	Ribosomal protein L6	Rpl6	-	-	-	-	-	-	2.8	Down
NM_025433	Ribosomal protein L7-like 1	Rpl7l1	-	-	-	-	-	-	2.4	Down
NM_013721	Ribosomal protein L7a	Rpl7a	-	-	-	-	1.7	Up	-	-
NM_025963	Ribosomal protein S10	Rps10	-	-	-	-	-	-	1.6	Down
NM_009091	Ribosomal protein S15	Rps15	1.5	Down	-	-	-	-	-	-
NM_013647	Ribosomal protein S16	Rps16	-	-	-	-	-	-	1.6	Down
NM_016959	Ribosomal protein S3a	Rps3a	-	-	-	-	-	-	1.7	Down
NM_025405	ribosomal protein S4, Y-linked 2	-	-	-	-	-	-	-	2.2	Down
NM_009095	Ribosomal protein S5	Rps5	-	-	-	-	-	-	2.0	Down

NM_009096	Ribosomal protein S6	Rps6	-	-	-	-	-	-	1.9	Down
NM_025949	Ribosomal protein S6 kinase polypeptide 6	Rps6ka6	-	-	-	-	2.1	Up	3.3	Up
NM_021485	Ribosomal protein S6 kinase, polypeptide 2	Ptprcap	-	-	-	-	-	-	2.4	Up
NM_011029	Ribosomal protein SA	Rpsa	-	-	-	-	-	-	1.7	Down
NM_026020	Ribosomal protein, large P2	Rplp2	-	-	-	-	-	-	2.3	Down
NM_010925	Ribosomal RNA processing 1 homolog (S. cerevisiae)	Rrp1	-	-	2.3	Up	2.7	Up	-	-
NM_212470	RIKEN cDNA 0610007C21 gene	0610007 C21Rik	-	-	-	-	2.0	Up	-	-
NM_027855	RIKEN cDNA 0610007C21 gene	0610007 C21Rik	-	-	-	-	-	-	2.9	Down
NM_024179	RIKEN cDNA 0610009O20 gene	0610009 O20Rik	-	-	-	-	1.5	Up	2.2	Up
XM_355548	RIKEN cDNA 0610025J13 gene	0610025 J13Rik	-	-	-	-	-	-	2.3	Up
NM_028754	RIKEN cDNA 0610037L13 gene	0610037 L13Rik	-	-	-	-	-	-	2.1	Down
NM_026306	RIKEN cDNA 0610038D11 gene	0610038 D11Rik	-	-	-	-	2.0	Up	-	-
NM_029554	RIKEN cDNA 0610040J01 gene	0610040 J01Rik	-	-	-	-	1.7	Up	1.9	Up
NM_183275	RIKEN cDNA 1110002N22 gene	1110002 N22Rik	-	-	-	-	-	-	2.1	Down
NM_021417	RIKEN cDNA 1110006O24 gene	-	-	-	-	-	-	-	1.8	Up
NM_028617	RIKEN cDNA 1110012M11 gene	1110012 M11Rik	-	-	-	-	-	-	1.5	Down
XM_126634	RIKEN cDNA 1110012N22 gene	-	-	-	2.6	Down	-	-	3.0	Down
NM_026808	RIKEN cDNA 1110028A07 gene	1110028 A07Rik	-	-	-	-	2.1	Up	1.8	Up
NM_177645	RIKEN cDNA 1110028C15 gene	1110028 C15Rik	-	-	-	-	-	-	1.5	Up
NM_025402	RIKEN cDNA 1110031I02 gene	1110031 I02Rik	-	-	-	-	-	-	1.9	Up
NM_199197	RIKEN cDNA 1110032A13 gene	1110032 A13Rik	-	-	-	-	-	-	2.1	Down
XM_193728	RIKEN cDNA 1110033M05 gene	1110033 M05Rik	-	-	-	-	-	-	2.5	Up
NM_027269	RIKEN cDNA 1110034A24 gene	1110034 A24Rik	-	-	-	-	-	-	1.9	Up
XM_135842	RIKEN cDNA 1110059M19 gene	-	-	-	-	-	-	-	1.7	Up
XM_130050	RIKEN cDNA 1190002A17 gene	-	-	-	-	-	1.5	Up	2.2	Up
XM_147036	RIKEN cDNA 1190002N15 gene	-	-	-	-	-	-	-	3.1	Up
NM_197988	RIKEN cDNA 1190005I06 gene	1190005I 06Rik	-	-	-	-	-	-	1.7	Up
XM_489067	RIKEN cDNA 1190007F08 gene	-	-	-	-	-	1.9	Up	1.7	Up

NM_024205	RIKEN cDNA 1200003C05 gene	1200003 C05Rik	-	-	1.6	Down	-	-	-	-
NM_028807	RIKEN cDNA 1200009I06 gene	1200009I 06Rik	-	-	-	-	-	-	2.2	Down
NM_025817	RIKEN cDNA 1200009O22 gene	1200009 O22Rik	-	-	-	-	-	-	3.3	Up
NM_024244	RIKEN cDNA 1200015N20 gene	1200015 N20Rik	-	-	-	-	-	-	1.8	Up
NM_028933	RIKEN cDNA 1300010M03 gene	1300010 M03Rik	-	-	-	-	-	-	2.0	Up
NM_023625	RIKEN cDNA 1300012G16 gene	1300012 G16Rik	-	-	-	-	1.7	Up	-	-
NM_025892	RIKEN cDNA 1500031L02 gene	1500031 L02Rik	-	-	-	-	1.5	Down	2.9	Down
NM_026451	RIKEN cDNA 1600012H06 gene	1600012 H06Rik	-	-	-	-	-	-	1.9	Down
XM_128667	RIKEN cDNA 1600014C23 gene	-	-	-	-	-	-	-	2.3	Up
XM_135038	RIKEN cDNA 1600029I14 gene	-	-	-	-	-	-	-	2.1	Up
XM_357859	RIKEN cDNA 1700003H04 gene	-	-	-	-	-	-	-	1.6	Up
XM_126493	RIKEN cDNA 1700006E09 gene	1700006 E09Rik	-	-	-	-	-	-	2.1	Up
XM_135691	RIKEN cDNA 1700007N14 gene	-	-	-	-	-	-	-	1.9	Up
XM_130726	RIKEN cDNA 1700010B08 gene	-	-	-	-	-	-	-	2.1	Up
XM_126647	RIKEN cDNA 1700012B07 gene	-	-	-	-	-	1.5	Up	3.4	Up
NM_028157	RIKEN cDNA 1700013B16 gene	1700013 B16Rik	-	-	-	-	-	-	1.9	Up
NM_027063	RIKEN cDNA 1700013G24 gene	1700013 G24Rik	-	-	-	-	-	-	2.7	Up
XM_487140	RIKEN cDNA 1700017N19 gene	-	-	-	-	-	-	-	1.8	Up
NM_029597	RIKEN cDNA 1700018B08 gene	1700018 B08Rik	-	-	-	-	-	-	2.0	Up
NM_025493	RIKEN cDNA 1700018B24 gene	-	-	-	-	-	-	-	1.6	Up
NM_023781	RIKEN cDNA 1700020D05 gene	1700020 D05Rik	-	-	-	-	-	-	3.5	Up
NM_023064	RIKEN cDNA 1700021K02 gene	1700021 K02Rik	-	-	1.7	Down	-	-	-	-
NM_172615	RIKEN cDNA 1700021K19 gene	1700021 K19Rik	-	-	-	-	1.7	Up	-	-
XM_129158	RIKEN cDNA 1700021P04 gene	-	-	-	-	-	-	-	3.2	Up
XM_133423	RIKEN cDNA 1700021P22 gene	-	-	-	-	-	-	-	2.0	Up
XM_132958	RIKEN cDNA 1700023A16 gene	1700023 A16Rik	-	-	-	-	-	-	1.7	Up
XM_284686	RIKEN cDNA 1700023I07 gene	-	-	-	-	-	-	-	1.5	Up
XM_485737	RIKEN cDNA 1700023L04 gene	1700023	-	-	-	-	-	-	2.5	Up



Gene ID	Gene Name	Accession	FC	Regulation	FC	Regulation	FC	Regulation
		L04Rik						
XM_147820	RIKEN cDNA 1700024G13 gene	-	-	-	-	-	-	3.6 Up
XM_147929	RIKEN cDNA 1700025B11 gene	-	-	-	-	-	-	1.9 Up
NM_026469	RIKEN cDNA 1700025D03 gene	1700025 D03Rik	-	-	-	-	-	3.0 Up
NM_182745	RIKEN cDNA 1700028K03 gene	1700028 K03Rik	-	-	-	-	-	2.6 Up
NM_025601	RIKEN cDNA 1700029H14 gene	1700029 H14Rik	-	-	-	-	-	2.1 Up
XM_354881	RIKEN cDNA 1700030F18 gene	-	-	-	-	-	-	2.2 Up
XM_145587	RIKEN cDNA 1700039E15 gene	-	-	-	1.6	Down	-	-
XM_485065	RIKEN cDNA 1700041B20 gene	1700041 B20Rik	-	-	-	-	-	2.2 Up
XM_136155	RIKEN cDNA 1700042B14 gene	-	-	-	-	-	-	2.3 Up
XM_149454	RIKEN cDNA 1700042G07 gene	-	-	-	-	-	-	3.6 Up
NM_028842	RIKEN cDNA 1700045I19 gene	-	-	-	1.5	Down	-	-
NM_175390	RIKEN cDNA 1700049L16 gene	-	-	-	-	-	2.0	Up
NM_028539	RIKEN cDNA 1700052K11 gene	-	-	-	-	-	-	3.2 Up
XM_485380	RIKEN cDNA 1700054F22 gene	1700054 F22Rik	-	-	1.6	Down	-	-
XM_484951	RIKEN cDNA 1700056E22 gene	-	-	-	-	-	-	2.0 Up
NM_183272	RIKEN cDNA 1700063I17 gene	1700063I 17Rik	-	-	-	-	-	2.1 Up
NM_029714	RIKEN cDNA 1700067C01 gene	1700067 C01Rik	-	-	-	-	-	1.6 Up
NM_028550	RIKEN cDNA 1700074P13 gene	1700074 P13Rik	-	-	1.6	Down	-	-
NM_028564	RIKEN cDNA 1700082M22 gene	-	-	-	-	-	-	2.4 Up
XM_355035	RIKEN cDNA 1700090G07 gene	1700090 G07Rik	-	-	-	-	-	3.7 Up
XM_484061	RIKEN cDNA 1700106J16 gene	-	-	-	-	-	-	2.3 Up
NM_026461	RIKEN cDNA 1700129C05 gene	-	-	-	2.4	Down	-	-
NM_026109	RIKEN cDNA 1810008K16 gene	1810008 K16Rik	-	-	-	-	-	2.3 Up
XM_286373	RIKEN cDNA 1810010H24 gene	1810010 H24Rik	-	-	-	-	-	2.7 Up
XM_150054	RIKEN cDNA 1810012K16 gene	-	-	-	-	-	-	3.2 Up
NM_133707	RIKEN cDNA 1810019J16 gene	1810019 J16Rik	-	-	-	-	-	2.8 Up
NM_145449	RIKEN cDNA 1810023F06 gene	1810023 F06Rik	-	-	-	-	-	1.6 Up
NM_025470	RIKEN cDNA 1810030J14 gene	1810030 J14Rik	-	-	-	-	-	2.8 Up
NM_025559	RIKEN cDNA 1810046J19 gene	1810046	-	-	-	-	2.0	Up

		J19Rik									
XM_131465	RIKEN cDNA 1810054D07 gene	-	-	-	-	-	-	-	-	1.7	Up
XM_484351	RIKEN cDNA 1810063B07 gene	-	-	-	-	-	-	-	-	1.9	Down
NM_029733	RIKEN cDNA 2010005H15 gene	2010005 H15Rik	-	-	-	-	1.8	Down	-	-	-
NM_026333	RIKEN cDNA 2010106E10 gene	2010106 E10Rik	-	-	-	-	-	-	-	2.3	Up
XM_132136	RIKEN cDNA 2010109A12 gene	-	-	-	-	-	-	-	-	2.7	Up
NM_025591	RIKEN cDNA 2010309E21 gene	2010309 E21Rik	-	-	-	-	-	-	-	1.5	Down
NM_133839	RIKEN cDNA 2010311D03 gene	2010311 D03Rik	-	-	-	-	-	-	-	2.1	Down
NM_175153	RIKEN cDNA 2010321M09 gene	2010321 M09Rik	-	-	-	-	-	-	-	1.7	Down
NM_028211	RIKEN cDNA 2210016L21 gene	2210016 L21Rik	-	-	-	-	-	-	-	2.4	Up
NM_183259	RIKEN cDNA 2210020M01 gene	-	-	-	-	-	1.8	Up	-	2.3	Up
NM_172929	RIKEN cDNA 2210418O10 gene	-	-	-	-	-	-	-	-	3.2	Up
NM_027104	RIKEN cDNA 2310002L09 gene	2310002 L09Rik	-	-	-	-	-	-	-	3.7	Up
NM_025510	RIKEN cDNA 2310004I24 gene	2310004I 24Rik	-	-	-	-	-	-	-	3.9	Up
NM_027310	RIKEN cDNA 2310005N01 gene	2310005 N01Rik	-	-	-	-	1.7	Up	-	-	-
XM_129448	RIKEN cDNA 2310006M14 gene	-	-	-	-	-	-	-	-	3.7	Up
NM_172411	RIKEN cDNA 2310007B03 gene	2310007 B03Rik	-	-	-	-	-	-	-	1.5	Up
NM_146068	RIKEN cDNA 2310008H04 gene	2310008 H04Rik	-	-	-	-	-	-	-	1.7	Up
NM_025990	RIKEN cDNA 2310021H06 gene	2310021 H06Rik	-	-	-	-	-	-	-	3.4	Up
NM_054100	RIKEN cDNA 2310034C09 gene	2310034 C09Rik	-	-	1.9	Down	-	-	-	-	-
NM_133714	RIKEN cDNA 2310037I24 gene	2310037I 24Rik	-	-	1.6	Down	-	-	-	1.7	Up
XM_484355	RIKEN cDNA 2310047A01 gene	-	-	-	-	-	-	-	-	1.8	Down
NM_027344	RIKEN cDNA 2310051M13 gene	2310051 M13Rik	-	-	-	-	-	-	-	3.0	Down
XM_358687	RIKEN cDNA 2400009B08 gene	-	-	-	-	-	-	-	-	1.8	Up
NM_025555	RIKEN cDNA 2410004B18 gene	2410004 B18Rik	-	-	-	-	1.7	Up	-	-	-
XM_486251	RIKEN cDNA 2410012M07 gene	-	-	-	-	-	-	-	-	2.6	Up
NM_026423	RIKEN cDNA 2410018C20 gene	2410018 C20Rik	-	-	-	-	3.6	Up	3.4	Up	-

NM_028596	RIKEN cDNA 2410025L10 gene	2410025						2.3	Up	
XM_149067	RIKEN cDNA 2410088K16 gene	L10Rik	-	-	-	-	-	2.0	Up	
XM_127911	RIKEN cDNA 2410089E03 gene	-	-	-	-	-	-	1.8	Up	
		2410127								
NM_026120	RIKEN cDNA 2410127L17 gene	L17Rik	-	-	-	-	-	3.5	Down	
XM_485677	RIKEN cDNA 2410131K14 gene	-	-	-	-	-	-	1.6	Up	
XM_128102	RIKEN cDNA 2410187C16 gene	-	-	-	-	-	-	1.7	Down	
NM_0010018		2510009								
81	RIKEN cDNA 2510009E07 gene	E07Rik	-	-	-	-	-	3.9	Up	
XM_131827	RIKEN cDNA 2610002J02 gene	-	-	-	-	2.1	Up	-	-	
XM_488549	RIKEN cDNA 2610036L11 gene	-	-	-	-	1.7	Up	1.5	Up	
		2610204								
NM_025997	RIKEN cDNA 2610204K14 gene	K14Rik	-	-	-	-	-	3.0	Down	
XM_134183	RIKEN cDNA 2700029M09 gene	-	-	-	-	-	-	2.1	Down	
		2810002I								
NM_172414	RIKEN cDNA 2810002I04 gene	04Rik	-	-	-	-	-	3.0	Up	
		2810007								
NM_175250	RIKEN cDNA 2810007J24 gene	J24Rik	-	-	-	-	-	2.3	Up	
		2810021								
NM_025479	RIKEN cDNA 2810021B07 gene	B07Rik	-	-	-	-	3.0	Up	1.5	Up
		2810030								
NM_028317	RIKEN cDNA 2810030E01 gene	E01Rik	-	-	-	-	-	1.7	Up	
		2810405								
NM_025582	RIKEN cDNA 2810405K02 gene	K02Rik	-	-	1.9	Down	-	2.6	Down	
XM_133164	RIKEN cDNA 2810409K11 gene	-	-	-	-	-	-	2.9	Up	
NM_175239	RIKEN cDNA 2810410L24 gene	-	-	-	-	-	-	2.3	Up	
		2810422								
NM_027279	RIKEN cDNA 2810422O20 gene	O20Rik	-	-	-	-	-	1.6	Down	
		2810485I								
NM_176836	RIKEN cDNA 2810485I05 gene	05Rik	-	-	-	-	-	1.8	Up	
		2900064								
NM_133749	RIKEN cDNA 2900064A13 gene	A13Rik	-	-	-	-	-	2.9	Down	
		3000004								
NM_197959	RIKEN cDNA 3000004C01 gene	C01Rik	-	-	-	-	-	1.7	Up	
		3110002								
NM_029623	RIKEN cDNA 3110002H16 gene	H16Rik	-	-	-	-	-	1.5	Down	
		3110006								
XM_127466	RIKEN cDNA 3110006E14 gene	E14Rik	-	-	-	-	-	3.2	Up	
		3110040								
NM_026077	RIKEN cDNA 3110040N11 gene	N11Rik	-	-	-	-	-	3.0	Up	
XM_484601	RIKEN cDNA 3110052M02 gene	-	-	-	-	-	-	2.6	Up	
XM_129926	RIKEN cDNA 3110079O15 gene	-	-	-	1.6	Down	-	-	-	
XM_135153	RIKEN cDNA 3222402P14 gene	-	-	-	-	-	-	1.6	Up	

NM_025699	RIKEN cDNA 3230401D17 gene	3230401 D17Rik	-	-	-	-	-	-	1.6	Down
NM_030093	RIKEN cDNA 3300001G02 gene	3300001 G02Rik	-	-	-	-	2.2	Up	-	-
XM_484361	RIKEN cDNA 3425401B19 gene	3425401 B19Rik	-	-	-	-	-	-	3.6	Up
NM_0010027 94	RIKEN cDNA 4631405J19 gene	-	-	-	-	-	-	-	2.3	Up
XM_485962	RIKEN cDNA 4632434I11 gene	-	-	-	-	-	-	-	1.5	Up
NM_172698	RIKEN cDNA 4732418C07 gene	4732418 C07Rik	-	-	-	-	-	-	2.0	Down
NM_177717	RIKEN cDNA 4732456N10 gene	4732456 N10Rik	-	-	-	-	-	-	3.8	Up
NM_0010014 99	RIKEN cDNA 4732465J04 gene	-	-	-	-	-	-	-	1.8	Up
NM_176987	RIKEN cDNA 4732471D19 gene	4732471 D19Rik	-	-	-	-	-	-	3.3	Up
XM_138397	RIKEN cDNA 4732474O15 gene	4732474 O15Rik	-	-	-	-	-	-	2.7	Up
NM_198005	RIKEN cDNA 4833418A01 gene	4833418 A01Rik	-	-	-	-	-	-	1.7	Up
NM_029021	RIKEN cDNA 4833422F24 gene	4833422 F24Rik	-	-	-	-	-	-	3.0	Up
NM_025723	RIKEN cDNA 4921515J06 gene	4921515 J06Rik	-	-	-	-	-	-	2.3	Up
NM_026256	RIKEN cDNA 4921537P18 gene	4921537 P18Rik	-	-	2.2	Down	-	-	-	-
NM_175176	RIKEN cDNA 4922501L14 gene	-	-	-	-	-	-	-	2.0	Up
XM_127955	RIKEN cDNA 4930401A09 gene	-	-	-	-	-	-	-	2.3	Up
NM_172895	RIKEN cDNA 4930401F20 gene	-	-	-	-	-	-	-	1.5	Up
XM_133905	RIKEN cDNA 4930404H21 gene	-	-	-	-	-	1.9	Up	3.3	Up
NM_175517	RIKEN cDNA 4930412F15 gene	4930412 F15Rik	-	-	-	-	-	-	1.8	Up
XM_128114	RIKEN cDNA 4930415O20 gene	4930415 O20Rik	-	-	-	-	-	-	2.7	Up
XM_485602	RIKEN cDNA 4930431F12 gene	-	-	-	-	-	-	-	1.8	Up
NM_207248	RIKEN cDNA 4930433I11 gene	4930433I 11Rik	-	-	-	-	-	-	3.9	Up
XM_127223	RIKEN cDNA 4930448F12 gene	4930448 F12Rik	-	-	-	-	-	-	2.3	Up
XM_127874	RIKEN cDNA 4930449E01 gene	-	-	-	-	-	-	-	2.5	Up
NM_183130	RIKEN cDNA 4930451E10 gene	-	-	-	1.9	Down	-	-	-	-
XM_148381	RIKEN cDNA 4930455F16 gene	-	-	-	-	-	-	-	2.0	Up
NM_175675	RIKEN cDNA 4930471M23 gene	4930471	-	-	-	-	-	-	1.6	Up

		M23Rik									
		4930474									
NM_175008	RIKEN cDNA 4930474N05 gene	N05Rik	-	-	-	-	-	-	-	3.3	Up
NM_026288	RIKEN cDNA 4930483J18 gene	-	-	-	-	-	-	-	-	2.0	Up
XM_131470	RIKEN cDNA 4930500O09 gene	-	-	-	-	-	-	-	-	3.0	Up
		4930503									
NM_172967	RIKEN cDNA 4930503L19 gene	L19Rik	-	-	-	-	-	-	-	2.6	Up
		4930513									
XM_136059	RIKEN cDNA 4930513O06 gene	O06Rik	-	-	-	-	-	-	-	1.6	Up
		4930522									
NM_026291	RIKEN cDNA 4930522H14 gene	H14Rik	-	-	-	-	-	-	-	3.5	Up
		4930529									
NM_175280	RIKEN cDNA 4930529M08 gene	M08Rik	-	-	-	-	-	-	-	2.7	Up
		4930539									
NM_172450	RIKEN cDNA 4930539E08 gene	E08Rik	-	-	-	-	-	-	-	3.4	Up
NM_183110	RIKEN cDNA 4930543L23 gene	-	-	-	-	-	-	-	-	1.6	Up
XM_283398	RIKEN cDNA 4930546H06 gene	-	-	-	-	-	-	-	-	1.6	Up
		4930548									
NM_026296	RIKEN cDNA 4930548H24 gene	H24Rik	-	-	-	-	-	-	-	2.0	Up
XM_283466	RIKEN cDNA 4930560E09 gene	-	-	-	-	-	-	-	-	2.3	Up
		4930562									
NM_177616	RIKEN cDNA 4930562D19 gene	D19Rik	-	-	-	-	-	-	-	1.9	Up
XM_484637	RIKEN cDNA 4930564C03 gene	-	-	-	-	-	-	-	-	2.5	Up
XM_130326	RIKEN cDNA 4930578N16 gene	-	-	-	1.5	Down	-	-	-	-	-
		4930579									
XM_131242	RIKEN cDNA 4930579F01 gene	F01Rik	-	-	-	-	-	-	-	1.7	Up
		4930583I									
XM_128729	RIKEN cDNA 4930583I09 gene	09Rik	-	-	-	-	-	-	-	4.1	Up
NM_183267	RIKEN cDNA 4930583K01 gene	-	-	-	1.9	Down	-	-	-	-	-
		4930595									
NM_173435	RIKEN cDNA 4930595M18 gene	M18Rik	-	-	-	-	-	-	-	2.0	Up
		4931406I									
NM_025739	RIKEN cDNA 4931406I20 gene	20Rik	-	-	-	-	2.5	Up	-	-	-
XM_132142	RIKEN cDNA 4931407G18 gene	-	-	-	-	-	-	-	-	4.0	Up
		4931409									
NM_177676	RIKEN cDNA 4931409K22 gene	K22Rik	-	-	-	-	-	-	-	2.4	Up
		4931414									
NM_028890	RIKEN cDNA 4931414P19 gene	P19Rik	-	-	-	-	2.0	Up	-	3.1	Up
NM_175161	RIKEN cDNA 4931422A03 gene	-	-	-	-	-	-	-	-	3.2	Up
XM_134806	RIKEN cDNA 4931429I11 gene	-	-	-	-	-	-	-	-	1.7	Up
		4932409I									
NM_198614	RIKEN cDNA 4932409I22 gene	22Rik	-	-	-	-	-	-	-	2.7	Up
		4932411									
NM_177705	RIKEN cDNA 4932411N23 gene	N23Rik	-	-	-	-	-	-	-	2.8	Up

XM_141917	RIKEN cDNA 4932429P05 gene	-	-	-	-	-	-	3.5	Up
NM_177801	RIKEN cDNA 4933400C05 gene	4933400	-	-	-	-	-	2.0	Up
NM_177901	RIKEN cDNA 4933402J07 gene	C05Rik	-	-	-	-	-	2.7	Up
XM_149613	RIKEN cDNA 4933402J10 gene	4933402	-	-	2.4	Down	-	-	-
NM_175368	RIKEN cDNA 4933402P03 gene	P03Rik	-	-	-	-	-	1.8	Up
NM_025744	RIKEN cDNA 4933404M02 gene	4933404	-	-	-	-	-	2.2	Up
NM_172901	RIKEN cDNA 4933405O20 gene	M02Rik	-	-	-	-	-	2.3	Up
NM_173771	RIKEN cDNA 4933406M09 gene	4933405	-	-	-	-	-	2.1	Up
XM_129929	RIKEN cDNA 4933407L21 gene	O20Rik	-	-	-	-	-	2.1	Up
NM_025750	RIKEN cDNA 4933417A18 gene	4933406	-	-	1.6	Down	-	-	-
XM_129743	RIKEN cDNA 4933424G06 gene	M09Rik	-	-	-	-	-	2.1	Up
XM_135711	RIKEN cDNA 4933430H15 gene	4933417	-	-	1.5	Down	-	-	-
XM_110919	RIKEN cDNA 4933433K01 gene	A18Rik	-	-	-	-	-	1.9	Up
NM_207657	RIKEN cDNA 5031410I06 gene	4933424	-	-	-	-	-	2.8	Up
NM_026362	RIKEN cDNA 5033414D02 gene	G06Rik	-	-	-	-	-	2.3	Up
XM_129208	RIKEN cDNA 5033428B15 gene	5031410I	-	-	-	-	-	2.8	Down
NM_172654	RIKEN cDNA 5330401P04 gene	06Rik	-	-	-	-	-	2.5	Up
XM_203978	RIKEN cDNA 5330417C22 gene	5033414	-	-	-	-	1.6	Down	2.1
NM_199365	RIKEN cDNA 5330438I03 gene	D02Rik	-	-	-	-	-	2.7	Up
NM_177314	RIKEN cDNA 5330439B14 gene	5033428	-	-	-	-	-	3.0	Up
NM_172418	RIKEN cDNA 5430432N15 gene	B15Rik	-	-	-	-	-	2.2	Up
XM_134954	RIKEN cDNA 5430433E21 gene	5330439	-	-	-	-	-	3.7	Up
NM_021552	RIKEN cDNA 5730427N09 gene	B14Rik	-	-	-	-	-	3.5	Up
XM_129261	RIKEN cDNA 5730455O13 gene	5730427	-	-	-	-	-	3.1	Down
NM_027478	RIKEN cDNA 5730494N06 gene	N09Rik	-	-	-	-	1.5	Up	-
NM_178243	RIKEN cDNA 5830403L16 gene	5730494	-	-	-	-	2.5	Up	-
NM_183264	RIKEN cDNA 5830405N20 gene	N06Rik	-	-	-	-	-	2.3	Down
NM_026583	RIKEN cDNA 5830415L20 gene	5830403	-	-	-	-	2.6	Up	-
		L16Rik	-	-	2.3	Down	-	-	-
		5830405	-	-	-	-	2.0	Up	-
		N20Rik	-	-	-	-	-	-	-
		-	-	-	-	-	-	-	-

XM_355322	RIKEN cDNA 5930434B04 gene	-	-	-	-	-	-	-	-	1.9	Down
XM_285987	RIKEN cDNA 6430526N21 gene	-	-	-	-	-	-	-	-	2.3	Up
		6430628									
XM_149458	RIKEN cDNA 6430628N08 gene	N08Rik	-	-	-	-	-	-	-	2.1	Up
NM_029541	RIKEN cDNA 6530401D17 gene	-	-	-	-	-	-	-	-	2.0	Up
		6530401									
NM_029545	RIKEN cDNA 6530401N04 gene	N04Rik	-	-	-	-	-	-	-	2.1	Down
		6530403									
NM_026382	RIKEN cDNA 6530403A03 gene	A03Rik	-	-	-	-	-	-	-	1.8	Down
NM_181587	RIKEN cDNA 6530404N21 gene	-	-	-	-	-	-	-	-	1.6	Up
		6720456									
NM_172600	RIKEN cDNA 6720456H20 gene	H20Rik	-	-	-	-	-	-	-	2.8	Up
XM_149265	RIKEN cDNA 7530422B04 gene	-	-	-	-	-	-	-	-	1.8	Up
XM_356343	RIKEN cDNA 8030474K03 gene	-	-	-	-	-	-	-	-	2.6	Up
		9030617									
NM_145448	RIKEN cDNA 9030617O03 gene	O03Rik	-	-	-	-	2.5	Up	-	-	-
		9030624									
NM_027815	RIKEN cDNA 9030624J02 gene	J02Rik	-	-	-	-	-	-	-	1.6	Down
		9130401									
NM_029418	RIKEN cDNA 9130401M01 gene	M01Rik	-	-	-	-	-	-	-	1.6	Down
		9230110									
NM_199017	RIKEN cDNA 9230110C19 gene	C19Rik	-	-	-	-	-	-	-	2.3	Up
		9230112									
XM_127665	RIKEN cDNA 9230112D13 gene	D13Rik	-	-	2.0	Down	-	-	-	-	-
NM_177044	RIKEN cDNA 9330119M13 gene	-	-	-	-	-	-	-	-	1.6	Up
NM_176961	RIKEN cDNA 9330132A10 gene	-	-	-	-	-	-	-	-	1.5	Up
NM_177011	RIKEN cDNA 9330154K18 gene	-	-	-	-	-	1.5	Down	-	-	-
XM_283579	RIKEN cDNA 9430016H08 gene	-	-	-	-	-	-	-	-	2.4	Down
XM_133396	RIKEN cDNA 9430025M13 gene	-	-	-	-	-	-	-	-	1.5	Up
		9430031									
NM_172849	RIKEN cDNA 9430031J16 gene	J16Rik	-	-	-	-	-	-	-	2.1	Up
		9430069									
NM_213727	RIKEN cDNA 9430069J07 gene	J07Rik	-	-	-	-	-	-	-	1.6	Up
NM_177095	RIKEN cDNA 9430076C15 gene	-	-	-	-	-	-	-	-	2.1	Up
		9530098									
NM_178786	RIKEN cDNA 9530098N22 gene	N22Rik	-	-	-	-	-	-	-	2.1	Up
NM_176943	RIKEN cDNA 9630028B13 gene	-	-	-	2.5	Down	-	-	-	-	-
		9930022									
NM_177363	RIKEN cDNA 9930022N03 gene	N03Rik	-	-	1.7	Down	1.5	Down	-	-	-
		9930032									
NM_177162	RIKEN cDNA 9930032O22 gene	O22Rik	-	-	-	-	-	-	-	2.7	Up
		9930039									
NM_177060	RIKEN cDNA 9930039A11 gene	A11Rik	-	-	-	-	1.8	Down	-	-	-
NM_177668	RIKEN cDNA A030001H23 gene	A030001	-	-	-	-	-	-	-	2.2	Up

		H23Rik									
NM_177864	RIKEN cDNA A030013N09 gene	A030013								1.8	Up
NM_0010027		N09Rik	-	-	-	-	-	-	-		
66	RIKEN cDNA A230052G05 gene		-	-	-	-	-	-	-	2.3	Up
NM_177037	RIKEN cDNA A230059G12 gene		-	-	-	2.0	Down	-	-	-	-
NM_177334	RIKEN cDNA A230074B11 gene		-	-	-	-	-	-	-	2.3	Up
NM_0010027											
85	RIKEN cDNA A230083G16 gene		-	-	-	-	-	-	-	1.7	Up
NM_175479	RIKEN cDNA A330008L17 gene		-	-	-	-	-	-	-	2.8	Up
NM_176967	RIKEN cDNA A430072C10 gene		-	-	-	-	-	-	-	3.1	Up
		A430090									
NM_177578	RIKEN cDNA A430090E18 gene	E18Rik	-	-	-	-	-	-	-	2.7	Up
XM_484623	RIKEN cDNA A430107D22 gene		-	-	-	-	-	-	-	1.7	Up
XM_145117	RIKEN cDNA A430107O13 gene		-	-	-	-	-	-	-	3.2	Up
NM_177048	RIKEN cDNA A530079E22 gene		-	-	-	-	-	1.5	Up	3.4	Up
		A630098									
NM_177669	RIKEN cDNA A630098G03 gene	G03Rik	-	-	-	-	-	2.0	Down	-	-
XM_485664	RIKEN cDNA A830023I12 gene		-	-	-	-	-	-	-	2.8	Up
		A830043									
NM_173425	RIKEN cDNA A830043J08 gene	J08Rik	-	-	-	-	-	-	-	2.0	Up
NM_177172	RIKEN cDNA A830054O04 gene		-	-	-	-	-	3.6	Up	-	-
NM_177118	RIKEN cDNA A830073O21 gene		-	-	-	-	-	-	-	2.4	Up
NM_175410	RIKEN cDNA A930002I21 gene		-	-	-	-	-	-	-	2.0	Up
NM_177202	RIKEN cDNA A930104D05 gene		-	-	-	-	-	-	-	3.5	Up
NM_177246	RIKEN cDNA B230220B15 gene		-	-	-	-	-	-	-	3.4	Up
NM_175693	RIKEN cDNA B230220N19 gene		-	-	-	-	-	-	-	1.8	Up
NM_177148	RIKEN cDNA B230317F23 gene		-	-	-	-	-	-	-	2.3	Up
NM_177234	RIKEN cDNA B230340J04 gene		-	-	-	-	-	-	-	4.0	Up
		B230358									
NM_172931	RIKEN cDNA B230358A15 gene	A15Rik	-	-	-	-	-	-	-	2.1	Up
		B430203									
NM_177096	RIKEN cDNA B430203M17 gene	M17Rik	-	-	-	-	-	-	-	1.6	Up
NM_177302	RIKEN cDNA B530045E10 gene		-	-	-	-	-	-	-	2.6	Up
		B830045									
NM_153539	RIKEN cDNA B830045N13 gene	N13Rik	-	-	-	-	-	-	-	2.1	Up
NM_177121	RIKEN cDNA B930095G15 gene		-	-	-	-	-	-	-	2.3	Up
XM_127766	RIKEN cDNA C030027K23 gene		-	-	-	-	-	-	-	1.5	Down
		C130050									
NM_177000	RIKEN cDNA C130050O18 gene	O18Rik	-	-	-	-	-	-	-	1.5	Up
NM_177100	RIKEN cDNA C130071C03 gene		-	-	-	-	-	-	-	1.9	Up
		C130074									
NM_178692	RIKEN cDNA C130074G19 gene	G19Rik	-	-	-	-	-	-	-	2.2	Up



NM_177916	RIKEN cDNA C230004F18 gene	-	-	-	-	-	-	-	-	2.5	Up
NM_172847	RIKEN cDNA C230030N03 gene	-	-	-	-	-	-	-	-	2.3	Up
XM_126866	RIKEN cDNA C330002I19 gene	-	-	-	-	-	-	-	-	2.5	Up
XM_135837	RIKEN cDNA C330007P06 gene	-	-	-	-	-	-	-	-	3.6	Up
NM_172616	RIKEN cDNA C330027C09 gene	C330027 C09Rik	-	-	-	-	-	-	-	1.7	Up
NM_177883	RIKEN cDNA C330043M08 gene	C330043 M08Rik	-	-	1.8	Up	-	-	-	-	-
NM_0010027 73	RIKEN cDNA D130007C19 gene	-	-	-	-	-	-	-	-	2.9	Up
NM_177185	RIKEN cDNA D130059P03 gene	D130059 P03Rik	-	-	-	-	-	-	-	2.8	Up
NM_177204	RIKEN cDNA D330017J20 gene	D330017 J20Rik	-	-	-	-	-	-	-	3.4	Up
NM_172737	RIKEN cDNA D430041B17 gene	D430041 B17Rik	-	-	-	-	-	-	-	2.5	Up
XM_485042	RIKEN cDNA D430041D05 gene	-	-	-	-	-	-	-	-	2.1	Up
NM_175293	RIKEN cDNA D630023F18 gene	D630023 F18Rik	-	-	-	-	-	-	-	3.1	Up
NM_172433	RIKEN cDNA D730001G18 gene	-	-	-	-	-	2.1	Down	-	-	-
NM_175518	RIKEN cDNA D730040F13 gene	D730040 F13Rik	-	-	-	-	-	-	-	2.1	Up
XM_354677	RIKEN cDNA D830013O20 gene	-	-	-	-	-	-	-	-	1.8	Up
NM_177135	RIKEN cDNA D830030K20 gene	D830030 K20Rik	-	-	-	-	-	-	-	3.6	Up
NM_177297	RIKEN cDNA D830039M14 gene	-	-	-	-	-	-	-	-	1.5	Up
NM_178702	RIKEN cDNA D930005D10 gene	D930005 D10Rik	-	-	-	-	-	-	-	1.9	Up
NM_020616	RIKEN cDNA D930014E17 gene	D930014 E17Rik	-	-	-	-	1.7	Up	-	-	-
NM_172921	RIKEN cDNA D930028F11 gene	D930028 F11Rik	-	-	-	-	-	-	-	2.2	Up
NM_172905	RIKEN cDNA E030002O03 gene	E030002 O03Rik	-	-	-	-	-	-	-	1.9	Up
XM_196056	RIKEN cDNA E030025P04 gene	-	-	-	2.3	Down	-	-	-	-	-
XM_355025	RIKEN cDNA E130009J12 gene	-	-	-	-	-	-	-	-	3.1	Up
XM_485355	RIKEN cDNA E130016E03 gene	-	-	-	1.5	Down	-	-	-	-	-
XM_149469	RIKEN cDNA E130102H24 gene	-	-	-	-	-	-	-	-	1.7	Up
XM_131404	RIKEN cDNA E130306D19 gene	-	-	-	-	-	-	-	-	2.0	Up
NM_153158	RIKEN cDNA E130308A19 gene	E130308 A19Rik	-	-	-	-	-	-	-	1.6	Up
NM_177069	RIKEN cDNA E330009P21 gene	E330009 P21Rik	-	-	1.6	Down	-	-	-	-	-
NM_175355	RIKEN cDNA E330013P04 gene	-	-	-	-	-	-	-	-	3.6	Up

NM_175527	RIKEN cDNA E330021D16 gene	-	-	-	-	-	-	2.4	Up
NM_001002780	RIKEN cDNA F830005K03 gene	-	-	-	-	-	-	2.4	Up
NM_026557	Ring finger and CHY zinc finger domain containing 1	Rchy1	-	-	-	-	-	2.0	Down
NM_028774	Ring finger protein (C3H2C3 type) 6	Rnf6	-	-	-	-	1.6	Up	-
NM_009548	Ring finger protein 112	Rnf112	-	-	-	-	-	3.0	Up
NM_144528	Ring finger protein 126	Rnf126	-	-	-	-	1.8	Up	-
XM_203376	ring finger protein 145	-	-	-	-	-	1.7	Up	-
NM_177378	Ring finger protein 150	Rnf150	-	-	-	-	-	2.7	Up
NM_025786	Ring finger protein 186	Rnf186	-	-	-	-	-	1.7	Up
NM_027859	Ring finger protein 215	Rnf215	-	-	-	-	1.8	Up	-
XM_193558	Ring finger protein 217	Rnf217	-	-	-	-	-	1.9	Up
NM_172448	Ring finger protein 43	Rnf43	-	-	-	-	-	1.8	Up
NM_019712	Ring-box 1	Rbx1	-	-	-	-	-	2.0	Down
NM_026440	RNA (guanine-7-) methyltransferase	Rnmt	-	-	-	-	2.0	Up	-
NM_029092	RNA (guanine-9-) methyltransferase domain containing 1	Rg9mtd1	-	-	-	-	-	3.8	Down
XM_486938	RNA binding motif 31, Y-linked	-	-	-	-	-	-	3.3	Up
NM_026434	RNA binding motif protein 18	Rbm18	-	-	-	-	-	2.3	Up
NM_028762	RNA binding motif protein 19	Rbm19	-	-	-	-	-	1.6	Down
XM_140742	RNA binding motif protein 20	-	-	-	-	-	-	3.3	Up
NM_194055	RNA binding motif protein 35A	Rbm35a	-	-	1.6	Down	-	-	-
NM_133242	RNA binding motif protein 39	Rbm39	-	-	-	-	-	1.8	Down
NM_019711	RNA binding motif, single stranded interacting protein 2	Rbms2	-	-	-	-	-	2.0	Up
NM_009087	RNA polymerase 1-3	Rpo1-3	-	-	-	-	1.8	Up	-
NM_009088	RNA polymerase 1-4	Rpo1-4	-	-	-	-	-	2.2	Up
NM_175542	Rotatin	Rttn	-	-	-	-	-	3.6	Up
XM_126152	RPA interacting protein	-	-	-	-	-	-	1.9	Down
NM_173431	Rpgrip1-like	Rpgrip1l	-	-	1.7	Down	-	-	-
XM_283757	Rtf1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	Rtf1	-	-	-	-	2.0	Up	-
NM_177652	Ryanodine receptor 3	Ryr3	-	-	-	-	2.0	Up	4.0
NM_009665	S-adenosylmethionine decarboxylase 1	Amd1	-	-	1.8	Up	1.6	Up	-
NM_011310	S100 calcium binding protein A3	S100a3	-	-	-	-	1.8	Up	2.3
NM_009114	S100 calcium binding protein A9 (calgranulin B)	S100a9	-	-	-	-	-	1.7	Up
NM_009789	S100 calcium binding protein G	S100g	-	-	-	-	-	1.9	Up
NM_009267	Salivary protein 1	Spt1	-	-	-	-	-	2.2	Up
NM_028773	SAM and SH3 domain containing 3	Sash3	-	-	-	-	2.4	Up	-
NM_032008	Sarcolemma associated protein	Simap	-	-	-	-	-	2.8	Down
NM_178677	SEC22 vesicle trafficking protein-like C (S. cerevisiae)	Sec22c	-	-	-	-	-	2.0	Up
NM_027135	SEC24 related gene family, member D (S. cerevisiae)	Sec24d	-	-	-	-	1.8	Up	-
NM_016906	Sec61 alpha 1 subunit (S. cerevisiae)	Sec61a1	-	-	-	-	2.1	Up	-
NM_024171	Sec61 beta subunit	Sec61b	-	-	-	-	-	2.1	Down

NM_146027	Secernin 2	Scrn2	-	-	-	-	-	-	2.0	Up
NM_018780	Secreted frizzled-related sequence protein 5	Sfrp5	-	-	-	-	-	-	3.8	Up
NM_013789	Secretion regulating guanine nucleotide exchange factor	Sergef	-	-	-	-	2.0	Up	-	-
NM_009129	Secretogranin II	Scg2	-	-	-	-	-	-	3.1	Up
NM_011352	Sema domain, immunoglobulin domain (Ig), and GPI membrane anchor, (semaphorin) 7A	Sema7a	-	-	-	-	-	-	2.2	Up
NM_009153	Sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3B	Sema3b	-	-	-	-	-	-	2.5	Up
NM_011349	Sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F	Sema3f	-	-	-	-	-	-	1.6	Up
NM_013659	Sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B	Sema4b	-	-	-	-	-	-	1.9	Up
NM_013662	Sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B	Sema6b	-	-	-	-	-	-	2.0	Up
NM_009299	Seminal vesicle antigen	Sva	-	-	-	-	-	-	2.2	Up
NM_027832	Seminal vesicle antigen-like 1	Sval1	-	-	-	-	-	-	2.0	Up
NM_173377	Seminal vesicle secretory protein 3B	Svs3b	-	-	-	-	-	-	3.0	Up
NM_009300	Seminal vesicle secretory protein 4	Svs4	-	-	2.7	Down	-	-	-	-
NM_013679	Seminal vesicle secretory protein 6	Svs6	-	-	-	-	-	-	2.0	Up
NM_213614	Septin 5	6-Sep	-	-	-	-	-	-	3.2	Up
NM_019942	Septin 6	7-Sep	-	-	-	-	-	-	1.9	Up
NM_009246	Serine (or cysteine) peptidase inhibitor, clade A, member 1d	Serpina1	-	-	-	-	-	-	2.3	Up
NM_009253	Serine (or cysteine) peptidase inhibitor, clade A, member 3K	Serpina3	-	-	-	-	-	-	2.3	Up
NM_009252	Serine (or cysteine) peptidase inhibitor, clade A, member 3K	Serpina3	-	-	-	-	-	-	2.6	Up
NM_007618	Serine (or cysteine) peptidase inhibitor, clade A, member 6	Serpina6	-	-	-	-	-	-	2.2	Up
NM_198680	Serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 3B	Serpinb3	-	-	1.6	Down	-	-	-	-
NM_012032	Serine incorporator 3	Serinc3	-	-	-	-	-	-	2.5	Down
NM_177829	Serine peptidase inhibitor, Kazal type 10	Spink10	-	-	-	-	-	-	1.7	Up
NM_183136	Serine peptidase inhibitor, Kazal type 8	Spink8	-	-	-	-	-	-	2.3	Up
NM_011464	Serine protease inhibitor, Kunitz type 2	Spint2	-	-	-	-	-	-	2.4	Down
NM_029916	Serine threonine kinase 31	Stk31	-	-	-	-	-	-	2.6	Down
NM_011492	Serine/threonine kinase 11	Stk11	-	-	-	-	-	-	1.9	Down
NM_026563	Serologically defined colon cancer antigen 3	Sdccag3	-	-	-	-	-	-	1.5	Down
NM_018820	SERTA domain containing 1	Sertad1	-	-	-	-	2.0	Up	-	-
NM_011315	Serum amyloid A 3	Saa3	-	-	-	-	-	-	1.9	Up
NM_023637	Seryl-aminoacyl-tRNA synthetase 2	Sars2	-	-	-	-	-	-	2.0	Up
NM_144907	Sestrin 2	Sesn2	-	-	-	-	-	-	2.8	Up
NM_009762	SET and MYND domain containing 1	Smyd1	-	-	-	-	-	-	2.9	Up
XM_358316	SET binding factor 1	-	-	-	-	-	-	-	3.0	Up

NM_177581	SET domain containing 1B	-	-	-	-	-	-	2.8	Up
XM_139089	SET domain, bifurcated 2	-	-	-	-	-	-	2.0	Down
NM_010623	SH2 domain containing 5	Kif17	-	-	-	-	-	2.1	Up
NM_011363	SH2B adaptor protein 1	Sh2b1	-	-	-	-	1.8	Up	-
NM_177707	SH3 and cysteine rich domain 3	Stac3	-	-	-	-	-	1.7	Up
NM_172507	SH3 domain binding glutamic acid-rich protein like 2	Sh3bgrl2	-	-	-	-	-	1.6	Up
NM_012059	SH3 domain protein D19	-	-	-	-	-	-	1.6	Up
NM_019989	SH3-binding domain glutamic acid-rich protein like	Sh3bgrl	-	-	-	-	-	2.9	Down
NM_011893	SH3-domain binding protein 2	Sh3bp2	-	-	-	-	1.8	Up	-
NM_019535	SH3-domain GRB2-like 2	Sh3gl2	-	-	3.0	Down	-	3.8	Down
NM_145581	Sialic acid binding Ig-like lectin 5	Siglec5	-	-	-	-	-	2.0	Up
NM_172800	Sidekick homolog 2 (chicken)	Sdk2	-	-	-	-	-	2.8	Up
NM_053198	Sideroflexin 4	Sfxn4	-	-	-	-	-	2.8	Up
NM_146032	Signal recognition particle 68	Srp68	-	-	-	-	1.7	Up	-
NM_025965	Signal sequence receptor, alpha	Ssr1	-	-	-	-	-	2.8	Down
NM_009279	Signal sequence receptor, delta	Ssr4	-	-	-	-	-	2.0	Down
NM_009284	Signal transducer and activator of transcription 6	Stat6	-	-	-	-	1.8	Up	-
NM_007547	Signal-regulatory protein alpha	Sirpa	-	-	-	-	-	1.5	Up
NM_178792	signal-regulatory protein beta 1	-	-	-	-	-	-	1.8	Up
XM_143763	similar to Chaperonin subunit 3 (gamma)	-	-	-	-	-	-	2.4	Up
		LOC2320							
XM_144880	Similar to hCG33270	77	-	-	-	-	-	1.9	Up
		LOC3821							
NM_207162	Similar to RIKEN cDNA 1700029H17	33	-	-	1.7	Down	-	2.2	Up
XM_354752	similar to RNA binding motif protein 24	-	-	-	-	-	-	1.5	Up
NM_011382	Sine oculis-related homeobox 4 homolog (Drosophila)	Six4	-	-	-	-	-	1.5	Up
NM_011384	Sine oculis-related homeobox 6 homolog (Drosophila)	Six6	-	-	-	-	-	1.7	Up
NM_011376	Single-minded homolog 1 (Drosophila)	Sim1	-	-	-	-	-	2.6	Up
NM_011377	Single-minded homolog 2 (Drosophila)	Sim2	-	-	-	-	-	2.1	Up
NM_024272	Single-stranded DNA binding protein 2	Ssbp2	-	-	-	-	-	2.4	Down
NM_022433	Sirtuin 3 (silent mating type information regulation 2, homolog) 3 (S. cerevisiae)	Sirt3	-	-	-	-	-	4.3	Down
	Sirtuin 6 (silent mating type information regulation 2, homolog) 6 (S. cerevisiae)	Sirt6	-	-	-	-	-	1.6	Up
NM_181586	Ski sarcoma viral oncogene homolog (avian)	Ski	-	-	-	-	-	1.9	Up
NM_029612	SLAM family member 9	Slamf9	-	-	2.1	Up	3.1	Up	-
NM_199065	SLIT and NTRK-like family, member 1	Sliitrk1	-	-	-	-	-	1.6	Up
NM_198864	SLIT and NTRK-like family, member 3	Sliitrk3	-	-	-	-	-	1.9	Up
NM_172718	Small G protein signaling modulator 1	Sgsm1	-	-	-	-	-	2.6	Up
NM_007926	Small inducible cytokine subfamily E, member 1	Scye1	-	-	-	-	-	2.5	Down
XM_133225	small nuclear ribonucleoprotein D2	-	-	-	-	-	-	2.4	Up
NM_172339	Small nuclear RNA activating complex, polypeptide 4	Snapc4	-	-	-	-	-	1.7	Down

NM_015830	Small optic lobes homolog (Drosophila)	Solh	-	-	-	-	-	-	2.7	Up
NM_009265	Small proline-rich protein 1B	Sprr1b	-	-	-	-	-	-	3.0	Up
NM_173070	Small proline-rich protein 4	Sprr4	-	-	-	-	-	-	4.2	Up
NM_175491	Smith-Magenis syndrome chromosome region, candidate 8 homolog (human)	Smcr8	-	-	-	-	-	-	3.0	Up
NM_024230	Smoothelin-like 1	Smtnl1	-	-	-	-	-	-	1.7	Up
NM_011427	Snail homolog 1 (Drosophila)	Snai1	-	-	-	-	-	-	1.8	Up
NM_133854	SNAP-associated protein	Snapi	-	-	-	-	2.0	Up	-	-
NM_172937	SNF2 histone linker PHD RING helicase	Shprh	-	-	-	-	-	-	4.2	Up
XM_355637	sno, strawberry notch homolog 1 (Drosophila)	-	-	-	-	-	-	-	3.3	Down
NM_011325	Sodium channel, nonvoltage-gated 1 beta	Scnn1b	-	-	-	-	-	-	2.6	Up
NM_011323	Sodium channel, voltage-gated, type VIII, alpha	Scn8a	-	-	-	-	-	-	1.7	Up
NM_011387	Solute carrier family 10 (sodium/bile acid cotransporter family), member 1	Slc10a1	-	-	-	-	-	-	1.9	Up
NM_013612	Solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	Slc11a1	-	-	-	-	2.2	Up	-	-
NM_053079	Solute carrier family 15 (oligopeptide transporter), member 1	Slc15a1	-	-	2.3	Down	-	-	-	-
NM_133895	Solute carrier family 15, member 4	Slc15a4	-	-	-	-	-	-	1.7	Down
NM_153081	Solute carrier family 16 (monocarboxylic acid transporters), member 11	Slc16a11	-	-	2.0	Down	-	-	-	-
NM_172838	Solute carrier family 16 (monocarboxylic acid transporters), member 12	Slc16a12	-	-	-	-	-	-	1.7	Up
NM_134038	Solute carrier family 16 (monocarboxylic acid transporters), member 6	Slc16a6	-	-	-	-	2.4	Up	1.8	Up
NM_144836	Solute carrier family 17 (sodium phosphate), member 2	Slc17a2	-	-	-	-	-	-	2.3	Up
NM_177016	Solute carrier family 17 (sodium phosphate), member 4	Slc17a4	-	-	-	-	-	-	1.7	Up
NM_031196	Solute carrier family 19 (sodium/hydrogen exchanger), member 1	Slc19a1	-	-	-	-	-	-	3.6	Up
NM_031194	Solute carrier family 22 (organic anion transporter), member 8	Slc22a8	-	-	-	-	-	-	1.9	Up
NM_144785	Solute carrier family 22 (organic anion transporter), member 9	Slc22a9	-	-	-	-	-	-	1.9	Up
XM_356200	solute carrier family 22 (organic cation transporter), member 14	-	-	-	1.6	Down	-	-	-	-
NM_008767	Solute carrier family 22 (organic cation transporter), member 18	Slc22a18	-	-	-	-	1.6	Up	-	-
NM_011396	Solute carrier family 22 (organic cation transporter), member 5	Slc22a5	-	-	-	-	1.7	Up	-	-
NM_144813	Solute carrier family 24 (sodium/potassium/calcium exchanger), member 1	Slc24a1	-	-	-	-	-	-	2.0	Up
NM_024211	Solute carrier family 25 (mitochondrial carrier oxoglutarate carrier), member 11	Slc25a11	-	-	-	-	2.2	Up	-	-
XM_134169	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 4	-	-	-	-	-	1.6	Up	-	-
NM_181328	Solute carrier family 25 (mitochondrial carrier, palmitoylcarnitine transporter), member 29	Slc25a29	-	-	-	-	1.8	Up	-	-
NM_011399	Solute carrier family 25 (mitochondrial carrier, peroxisomal membrane protein), member 17	Slc25a17	-	-	-	-	2.6	Up	-	-
NM_172685	Solute carrier family 25 (mitochondrial carrier, phosphate carrier),	Slc25a24	-	-	-	-	-	-	2.3	Down

	member 24										
NM_028711	Solute carrier family 25, member 27	Slc25a27	-	-	-	-	-	-	-	2.0	Up
XM_110743	solute carrier family 25, member 43	-	-	-	-	-	-	-	-	1.5	Up
NM_178696	Solute carrier family 25, member 44	Slc25a44	-	-	-	-	-	-	-	1.7	Up
NM_009512	Solute carrier family 27 (fatty acid transporter), member 5	Slc27a5	-	-	-	-	-	-	-	2.4	Up
NM_007854	Solute carrier family 29 (nucleoside transporters), member 2	Slc29a2	-	-	-	-	-	-	-	2.9	Up
XM_136506	solute carrier family 30, member 10	-	-	-	-	-	-	1.6	Up	2.8	Up
NM_015728	Solute carrier family 33 (acetyl-CoA transporter), member 1	Slc33a1	-	-	-	-	-	-	-	2.8	Down
NM_011402	Solute carrier family 34 (sodium phosphate), member 2	Slc34a2	-	-	-	-	-	-	-	1.9	Up
NM_026404	Solute carrier family 35, member A4	Slc35a4	-	-	-	-	-	-	-	1.5	Up
NM_177766	Solute carrier family 35, member E1	Slc35e1	-	-	-	-	-	-	-	1.6	Up
NM_178675	Solute carrier family 35, member F1	Slc35f1	-	-	-	-	-	-	-	2.0	Up
XM_127701	solute carrier family 35, member F4	-	-	-	-	-	-	-	-	2.4	Up
NM_153139	Solute carrier family 36 (proton/amino acid symporter), member 1	Slc36a1	-	-	-	-	-	-	-	2.1	Up
NM_134086	Solute carrier family 38, member 1	Slc38a1	-	-	-	-	-	2.4	Up	-	-
NM_024249	Solute carrier family 38, member 10	Slc38a10	-	-	-	-	-	2.3	Up	-	-
NM_027052	Solute carrier family 38, member 4	Slc38a4	-	-	-	-	-	-	-	1.5	Up
XM_139051	solute carrier family 39 (zinc transporter), member 2	-	-	-	-	-	-	-	-	2.9	Up
NM_134135	Solute carrier family 39 (zinc transporter), member 3	Slc39a3	-	-	-	-	-	2.0	Up	1.6	Up
NM_008202	Solute carrier family 39 (zinc transporter), member 7	Slc39a7	-	-	-	-	-	-	-	2.1	Down
XM_484158	solute carrier family 39 (zinc transporter), member 9	-	-	-	-	-	-	-	-	2.8	Up
NM_018760	Solute carrier family 4 (anion exchanger), member 4	Slc4a4	-	-	-	-	-	-	-	1.8	Up
XM_147798	solute carrier family 4, sodium bicarbonate cotransporter, member 7	-	-	-	-	-	-	-	-	1.6	Up
NM_145977	Solute carrier family 45, member 3	Slc45a3	-	-	-	-	-	2.1	Up	-	-
NM_133254	Solute carrier family 5 (sodium/glucose cotransporter), member 2	Slc5a2	-	-	-	-	-	1.9	Up	1.6	Up
NM_172890	Solute carrier family 6 (neurotransmitter transporter, GABA), member 11	Slc6a11	-	-	-	-	-	-	-	2.1	Up
NM_172861	Solute carrier family 7 (cationic amino acid transporter, y+ system), member 14	Slc7a14	-	-	1.8	Down	-	-	-	-	-
NM_011404	Solute carrier family 7 (cationic amino acid transporter, y+ system), member 5	Slc7a5	-	-	-	-	-	1.5	Up	-	-
NM_021291	Solute carrier family 7 (cationic amino acid transporter, y+ system), member 9	Slc7a9	-	-	-	-	-	-	-	2.1	Up
XM_127434	solute carrier family 9 (sodium/hydrogen exchanger), member 3	-	-	-	-	-	-	-	-	2.5	Up
NM_177353	Solute carrier family 9 (sodium/hydrogen exchanger), member 7	Slc9a7	-	-	-	-	-	-	-	1.9	Up
NM_013797	Solute carrier organic anion transporter family, member 1a1	Slco1a1	-	-	-	-	-	-	-	1.7	Up
NM_130861	Solute carrier organic anion transporter family, member 1a5	Slco1a5	-	-	-	-	-	-	-	3.0	Up
NM_023718	Solute carrier organic anion transporter family, member 1a6	Slco1a6	-	-	-	-	-	-	-	1.7	Up
NM_172658	Solute carrier organic anion transporter family, member 4C1	Slco4c1	-	-	1.9	Down	-	-	-	-	-
NM_172841	Solute carrier organic anion transporter family, member 5A1	Slco5a1	-	-	-	-	-	-	-	2.4	Up
NM_009215	Somatostatin	Sst	-	-	-	-	-	-	-	2.7	Up
NM_009170	Sonic hedgehog	Shh	-	-	-	-	-	-	-	2.0	Up

XM_486103	sorbin and SH3 domain containing 2	-	-	-	-	-	-	-	-	1.5	Up
XM_134171	sorting nexin 25	-	-	-	-	-	-	-	-	2.1	Up
NM_024225	Sorting nexin 5	Snx5	-	-	-	-	-	-	-	2.1	Down
NM_009262	Sparc/osteonectin, cwcv and kazal-like domains proteoglycan 1	Spock1	-	-	-	-	-	-	-	2.5	Up
NM_013675	Spectrin beta 1	Spnb1	-	-	-	-	-	-	-	1.6	Up
NM_032610	Spectrin beta 4	Spnb4	-	-	-	-	-	-	-	1.5	Up
XM_354632	sperm acrosome associated 3	-	-	-	-	-	-	-	-	1.8	Up
XM_205301	sperm acrosome associated 5	-	-	-	-	-	-	-	-	1.9	Up
NM_009241	Sperm adhesion molecule 1	Spam1	-	-	-	-	-	-	-	2.2	Up
NM_029160	Sperm associated antigen 16	Spag16	-	-	-	-	-	-	-	2.9	Up
NM_139151	Sperm associated antigen 4	Spag4	-	-	-	-	-	-	-	3.6	Up
XM_357260	sperm flagellar 1	-	-	-	-	-	-	-	-	1.7	Up
XM_128015	spermatogenesis and centriole associated 1	-	-	-	2.7	Down	-	-	-	-	-
NM_029299	Spermatogenesis associated 19	Spata19	-	-	-	-	-	-	-	2.5	Up
NM_177867	Spermatogenesis associated 21	Spata21	-	-	-	-	-	-	-	3.1	Up
NM_026470	Spermatogenesis associated 6	Spata6	-	-	-	-	-	-	-	2.8	Up
NM_173069	Spermatogenesis associated glutamate (E)-rich protein 2	Speer2	-	-	-	-	-	-	-	3.4	Up
NM_029376	Spermatogenesis associated glutamate (E)-rich protein 4a	Speer4a	-	-	-	-	-	-	-	3.0	Up
NM_025759	Spermatogenesis associated glutamate (E)-rich protein 4d	Speer4d	-	-	-	-	-	-	-	2.0	Up
NR_001582	spermatogenesis associated glutamate (E)-rich protein 5, pseudogene 1	-	-	-	-	-	-	-	-	2.4	Up
NR_001585	spermatogenesis associated glutamate (E)-rich protein 7, pseudogene 1	-	-	-	-	-	-	-	-	3.2	Up
NR_001583	spermatogenesis associated glutamate (E)-rich protein 9, pseudogene 1	-	-	-	-	-	-	-	-	2.2	Up
NM_027649	Spermatogenesis associated, serine-rich 1	Spats1	-	-	-	-	2.1	Up	-	3.4	Up
NM_139140	Spermatogenesis associated, serine-rich 2	Spats2	-	-	-	-	-	-	-	1.7	Up
NM_030237	Spermatogenic Zip 1	Spz1	-	-	-	-	-	-	-	3.1	Up
NM_009220	Spermiogenesis specific transcript on the Y 1	Ssty1	-	-	-	-	-	-	-	2.6	Up
NM_020561	Sphingomyelin phosphodiesterase, acid-like 3A	Smpdl3a	-	-	-	-	-	-	-	2.3	Down
NM_028943	Sphingomyelin synthase 2	Sgms2	-	-	-	-	-	-	-	1.8	Up
NM_007901	Sphingosine-1-phosphate receptor 1	S1pr1	-	-	-	-	-	-	-	2.2	Down
NM_172430	SPHK1 interactor, AKAP domain containing	Sphkap	-	-	-	-	-	-	-	1.9	Up
XM_126365	spinster homolog 3 (Drosophila)	-	-	-	-	-	-	-	-	1.5	Up
NM_027141	SplA/ryanodine receptor domain and SOCS box containing 3	Spsb3	-	-	-	-	2.8	Up	-	-	-
NM_011750	Splicing factor 1	Sf1	-	-	-	-	-	-	-	1.9	Up
NM_030109	Splicing factor 3b, subunit 2	Sf3b2	-	-	-	-	-	-	-	2.0	Down
NM_020587	Splicing factor, arginine/serine-rich 4 (SRp75)	Sfrs4	-	-	1.6	Up	-	-	-	-	-
NM_172276	Splicing factor, arginine/serine-rich 8	Sfrs8	-	-	-	-	-	-	-	2.1	Up
NM_011898	Sprouty homolog 4 (Drosophila)	Spry4	-	-	-	-	-	-	-	1.8	Up
NM_016926	Squamous cell carcinoma antigen recognized by T-cells 3	Sart3	-	-	-	-	2.7	Up	-	-	-
NM_009192	Src-like adaptor	Sla	-	-	-	-	2.7	Up	-	-	-

NM_011481	Src-related kinase lacking C-terminal regulatory tyrosine and N-terminal myristylation sites	Srms	-	-	-	-	-	-	2.1	Up
XM_128139	SRY-box containing gene 10	Sox10	-	-	-	-	-	-	3.2	Up
NM_024239	Stam binding protein	Stampb	-	-	-	-	-	-	2.0	Down
NM_029682	Stam binding protein like 1	Stampb1	-	-	-	-	-	-	2.3	Down
NM_019776	Staphylococcal nuclease and tudor domain containing 1	Snd1	-	-	-	-	1.9	Up	-	-
NM_019675	Stathmin-like 4	Stmn4	-	-	2.2	Down	-	-	-	-
NM_011490	Staufen (RNA binding protein) homolog 1 (Drosophila)	Stau1	-	-	-	-	-	-	1.8	Up
NM_009289	STE20-like kinase (yeast)	Slk	-	-	-	-	-	-	1.8	Down
NM_009127	Stearoyl-Coenzyme A desaturase 1	Scd1	-	-	-	-	-	-	2.4	Down
NM_080459	Stereocilin	Strc	-	-	-	-	-	-	1.6	Up
NM_172676	Sterile alpha motif domain containing 10	Samd10	-	-	-	-	2.1	Up	1.8	Up
NM_178049	sterile alpha motif domain containing 14	-	-	-	-	-	-	-	2.8	Up
NM_175021	Sterile alpha motif domain containing 4B	Samd4b	-	-	-	-	-	-	3.2	Up
NM_053188	Steroid 5 alpha-reductase 2	Srd5a2	-	-	-	-	-	-	1.8	Up
NM_009230	Sterol O-acyltransferase 1	Soat1	-	-	-	-	1.5	Up	-	-
NM_018754	Stratifin	Sfn	-	-	-	-	-	-	2.4	Up
NM_052973	Striatin, calmodulin binding protein 3	Strn3	-	-	-	-	-	-	2.0	Down
NM_021465	Stromal antigen 2	Stag2	-	-	-	-	-	-	1.8	Down
NM_009143	Stromal cell derived factor 2	Sdf2	-	-	-	-	-	-	2.0	Down
NM_011341	Stromal cell derived factor 4	Sdf4	-	-	-	-	-	-	2.2	Down
NM_008408	STT3, subunit of the oligosaccharyltransferase complex, homolog A (S. cerevisiae)	Stt3a	-	-	-	-	-	-	1.7	Down
NM_207243	Submandibular gland protein C	Muc19	-	-	-	-	-	-	2.7	Up
NM_021289	Submaxillary gland androgen regulated protein 2	Smr2	-	-	-	-	-	-	1.6	Up
NM_011422	Submaxillary gland androgen regulated protein 3A	Smr3a	-	-	-	-	-	-	1.5	Up
NM_029688	Sulfiredoxin 1 homolog (S. cerevisiae)	Srxn1	-	-	-	-	-	-	1.5	Down
NM_146003	SUMO/sentrin specific peptidase 6	Senp6	-	-	-	-	-	-	2.0	Down
NM_013671	Superoxide dismutase 2, mitochondrial	Sod2	-	-	-	-	-	-	2.2	Down
NM_019436	Suppression inducing transmembrane adaptor 1	Sit1	-	-	-	-	-	-	1.8	Up
NM_007706	Suppressor of cytokine signaling 2	Socs2	-	-	-	-	-	-	3.2	Down
NM_019654	Suppressor of cytokine signaling 5	Socs5	-	-	-	-	-	-	2.4	Up
NM_011509	Suppressor of Ty 4 homolog 1 (S. cerevisiae)	Supt4h1	-	-	-	-	-	-	2.2	Down
NM_013676	Suppressor of Ty 5 homolog (S. cerevisiae)	Supt5h	-	-	-	-	-	-	1.6	Down
NM_144871	Suppressor of variegation 4-20 homolog 1 (Drosophila)	Suv420h1	-	-	-	-	-	-	2.1	Up
NM_147779	Surfactant associated protein B	Sftpb	-	-	-	-	-	-	3.5	Up
NM_025891	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3	Smarcd3	-	-	-	-	-	-	1.9	Up
XM_143616	synapse defective 1, Rho GTPase, homolog 2 (C. elegans)	-	-	-	-	-	-	-	2.9	Up
NM_022027	Synaptic nuclear envelope 1	Syne1	-	-	-	-	-	-	1.7	Up
NM_011516	Synaptonemal complex protein 1	Sycp1	-	-	-	-	-	-	2.2	Up



NM_175132	Synaptopodin 2-like	Synpo2l	-	-	-	-	-	-	3.8	Up
NM_021889	Synaptotagmin IX	Syt9	-	-	-	-	-	-	2.0	Up
NM_016908	Synaptotagmin V	Syt5	-	-	-	-	-	-	1.8	Up
NM_023485	Syncoilin	Sync	-	-	-	-	-	-	1.7	Up
NM_016807	Syndecan binding protein	Sdcbp	-	-	-	-	-	-	2.2	Down
NM_198898	Synovial sarcoma, X member B, breakpoint 10	Ssxb10	-	-	-	-	-	-	3.6	Up
NM_199066	Synovial sarcoma, X member B, breakpoint 3	Ssxb2	-	-	-	-	-	-	1.7	Up
NM_026588	Syntaxin 19	Stx19	-	-	-	-	-	-	1.5	Up
NM_018768	Syntaxin 8	Stx8	-	-	-	-	-	-	2.3	Down
NM_011503	Syntaxin binding protein 2	Stxbp2	-	-	2.3	Up	-	-	2.1	Up
NM_009221	Synuclein, alpha	Snca	-	-	-	-	2.9	Up	1.7	Up
NM_145968	T-cell activation Rho GTPase-activating protein	Tagap	-	-	-	-	-	-	3.7	Down
NM_133986	T-cell leukemia translocation altered gene	Tcta	-	-	-	-	-	-	1.8	Down
NM_011553	T-complex protein 10b	Tcp10b	-	-	-	-	-	-	2.4	Up
NM_022311	T-complex-associated testis expressed 2	Tcte2	-	-	-	-	-	-	1.7	Up
NM_009311	Tachykinin 1	Tac1	-	-	-	-	-	-	3.1	Up
NM_009313	Tachykinin receptor 1	Tacr1	-	-	-	-	-	-	1.9	Up
NM_009314	Tachykinin receptor 2	Tacr2	-	-	-	-	-	-	2.4	Up
XM_194622	TAF1 RNA polymerase II, TATA box binding protein (TBP)-associated factor	-	-	-	-	-	-	-	1.6	Down
NM_133966	TAF5-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor	Taf5l	-	-	-	-	1.9	Up	-	-
NM_028958	TAF7-like RNA polymerase II, TATA box binding protein (TBP)-associated factor	Taf7l	-	-	-	-	-	-	2.7	Up
NM_175091	Tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase	Tnks	-	-	-	-	-	-	2.8	Up
NM_026654	Target of EGR1, member 1 (nuclear)	Toe1	-	-	-	-	2.5	Up	-	-
NM_020502	Taste receptor, type 2, member 108	Tas2r108	-	-	-	-	-	-	3.5	Up
NM_207025	Taste receptor, type 2, member 123	Tas2r123	-	-	1.7	Down	-	-	-	-
NM_020614	TATA box binding protein (Tbp)-associated factor, RNA polymerase I, B	Taf1b	-	-	3.0	Up	3.1	Up	2.5	Up
NM_138628	Taxilin beta	Txlnb	-	-	-	-	-	-	2.3	Up
NM_134023	TBC1 domain family, member 10a	Tbc1d10a	-	-	-	-	1.5	Up	-	-
NM_144522	TBC1 domain family, member 10b	Tbc1d10b	-	-	-	-	1.6	Up	-	-
NM_024196	TBC1 domain family, member 20	Tbc1d20	-	-	-	-	-	-	1.5	Up
NM_172478	TBC1 domain family, member 25	Tbc1d25	-	-	-	-	-	-	1.7	Up
XM_137322	TBC1 domain family, member 30	Tbc1d30	-	-	-	-	-	-	1.9	Up
XM_109880	TBC1 domain family, member 9B	-	-	-	-	-	-	-	1.8	Up
NM_023524	TCF3 (E2A) fusion partner	Tfpt	-	-	-	-	2.3	Up	1.8	Up
NM_172298	Teashirt zinc finger family member 3	Tshz3	-	-	-	-	-	-	1.7	Up
NM_011607	Tenascin C	Tnc	-	-	-	-	-	-	3.3	Up

XM_109868	tensin 3	-	-	-	-	-	-	1.8	Up	
NM_197993	Terminal uridylyl transferase 1, U6 snRNA-specific	Tut1	-	-	-	-	1.9	Up	2.1	Up
XM_357873	testase-8	-	-	-	-	-	-	-	1.6	Up
NM_031385	testis expressed gene 18	-	-	-	-	-	-	-	2.7	Up
NM_009357	Testis expressed gene 261	Tex261	-	-	-	-	-	-	2.0	Down
NM_011573	Testis expressed gene 264	Tex264	-	-	-	-	-	-	3.3	Up
NM_199471	Testis serine protease 3	Tessp3	-	-	-	-	-	-	3.6	Up
NM_021898	testis specific gene A8	-	-	-	-	-	-	-	2.6	Up
NM_009440	Testis specific X-linked gene	Tsx	-	-	-	-	-	-	2.0	Up
NM_009433	Testis-specific protein, Y-encoded-like 1	Tspyl1	-	-	-	-	-	-	2.5	Down
XM_125673	Tet oncogene 1	Tet1	-	-	-	-	-	-	2.1	Up
NM_145928	Tetraspanin 14	Tspan14	-	-	-	-	1.6	Up	-	-
NM_183180	Tetraspanin 18	Tspan18	-	-	-	-	-	-	1.6	Up
NM_053082	Tetraspanin 4	Tspan4	-	-	-	-	1.8	Up	-	-
NM_019634	Tetraspanin 7	Tspan7	-	-	-	-	1.7	Up	2.6	Up
NM_133795	Tetratricopeptide repeat domain 1	Ttc1	-	-	-	-	-	-	2.5	Down
NM_172526	Tetratricopeptide repeat domain 24	Ttc24	-	-	-	-	-	-	2.7	Up
XM_126529	tetratricopeptide repeat domain 25	-	-	-	-	-	-	-	3.1	Up
NM_153600	Tetratricopeptide repeat domain 26	Ttc26	-	-	-	-	-	-	1.5	Up
NM_024477	tetratricopeptide repeat domain 28	-	-	-	-	-	-	-	1.8	Up
NM_028639	Tetratricopeptide repeat domain 7	Ttc7	-	-	-	-	2.2	Up	-	-
NM_153061	TGF-beta1-induced anti-apoptotic factor 2	-	-	-	-	-	-	-	2.8	Up
NM_153109	TGFB-induced factor homeobox 2-like, X-linked	Tgif2lx	-	-	-	-	-	-	2.0	Up
NM_021513	THAP domain containing 11	Thap11	-	-	-	-	-	-	1.7	Down
NM_011660	Thioredoxin 1	Txn1	-	-	-	-	-	-	1.9	Up
NM_029572	Thioredoxin domain containing 4 (endoplasmic reticulum)	Txndc4	-	-	-	-	-	-	1.8	Down
NM_178604	Thioredoxin-like 4A	Txn14a	-	-	-	-	1.7	Up	-	-
NM_009437	Thiosulfate sulfurtransferase, mitochondrial	Tst	-	-	-	-	-	-	3.2	Up
NM_011637	Three prime repair exonuclease 1	Trex1	-	-	-	-	1.8	Up	-	-
NM_027931	Threonyl-tRNA synthetase 2, mitochondrial (putative)	Tars2	-	-	-	-	1.6	Up	2.1	Up
NM_009378	Thrombomodulin	Thbd	-	-	-	-	-	-	2.8	Up
NM_009379	Thrombopoietin	Thpo	-	-	2.0	Down	-	-	-	-
NM_011580	Thrombospondin 1	Thbs1	-	-	-	-	-	-	1.7	Up
NM_172485	Thrombospondin, type I, domain containing 7B	Thsd7b	-	-	-	-	-	-	2.0	Up
NR_000040	thymidylate synthase, pseudogene	-	-	-	1.9	Down	-	-	-	-
NM_172552	Thymine DNA glycosylase	Tdg	-	-	-	-	-	-	2.8	Up
NM_009380	Thyroid hormone receptor beta	Thrb	-	-	-	-	-	-	3.5	Up
NM_009417	Thyroid peroxidase	Tpo	-	-	-	-	-	-	2.6	Up
NM_009426	Thyrotropin releasing hormone	Trh	-	-	-	-	-	-	2.4	Up
NM_009383	Tia1 cytotoxic granule-associated RNA binding protein-like 1	Tial1	-	-	-	-	-	-	2.0	Down
AF247559	TIM (TRIOSEPHOSPHATE ISOMERASE)	TIM	-	-	-	-	-	-	1.9	Up

NM_053157	TM2 domain containing 1	Tm2d1	-	-	-	-	-	-	2.2	Down
NM_009422	Tnf receptor-associated factor 2	Traf2	-	-	-	-	1.8	Up	-	-
NM_001001495	TNFAIP3 interacting protein 3	Tnip3	-	-	-	-	-	-	2.5	Up
NM_011905	Toll-like receptor 2	Tlr2	-	-	-	-	-	-	1.5	Down
NM_174989	Toll-like receptor adaptor molecule 1	Ticam1	-	-	-	-	-	-	2.7	Up
NM_011623	Topoisomerase (DNA) II alpha	Top2a	-	-	-	-	2.4	Up	1.8	Up
NM_009409	Topoisomerase (DNA) II beta	Top2b	-	-	-	-	-	-	1.9	Down
NM_144791	Torsin A interacting protein 1	Tor1aip1	-	-	-	-	-	-	2.2	Down
NM_133673	Torsin family 1, member B	Tor1b	-	-	-	-	1.6	Up	-	-
NM_026933	TP53 regulated inhibitor of apoptosis 1	Triap1	-	-	-	-	2.1	Up	2.0	Up
NM_053205	Trace amine-associated receptor 1	Taar1	-	-	-	-	-	-	1.9	Up
XM_136993	trace amine-associated receptor 6	-	-	-	-	-	-	-	1.5	Up
NM_011529	TRAF family member-associated Nf-kappa B activator	Tank	-	-	-	-	-	-	2.3	Down
NM_021502	Trafficking protein particle complex 2-like	Trappc2l	-	-	-	-	2.0	Up	-	-
NM_029640	Trafficking protein particle complex 9	Trappc9	-	-	-	-	-	-	1.9	Down
NM_031183	Trans-acting transcription factor 6	Sp6	-	-	-	-	-	-	2.3	Up
NM_177082	Trans-acting transcription factor 8	Sp8	-	-	-	-	-	-	3.0	Up
NM_015749	Transcobalamin 2	Tcn2	-	-	-	-	1.7	Up	-	-
NM_011541	Transcription elongation factor A (SII) 1	Tcea1	-	-	-	-	-	-	3.5	Down
NM_025355	Transcription elongation factor A (SII)-like 6	Tcea6	-	-	-	-	-	-	1.7	Up
NM_013736	Transcription elongation factor B (SIII), polypeptide 3	Tceb3	-	-	-	-	2.0	Up	-	-
NM_019512	transcription elongation regulator 1 (CA150)	-	-	-	-	-	-	-	1.9	Up
NM_011544	Transcription factor 12	Tcf12	-	-	-	-	-	-	1.7	Down
NM_013685	Transcription factor 4	Tcf4	-	-	-	-	2.5	Up	-	-
NM_009331	Transcription factor 7, T-cell specific	Tcf7	-	-	-	-	-	-	1.6	Down
NM_009361	Transcription factor Dp 1	Tfdp1	-	-	-	-	-	-	3.3	Up
NM_011549	Transcription factor EB	Tcfef	-	-	-	-	1.5	Up	2.7	Up
NM_133932	Transcriptional adaptor 3 (NGG1 homolog, yeast)-like	Tada3l	-	-	-	-	2.5	Up	-	-
NM_011599	Transducin-like enhancer of split 1, homolog of Drosophila E(spl)	Tle1	-	-	-	-	-	-	2.1	Up
NM_053254	Transducin-like enhancer of split 6, homolog of Drosophila E(spl)	Tle6	-	-	-	-	-	-	2.4	Up
NM_011641	Transformation related protein 63	Trp63	-	-	-	-	-	-	2.0	Up
NM_175165	Transformation related protein 63 regulated	Tprg	-	-	-	-	-	-	1.8	Up
NM_010786	Transformed mouse 3T3 cell double minute 2	Mdm2	-	-	-	-	-	-	1.7	Down
NM_025289	Transforming growth factor beta regulated gene 1	Tbrg1	-	-	-	-	-	-	1.6	Down
NM_011526	Transgelin	Tagln	-	-	-	-	-	-	1.5	Down
NM_009373	Transglutaminase 2, C polypeptide	Tgm2	-	-	-	-	1.9	Up	-	-
NM_024445	Translin-associated factor X (Tsnax) interacting protein 1	Tsnaxip1	-	-	-	-	-	-	2.1	Up
NM_013898	Translocase of inner mitochondrial membrane 8 homolog a1 (yeast)	Timm8a1	-	-	-	-	-	-	2.4	Down
XM_127887	translocase of inner mitochondrial membrane 8 homolog a2 (yeast)	-	-	-	-	-	-	-	1.5	Up
NM_013896	Translocase of inner mitochondrial membrane 9 homolog (yeast)	Timm9	-	-	-	-	-	-	1.8	Down

NM_024214	Translocase of outer mitochondrial membrane 20 homolog (yeast)	Tomm20	-	-	-	-	-	-	2.7	Down
NM_133780	Translocated promoter region	Tpr	-	-	-	-	1.8	Down	1.9	Up
NM_009775	Translocator protein	Tspo	-	-	-	-	1.8	Up	-	-
NM_172051	Transmembrane and coiled coil domains 3	Tmcc3	-	-	-	-	-	-	2.5	Up
NM_026104	Transmembrane and coiled-coil domains 5	Tmco5	2.4	Down	-	-	-	-	-	-
NM_173037	Transmembrane and coiled-coil domains 7	Tmco7	-	-	-	-	-	-	1.6	Up
XM_127899	transmembrane and tetratricopeptide repeat containing 4	-	-	-	-	-	-	-	3.4	Up
NM_022418	Transmembrane and ubiquitin-like domain containing 1	Tmub1	-	-	-	-	1.7	Up	-	-
NM_181820	Transmembrane channel-like gene family 4	Tmc4	-	-	-	-	-	-	1.9	Up
NM_028930	Transmembrane channel-like gene family 5	Tmc5	-	-	-	-	-	-	1.8	Up
NM_172476	Transmembrane channel-like gene family 7	Tmc7	-	-	-	-	-	-	2.0	Up
XM_128959	transmembrane emp24 protein transport domain containing 7	-	-	-	1.9	Down	-	-	1.5	Up
NM_177024	Transmembrane protease, serine 11b	Tmprss1 1b	-	-	-	-	-	-	2.0	Up
NM_178730	Transmembrane protease, serine 11f	Tmprss1 1f	-	-	-	-	-	-	1.6	Up
NM_030709	Transmembrane protease, serine 5 (spinesin)	Tmprss5	-	-	-	-	-	-	2.1	Up
NM_027992	Transmembrane protein 106B	Tmem10 6b	-	-	-	-	-	-	1.6	Down
NM_201359	Transmembrane protein 106C	Tmem10 6c	-	-	-	-	-	-	2.4	Up
NM_178789	Transmembrane protein 117	Tmem11 7	-	-	-	-	-	-	4.0	Up
NM_133739	Transmembrane protein 123	Tmem12 3	-	-	-	-	1.5	Up	2.1	Down
NM_172383	Transmembrane protein 125	Tmem12 5	-	-	-	-	-	-	3.0	Up
NM_025460	Transmembrane protein 126A	Tmem12 6a	-	-	-	-	-	-	1.8	Down
XM_485684	transmembrane protein 132C	-	-	-	-	-	-	-	2.2	Up
NM_183311	Transmembrane protein 145	Tmem14 5	-	-	1.7	Down	-	-	-	-
NM_025387	Transmembrane protein 14C	Tmem14 c	-	-	-	-	-	-	2.4	Down
XM_144292	Transmembrane protein 156	Tmem15 6	-	-	-	-	-	-	2.2	Up
NM_0010022 67	Transmembrane protein 158	Tmem15 8	-	-	-	-	-	-	1.9	Up
NM_011626	Transmembrane protein 165	Tmem16 5	-	-	-	-	-	-	1.8	Down
NM_153589	Transmembrane protein 16B	Tmem16 b	-	-	-	-	-	-	2.2	Up
NM_178773	Transmembrane protein 16D (eight membrane-spanning domains)	Tmem16 d	-	-	-	-	-	-	1.5	Up

NM_025326	Transmembrane protein 176A	Tmem17										
NM_172049	Transmembrane protein 18	6a	-	-	-	-	1.7	Up	-	-	-	-
		Tmem18	-	-	-	-	-	-	-	-	1.6	Down
		Tmem18										
NM_020588	Transmembrane protein 183A	3a	-	-	-	-	-	-	-	-	1.5	Down
		Tmem18										
NM_146103	Transmembrane protein 185B	5b	-	-	-	-	-	-	-	-	1.8	Up
XM_134198	transmembrane protein 192	-	-	-	-	-	-	-	-	-	1.6	Down
		Tmem20										
NM_177672	Transmembrane protein 201	1	-	-	-	-	-	-	-	-	2.0	Up
		Tmem30										
NM_133718	Transmembrane protein 30A	a	-	-	-	-	-	-	-	-	3.0	Down
NM_146234	Transmembrane protein 32	Tmem32	-	-	-	-	1.7	Up	-	-	-	-
NM_028355	Transmembrane protein 48	Tmem48	-	-	-	-	1.7	Up	-	-	-	-
		Tmem50										
NM_027935	Transmembrane protein 50A	a	-	-	-	-	-	-	-	-	1.9	Down
NM_025452	Transmembrane protein 54	Tmem54	-	-	-	-	-	-	-	-	2.0	Up
		Tmem55										
NM_028264	Transmembrane protein 55A	a	-	-	-	-	1.5	Up	-	-	-	-
NM_029565	Transmembrane protein 59	Tmem59	-	-	-	-	-	-	-	-	1.7	Down
NM_182991	Transmembrane protein 59-like	Tmem59l	-	-	1.5	Down	1.5	Down	-	-	-	-
NM_175285	Transmembrane protein 62	Tmem62	-	-	-	-	-	-	-	-	1.7	Down
		Tmem63										
NM_198167	Transmembrane protein 63b	b	-	-	-	-	-	-	-	-	2.4	Up
NM_026013	Transmembrane protein 77	Tmem77	-	-	-	-	1.6	Up	-	-	-	-
NM_145987	Transmembrane protein 82	Tmem82	-	-	-	-	-	-	-	-	2.7	Up
		Tmem86										
NM_026436	Transmembrane protein 86A	a	-	-	-	-	1.9	Up	-	-	-	-
NM_144551	Tribbles homolog 2 (Drosophila)	Trib2	-	-	-	-	-	-	-	-	4.1	Down
NM_027762	Trichohyalin-like 1	Tchhl1	-	-	1.8	Down	-	-	-	-	-	-
NM_138758	Trimethyllysine hydroxylase, epsilon	Tmlhe	-	-	-	-	-	-	-	-	2.8	Up
NM_053168	Tripartite motif-containing 11	Trim11	-	-	-	-	-	-	-	-	1.7	Up
NM_030731	Tripartite motif-containing 23	Trim23	-	-	-	-	-	-	-	-	2.6	Up
NM_009054	Tripartite motif-containing 27	Trim27	-	-	-	-	-	-	-	-	2.9	Down
NM_011588	Tripartite motif-containing 28	Trim28	-	-	-	-	2.2	Up	-	-	-	-
NM_023655	Tripartite motif-containing 29	Trim29	-	-	-	-	-	-	-	-	2.5	Up
NM_146077	Tripartite motif-containing 31	Trim31	-	-	2.3	Down	-	-	-	-	-	-
NM_029979	Tripartite motif-containing 35	Trim35	-	-	-	-	-	-	-	-	4.0	Up
XM_286106	tripartite motif-containing 75	-	-	-	-	-	-	-	-	-	3.1	Up
NM_025873	TRNA isopentenyltransferase 1	Trit1	-	-	-	-	3.0	Up	-	-	-	-
XM_283286	Trophinin associated protein	Troap	-	-	1.5	Down	-	-	-	-	-	-
NM_024427	Tropomyosin 1, alpha	Tpm1	-	-	-	-	-	-	-	-	2.9	Down
NM_009394	Troponin C2, fast	Tnnc2	-	-	1.6	Down	-	-	-	-	-	-

NM_023910	TSC22 domain family 4	Tsc22d4	-	-	-	-	1.5	Up	-	-
NM_009366	TSC22 domain family, member 1	Tsc22d1	-	-	-	-	2.5	Up	1.7	Down
NM_175146	TSR2, 20S rRNA accumulation, homolog (S. cerevisiae)	Tsr2	-	-	-	-	1.9	Up	-	-
NM_025548	Tubulin folding cofactor B	Tbcb	-	-	-	-	-	-	1.7	Down
NM_173038	Tubulin folding cofactor E-like	Tbcel	-	-	-	-	-	-	2.3	Down
NM_183017	Tubulin tyrosine ligase-like family, member 12	Ttl12	-	-	-	-	-	-	1.8	Up
XM_126935	tubulin tyrosine ligase-like family, member 5	-	-	-	-	-	1.9	Up	3.5	Up
NM_011653	Tubulin, alpha 1A	Tuba1a	-	-	-	-	-	-	3.1	Down
NM_009446	Tubulin, alpha 3A	Tuba3a	-	-	-	-	-	-	2.2	Up
NM_017379	Tubulin, alpha 8	Tuba8	-	-	-	-	-	-	1.7	Up
NM_011655	Tubulin, beta 5	Tubb5	-	-	-	-	-	-	1.5	Down
NM_198418	Tudor domain containing 6	Tdrd6	-	-	-	-	-	-	2.1	Up
NM_009399	tumor necrosis factor receptor superfamily, member 11a	-	-	-	-	-	2.2	Up	3.0	Up
NM_023680	Tumor necrosis factor receptor superfamily, member 22	Tnfrsf22	-	-	-	-	-	-	2.1	Up
NM_033042	Tumor necrosis factor receptor superfamily, member 25	Tnfrsf25	-	-	-	-	-	-	2.2	Up
NM_025482	Tumor protein D52-like 2	Trpd52l2	-	-	-	-	-	-	2.4	Down
NM_025741	Tumor protein D52-like 3	Trpd52l3	-	-	-	-	-	-	1.6	Up
NM_011635	Tumor rejection antigen P1A	Trap1a	-	-	-	-	-	-	4.0	Up
NM_145853	Two pore channel 1	Tpcn1	-	-	-	-	-	-	2.8	Up
NM_146206	Two pore segment channel 2	Tpcn2	-	-	-	-	-	-	3.8	Up
NM_011738	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	Ywhah	-	-	-	-	1.8	Up	-	-
NM_009377	Tyrosine hydroxylase	Th	-	-	-	-	-	-	1.9	Up
NM_001002900	UbiE-YGHL1 fusion protein	LOC554292	-	-	1.6	Down	-	-	-	-
NM_025407	Ubiquinol-cytochrome c reductase core protein 1	Uqcrc1	-	-	-	-	-	-	4.3	Down
NM_019639	Ubiquitin C	Ubc	-	-	-	-	-	-	2.3	Down
NM_011670	Ubiquitin carboxy-terminal hydrolase L1	Uchl1	-	-	-	-	-	-	2.5	Up
NM_145500	Ubiquitin domain containing 1	Ubt1	-	-	-	-	1.8	Up	1.5	Up
NM_173784	Ubiquitin domain containing 2	Ubt2	-	-	-	-	-	-	1.8	Up
NM_011672	Ubiquitin fusion degradation 1 like	Ufd1l	-	-	-	-	-	-	2.3	Down
XM_355528	ubiquitin protein ligase E3 component n-recognin 4	-	-	-	-	-	1.9	Up	-	-
XM_130826	ubiquitin specific peptidase 13 (isopeptidase T-3)	-	-	-	-	-	-	-	2.9	Up
NM_021522	Ubiquitin specific peptidase 14	Usp14	-	-	-	-	2.9	Up	-	-
NM_028846	Ubiquitin specific peptidase 20	Usp20	-	-	-	-	-	-	3.1	Up
NM_001004143	Ubiquitin specific peptidase 22	Usp22	-	-	-	-	-	-	3.1	Up
XM_131566	ubiquitin specific peptidase 24	-	-	-	-	-	-	-	4.1	Up
NM_019461	ubiquitin specific peptidase 27, X chromosome	-	-	-	-	-	-	-	2.1	Up
XM_357781	Ubiquitin specific peptidase 31	Usp31	-	-	-	-	-	-	2.7	Up
NM_133247	Ubiquitin specific peptidase 33	Usp33	-	-	-	-	-	-	1.7	Down
NM_183199	Ubiquitin specific peptidase 44	Usp44	-	-	-	-	-	-	2.1	Up

NM_029163	Ubiquitin specific peptidase 50	Usp50	-	-	-	-	-	-	-	3.9	Up
NM_011908	Ubiquitin-like 3	Ubl3	-	-	-	-	-	-	-	1.7	Down
NM_010931	Ubiquitin-like, containing PHD and RING finger domains, 1	Uhrf1	-	-	-	-	-	-	-	2.9	Up
NM_201642	UDP glucuronosyltransferase 1 family, polypeptide A6B	Ugt1a6a	-	-	-	-	-	-	-	2.0	Up
NM_013701	UDP glucuronosyltransferase 1 family, polypeptide A6B	Ugt1a6a	-	-	-	-	-	-	-	2.1	Up
NM_153598	UDP glucuronosyltransferase 2 family, polypeptide B34	Ugt2b34	-	-	-	-	-	-	-	2.0	Up
NM_181069	UDP glycosyltransferases 3 family, polypeptide A2	-	-	-	-	-	-	-	-	3.0	Up
NM_020283	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1	B3galt1	-	-	-	-	-	-	-	3.2	Up
NM_033149	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5	B3galt5	-	-	-	-	-	-	-	2.3	Up
NM_138668	UFM1-specific peptidase 2	Ufsp2	-	-	-	-	-	-	-	2.5	Down
XM_356087	unc-13 homolog A (C. elegans)	-	-	-	1.7	Up	-	-	-	4.2	Up
NM_021468	unc-13 homolog B (C. elegans)	-	-	-	-	-	-	-	-	2.8	Up
NM_177589	unc-51-like kinase 4 (C. elegans)	-	-	-	-	-	-	-	-	1.7	Up
NM_024451	Unc-84 homolog A (C. elegans)	Unc84a	-	-	1.7	Down	-	-	-	-	-
NM_178918	UTP15, U3 small nucleolar ribonucleoprotein, homolog (yeast)	Utp15	-	-	-	-	2.2	Up	-	-	-
NM_178635	UV radiation resistance associated gene	Uvrag	-	-	-	-	2.0	Up	-	-	-
NM_010658	V-maf musculoaponeurotic fibrosarcoma oncogene family, protein B (avian)	Mafb	-	-	-	-	-	-	-	3.1	Down
NM_030181	V-set and immunoglobulin domain containing 1	Vsig1	-	-	-	-	-	-	-	2.6	Up
NM_177723	V-set and immunoglobulin domain containing 8	Vsig8	-	-	-	-	-	-	-	1.7	Up
NM_133945	Vaccinia related kinase 3	Vrk3	-	-	-	-	-	-	-	2.1	Down
NM_029929	Vacuolar protein sorting 33A (yeast)	Vps33a	-	-	-	-	-	-	-	1.8	Down
NM_022997	Vacuolar protein sorting 35	Vps35	-	-	-	-	1.6	Up	-	-	-
NM_172120	Vacuolar protein sorting 41 (yeast)	Vps41	-	-	-	-	-	-	-	2.1	Down
NM_009190	Vacuolar protein sorting 4b (yeast)	Vps4b	-	-	-	-	-	-	-	2.4	Down
NM_139061	Vacuolar protein sorting 54 (yeast)	Vps54	-	-	-	-	-	-	-	2.3	Down
NM_009336	Vacuolar protein sorting 72 (yeast)	Vps72	-	-	-	-	1.8	Up	-	-	-
NM_175137	Valyl-tRNA synthetase 2, mitochondrial (putative)	Vars2	-	-	-	-	-	-	-	2.4	Up
NM_011979	Vanin 3	Vnn3	-	-	-	-	3.0	Up	-	2.3	Up
NM_011693	Vascular cell adhesion molecule 1	Vcam1	1.6	Up	-	-	-	-	-	3.8	Down
NM_009505	Vascular endothelial growth factor A	Vegfa	-	-	-	-	-	-	-	2.8	Up
NM_011697	Vascular endothelial growth factor B	Vegfb	-	-	-	-	-	-	-	1.9	Down
NM_139307	Vasorin	Dnaja3	-	-	-	-	-	-	-	1.9	Up
NM_145820	Ventricular zone expressed PH domain homolog 1 (zebrafish)	Veph1	-	-	-	-	1.7	Up	-	3.0	Up
NM_016794	Vesicle-associated membrane protein 8	Vamp8	-	-	-	-	-	-	-	2.1	Down
NM_013933	Vesicle-associated membrane protein, associated protein A	Vapa	-	-	-	-	-	-	-	2.0	Up
NM_019806	Vesicle-associated membrane protein, associated protein B and C	Vapb	-	-	-	-	2.9	Up	-	-	-
NM_133251	Vestigial like 1 homolog (Drosophila)	Vgll1	-	-	-	-	-	-	-	1.5	Up
NM_178600	Vitamin K epoxide reductase complex, subunit 1	Vkorc1	-	-	-	-	-	-	-	2.2	Down
NM_053221	Vomer nasal 1 receptor, A6	V1ra6	-	-	1.6	Down	-	-	-	-	-
NM_134174	Vomer nasal 1 receptor, C19	V1rc19	-	-	-	-	-	-	-	3.4	Up

NM_134175	Vomeronasal 1 receptor, C20	V1rc20	-	-	-	-	-	-	-	1.8	Up
NM_134180	Vomeronasal 1 receptor, C25	V1rc25	-	-	-	-	-	-	-	2.0	Up
NM_134181	Vomeronasal 1 receptor, C26	V1rc26	-	-	-	-	-	-	-	2.6	Up
NM_134185	Vomeronasal 1 receptor, C30	V1rc30	-	-	-	-	-	-	-	3.3	Up
NM_134436	Vomeronasal 1 receptor, C33	V1rc33	-	-	-	-	-	-	-	2.8	Up
NM_207543	Vomeronasal 1 receptor, D10	V1rd10	-	-	-	-	-	-	-	2.4	Up
NM_203489	Vomeronasal 1 receptor, D15	V1rd15	-	-	-	-	-	-	-	2.2	Up
NM_030741	Vomeronasal 1 receptor, D2	V1rd2	-	-	-	-	-	-	-	2.3	Up
NM_207548	Vomeronasal 1 receptor, D22	V1rd22	-	-	-	-	-	-	-	4.3	Up
XM_357688	vomeronasal 1 receptor, D5	-	-	-	-	-	-	-	-	1.9	Up
NM_134194	Vomeronasal 1 receptor, E5	V1re5	-	-	-	-	-	-	-	2.1	Up
NM_145842	Vomeronasal 1 receptor, E9	V1re9	-	-	-	-	-	-	-	2.4	Up
NM_134198	Vomeronasal 1 receptor, F1	V1rf1	-	-	-	-	-	1.9	Up	3.5	Up
NM_134201	Vomeronasal 1 receptor, F4	V1rf4	-	-	-	-	-	-	-	1.8	Up
NM_134233	Vomeronasal 1 receptor, G11	V1rg11	-	-	-	-	-	-	-	2.8	Up
NM_134204	Vomeronasal 1 receptor, G3	V1rg3	-	-	-	-	-	-	-	1.8	Up
NM_134210	Vomeronasal 1 receptor, G9	V1rg9	-	-	-	-	-	-	-	2.0	Up
NM_134211	vomeronasal 1 receptor, H1	-	-	-	-	-	-	-	-	2.6	Up
NM_134238	Vomeronasal 1 receptor, H13	V1rh13	-	-	-	-	-	-	-	3.5	Up
NM_134212	Vomeronasal 1 receptor, H3	V1rh3	-	-	-	-	-	-	-	3.2	Up
NM_134218	Vomeronasal 1 receptor, H9	V1rh9	-	-	-	-	-	-	-	1.7	Up
XM_139786	vomeronasal 2, receptor 102	-	-	-	-	-	-	-	-	3.0	Up
XM_356949	vomeronasal 2, receptor 118	-	-	-	-	-	-	-	-	2.9	Up
XM_140062	vomeronasal 2, receptor 120	-	-	-	-	-	-	-	-	2.1	Up
XM_142477	vomeronasal 2, receptor 15	-	-	-	-	-	-	-	-	2.5	Up
NM_009490	Vomeronasal 2, receptor 30	Vmn2r30	-	-	-	-	-	-	-	2.4	Up
NM_009489	Vomeronasal 2, receptor 37	Vmn2r37	-	-	-	-	-	-	-	1.5	Up
XM_145883	vomeronasal 2, receptor 66	-	-	-	1.6	Down	-	-	-	-	-
NM_175936	Vomeronasal 2, receptor 81	Vmn2r81	-	-	-	-	-	-	-	2.8	Up
NM_009492	Vomeronasal 2, receptor, 122	Vmn2r89	-	-	-	-	-	-	-	2.6	Up
NM_198676	vomeronasal 2, receptor, pseudogene 105	-	-	-	-	-	-	-	-	2.7	Up
XM_144973	vomeronasal 2, receptor27	-	-	-	-	-	-	-	-	2.9	Up
NM_011692	Von Hippel-Lindau binding protein 1	Vbp1	-	-	-	-	-	-	-	2.7	Down
NM_177697	Von Willebrand factor A domain containing 3A	Vwa3a	-	-	-	-	-	-	-	3.2	Up
NM_177033	Von Willebrand factor C domain containing 2	Vwc2	-	-	-	-	-	-	-	2.1	Up
XM_356186	Vpr (HIV-1) binding protein	-	-	-	-	-	-	-	-	2.7	Up
NM_025418	Vps20-associated 1 homolog (S. cerevisiae)	Vta1	-	-	-	-	-	-	-	1.7	Down
XM_130716	WAP four-disulfide core domain 6A	-	-	-	2.7	Down	-	-	-	2.0	Up
NM_153423	WAS protein family, member 2	Wasf2	-	-	-	-	-	-	-	1.7	Up
NM_019653	WD repeat and SOCS box-containing 1	Wsb1	-	-	-	-	-	-	-	2.9	Down
NM_028220	WD repeat domain 17	Wdr17	-	-	-	-	-	-	-	2.2	Up



NM_133734	WD repeat domain 23	Wdr23	-	-	-	-	-	-	2.4	Down
NM_173741	WD repeat domain 24	Wdr24	-	-	-	-	-	-	1.7	Down
NM_172470	WD repeat domain 35	Wdr35	-	-	-	-	-	-	2.9	Up
NM_172372	WD repeat domain 45	Wdr45	-	-	-	-	-	-	1.9	Down
NM_020603	WD repeat domain 46	Wdr46	-	-	-	-	-	-	2.6	Up
NM_023790	WD repeat domain 54	Wdr54	-	-	-	-	-	-	1.8	Up
NM_023191	WD repeat domain 61	Wdr61	-	-	-	-	-	-	2.0	Down
XM_140391	WD repeat domain 7	Wdr7	-	-	2.0	Down	-	-	-	-
NM_025793	Wdr45 like	Wdr45l	-	-	-	-	-	-	2.1	Down
NM_009522	Wingless-related MMTV integration site 3A	Wnt3a	-	-	-	-	-	-	1.9	Up
NM_009524	Wingless-related MMTV integration site 5A	Wnt5a	-	-	1.5	Down	-	-	-	-
XM_133026	Wiskott-Aldrich syndrome-like (human)	-	-	-	-	-	1.6	Up	-	-
NM_175638	WNK lysine deficient protein kinase 4	Wnk4	-	-	-	-	-	-	2.2	Up
NM_018865	WNT1 inducible signaling pathway protein 1	Wisp1	-	-	-	-	-	-	2.3	Up
NM_177618	WSC domain containing 1	Wscd1	-	-	-	-	-	-	2.7	Up
NM_177292	WSC domain containing 2	Wscd2	-	-	-	-	-	-	2.3	Up
NM_016757	WW domain binding protein 1	Wbp1	-	-	-	-	-	-	1.5	Down
NM_021714	WW domain binding protein 11	Wbp11	-	-	-	-	-	-	2.2	Down
NM_016852	WW domain binding protein 2	Wbp2	-	-	-	-	-	-	2.4	Up
NM_173393	X Kell blood group precursor related family member 6 homolog	Xkr6	-	-	-	-	-	-	2.4	Up
XM_141539	X Kell blood group precursor related family member 7 homolog	-	-	-	-	-	-	-	1.8	Up
XM_194369	X-ray radiation resistance associated 1	Xrra1	-	-	-	-	-	-	1.6	Up
XM_141283	xin actin-binding repeat containing 2	-	-	-	-	-	-	-	2.5	Up
NM_026570	YEATS domain containing 4	Yeats4	-	-	-	-	-	-	2.1	Down
NM_023249	Yippee-like 1 (Drosophila)	Ypel1	-	-	2.0	Down	-	-	-	-
NM_146090	Zinc binding alcohol dehydrogenase, domain containing 2	Zadh2	-	-	-	-	-	-	2.0	Down
NM_198644	Zinc finger and AT hook domain containing	Zfat	-	-	-	-	2.0	Up	2.0	Up
XM_134826	zinc finger and BTB domain containing 16	-	-	-	2.3	Down	-	-	-	-
NM_173424	Zinc finger and BTB domain containing 37	Zbtb37	-	-	-	-	-	-	2.8	Up
NM_198035	Zinc finger and BTB domain containing 39	Zbtb39	-	-	-	-	-	-	1.5	Up
NM_009565	Zinc finger and BTB domain containing 7B	Zbtb7b	-	-	-	-	1.8	Up	1.8	Up
NM_028603	Zinc finger and BTB domain containing 8a	Zbtb8a	-	-	-	-	-	-	1.8	Down
NM_0010014	Zinc finger and SCAN domain containing 22	Zscan22	-	-	-	-	-	-	2.3	Up
47										
XM_146893	Zinc finger CCCH type containing 12C	Zc3h12c	-	-	-	-	-	-	3.3	Up
XM_141968	zinc finger CCCH-type containing 12B	-	-	-	-	-	-	-	2.1	Up
NM_198631	Zinc finger CCCH-type containing 4	Zc3h4	-	-	-	-	-	-	3.6	Up
XM_139193	zinc finger homeobox 2	-	-	-	-	-	-	-	2.0	Up
NM_011980	Zinc finger protein 146	Zfp146	-	-	-	-	2.1	Up	2.6	Up
XM_147946	zinc finger protein 251	-	-	-	-	-	-	-	2.7	Up
NM_031494	Zinc finger protein 275	Zfp275	-	-	-	-	2.2	Up	-	-

NM_172586	Zinc finger protein 322a	Zfp322a	-	-	-	-	-	-	1.8	Up
NM_178732	Zinc finger protein 324	Zfp324	-	-	-	-	-	-	3.8	Up
NM_145600	Zinc finger protein 330	Zfp330	-	-	-	-	-	-	3.4	Down
NM_011755	Zinc finger protein 35	Zfp35	-	-	-	-	-	-	2.8	Up
NM_009329	Zinc finger protein 354A	Zfp354a	-	-	-	-	-	-	2.9	Up
NM_178679	Zinc finger protein 365	Zfp365	-	-	-	-	-	-	2.9	Up
NM_175557	Zinc finger protein 384	Zfp384	-	-	-	-	-	-	1.7	Up
NM_178723	Zinc finger protein 385B	Zfp385b	-	-	-	-	-	-	2.3	Up
NM_146179	Zinc finger protein 418	Zfp418	-	-	-	-	-	-	3.1	Up
NM_172740	zinc finger protein 420	-	-	-	-	-	-	-	1.6	Down
NM_026057	Zinc finger protein 422	Zfp422	-	-	1.6	Down	-	-	-	-
NM_175558	Zinc finger protein 446	Zfp446	-	-	-	-	-	-	3.2	Up
NM_001003666	Zinc finger protein 457	Zfp457	-	-	-	-	-	-	2.1	Up
NM_172617	Zinc finger protein 523	Zfp523	-	-	-	-	-	-	2.9	Up
NM_172385	Zinc finger protein 536	Zfp536	-	-	-	-	-	-	2.1	Up
NM_146201	Zinc finger protein 553	Zfp553	-	-	-	-	-	-	2.1	Up
XM_356228	Zinc finger protein 558	Zfp558	-	-	-	-	-	-	3.2	Up
XM_139876	zinc finger protein 563	-	-	-	-	-	-	-	2.7	Up
NM_172536	Zinc finger protein 609	Zfp609	-	-	-	-	-	-	2.3	Up
NM_001004139	Zinc finger protein 619	Zfp619	-	-	-	-	-	-	1.7	Up
NM_170759	Zinc finger protein 628	Zfp628	-	-	1.8	Down	-	-	-	-
NM_009564	Zinc finger protein 64	Zfp64	-	-	-	-	-	-	3.4	Up
NM_172486	Zinc finger protein 677	Zfp677	-	-	-	-	-	-	1.7	Down
NM_183140	Zinc finger protein 691	Zfp691	-	-	-	-	-	-	2.2	Up
NM_175433	Zinc finger protein 710	Zfp710	-	-	-	-	-	-	1.8	Up
XM_145574	Zinc finger protein 719	Zfp719	-	-	-	-	-	-	2.1	Up
NM_146203	Zinc finger protein 764	Zfp764	-	-	-	-	1.9	Up	-	-
NM_177889	Zinc finger protein 82	Zfp82	-	-	-	-	-	-	1.6	Up
NM_009577	Zinc finger protein interacting with K protein 1	Zik1	-	-	-	-	-	-	2.9	Up
NM_009576	Zinc finger protein of the cerebellum 4	Zic4	-	-	-	-	-	-	2.0	Up
NM_022987	Zinc finger protein of the cerebellum 5	Zic5	-	-	-	-	-	-	1.7	Up
NM_023322	Zinc finger with KRAB and SCAN domains 14	Zkscan14	-	-	-	-	-	-	2.5	Down
NM_133349	Zinc finger, AN1-type domain 2A	Zfand2a	-	-	-	-	-	-	1.9	Down
NM_148926	Zinc finger, AN1-type domain 3	Zfand3	-	-	-	-	-	-	1.5	Down
NM_175472	Zinc finger, CCHC domain containing 11	Zcchc11	-	-	-	-	-	-	2.2	Down
NM_172554	Zinc finger, DHHC domain containing 17	Zdhhc17	-	-	-	-	-	-	2.2	Up
NM_029492	Zinc finger, DHHC domain containing 20	Zdhhc20	-	-	-	-	-	-	2.3	Down
NM_011769	Zinc finger, imprinted 1	Zim1	-	-	-	-	-	-	1.7	Up
NM_177086	Zinc finger, matrin type 4	Zmat4	-	-	-	-	-	-	2.7	Up

NM_053253	Zinc finger, MYND domain containing 10	Zmynd10	-	-	-	-	-	-	-	2.9	Up
NM_028028	Zinc finger, SWIM domain containing 1	Zswim1	-	-	-	-	-	-	-	1.9	Down
XM_204114	zinc finger, SWIM domain containing 5	-	-	-	-	-	-	-	-	2.7	Up
XM_111053	zinc finger, ZZ-type with EF hand domain 1	-	-	-	-	-	-	-	-	2.0	Up
NM_011775	Zona pellucida glycoprotein 2	Zp2	-	-	-	-	-	-	-	2.0	Up
XM_131619	Zyg-11 homolog A (C. elegans)	Zyg11a	-	-	-	-	-	-	-	1.6	Up

## APPENDIX III

**Appendix III: Active *F. tularensis* transcripts during mid logarithmic growth in broth culture.** Raw sequence reads from *F. tularensis* transcripts isolated from growth in broth culture were mapped to the *F. tularensis* Schu4 gene bank reference file and expression reports for each organ and time point were exported in text format. Global means for each expression report were calculated using RPKM values and genes that fell below the global mean were removed to remove background noise and potential DNA contamination.

Locus	Gene Symbol	Annotation	RPKM
FTT_0004c	<i>isftu1</i>	Transposase	7211.07
FTT_0009	<i>isftu1</i>	Transposase, fragment	4060.46
FTT_0016		hypothetical protein	713.43
FTT_0018		Secretion protein	289.70
FTT_0019	<i>gatC</i>	Glu-tRNA <sup>Gln</sup> amidotransferase C subunit	266.15
FTT_0032	<i>nuoB</i>	NADH dehydrogenase I, B subunit	1382.65
FTT_0033	<i>nuoC</i>	NADH dehydrogenase I	415.13
FTT_0036	<i>nuoF</i>	NADH dehydrogenase I, F subunit	496.19
FTT_0038	<i>nuoH</i>	NADH dehydrogenase I, H subunit	382.27
FTT_0042	<i>nuoL</i>	NADH dehydrogenase I, L subunit	570.14
FTT_0043	<i>nuoM</i>	NADH dehydrogenase I, M subunit	377.28
FTT_0044	<i>nuoN</i>	NADH dehydrogenase I, N subunit	271.02
FTT_0048		conserved hypothetical protein	283.71
FTT_0050	<i>infB</i>	translation initiation factor IF-2	273.88
FTT_0051	<i>rbfA</i>	Ribosome-binding factor A	390.91
FTT_0054		ATPase	475.93
FTT_0055	<i>rluC</i>	ribosomal large subunit pseudouridine synthase C	326.43
FTT_0056c		major facilitator superfamily (MFS) transport protein	424.69
FTT_0057		hypothetical membrane protein	2023.90
FTT_0058	<i>atpB</i>	ATP synthase A chain	646.74
FTT_0059	<i>atpE</i>	ATP synthase C chain	269.07
FTT_0060	<i>atpF</i>	ATP synthase B chain	291.94
FTT_0062	<i>atpA</i>	ATP synthase alpha chain	330.72
FTT_0063	<i>atpG</i>	ATP synthase gamma chain	292.54
FTT_0064	<i>atpD</i>	ATP synthase beta chain	498.48
FTT_0065	<i>atpC</i>	ATP synthase epsilon chain	519.18

FTT_0066		hypothetical protein	294.92
FTT_0068	<i>sodB</i>	superoxide dismutase [Fe]	646.68
FTT_0069c		hypothetical protein	2023.60
FTT_0070c	<i>ampG</i>	major facilitator superfamily (MFS) transport protein	321.20
FTT_0071c	<i>gltA</i>	citrate synthase	405.03
FTT_0072	<i>sdhC</i>	succinate dehydrogenase, cytochrome b556	430.71
FTT_0073	<i>sdhD</i>	succinate dehydrogenase hydrophobic membrane anchor protein	429.57
FTT_0075	<i>sdhB</i>	succinate dehydrogenase iron-sulfur protein	425.66
FTT_0076	<i>sucA</i>	2-oxoglutarate dehydrogenase E1 component	313.25
FTT_0080	<i>tpiA</i>	triosephosphate isomerase	306.15
FTT_0086		conserved hypothetical protein	420.56
FTT_0094c	<i>qseC</i>	sensor histidine kinase	255.73
FTT_0098c	<i>isftu1</i>	Transposase	471.27
FTT_0099	<i>isftu2</i>	Transposase	2866.77
FTT_0101		conserved membrane hypothetical protein	1047.02
FTT_0104c		major facilitator superfamily (MFS) transport protein	332.64
FTT_0106c		Efflux protein, RND family, MFP subunit	791.24
FTT_0107c	<i>dsbB</i>	disulfide bond formation protein	327.30
FTT_0109	<i>valA</i>	Lipid A transport protein, ABC transporter, ATP-binding and membrane protein	441.96
FTT_0119		hypothetical membrane protein	415.29
FTT_0131c	<i>isftu1</i>	Transposase	447.37
FTT_0132	<i>glpA</i>	anaerobic glycerol-3-phosphate dehydrogenase	262.88
FTT_0133	<i>glpF</i>	glycerol uptake facilitator protein	301.65
FTT_0135		ion channel protein, fragment	282.86
FTT_0137	<i>tufA</i>	elongation factor Tu (EF-Tu)	405.31
FTT_0138	<i>secE</i>	preprotein translocase, subunit E, membrane protein	491.13
FTT_0139	<i>nusG</i>	transcription antitermination protein nusG	498.22
FTT_0141	<i>rplA</i>	50S ribosomal protein L1	293.33
FTT_0142	<i>rplJ</i>	50S ribosomal protein L10	507.76
FTT_0143	<i>rplL</i>	50S ribosomal protein L7/L12	252.64
FTT_0144	<i>rpoB</i>	DNA-directed RNA polymerase beta chain	328.41
FTT_0145	<i>rpoC</i>	DNA-directed RNA polymerase, beta subunit	647.86
FTT_0150	<i>rpsP</i>	30S ribosomal protein S16	402.65
FTT_0151	<i>rimM</i>	16S rRNA processing protein rimM	521.67
FTT_0152	<i>trmD</i>	tRNA (Guanine-N(1)-)-methyltransferase	596.35
FTT_0153	<i>rplS</i>	50S ribosomal protein L19	499.75
FTT_0160	<i>nudH</i>	(Di)nucleoside polyphosphate hydrolase	415.29
FTT_0164c		Efflux protein	317.72
FTT_0165c		conserved hypothetical lipoprotein	646.51
FTT_0166c		conserved hypothetical membrane protein	398.55
FTT_0171	<i>isftu1</i>	Transposase	3745.21
FTT_0181c		conserved membrane protein	412.52
FTT_0184		Zinc-binding domain protein	438.26
FTT_0187	<i>ftsA</i>	cell division protein FtsA	475.62
FTT_0189	<i>lpxC</i>	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase	296.97
FTT_0194c		conserved hypothetical membrane protein	274.92
FTT_0196c	<i>glnA</i>	glutamine synthetase	311.08
FTT_0200		hypothetical protein	285.04
FTT_0202c	<i>isftu2</i>	Transposase	1076.61
FTT_0201		Transporter protein, pseudogene	2488.10
FTT_0207c		permease of ABC transporter	295.00
FTT_0208c		ABC transporter, ATP-binding protein	283.36
FTT_0209c		periplasmic solute binding family protein	285.54
FTT_0211c		outer membrane lipoprotein	292.10
FTT_0212c	<i>wrbA</i>	trp repressor binding protein	388.88
FTT_0214		Transport protein, pseudogene	281.06
FTT_0216	<i>isftu1</i>	Transposase	287.19
FTT_0221	<i>acpA</i>	acid phosphatase (precursor)	346.94

FTT_0222c	<i>ybgK</i>	hydrolase subunit	257.71
FTT_0226c	<i>isftu1</i>	Transposase	447.73
FTT_0227c		hypothetical protein	331.75
FTT_0232c	<i>ddg</i>	Acyltransferase	348.20
FTT_0233c	<i>yidC</i>	Inner-membrane protein	251.98
FTT_0234c		conserved hypothetical protein	386.55
FTT_0235c	<i>rnpA</i>	Ribonuclease P protein component	420.77
FTT_0236c	<i>rpmH</i>	50S ribosomal protein L34	1935.47
FTT_0237c		hypothetical protein	299.58
FTT_0244		DNA/RNA helicase	255.54
FTT_0245	<i>usp</i>	universal stress protein	482.48
FTT_0246c		Hypothetical protein, pseudogene	258.01
FTT_0247	<i>isftu1</i>	Transposase	349.26
FTT_0253c	<i>isftu1</i>	Transposase	423.47
FTT_0255c		hypothetical protein	253.30
FTT_0264c		conserved hypothetical protein	325.12
FTT_0266		ABC transporter, ATP-binding protein	266.23
FTT_0269		carbonic anhydrase, family 3	1360.33
FTT_0270	<i>lolB</i>	lipoprotein releasing system, subunit B, outer membrane lipoprotein	711.14
FTT_0272		hypothetical membrane protein	276.56
FTT_0273	<i>isftu1</i>	Transposase	290.40
FTT_0277c		conserved hypothetical membrane protein	280.05
FTT_0278c	<i>cydB</i>	cytochrome d terminal oxidase, polypeptide subunit II	432.27
FTT_0279c	<i>cydA</i>	cytochrome d terminal oxidase, polypeptide subunit I	424.09
FTT_0281	<i>cyoA</i>	Cytochrome O ubiquinol oxidase subunit II	310.14
FTT_0282	<i>cyoB</i>	Cytochrome O ubiquinol oxidase subunit I	267.37
FTT_0283	<i>cyoC</i>	Cytochrome O ubiquinol oxidase, subunit III	261.01
FTT_0284	<i>cyoD</i>	Cytochrome O ubiquinol oxidase subunit IV	280.89
FTT_0285	<i>cyoE</i>	Protoheme IX farnesyltransferase	265.21
FTT_0286c	<i>lpxD1</i>	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	314.66
FTT_0288c	<i>pdxY</i>	Pyridoxal/pyridoxine/pyridoxamine kinase	838.51
FTT_0289c		hypothetical lipoprotein	497.66
FTT_0290	<i>moxR</i>	methanol dehydrogenase regulatory protein	465.00
FTT_0296	<i>pcp</i>	Pyrrolidone-carboxylate peptidase	457.25
FTT_0297		hypothetical membrane protein	296.29
FTT_0298	<i>holC</i>	DNA polymerase III (CHI subunit) protein	295.93
FTT_0310		amino acid permease	320.09
FTT_0311c		conserved hypothetical protein	385.83
FTT_0315	<i>pyrH</i>	uridylyate kinase	340.54
FTT_0321	<i>rpsL</i>	30S ribosomal protein S12	445.84
FTT_0322	<i>rpsG</i>	30S ribosomal protein S7	306.64
FTT_0323	<i>fusA</i>	elongation factor G (EF-G)	401.61
FTT_0325	<i>rplC</i>	50S ribosomal protein L3	262.00
FTT_0326	<i>rplD</i>	50S ribosomal protein L4	527.79
FTT_0328	<i>rplB</i>	50S ribosomal protein L2	484.74
FTT_0329	<i>rpsS</i>	30S ribosomal protein S19	502.89
FTT_0330	<i>rplV</i>	50S ribosomal protein L22	425.91
FTT_0331	<i>rpsC</i>	30S ribosomal protein S3	541.27
FTT_0332	<i>rplP</i>	50S ribosomal protein L16	856.39
FTT_0335	<i>rplN</i>	50S ribosomal protein L14	2228.27
FTT_0336	<i>rplX</i>	50S ribosomal protein L24	730.07
FTT_0337	<i>rplE</i>	50S ribosomal protein L5	278.50
FTT_0338	<i>rpsN</i>	30S ribosomal protein S14	260.83
FTT_0339	<i>rpsH</i>	30S ribosomal protein S8	538.35
FTT_0340	<i>rplF</i>	50S ribosomal protein L6	324.38
FTT_0341	<i>rplR</i>	50S ribosomal protein L18	251.57
FTT_0342	<i>rpsE</i>	30S ribosomal protein S5	1572.43
FTT_0345	<i>secY</i>	preprotein translocase, subunit Y, membrane protein	428.74

FTT_0346	<i>rpmJ</i>	50S ribosomal protein L36	302.16
FTT_0347	<i>rpsM</i>	30S ribosomal protein S13	620.51
FTT_0349	<i>rpsD</i>	30S ribosomal protein S4	384.68
FTT_0350	<i>rpoA1</i>	DNA-directed RNA polymerase, alpha subunit	252.68
FTT_0351	<i>rplQ</i>	50S ribosomal protein L17	427.11
FTT_0352	<i>isftu1</i>	Transposase	286.47
FTT_0354		hypothetical protein	2324.77
FTT_0355c	<i>isftu1</i>	Transposase	423.82
FTT_0357c	<i>isftu1</i>	Transposase	418.83
FTT_0363	<i>isftu1</i>	Transposase	271.13
FTT_0366	<i>rpmE</i>	50S ribosomal protein L31	342.29
FTT_0371c	<i>folC</i>	FolC Bifunctional protein	275.08
FTT_0377	<i>isftu1</i>	Transposase	279.34
FTT_0378c		hypothetical protein	1051.60
FTT_0380c	<i>gdh</i>	NAD(P)-specific glutamate dehydrogenase	261.59
FTT_0383		hypothetical protein	430.91
FTT_0384c	<i>psd</i>	phosphatidylserine decarboxylase proenzyme	324.43
FTT_0388	<i>glmS</i>	Glucosamine--fructose-6-phosphate aminotransferase	411.17
FTT_0389		Acetyltransferase	365.40
FTT_0390c	<i>rpsU1</i>	30S ribosomal protein S21	339.46
FTT_0391c	<i>cspC</i>	cold shock protein	295.15
FTT_0394		hypothetical protein	327.55
FTT_0397	<i>mtn</i>	5-methylthioadenosine\S-adenosylhomocysteine nucleosidase	299.62
FTT_0403	<i>def1</i>	peptide deformylase	454.86
FTT_0407	<i>gcvT</i>	glycine cleavage complex protein T (aminomethyltransferase)	265.49
FTT_0408	<i>gcvH</i>	glycine cleavage system H protein	411.33
FTT_0409	<i>gcvP1</i>	glycine cleavage system P protein, subunit 1	295.41
FTT_0410	<i>gcvP2</i>	glycine cleavage system P protein, subunit 2	635.83
FTT_0412c	<i>pulB</i>	pullulanase	280.31
FTT_0421		outer membrane lipoprotein, pseudogene	386.25
FTT_0430	<i>speH</i>	S-adenosylmethionine decarboxylase	477.05
FTT_0431	<i>speE</i>	spermidine synthase	287.78
FTT_0433		hypothetical protein	1349.88
FTT_0434		conserved hypothetical protein	1221.79
FTT_0435		Carbon-nitrogen hydrolase family protein	411.46
FTT_0440c	<i>isftu1</i>	Transposase	460.93
FTT_0441c		NADH dehydrogenase subunit, pseudogene	268.69
FTT_0444	<i>tet</i>	multidrug transporter (tetracycline resistance protein)	321.87
FTT_0459	<i>sohB</i>	peptidase family S49 protein	300.64
FTT_0460	<i>holB</i>	DNA polymerase III, delta prime subunit	268.38
FTT_0462	<i>hemB</i>	Delta-aminolevulinic acid dehydratase	342.67
FTT_0465		hypothetical protein	321.54
FTT_0472	<i>accB</i>	Acetyl-CoA carboxylase, biotin carboxyl carrier protein subunit	404.13
FTT_0474		hypothetical membrane protein	267.72
FTT_0478c	<i>recJ</i>	Single-stranded-DNA-specific exonuclease	288.25
FTT_0481	<i>potF</i>	Putrescine-binding periplasmic protein	349.71
FTT_0486	<i>mutL</i>	DNA mismatch repair protein	258.00
FTT_0489c	<i>trxB</i>	thioredoxin reductase	253.55
FTT_0501c		conserved hypothetical membrane protein	344.35
FTT_0506c		hypothetical protein	288.05
FTT_0509c		conserved hypothetical protein	359.07
FTT_0510	<i>gyrB</i>	DNA gyrase subunit B	256.54
FTT_0511		Pyridoxine/pyridoxal 5-phosphate biosynthesis protein	347.47
FTT_0513c	<i>isftu1</i>	Transposase	434.88
FTT_0535c	<i>mdh</i>	lactate dehydrogenase	276.26
FTT_0537		ubiquinone biosynthesis protein	259.80
FTT_0540c		hypothetical protein	257.70
FTT_0544	<i>phnA</i>	phosphonoacetate hydrolase	284.26

FTT_0554		conserved hypothetical protein	261.59
FTT_0558		conserved hypothetical protein	279.59
FTT_0559c	<i>cmk</i>	cytidylate kinase	299.40
FTT_0560c	<i>serC</i>	phosphoserine aminotransferase	314.36
FTT_0561	<i>isftu1</i>	Transposase	289.33
FTT_0563	<i>potH</i>	polyamine transporter, subunit H, ABC transporter, membrane protein	284.02
FTT_0564	<i>potI</i>	polyamine transporter, subunit I, ABC transporter, membrane protein	332.45
FTT_0570		hypothetical lipoprotein	508.87
FTT_0573	<i>alr</i>	alanine racemase	325.96
FTT_0581	<i>coaD</i>	phosphopantetheine adenylyltransferase	290.93
FTT_0582	<i>fdx</i>	Ferredoxin	495.21
FTT_0583	<i>fopA</i>	outer membrane associated protein	649.19
FTT_0590	<i>rnhA</i>	Ribonuclease H	258.60
FTT_0596c		hypothetical protein	433.22
FTT_0600		major facilitator superfamily (MFS) transport protein, pseudogene	418.29
FTT_0601		hypothetical protein	378.07
FTT_0607	<i>ispG</i>	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase	743.13
FTT_0609		Peptidase, M24 family protein	379.02
FTT_0610		DNA/RNA endonuclease family protein	277.42
FTT_0614c		Apolipoprotein N-acyltransferase	336.03
FTT_0616c		cconserved hypothetical protein, UPF0054 family	256.30
FTT_0619		o-methyltransferase family protein	424.02
FTT_0622c		hypothetical membrane protein	1058.18
FTT_0629	<i>miaA</i>	tRNA delta(2)-isopentenylpyrophosphate transferase	308.45
FTT_0645c		conserved hypothetical membrane protein	251.92
FTT_0654	<i>elbB</i>	DJ-1/PfpI family protein	381.04
FTT_0655		conserved hypothetical protein	413.89
FTT_0661c		conserved hypothetical protein	887.30
FTT_0662c		conserved hypothetical protein	536.77
FTT_0665c		Aldolase/adducin class II family protein	295.76
FTT_0667		hypothetical protein	891.28
FTT_0673c		conserved hypothetical protein	276.72
FTT_0674	<i>prsA</i>	Ribose-phosphate pyrophosphokinase	326.87
FTT_0675	<i>rplY</i>	50S ribosomal protein L25	261.77
FTT_0680c	<i>pth</i>	Peptidyl-tRNA hydrolase	620.39
FTT_0683c	<i>pilD</i>	Type IV pili leader peptidase and methylase.	353.23
FTT_0692c	<i>isftu1</i>	Transposase	460.93
FTT_0695	<i>mraW</i>	S-adenosyl-methyltransferase	251.68
FTT_0697	<i>ftsI</i>	penicillin binding protein (peptidoglycan synthetase)	266.83
FTT_0700		conserved hypothetical protein	256.12
FTT_0701	<i>kdsA</i>	2-dehydro-3-deoxyphosphooctonate aldolase	469.39
FTT_0702	<i>udk</i>	uridine kinase	253.98
FTT_0705	<i>rumA</i>	23S rRNA (Uracil-5-)-methyltransferase	309.72
FTT_0709	<i>eno</i>	Enolase (2-phosphoglycerate dehydratase)	269.84
FTT_0721c	<i>katG</i>	Peroxidase/catalase	352.52
FTT_0722c	<i>isftu1</i>	Transposase	436.31
FTT_0725c	<i>glpT</i>	Glycerol-3-phosphate transporter	554.79
FTT_0748		conserved hypothetical protein	961.51
FTT_0756		Cation-efflux family protein	322.31
FTT_0759		conserved hypothetical membrane protein	407.27
FTT_0760c		hypothetical lipoprotein	286.82
FTT_0765	<i>isftu1</i>	Transposase	274.70
FTT_0766	<i>deoD</i>	purine nucleoside phosphorylase	381.15
FTT_0767c		hypothetical protein	398.92
FTT_0769	<i>secA</i>	preprotein translocase, subunit A, ATPase secretion protein	277.79
FTT_0772	<i>rplU</i>	50S ribosomal protein L21	379.63
FTT_0773	<i>rpmA</i>	50S ribosomal protein L27	397.56
FTT_0775c	<i>bcr2</i>	major facilitator superfamily (MFS) transport protein, pseudogene	541.83



FTT_0779	<i>isftu1</i>	Transposase	283.62
FTT_0781c		conserved hypothetical protein	1437.91
FTT_0792		glycosyl transferases group 1 family protein	304.64
FTT_0812	<i>gcvH1</i>	glycine cleavage system protein H	252.86
FTT_0818	<i>infC</i>	translation initiation factor IF-3	276.46
FTT_0822	<i>isftu1</i>	Transposase	347.12
FTT_0824	<i>arsC1</i>	arsenate reductase	325.94
FTT_0825c		hypothetical protein	388.41
FTT_0830c		Smf protein DNA processing chain A, pseudogene	276.52
FTT_0831c		OmpA family protein	335.44
FTT_0833	<i>ispH</i>	IspH protein	290.29
FTT_0834	<i>aroQ</i>	chorismate mutase	301.65
FTT_0836c		hypothetical protein	702.00
FTT_0837	<i>tolQ</i>	TolQ protein	293.28
FTT_0840	<i>tolB</i>	TolB protein precursor	290.24
FTT_0880		conserved hypothetical transmembrane protein,fragment	311.60
FTT_0881c		amino acid permease	282.46
FTT_0886		DNA repair protein recN	294.65
FTT_0889c		Type IV pili fiber building block protein	428.02
FTT_0890c		Type IV pili fiber building block protein methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase putative bifunctional protein	341.14
FTT_0892	<i>folD</i>		354.60
FTT_0901	<i>lpnA</i>	conserved hypothetical lipoprotein	280.67
FTT_0902		hypothetical protein	400.82
FTT_0904	<i>lpnB</i>	conserved hypothetical lipoprotein	401.53
FTT_0905		Type IV pili glycosylation protein	283.35
FTT_0910		hypothetical protein	310.53
FTT_0913		hypothetical protein	603.79
FTT_0914c	<i>lspA</i>	lipoprotein signal peptidase II	253.55
FTT_0915c	<i>ileS</i>	Isoleucyl-tRNA synthetase	318.85
FTT_0917	<i>maeA</i>	NAD-dependent malic enzyme	1038.89
FTT_0918		hypothetical protein	6125.35
FTT_0920	<i>isftu1</i>	Transposase	391.72
FTT_0927	<i>hemL</i>	Glutamate-1-semialdehyde-2,1-aminomutase	320.68
FTT_0936c	<i>bioF</i>	8-amino-7-oxononanoate synthase	289.24
FTT_0937c	<i>bioB</i>	biotin synthase	385.89
FTT_0939c	<i>add</i>	adenosine deaminase	439.49
FTT_0941c		Lipase/esterase	333.27
FTT_0948c		Aldo/keto reductase	251.92
FTT_0953c		Proton-dependent oligopeptide transport (POT) family protein	277.51
FTT_0960		conserved hypothetical protein	329.86
FTT_0964c	<i>ffh</i>	signal recognition particle protein, Ffh	288.59
FTT_0966	<i>infA</i>	translation initiation factor IF	253.20
FTT_0980		Aminotransferase, class II	473.97
FTT_0990	<i>leuS</i>	Leucyl-tRNA synthetase	293.36
FTT_0991		hypothetical lipoprotein	477.45
FTT_0995		major facilitator superfamily (MFS) transport protein	367.27
FTT_1014c		short chain dehydrogenase family protein	253.82
FTT_1015		hypothetical protein	260.15
FTT_1016c		GDSL-like Lipase/Acylhydrolase family protein	314.73
FTT_1027c	<i>yrbI</i>	3-deoxy-D-manno-octulosonate 8-phosphate phosphatase	252.51
FTT_1032		conserved hypothetical membrane protein,pseudogene	314.86
FTT_1039	<i>dacB</i>	D-alanyl-D-alanine carboxypeptidase (Penicillin binding protein) family protein	294.61
FTT_1040		conserved hypothetical lipoprotein	404.06
FTT_1041		conserved hypothetical protein	380.12
FTT_1043		FKBP-type peptidyl-prolyl cis-trans isomerase family protein	321.73
FTT_1045c		hypothetical protein	263.20
FTT_1048c		hypothetical protein	362.04
FTT_1051c		hypothetical protein	324.18

FTT_1057c		Type IV pili lipoprotein	263.67
FTT_1059c	<i>dnaB</i>	Replicative DNA helicase	256.61
FTT_1060c	<i>rplI</i>	50S ribosomal protein L9	259.79
FTT_1062c	<i>rpsF</i>	30S ribosomal protein S6	258.38
FTT_1089		isochorismatase hydrolase family protein	349.80
FTT_1093c	<i>talA</i>	Transaldolase	328.18
FTT_1095c		conserved hypothetical protein	346.27
FTT_1097		hypothetical protein	270.65
FTT_1099c		hypothetical protein	545.10
FTT_1100		conserved hypothetical protein	1232.73
FTT_1101	<i>yjeS</i>	4Fe-4S ferredoxin (electron transport) family protein, pseudogene	274.42
FTT_1103		conserved hypothetical lipoprotein	372.13
FTT_1110		hypothetical protein	388.43
FTT_1112c	<i>rpoH</i>	RNA polymerase sigma-32 factor	266.03
FTT_1113c		hypothetical protein	292.71
FTT_1114c	<i>secF</i>	preprotein translocase, subunit F, membrane protein	644.27
FTT_1115c	<i>secD</i>	preprotein translocase, subunit D, membrane protein	254.62
FTT_1116c	<i>yajC</i>	preprotein translocase family protein	262.01
FTT_1121		Transposase, fragment	315.76
FTT_1124	<i>metN</i>	D-methionine transport protein, ABC transporter,ATP-binding subunit D-methionine binding transport protein, ABC transporter, membrane and periplasmic protein	333.36
FTT_1125	<i>metIQ</i>		450.97
FTT_1128	<i>ispF</i>	2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	532.68
FTT_1137c		hypothetical protein	314.39
FTT_1140		hypothetical protein	485.14
FTT_1146c	<i>galM</i>	Aldose 1-epimerase (pseudogene) 4-phosphopantothenoylecysteine decarboxylase,phosphopantothenoylecysteine synthetase,FMN-binding (bifunctional protein)	512.90
FTT_1147c	<i>dfp</i>		269.10
FTT_1155c	<i>aroK</i>	shikimate kinase I	260.01
FTT_1156c	<i>pilQ</i>	Type IV pilin multimeric outer membrane protein	686.40
FTT_1161	<i>adk</i>	adenylate kinase	294.97
FTT_1166c		glutamine amidotransferases class-II family protein	676.01
FTT_1167c		glycoprotease family protein	285.31
FTT_1181c	<i>ggt</i>	Gamma-glutamyltranspeptidase	301.30
FTT_1190c	<i>xseA</i>	Exodeoxyribonuclease VII large subunit	323.70
FTT_1196c		major facilitator superfamily (MFS) transport protein	298.37
FTT_1202		transcriptional regulator, LysR family	438.44
FTT_1205	<i>gidA</i>	glucose inhibited division protein A	275.74
FTT_1208	<i>rpiA</i>	Ribose 5-phosphate isomerase A	318.64
FTT_1211c		hypothetical protein	290.03
FTT_1212c	<i>gloA</i>	lactoylglutathione lyase	323.08
FTT_1216c		hypothetical protein	251.56
FTT_1219c		conserved hypothetical protein	275.36
FTT_1221		hypothetical protein	615.70
FTT_1226c	<i>iscS</i>	cysteine desulfurase	262.19
FTT_1229	<i>thyA</i>	thymidylate synthase	348.96
FTT_1230	<i>serA</i>	D-3-phosphoglycerate dehydrogenase	276.00
FTT_1244c	<i>yfiO</i>	conserved hypothetical lipoprotein	478.97
FTT_1253		Proton-dependent oligopeptide transport (POT) family protein	644.23
FTT_1258		outer membrane efflux protein	347.17
FTT_1273	<i>rplM</i>	50S ribosomal subunit protein L13	1248.57
FTT_1274	<i>rpsI</i>	30S ribosomal protein S9	256.89
FTT_1275	<i>mglA</i>	macrophage growth locus, subunit A	259.21
FTT_1279c	<i>yfhQ</i>	SpoU rRNA methylase family protein	1075.79
FTT_1287	<i>cbs</i>	cystathionine beta-synthase (cystein synthase)	273.08
FTT_1288		conserved hypothetical membrane protein	284.97
FTT_1296	<i>ubiE</i>	menaquinone biosynthesis methyltransferase	435.14
FTT_1303c		hypothetical protein	359.34
FTT_1304c	<i>murB</i>	UDP-N-acetylenolpyruvoylglucosamine reductase	352.62

FTT_1314c		Type IV pili fiber building block protein	370.53
FTT_1324		conserved hypothetical membrane protein	320.49
FTT_1331	<i>cscK</i>	Fructokinase	292.50
FTT_1339c		sulfate permease family protein	340.78
FTT_1341		Membrane protein	465.05
FTT_1344	<i>pdpA</i>	conserved hypothetical protein	801.16
FTT_1345	<i>pdpB</i>	conserved hypothetical protein	399.86
FTT_1347		conserved hypothetical protein	4504.60
FTT_1348		conserved hypothetical protein	314.19
FTT_1349		conserved hypothetical protein	904.54
FTT_1350		conserved hypothetical protein	876.56
FTT_1351		conserved hypothetical protein	276.01
FTT_1352		conserved hypothetical protein	254.77
FTT_1353		conserved hypothetical protein	266.30
FTT_1354		conserved hypothetical protein	363.78
FTT_1355		conserved hypothetical protein	727.84
FTT_1356c	<i>iglD</i>	intracellular growth locus, subunit D	900.07
FTT_1357c	<i>iglC</i>	intracellular growth locus, subunit C	1589.16
FTT_1358c	<i>iglB</i>	intracellular growth locus, subunit B	1051.51
FTT_1359c	<i>iglA</i>	intracellular growth locus, subunit A	991.79
FTT_1360c	<i>pdpD</i>	conserved hypothetical protein	444.12
FTT_1365c	<i>fbaB</i>	Fructose-1,6-bisphosphate aldolase	264.80
FTT_1366c	<i>pyk</i>	pyruvate kinase	381.39
FTT_1367c	<i>pgk</i>	phosphoglycerate kinase	1109.04
FTT_1368c	<i>gapA</i>	Glyceraldehyde-3-phosphate dehydrogenase	321.78
FTT_1369c	<i>tktA</i>	Transketolase	472.80
FTT_1373	<i>fabH</i>	3-oxoacyl-[acyl carrier protein] synthase III	321.25
FTT_1376	<i>acpP</i>	acyl carrier protein	286.93
FTT_1377	<i>fabF</i>	3-oxoacyl-[acyl-carrier-protein] synthase II	288.28
FTT_1380		conserved hypothetical membrane protein,pseudogene	299.33
FTT_1382	<i>suhB</i>	Inositol-1-monophosphatase	328.32
FTT_1388		conserved hypothetical protein	324.97
FTT_1392		transcriptional regulator	270.61
FTT_1409c		conserved hypothetical protein	355.27
FTT_1416c		Hypothetical lipoprotein	717.04
FTT_1418c	<i>nusB</i>	N utilisation substance protein B	285.97
FTT_1423c		conserved hypothetical membrane protein	301.71
FTT_1424c		conserved hypothetical protein	2022.05
FTT_1432c	<i>ppnK</i>	inorganic phosphate/ATP-NAD kinase	252.71
FTT_1441		conserved hypothetical protein	413.16
FTT_1442c	<i>rpoA2</i>	DNA-directed RNA polymerase, alpha subunit	368.72
FTT_1446	<i>rho</i>	transcription termination factor Rho	262.09
FTT_1449c	<i>isftu1</i>	Transposase	481.57
FTT_1451c	<i>wbtL</i>	Glucose-1-phosphate thymidyltransferase	368.97
FTT_1453c	<i>wzx</i>	O-antigen flippase	275.72
FTT_1455c	<i>wbtI</i>	sugar transamine/perosamine synthetase	333.32
FTT_1459c	<i>wbtF</i>	NAD dependent epimerase	362.17
FTT_1462c	<i>wbtC</i>	UDP-glucose 4-epimerase	559.40
FTT_1463c	<i>wbtB</i>	galactosyl transferase	540.62
FTT_1470c	<i>gmk</i>	guanylate kinase	298.14
FTT_1475	<i>galT</i>	Galactose-1-phosphate uridylyltransferase	317.17
FTT_1477c		conserved hypothetical protein	303.39
FTT_1482		Transposase, fragmentation	636.83
FTT_1484c	<i>aceF</i>	pyruvate dehydrogenase, E2 component	296.60
FTT_1493c		hypothetical protein	632.24
FTT_1494c		glucokinase regulatory protein	738.26
FTT_1498c	<i>accA</i>	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha	558.04
FTT_1500	<i>secB2</i>	preprotein translocase, subunit B, chaperone protein	434.59

FTT_1511		conserved hypothetical membrane protein	331.00
FTT_1513		amino acid permease, fragment	272.63
FTT_1514c		hypothetical membrane protein	529.99
FTT_1516c	<i>merA</i>	mercuric reductase protein, pseudogene	296.86
FTT_1519		conserved hypothetical protein, pseudogene	333.17
FTT_1532		conserved hypothetical protein	305.25
FTT_1535c		ornithine cyclodeaminase, pseudogene	591.35
FTT_1536c		conserved hypothetical protein	308.52
FTT_1537c		conserved hypothetical protein	261.18
FTT_1538c		hypothetical protein	291.15
FTT_1540c		conserved hypothetical protein	568.84
FTT_1541c		hypothetical protein	675.86
FTT_1542c	<i>omp26</i>	outer membrane protein 26	694.13
FTT_1553c	<i>rnr</i>	Ribonuclease R	365.85
FTT_1554c	<i>truB</i>	tRNA pseudouridine synthetase B	336.43
FTT_1556c	<i>lepB</i>	signal peptidase I	280.38
FTT_1557c		Two-component response regulator	254.78
FTT_1569c	<i>lpxA</i>	Acyl-(acyl-carrier-protein)--UDP-N-acetylglucosamine O-acyltransferase	462.80
FTT_1570c	<i>fabZ</i>	(3R)-hydroxymyristoyl-(acyl-carrier protein) dehydratase	330.71
FTT_1571c	<i>lpxD</i>	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	418.97
FTT_1573c		outer membrane protein	296.18
FTT_1574c	<i>dxr</i>	1-deoxy-D-xylulose 5-phosphate reductoisomerase	574.37
FTT_1575c	<i>gyrA</i>	DNA gyrase, subunit A	457.09
FTT_1577		hypothetical protein	268.96
FTT_1587c		amino acid transporter protein, fragment	512.96
FTT_1590c	<i>ubiG</i>	3-demethylubiquinone-9 3-methyltransferase	264.36
FTT_1602		hypothetical lipoprotein	439.97
FTT_1603	<i>rpmB</i>	50S ribosomal protein L28	280.05
FTT_1604	<i>rpmG</i>	50S ribosomal protein L33	262.10
FTT_1605	<i>minC</i>	septum site-determining protein MinC	584.16
FTT_1606	<i>minD</i>	septum site-determining protein MinD	467.77
FTT_1608		ABC transporter, ATP-binding protein	358.42
FTT_1609		ABC transporter, membrane protein	255.16
FTT_1617	<i>hemK</i>	Adenine-specific methylase, HemK family	292.50
FTT_1622c		hypothetical membrane protein	337.52
FTT_1624c		hypothetical protein	293.14
FTT_1632c		conserved hypothetical protein	350.61
FTT_1638	<i>trkH</i>	potassium uptake protein	264.08
FTT_1653		hypothetical membrane protein	504.51
FTT_1654	<i>emrA2</i>	HlyD family secretion protein	289.04
FTT_1659		hypothetical protein	277.32
FTT_1674	<i>ribH</i>	riboflavin synthase beta subunit (6,7-dimethyl-8-ribityllumazine synthase)	264.28
FTT_1676		hypothetical membrane protein	514.13
FTT_1677c	<i>trmU</i>	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	624.13
FTT_1679	<i>rpsT</i>	30S ribosomal protein S20	285.18
FTT_1680c	<i>olmA</i>	outer membrane lipoprotein	531.08
FTT_1681c	<i>lpcA</i>	phosphoheptose isomerase	344.32
FTT_1696	<i>groL</i>	Chaperone protein, groEL	329.55
FTT_1724c	<i>tolC</i>	outer membrane protein tolC precursor	252.23
FTT_1734c	<i>fopA1</i>	outer membrane associated protein, fragment	610.90
FTT_1750	<i>recA</i>	Recombinase A protein	255.68
FTT_1751	<i>recX</i>	Regulatory protein recX	263.36
FTT_1752	<i>ssb</i>	Single-strand binding protein	290.03
FTT_1753	<i>tdcD</i>	propionate kinase	260.90
FTT_1769c	<i>clpB</i>	ClpB protein	261.49
FTT_1771		hypothetical protein	543.49
FTT_1772c	<i>trpA</i>	tryptophan synthase alpha chain	429.07
FTT_1776c		hypothetical membrane protein	316.55

FTT\_1778c  
FTT\_1789

hypothetical membrane protein  
conserved hypothetical membrane protein

897.16  
252.93

## APPENDIX IV

**Appendix IV: Active *F. tularensis* transcripts 48 hours post infection in the lungs of infected mice.** Raw sequence reads from *F. tularensis* transcripts isolated lungs of mice 48 hours post infection were mapped to the *F. tularensis* Schu4 gene bank reference file and expression reports for each organ and time point were exported in text format. Global means for each expression report were calculated using RPKM values and genes that fell below the global mean were removed to remove background noise and potential DNA contamination.

Locus	Gene Symbol	Common Name	RPKM
FTT_0004c	isftu1	Transposase	10471.8559
FTT_0005	gabD1	Succinate-semialdehyde dehydrogenase, fragment	618.6091
FTT_0007	aspS	Aspartyl-tRNA synthetase	589.5823
FTT_0009	isftu1	Transposase, fragment	10692.2919
FTT_0010		modification methylase, fragment	622.0136
FTT_0011		restriction endonuclease, pseudogene	596.0844
FTT_0012		conserved hypothetical protein, pseudogene	602.4007
FTT_0013c		hypothetical lipoprotein	614.5815
FTT_0014c		hypothetical protein	597.1746
FTT_0018		Secretion protein	635.1154
FTT_0019	gatC	Glu-tRNA <sup>Gln</sup> amidotransferase C subunit	629.562
FTT_0020	gatA	Glutamyl-tRNA(Gln) amidotransferase subunit A	552.4995
FTT_0021	gatB	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B	617.6782
FTT_0023c		Lipase/acyltransferase	587.9744
FTT_0024c		hypothetical protein	602.622
FTT_0025c		hypothetical membrane protein	569.497
FTT_0027c	lysA	diaminopimelate decarboxylase	584.933
FTT_0029c		conserved hypothetical protein	577.9183
FTT_0030c	fur	ferric uptake regulation protein	552.2474
FTT_0032	nuoB	NADH dehydrogenase I, B subunit	582.7773
FTT_0033	nuoC	NADH dehydrogenase I	595.6637
FTT_0034	nuoD	NADH dehydrogenase I, D subunit	631.5042

FTT_0035	nuoE	NADH dehydrogenase I, E subunit	578.0302
FTT_0036	nuoF	NADH dehydrogenase I, F subunit	551.4808
FTT_0037	nuoG	NADH dehydrogenase I, G subunit	590.1698
FTT_0038	nuoH	NADH dehydrogenase I, H subunit	644.6546
FTT_0039	nuoI	NADH dehydrogenase I, I subunit	687.9038
FTT_0042	nuoL	NADH dehydrogenase I, L subunit	575.2852
FTT_0043	nuoM	NADH dehydrogenase I, M subunit	686.1101
FTT_0044	nuoN	NADH dehydrogenase I, N subunit	684.1391
FTT_0045		conserved hypothetical protein	575.017
FTT_0046		chelatae family protein, pseudogene	585.1783
FTT_0047	hemE	uroporphyrinogen decarboxylase	636.4771
FTT_0048		conserved hypothetical protein	656.5247
FTT_0050	infB	translation initiation factor IF-2	544.2408
FTT_0053		major facilitator superfamily (MFS) transport protein	597.0394
FTT_0055	rluC	ribosomal large subunit pseudouridine synthase C	582.7457
FTT_0056c		major facilitator superfamily (MFS) transport protein	567.4437
FTT_0058	atpB	ATP synthase A chain	657.7392
FTT_0063	atpG	ATP synthase gamma chain	658.8736
FTT_0064	atpD	ATP synthase beta chain	658.2211
FTT_0068	sodB	superoxide dismutase [Fe]	572.9066
FTT_0071c	gltA	citrate synthase	635.7602
FTT_0072	sdhC	succinate dehydrogenase, cytochrome b556	655.4617
FTT_0075	sdhB	succinate dehydrogenase iron-sulfur protein	668.8566
FTT_0076	sucA	2-oxoglutarate dehydrogenase E1 component	576.9754
FTT_0078	apt	adenine phosphoribosyltransferase	548.6076
FTT_0080	tpiA	triosephosphate isomerase	551.8126
FTT_0084c	hemN	Oxygen-independent coproporphyrinogen III oxidase	600.8626
FTT_0087	acnA	aconitate hydratase	602.6797
FTT_0088	pilT	Type IV pili nucleotide-binding protein	569.8131
FTT_0089c		conserved hypothetical protein, pseudogene	593.9396
FTT_0092c	appC	cytochrome oxidase bd-II, subunit I, pseudogene	552.5488
FTT_0094c	qseC	sensor histidine kinase	567.643
FTT_0095		hypothetical protein	627.3288
FTT_0096		hypothetical protein	711.3488
FTT_0098c	isftu1	Transposase	1553.3699
FTT_0099	isftu2	Transposase	8763.1642
FTT_0105c		Transporter AcrB/AcrD/AcrF family	707.4034
FTT_0106c		Efflux protein, RND family, MFP subunit	615.4544
FTT_0107c	dsbB	disulfide bond formation protein Lipid A transport protein, ABC transporter, ATP-binding and membrane protein	541.2698
FTT_0109	valA		576.9808
FTT_0111	polA	DNA polymerase I	645.1332
FTT_0112		transcriptional regulator	613.3144
FTT_0113	deoB	Phosphopentomutase	581.6562
FTT_0114	deoC	Deoxyribose-phosphate aldolase	554.8782
FTT_0115	nupC1	nucleoside permease NUP family protein	574.2683
FTT_0118	prfC	peptide chain release factor 3	540.331
FTT_0119		hypothetical membrane protein	551.631
FTT_0121	uvrD	DNA helicase II	582.1627
FTT_0122	oppA	Similar to OPPA_HAEIN (P71370) Periplasmic oligopeptide-binding protein (precursor) from Haemophilus influenzae (541 aa). FASTA: opt: 924 Z-	652.0951

FTT ID	Gene Name	Description	Score
FTT_0123	oppB	score: 1112.1 E(): 4.7e-54 Smith-Waterman score: 924; 34.490identity in 461 aa overlap oligopeptide transporter, subunit B, ABC transporter, membrane protein, pseudogene	622.1023
FTT_0124	oppC	oligopeptide transporter, subunit C, ABC transporter, membrane protein, pseudogene	566.6286
FTT_0128		hypothetical protein	670.2974
FTT_0129		major facilitator superfamily (MFS) transport protein	544.8841
FTT_0130	glpK	glycerol kinase	616.1237
FTT_0131c	isftu1	Transposase	1458.1442
FTT_0133	glpF	glycerol uptake facilitator protein	735.9184
FTT_0135		ion channel protein, fragment	689.5441
FTT_0137	tufA	elongation factor Tu (EF-Tu)	555.9104
FTT_0141	rplA	50S ribosomal protein L1	540.3693
FTT_0142	rplJ	50S ribosomal protein L10	724.6571
FTT_0144	rpoB	DNA-directed RNA polymerase beta chain	559.7936
FTT_0145	rpoC	DNA-directed RNA polymerase, beta subunit	587.571
FTT_0147	gcp	O-sialoglycoprotein endopeptidase	640.0334
FTT_0149c	metK	S-adenosylmethionine synthetase	551.3056
FTT_0154	xerD	Integrase/recombinase	600.6115
FTT_0155		oxidoreductase iron/ascorbate family protein	674.4808
FTT_0156		acid phosphatase	555.0511
FTT_0158c		hypothetical protein	552.3562
FTT_0162	ampD	N-acetylmuramoyl-L-alanine amidase	569.5406
FTT_0163c	parE	Topoisomerase IV, subunit B	590.2012
FTT_0165c		conserved hypothetical lipoprotein	664.5095
FTT_0169		hemK protein homolog	595.6134
FTT_0170c		conserved hypothetical protein	588.0856
FTT_0171	isftu1	Transposase	4472.6341
FTT_0173		conserved hypothetical protein, pseudogene	647.4519
FTT_0175c		ABC transporter, ATP-binding protein	608.6147
FTT_0176c		ABC transporter, membrane protein, pseudogene	568.326
FTT_0183c	rpsA	30S ribosomal protein S1	578.7592
FTT_0185	ddlB	D-alanine--D-alanine ligase B	626.6056
FTT_0186	ftsQ	cell division protein FtsQ	556.6799
FTT_0187	ftsA	cell division protein FtsA	660.2964
FTT_0189	lpxC	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase	686.4224
FTT_0190c	dnaX	DNA polymerase III, gamma/tau subunits	585.0693
FTT_0191	prfB	peptide chain release factor 2	597.1387
FTT_0192	lysU	Lysyl-tRNA synthetase	618.0768
FTT_0196c	glnA	glutamine synthetase	666.1444
FTT_0199		hypothetical protein	686.2369
FTT_0200		hypothetical protein	559.432
FTT_0201	isftu2	Transposase	3036.6926
FTT_0202c		Transporter protein, pseudogene	6800.7931
FTT_0204	purA	adenylosuccinate synthetase	640.7228
FTT_0205	hpt	Hypoxanthine-guanine phosphoribosyltransferase	559.9416
FTT_0209c		periplasmic solute binding family protein	694.6947
FTT_0211c		outer membrane lipoprotein	592.793
FTT_0212c	wrbA	trp repressor binding protein	586.9363
FTT_0214		Transport protein, pseudogene	565.1629



FTT_0215	priA	Primosomal protein N	586.7129
FTT_0216	isftu1	Transposase	993.9187
FTT_0218c		cytochrome b561 family protein, pseudogene	573.756
FTT_0219c		phosphate transport protein	612.1463
FTT_0221	acpA	acid phosphatase (precursor)	559.432
FTT_0222c	ybgK	hydrolase subunit	631.3531
FTT_0226c	isftu1	Transposase	1529.5635
FTT_0227c		hypothetical protein	862.5255
FTT_0229c	efp	elongation factor P	639.3281
FTT_0230c		Type IV pili fiber building block protein	543.9231
FTT_0233c	yidC	Inner-membrane protein	600.9292
FTT_0234c		conserved hypothetical protein	734.8002
FTT_0237c		hypothetical protein	554.7379
FTT_0238	aroE1	Shikimate 5-dehydrogenase	603.6193
FTT_0239	murC	UDP-N-acetylmuramate--alanine ligase	699.4238
FTT_0240		tetrapyrrole methyltransferase family protein	599.3877
FTT_0241c		hypothetical protein	565.4028
FTT_0244		DNA/RNA helicase	540.127
FTT_0245	usp	universal stress protein	597.2585
FTT_0247	isftu1	Transposase	1196.2734
FTT_0253c	isftu1	Transposase	1434.3378
FTT_0258		Carboxylesterase/phospholipase family protein	579.6369
FTT_0259	hemC	hydroxymethylbilane synthase (porphobilinogen deaminase)	796.7774
FTT_0260	crcB	CrcB family protein	564.6835
FTT_0261		hypothetical membrane protein	555.3741
FTT_0265		ABC transporter, membrane protein	609.9573
FTT_0266		ABC transporter, ATP-binding protein	594.2006
FTT_0269		carbonic anhydrase, family 3	674.8463
FTT_0272		hypothetical membrane protein	785.9461
FTT_0273	isftu1	Transposase	1217.104
FTT_0274		hypothetical membrane protein	554.6682
FTT_0275c		major facilitator superfamily (MFS) transport protein, fragment	589.0299
FTT_0278c	cydB	cytochrome d terminal oxidase, polypeptide subunit II	635.8477
FTT_0279c	cydA	cytochrome d terminal oxidase, polypeptide subunit I	659.1767
FTT_0281	cyoA	Cytochrome O ubiquinol oxidase subunit II	701.0606
FTT_0282	cyoB	Cytochrome O ubiquinol oxidase subunit I	604.9923
FTT_0283	cyoC	Cytochrome O ubiquinol oxidase, subunit III	681.8195
FTT_0284	cyoD	Cytochrome O ubiquinol oxidase subunit IV	673.4433
FTT_0287c		conserved hypothetical protein	570.5763
FTT_0288c	pdxY	Pyridoxal/pyridoxine/pyridoxamine kinase	605.936
FTT_0289c		hypothetical lipoprotein	606.8247
FTT_0291		conserved hypothetical protein	601.9315
FTT_0293		hypothetical membrane protein	668.7391
FTT_0296	pcp	Pyrrolidone-carboxylate peptidase	578.8335
FTT_0297		hypothetical membrane protein	590.0472
FTT_0299	valS	Valyl-tRNA synthetase	650.0192
FTT_0305		MutT/nudix family protein	587.0916
FTT_0306	fumC	fumarate hydratase, Class II	543.7257
FTT_0308		hypothetical protein	601.9158

FTT_0309c	isftu2	Transposase	854.0239
FTT_0310		amino acid permease	550.6874
FTT_0313	rpsB	30S ribosomal protein S2	593.735
FTT_0317	uppS	undecaprenyl pyrophosphate synthetase	606.6373
FTT_0318	cdsA	phosphatidate cytidyltransferase	619.9967
FTT_0319	dut	dUTP pyrophosphatase (Deoxyuridine 5-triphosphate nucleotidohydrolase)	580.0822
FTT_0321	rpsL	30S ribosomal protein S12	660.3112
FTT_0322	rpsG	30S ribosomal protein S7	620.9638
FTT_0323	fusA	elongation factor G (EF-G)	576.5463
FTT_0325	rplC	50S ribosomal protein L3	712.5554
FTT_0328	rplB	50S ribosomal protein L2	574.7992
FTT_0334	rpsQ	30S ribosomal protein S17	556.192
FTT_0335	rplN	50S ribosomal protein L14	544.4351
FTT_0336	rplX	50S ribosomal protein L24	558.2909
FTT_0338	rpsN	30S ribosomal protein S14	572.5506
FTT_0340	rplF	50S ribosomal protein L6	661.216
FTT_0341	rplR	50S ribosomal protein L18	620.2955
FTT_0342	rpsE	30S ribosomal protein S5	629.4628
FTT_0343	rpmD	50S ribosomal protein L30	552.6037
FTT_0345	secY	preprotein translocase, subunit Y, membrane protein	628.9248
FTT_0346	rpmJ	50S ribosomal protein L36	573.756
FTT_0347	rpsM	30S ribosomal protein S13	628.1698
FTT_0350	rpoA1	DNA-directed RNA polymerase, alpha subunit	562.3719
FTT_0352	isftu1	Transposase	1089.1444
FTT_0353c	isftu2	Transposase, fragment	864.6258
FTT_0355c	isftu1	Transposase	1416.4829
FTT_0356	htpG	Chaperone Hsp90, heat shock protein HtpG	553.3624
FTT_0357c	isftu1	Transposase	1440.2894
FTT_0360		Short-chain dehydrogenase/reductase	540.8209
FTT_0363	isftu1	Transposase	940.3542
FTT_0365	poxF	phenol hydroxylase	574.4278
FTT_0370c	yjeE	Nucleotide-binding protein, yjeE	920.7617
FTT_0371c	folC	FolC Bifunctional protein	697.6398
FTT_0372c	accD	Acetyl-CoA carboxylase beta subunit	627.0469
FTT_0373c	ndk	nucleoside diphosphate kinase	695.8317
FTT_0374c	pyrG	CTP synthase	592.1869
FTT_0377	isftu1	Transposase	937.3784
FTT_0379	isftu2	Transposase, fragment	675.1749
FTT_0380c	gdh	NAD(P)-specific glutamate dehydrogenase	545.0682
FTT_0381	isftu2	Transposase	791.228
FTT_0385		hypothetical protein	571.5001
FTT_0389		Acetyltransferase	582.8892
FTT_0390c	rpsU1	30S ribosomal protein S21	672.4867
FTT_0391c	cspC	cold shock protein	698.5117
FTT_0392c		conserved hypothetical protein	729.1172
FTT_0396	parC	DNA topoisomerase IV subunit A	576.131
FTT_0399c		BNR/Asp-box repeat protein	590.7863
FTT_0404	lolC	lipoprotein releasing system, subunit C, putative membrane protein	573.3666
FTT_0406	cadA	lysine decarboxylase, inducible	591.0903

FTT_0407	gcvT	glycine cleavage complex protein T (aminomethyltransferase)	626.8393
FTT_0408	gcvH	glycine cleavage system H protein	553.5849
FTT_0409	gcvP1	glycine cleavage system P protein, subunit 1	566.9256
FTT_0410	gcvP2	glycine cleavage system P protein, subunit 2	573.5009
FTT_0412c	pulB	pullulanase	589.6363
FTT_0413c	glgB	1,4-alpha-glucan branching enzyme	628.0371
FTT_0415	glgC	Glucose-1-phosphate adenyltransferase,pseudogene	625.3876
FTT_0419	glyQ	Glycyl-tRNA synthetase alpha chain	591.0688
FTT_0420	murE	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6- diaminopimelate ligase	551.5571
FTT_0422	murF	UDP-N--acetylmuramoylalanyl-D-glutamyl-2,6- diaminopimelate-D-alanyl-D-alanyl ligase	608.4962
FTT_0424		hypothetical protein	549.6486
FTT_0425c	asd	aspartate semialdehyde dehydrogenase	571.7349
FTT_0428	thrC	threonine synthase	582.6403
FTT_0433		hypothetical protein	716.8697
FTT_0435		Carbon-nitrogen hydrolase family protein	548.0526
FTT_0438	mpl	UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-me so-diaminopimelate ligase	606.5779
FTT_0440c	isftu1	Transposase	1660.4989
FTT_0442c		major facilitator superfamily (MFS) transport protein	608.4573
FTT_0444	tet	multidrug transporter (tetracycline resistance protein)	612.7539
FTT_0448c	glnS	Glutaminyl-tRNA synthetase	554.5711
FTT_0452	ftsW	cell division protein FtsW	571.4112
FTT_0457c	ycck	anaerobic sulfite reductase subunit	578.4397
FTT_0458	sspA	stringent starvation protein A, regulator of transcription	590.4598
FTT_0459	sohB	peptidase family S49 protein	547.3584
FTT_0461	yhbY	RNA-binding protein	544.2309
FTT_0462	hemB	Delta-aminolevulinic acid dehydratase	591.7883
FTT_0465		hypothetical protein	543.8322
FTT_0467	ostA1	organic solvent tolerance protein	569.8888
FTT_0475	msc	mechanosensitive ion channel protein	551.1222
FTT_0478c	recJ	Single-stranded-DNA-specific exonuclease	699.5958
FTT_0480c	xasA	Glutamate:gamma-aminobutyric acid antiporter family protein (APC family protein)	617.9648
FTT_0485		hypothetical protein	581.3591
FTT_0486	mutL	DNA mismatch repair protein	628.3767
FTT_0487		hypothetical membrane protein	581.6179
FTT_0489c	trxB	thioredoxin reductase	560.052
FTT_0493		major facilitator superfamily (MFS) transport protein, pseudogene	651.7697
FTT_0494c	cutC	CutC family protein	546.0375
FTT_0495		conserved hypothetical protein	621.0811
FTT_0496		conserved hypothetical protein	717.5968
FTT_0497c		Asparaginase 2 family protein, pseudogene	587.8522
FTT_0502c		hypothetical membrane protein	542.8748
FTT_0503c	sucD	Succinyl-CoA synthetase, alpha subunit	778.6688
FTT_0506c		hypothetical protein	556.192
FTT_0507		conserved hypothetical lipoprotein	647.8768
FTT_0509c		conserved hypothetical protein	586.1889
FTT_0511		Pyridoxine/pyridoxal 5-phosphate biosynthesis protein	567.7794
FTT_0513c	isftu1	Transposase	1449.2168
FTT_0514	lldD1	L-lactate dehydrogenase, pseudogene	574.156

FTT_0515		hypothetical membrane protein	633.4933
FTT_0518	prmA	50S ribosomal protein L11, methyltransferase	563.2923
FTT_0534c	nrdA	Ribonucleoside-diphosphate reductase, alpha subunit	629.7863
FTT_0535c	mdh	lactate dehydrogenase	608.335
FTT_0537		ubiquinone biosynthesis protein	650.115
FTT_0543		hypothetical protein	578.4882
FTT_0544	phnA	phosphonoacetate hydrolase	743.5937
FTT_0546		hypothetical protein	793.9369
FTT_0547		hypothetical protein	546.818
FTT_0550		conserved hypothetical protein	671.3783
FTT_0552		aldehyde dehydrogenase	717.8109
FTT_0554		conserved hypothetical protein	581.8624
FTT_0555		conserved hypothetical membrane protein	590.3842
FTT_0558		conserved hypothetical protein	587.8186
FTT_0559c	cmk	cytidylate kinase	599.7855
FTT_0561	isftu1	Transposase	1065.338
FTT_0563	potH	polyamine transporter, subunit H, ABC transporter, membrane protein	582.7293
FTT_0564	potI	polyamine transporter, subunit I, ABC transporter, membrane protein	619.4615
FTT_0565c	isftu2	Transposase	850.8841
FTT_0567c		conserved hypothetical membrane protein,pseudogene	569.6016
FTT_0569c		conserved hypothetical membrane protein	593.7064
FTT_0570		hypothetical lipoprotein	784.5235
FTT_0571		conserved hypothetical protein	653.29
FTT_0573	alr	alanine racemase	557.4077
FTT_0574		amino acid permease family protein, pseudogene	576.2248
FTT_0577	sdaA	L-serine dehydratase 1	629.0556
FTT_0578	csdB	selenocysteine lyase	671.7927
FTT_0580		conserved hypothetical protein	554.3784
FTT_0581	coaD	phosphopantetheine adenylyltransferase	821.6628
FTT_0582	fdx	Ferredoxin	655.2213
FTT_0583	fopA	outer membrane associated protein	583.0135
FTT_0586		conserved hypothetical protein	714.116
FTT_0587c	isftu2	Transposase	857.1637
FTT_0591	ansA	L-asparaginase	630.1366
FTT_0592	cynT	carbonic anhydrase	632.4559
FTT_0595c	rubA	Rubredoxin	573.756
FTT_0597		conserved hypothetical protein	550.9291
FTT_0600		major facilitator superfamily (MFS) transport protein, pseudogene	568.2178
FTT_0607	ispG	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase	596.468
FTT_0610		DNA/RNA endonuclease family protein	559.3255
FTT_0616c		cconserved hypothetical protein, UPF0054 family	603.5835
FTT_0618c	yleA	conserved hypothetical protein yleA	657.3863
FTT_0619		o-methyltransferase family protein	640.2388
FTT_0620		HAD superfamily protein	631.0985
FTT_0621	tdk	thymidine kinase	578.1026
FTT_0622c		hypothetical membrane protein	758.5742
FTT_0629	miaA	tRNA delta(2)-isopentenylpyrophosphate transferase	597.2314
FTT_0630	hfq	host factor I for bacteriophage Q beta replication	700.802
FTT_0632c		monooxygenase family protein	594.2989

FTT_0634	hflC	SPFH domain, band 7 family protein	713.1498
FTT_0636	engB	ATP/GTP-binding protein	558.4393
FTT_0637	thrC1	threonine synthase, pseudogene	567.5946
FTT_0638		hypothetical protein	645.5631
FTT_0643	ilvC	Ketol-acid reductoisomerase, pseudogene	590.149
FTT_0647c		conserved hypothetical protein	600.2239
FTT_0648c	nth	Endonuclease III	683.6201
FTT_0650c	grxB	Glutaredoxin 2	561.3659
FTT_0653	lipA	lipoic acid synthetase	548.3918
FTT_0655		conserved hypothetical protein	703.6164
FTT_0656	ruvC	holliday junction endodeoxyribonuclease	609.0147
FTT_0658	ruvA	holliday junction DNA helicase, subunit A	596.5032
FTT_0660		hypothetical membrane protein	611.8112
FTT_0665c		Aldolase/adducin class II family protein	686.1537
FTT_0674	prsA	Ribose-phosphate pyrophosphokinase	691.8822
FTT_0682c		hypothetical protein	612.9946
FTT_0683c	pilD	Type IV pili leader peptidase and methylase.	556.192
FTT_0684c	sthA	soluble pyridine nucleotide transhydrogenase	565.8547
FTT_0685c		potassium channel protein	588.7496
FTT_0686c		Proton-dependent oligopeptide transport (POT) family protein	547.7532
FTT_0687c	hslU	ATP-dependent protease, ATP-binding subunit	554.9723
FTT_0690c	lplA	Lipoate-protein ligase A	576.8875
FTT_0692c	isftu1	Transposase	1434.3378
FTT_0694		conserved hypothetical protein	605.1369
FTT_0695	mraW	S-adenosyl-methyltransferase	692.1501
FTT_0697	ftsI	penicillin binding protein (peptidoglycan synthetase)	589.8589
FTT_0701	kdsA	2-dehydro-3-deoxyphosphooctonate aldolase	624.586
FTT_0708		major facilitator superfamily (MFS) transport protein	625.9156
FTT_0709	eno	Enolase (2-phosphoglycerate dehydratase)	603.1702
FTT_0711	ispD	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase	687.2599
FTT_0712c	sdaC1	serine transporter	747.2261
FTT_0713c	tdh	L-threonine 3-dehydrogenase	650.3654
FTT_0715		chitinase family 18 protein	626.2094
FTT_0722c	isftu1	Transposase	1324.233
FTT_0723c		Short-chain dehydrogenase/reductase family protein	612.8686
FTT_0724c	dacB1	D-alanyl-D-alanine carboxypeptidase (Penicillin binding protein) family protein, pseudogene	553.0001
FTT_0725c	glpT	Glycerol-3-phosphate transporter	610.1642
FTT_0728	ybhF	ABC transporter, ATP-binding protein	686.0298
FTT_0730	isftu2	Transposase	825.7657
FTT_0732		hypothetical protein	671.2662
FTT_0733		glutathione peroxidase	560.4432
FTT_0734		conserved hypothetical membrane protein,pseudogene	542.4659
FTT_0735		mandelate racemase/muconate lactonizing enzyme family protein, pseudogene	586.7281
FTT_0736		conserved hypothetical protein	551.5571
FTT_0738	yjeF	carbohydrate kinase family protein (YjeF-related protein)	576.0637
FTT_0742		hypothetical lipoprotein	554.3464
FTT_0743		conserved hypothetical protein	552.5113
FTT_0745c		hypothetical protein	641.2567
FTT_0747c		conserved hypothetical protein	621.1519

FTT_0756		Cation-efflux family protein	547.1173
FTT_0758	acs	Acetyl-coenzyme A synthetase, pseudogene	624.0973
FTT_0764	glyS	Glycyl-tRNA synthetase beta subunit	542.2672
FTT_0765	isftu1	Transposase	967.1365
FTT_0769	secA	preprotein translocase, subunit A, ATPase secretion protein	546.8711
FTT_0770	tag	DNA-3-methyladenine glycosylase I (pseudogene)	692.1501
FTT_0774		conserved hypothetical protein	655.0706
FTT_0775c	bcr2	major facilitator superfamily (MFS) transport protein, pseudogene	543.9751
FTT_0779	isftu1	Transposase	1011.7735
FTT_0780c		hypothetical membrane protein	761.3651
FTT_0781c		conserved hypothetical protein	549.6486
FTT_0782	fabI	Enoyl-[acyl-carrier-protein] reductase (NADH)	596.6811
FTT_0783	ars	Arylsulfatase	579.7565
FTT_0784		hypothetical protein	552.147
FTT_0785		conserved hypothetical protein	591.1063
FTT_0789	rpe	D-ribulose-phosphate 3-epimerase	666.9316
FTT_0791	galE	UDP-glucose 4-epimerase	641.2567
FTT_0792		glycosyl transferases group 1 family protein	562.1609
FTT_0801c		Carbohydrate/purine kinase pfkB family protein	607.7415
FTT_0802	cphB	Cyanophycinase	576.1579
FTT_0803	ans	Asparaginase	578.5942
FTT_0804		major facilitator superfamily (MFS) transport protein	594.6874
FTT_0805	capB	capsule biosynthesis protein capB Guanosine-3,5-bis(Diphosphate) 3-pyrophosphohydrolase/(p)ppGpp synthase	552.3562
FTT_0808	spoT		797.3657
FTT_0809c	recR	Recombination protein recR	573.3482
FTT_0814c		hypothetical protein	661.8685
FTT_0816c		chitin binding protein	627.1158
FTT_0817	thrS	Threonyl-tRNA synthetase	621.7088
FTT_0822	isftu1	Transposase	1163.5395
FTT_0824	arsC1	arsenate reductase	554.3066
FTT_0825c		hypothetical protein	709.1448
FTT_0828c		L-aspartate-beta-decarboxylase, pseudogene	616.8356
FTT_0829c		Aspartate:alanine antiporter	579.9177
FTT_0830c		Smf protein DNA processing chain A, pseudogene	549.7725
FTT_0832	fkpB	FKBP-type 16 kDa peptidyl-prolyl cis-transisomerase	597.8167
FTT_0833	ispH	IspH protein	558.9817
FTT_0834	aroQ	chorismate mutase	656.3985
FTT_0835		CDP-alcohol phosphatidyltransferase	636.576
FTT_0837	tolQ	TolQ protein	558.046
FTT_0838	tolR	TolR protein	721.1832
FTT_0840	tolB	TolB protein precursor	619.3957
FTT_0841		hypothetical lipoprotein	630.351
FTT_0842		Peptidoglycan-associated lipoprotein	625.1812
FTT_0843		conserved hypothetical protein, pseudogene	601.0368
FTT_0844		rossman fold oxidoreductase, pseudogene	588.0404
FTT_0846		deoxyribodipyrimidine photolyase	621.3777
FTT_0847		conserved hypothetical protein	647.308
FTT_0861c		Type IV pili fiber building block protein	672.4867
FTT_0863c		LemA-like protein	584.0016

FTT_0864c		transcriptional regulator, LysR family	546.8912
FTT_0865		conserved hypothetical protein, pseudogene	576.2445
FTT_0866c	isftu2	Transposase	632.8131
FTT_0867		Cadmium-transporting ATPase (pseudogene)	819.4862
FTT_0868c		arsenical resistance operon repressor	1129.7081
FTT_0871	gpsA	Glycerol-3-phosphate dehydrogenase [NAD(P)+]	876.8793
FTT_0876c	aroC	chorismate synthase	551.4652
FTT_0880		conserved hypothetical transmembrane protein, fragment	635.7486
FTT_0881c		amino acid permease	579.3966
FTT_0882		Mannose-6-phosphate isomerase, fragment	691.4579
FTT_0884c	aspC1	aspartate transaminase	549.1871
FTT_0885		cation transporter	560.0426
FTT_0886		DNA repair protein recN	563.4731
FTT_0887c		hypothetical protein	560.6416
FTT_0888c		Type IV pili fiber building block protein	661.2816
FTT_0889c		Type IV pili fiber building block protein	593.2715
FTT_0892	folD	methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase putative bifunctional protein	577.8108
FTT_0895	purN	phosphoribosylglycinamide formyltransferase	575.8905
FTT_0898c		conserved hypothetical protein	580.7022
FTT_0899c	prfC	Oligopeptidase A	583.424
FTT_0904	lpnB	conserved hypothetical lipoprotein	564.0358
FTT_0906c	topA	DNA topoisomerase I	600.542
FTT_0907	parA	chromosome partition protein A	560.3505
FTT_0909		glutamine amidotransferase, class I	541.1089
FTT_0910		hypothetical protein	574.7318
FTT_0912c	rrmJ	ribosomal large subunit methyltransferase J	579.2995
FTT_0914c	lspA	lipoprotein signal peptidase II	610.4379
FTT_0915c	ileS	Isoleucyl-tRNA synthetase	564.8677
FTT_0917	maeA	NAD-dependent malic enzyme	544.4247
FTT_0918		hypothetical protein	676.8
FTT_0919		hypothetical protein	568.6544
FTT_0920	isftu1	Transposase	907.6204
FTT_0924		hypothetical membrane protein	585.4653
FTT_0927	hemL	Glutamate-1-semialdehyde-2,1-aminomutase	542.5447
FTT_0928c		Beta-glucosidase-related glycosidase	596.606
FTT_0929c		D-Beta-hydroxybutyrate dehydrogenase, pseudogene	601.9709
FTT_0930c		acetoacetate decarboxylase, fragment	584.9156
FTT_0932		ROK family protein	594.9688
FTT_0936c	bioF	8-amino-7-oxononanoate synthase	577.7888
FTT_0937c	bioB	biotin synthase	550.5238
FTT_0939c	add	adenosine deaminase	585.8556
FTT_0942c	folK	2-amino-4-hydroxy-6-hydroxymethyl-dihydropteridine pyrophosphokinase/dihydropteroate synthase	594.1502
FTT_0946	trpG	anthranilate synthase component II	631.3531
FTT_0947c		major facilitator superfamily (MFS) transport protein, pseudogene	540.364
FTT_0948c		Aldo/keto reductase	686.5446
FTT_0953c		Proton-dependent oligopeptide transport (POT) family protein	630.2067
FTT_0955c	gor	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase component	564.2776
FTT_0959c	xthA	Exodeoxyribonuclease III	651.358

FTT_0963c	aroG	Phospho-2-dehydro-3-deoxyheptonate aldolase	629.6513
FTT_0966	infA	translation initiation factor IF	544.0015
FTT_0969c	trkA	potassium uptake protein TrkA	606.9537
FTT_0971		ABC transporter, membrane protein	573.5009
FTT_0974		amidinotransferase family protein, pseudogene	566.847
FTT_0980		Aminotransferase, class II	560.4911
FTT_0985		conserved hypothetical protein	583.0033
FTT_0986		conserved hypothetical protein	596.79
FTT_0990	leuS	Leucyl-tRNA synthetase	568.2178
FTT_0991		hypothetical lipoprotein	543.446
FTT_0994c		MRP like protein	542.6264
FTT_0997	ybhO	cardiolipin synthetase	563.1882
FTT_0998		hypothetical lipoprotein	549.7874
FTT_0999c		ZIP metal transporter family protein,pseudogene	576.3776
FTT_1002c	pheT	Phenylalanyl-tRNA synthetase, beta subunit	540.4415
FTT_1003c	pheS	Phenylalanyl-tRNA synthetase, alpha subunit	555.2047
FTT_1006		hypothetical membrane protein	573.8577
FTT_1013c	ruvB	holliday junction DNA helicase, subunit B	618.0266
FTT_1014c		short chain dehydrogenase family protein	556.6517
FTT_1018c	dxs	1-deoxy-D-xylulose 5-phosphate synthase	558.7202
FTT_1019c	guaA	GMP synthase (glutamine-hydrolyzing)	578.3536
FTT_1022c		conserved hypothetical protein	612.9946
FTT_1028c	ppa	inorganic pyrophosphatase D-alanyl-D-alanine carboxypeptidase (Penicillin binding protein) family protein	832.3701
FTT_1029	dacD		698.1772
FTT_1031	lipB	Lipoate-protein ligase B	616.9164
FTT_1033	yihQ	glycosyl hydrolases family 31 protein,pseudogene	578.7718
FTT_1037c		conserved hypothetical protein	600.986
FTT_1042		conserved hypothetical protein	639.2058
FTT_1043		FKBP-type peptidyl-prolyl cis-trans isomerase family protein	591.9032
FTT_1044c	ispB	Octaprenyl-diphosphate synthase	578.0302
FTT_1050c	cysN	sulfate adenylate transferase subunit 1	578.6286
FTT_1053c		Transposase, pseudogene	628.2821
FTT_1056c	rluB	ribosomal large subunit pseudouridine synthase B	575.4134
FTT_1058c		Radical SAM superfamily protein	648.5409
FTT_1059c	dnaB	Replicative DNA helicase	656.6885
FTT_1062c	rpsF	30S ribosomal protein S6	674.3828
FTT_1064		hypothetical protein	581.0372
FTT_1070c		conserved hypothetical protein, pseudogene	556.4387
FTT_1072		hypothetical protein	589.5635
FTT_1073c		hypothetical protein	728.4321
FTT_1075		transcriptional regulator	604.4929
FTT_1077c		hypothetical protein	567.4021
FTT_1081c		hypothetical protein	595.6235
FTT_1086c		conserved hypothetical protein	542.5382
FTT_1094c		cytosol aminopeptidase family protein	564.205
FTT_1095c		conserved hypothetical protein	559.0876
FTT_1096c	alaS	Alanyl-tRNA synthetase	542.1909
FTT_1097		hypothetical protein	590.5341
FTT_1100		conserved hypothetical protein	625.716



FTT_1102		macrophage infectivity potentiator, fragment	545.8709
FTT_1103		conserved hypothetical lipoprotein	616.978
FTT_1105c	msrA1	peptide methionine sulfoxide reductase	560.0951
FTT_1106	tspO	Tryptophan-rich sensory protein	710.1068
FTT_1107c	betT	Betaine/carnitine/choline transporter (BCCT) family protein, pseudogene	551.6901
FTT_1111	isftu2	Transposase	797.5076
FTT_1112c	rpoH	RNA polymerase sigma-32 factor	597.9539
FTT_1114c	secF	preprotein translocase, subunit F, membrane protein	657.5426
FTT_1115c	secD	preprotein translocase, subunit D, membrane protein	572.5506
FTT_1116c	yajC	preprotein translocase family protein	543.1052
FTT_1117c		isochorismatase hydrolase family protein	595.2128
FTT_1119		LysR transcriptional regulator family protein	589.335
FTT_1120c	tgt	queuine tRNA-ribosyltransferase.	653.8279
FTT_1121		Transposase, fragment	548.7264
FTT_1123	ygiH	conserved hypothetical protein	569.7577
FTT_1124	metN	D-methionine transport protein, ABC transporter,ATP-binding subunit	681.0641
FTT_1127		Rhodanese-like family protein	563.2269
FTT_1129c		conserved hypothetical protein	547.285
FTT_1131		molybdopterin binding family protein, fragment	637.3781
FTT_1134	pilC	Type IV pili polytopic inner membrane protein	586.8504
FTT_1140		hypothetical protein	578.1026
FTT_1143		hypothetical protein	645.7254
FTT_1146c	galM	Aldose 1-epimerase (pseudogene)	606.0732
FTT_1150c	putA	Multifunctional protein, transcriptional repressor of proline utilization, proline dehydrogenase,pyrroline-5-carboxylate dehydrogenase	588.3021
FTT_1156c	pilQ	Type IV pilin multimeric outer membrane protein	584.9831
FTT_1161	adk	adenylate kinase	707.5575
FTT_1162c		FAD-binding family protein, pseudogene	578.4234
FTT_1165c	aspC2	aspartate aminotransferase	543.8943
FTT_1166c		glutamine amidotransferases class-II family protein	541.3051
FTT_1168c	nagA	N-acetylglucosamine-6-phosphate deacetylase	624.171
FTT_1176c	hsdR1	Type I restriction enzyme subunit R, pseudogene	657.6236
FTT_1178c		hypothetical membrane protein	591.0378
FTT_1179	bipA	GTP binding translational elongation factor Tu and G family protein	578.2194
FTT_1180		conserved hypothetical protein, pseudogene	599.4514
FTT_1182c	vacJ	VacJ lipoprotein, pseudogene	563.0765
FTT_1183c		conserved hypothetical lipoprotein	602.403
FTT_1184c		conserved hypothetical protein	740.4988
FTT_1187		conserved hypothetical protein	590.1815
FTT_1191		Aminoacylase	601.6072
FTT_1195c		conserved hypothetical protein, pseudogene	548.7048
FTT_1196c		major facilitator superfamily (MFS) transport protein	618.5687
FTT_1197c	murl	glutamate racemase	582.538
FTT_1199c	uvrB	DNA excision repair enzyme, subunit B (UvrABC system protein B)	584.2926
FTT_1201c		Oxidoreductase, short-chain dehydrogenase family protein	542.8065
FTT_1202		transcriptional regulator, LysR family	542.4726
FTT_1205	gidA	glucose inhibited division protein A	626.1589
FTT_1208	rpiA	Ribose 5-phospate isomerase A	588.3276
FTT_1209c		metallopeptidase family M13 protein, pseudogene	1454.0821
FTT_1214c		haloacid dehalogenase-like hydrolase family protein	722.6283

FTT_1215c	queA	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	614.2578
FTT_1217c	visC	monooxygenase family protein	551.8721
FTT_1218c	ubiH	2-octaprenyl-6-methoxyphenyl hydroxylase	589.7838
FTT_1229	thyA	thymidylate synthase	566.3046
FTT_1233c	yjdL	Proton-dependent oligopeptide transport (POT) family protein	578.289
FTT_1241	glyA	serine hydroxymethyltransferase	547.6762
FTT_1244c	yfiO	conserved hypothetical lipoprotein	639.9242
FTT_1245	rluD	ribosomal large subunit pseudouridine synthase D	617.323
FTT_1247		ABC transporter, membrane protein	672.5832
FTT_1248		ABC transporter, ATP-binding protein	561.0094
FTT_1249		mycobacterial cell entry (mce) related family protein	550.2164
FTT_1253		Proton-dependent oligopeptide transport (POT) family protein	646.7975
FTT_1254	fadD1	Acyl-CoA synthetase (long-chain-fatty-acid--CoA ligase)	659.9356
FTT_1255c		transcriptional regulator araC family protein	616.3315
FTT_1256	emrB	major facilitator superfamily (MFS) transport protein	545.0682
FTT_1257	emrA1	HlyD family secretion protein	616.5413
FTT_1264	isftu2	Transposase	629.6643
FTT_1273	rplM	50S ribosomal subunit protein L13	578.8788
FTT_1274	rpsI	30S ribosomal protein S9	608.8839
FTT_1275	mgIA	macrophage growth locus, subunit A	616.1312
FTT_1276	mgIB	macrophage growth locus, subunit B	669.8842
FTT_1279c	yfhQ	SpoU rRNA methylase family protein	577.722
FTT_1285c		LysR transcriptional regulator family protein	665.9323
FTT_1286		choloylglycine hydrolase family protein,pseudogene	546.3955
FTT_1290	metG	Methionyl-tRNA synthetase	572.1774
FTT_1292c		conserved hypothetical protein	581.0961
FTT_1295c	glk	glucose kinase	643.1483
FTT_1296	ubiE	menaquinone biosynthesis methyltransferase	648.3737
FTT_1297		hypothetical protein	589.7838
FTT_1299	hitA	histidine triad (HIT) family protein	599.5061
FTT_1304c	murB	UDP-N-acetylenolpyruvoylglucosamine reductase	2380.0302
FTT_1307c		hypothetical protein	617.7149
FTT_1312c	uvrA	DNA excision repair enzyme, subunit A (UvrABC system protein A), ABC transporter, ATP-binding protein	565.1762
FTT_1313c	greA	transcriptional elongation factor	686.7762
FTT_1314c		Type IV pili fiber building block protein	630.9214
FTT_1315c	pgi	Glucose-6-phosphate isomerase	572.8469
FTT_1318c	pepA	cytosol aminopeptidase	592.1128
FTT_1319		Permease YjgP/YjgQ family protein	569.442
FTT_1321		Peptidase M16 family protein	560.7161
FTT_1326	udp	uridine phosphorylase	624.6784
FTT_1327	cdd	cytidine deaminase	586.9071
FTT_1328c		FAD-binding family protein, pseudogene	558.1745
FTT_1329	gpml	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	623.8458
FTT_1336	cydC	ABC transporter, ATP-binding and membrane protein	543.6524
FTT_1337c	dctA	C4-dicarboxylate transport protein	601.2743
FTT_1338c		translation initiation inhibitor	570.2063
FTT_1339c		sulfate permease family protein	550.3601
FTT_1340c	isftu2	Transposase	863.4433
FTT_1343c		hypothetical protein	697.918

FTT_1344	pdpA	conserved hypothetical protein	1033.7991
FTT_1345	pdpB	conserved hypothetical protein	664.075
FTT_1347		conserved hypothetical protein	783.388
FTT_1349		conserved hypothetical protein	1056.1255
FTT_1350		conserved hypothetical protein	783.5661
FTT_1351		conserved hypothetical protein	722.5148
FTT_1352		conserved hypothetical protein	586.0294
FTT_1354		conserved hypothetical protein	1154.8204
FTT_1356c	iglD	intracellular growth locus, subunit D	1003.3593
FTT_1357c	iglC	intracellular growth locus, subunit C	1043.1224
FTT_1358c	iglB	intracellular growth locus, subunit B	960.1062
FTT_1359c	iglA	intracellular growth locus, subunit A	1063.2585
FTT_1366c	pyk	pyruvate kinase	542.9549
FTT_1367c	pgk	phosphoglycerate kinase	602.3291
FTT_1368c	gapA	Glyceraldehyde-3-phosphate dehydrogenase	557.7857
FTT_1369c	tktA	Transketolase	620.3551
FTT_1373	fabH	3-oxoacyl-[acyl carrier protein] synthase III	564.7752
FTT_1374		malonyl coA-acyl carrier protein transacylase	583.3675
FTT_1375	fabG	3-oxoacyl-(acyl-carrier-protein) reductase	637.3781
FTT_1377	fabF	3-oxoacyl-[acyl-carrier-protein] synthase II	596.9794
FTT_1379c		conserved hypothetical protein, pseudogene	633.3315
FTT_1382	suhB	Inositol-1-monophosphatase	598.065
FTT_1387c	ligN	DNA ligase	587.1553
FTT_1390	panC	Pantoate-beta-alanine ligase	543.8794
FTT_1392		transcriptional regulator	593.8486
FTT_1398c		conserved hypothetical membrane, pseudogene	544.5271
FTT_1402c		hypothetical protein	557.2126
FTT_1406c		hypothetical membrane protein	645.5286
FTT_1409c		conserved hypothetical protein	694.6398
FTT_1412	proS	Prolyl-tRNA synthetase	628.7132
FTT_1413		Aminotransferase	673.3317
FTT_1418c	nusB	N utilisation substance protein B	751.2509
FTT_1419		hypothetical lipoprotein	692.9438
FTT_1420		hypothetical protein	579.0102
FTT_1422		Oxidoreductase	564.2528
FTT_1423c		conserved hypothetical membrane protein	610.4764
FTT_1425c	naoX	NADH oxidase	581.5898
FTT_1430c		Methyltransferase, fragment	580.1846
FTT_1432c	ppnK	inorganic phosphate/ATP-NAD kinase	561.061
FTT_1433	gtrB	glycosyl transferase	642.7108
FTT_1434c	yadH	ABC transporter, membrane protein	697.8071
FTT_1435c	yagD	ABC transporter, ATP-binding protein	576.4172
FTT_1436	isftu2	Transposase	791.228
FTT_1439c		Deoxyribonuclease	568.7933
FTT_1445	trxA1	Thioredoxin	540.7422
FTT_1448c	manC	Mannose-1-phosphate guanylttransferase	567.8139
FTT_1449c	isftu1	Transposase	3530.5006
FTT_1451c	wbtL	Glucose-1-phosphate thymidyltransferase	578.0626
FTT_1459c	wbtF	NAD dependent epimerase	622.4544

FTT_1460c	wbtE	UDP-glucose/GDP-mannose dehydrogenase	625.4297
FTT_1461c	wbtD	galacturonosyl transferase	714.4928
FTT_1462c	wbtC	UDP-glucose 4-epimerase	554.5066
FTT_1465c	isftu2	Transposase	850.8841
FTT_1467c	nadB	L-aspartate oxidase	547.894
FTT_1468c	nadC	Nicotinate-nucleotide pyrophosphorylase	578.5942
FTT_1469c	nadA	quinolinate sythetase A	555.5415
FTT_1470c	gmk	guanylate kinase	680.8256
FTT_1471c	deaD	Cold-shock DEAD-box protein A	569.6577
FTT_1474c	galP1	Galactose-proton symporter, major facilitator superfamily (MFS) transport protein	560.7767
FTT_1475	galT	Galactose-1-phosphate uridylyltransferase	591.9705
FTT_1479c		conserved hypothetical protein	556.192
FTT_1483c	lpd	dihydrolipoamide dehydrogenase	626.5722
FTT_1485c	aceE	pyruvate dehydrogenase, E1 component	631.4708
FTT_1486c		conserved hypothetical protein	581.4335
FTT_1490		Na <sup>+</sup> /H <sup>+</sup> antiporter	636.6022
FTT_1493c		hypothetical protein	725.5778
FTT_1494c		glucokinase regulatory protein	591.2604
FTT_1497c		hypothetical membrane protein	551.5571
FTT_1498c	accA	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha	611.1072
FTT_1503	xerC	Integrase/recombinase XerC	613.8993
FTT_1506		hypothetical protein	564.8375
FTT_1507		hypothetical protein	619.9828
FTT_1508c	relA	GTP pyrophosphokinase	650.0923
FTT_1510c		aromatic amino acid transporter of the HAAAP family	571.8044
FTT_1511		conserved hypothetical membrane protein	554.3066
FTT_1513		amino acid permease, fragment	553.8649
FTT_1514c		hypothetical membrane protein	866.5831
FTT_1516c	merA	mercuric reductase protein, pseudogene	555.9564
FTT_1517c		conserved hypothetical membrane protein	574.2683
FTT_1520c	gabP	Glutamate/gamma-aminobutyrate anti-porter	632.0137
FTT_1521c	lysA1	diaminopimelate decarboxylase, pseudogene	574.6221
FTT_1522c		conserved hypothetical protein	553.3687
FTT_1523c	isftu2	Transposase	857.1637
FTT_1526c	idh	isocitrate dehydrogenase	578.7966
FTT_1529	fadE	Acyl-CoA dehydrogenase	552.5037
FTT_1530	fadB/acbP	fusion product of 3-hydroxacyl-CoA dehydrogenase and acyl-CoA-binding protein	635.7541
FTT_1531	fadA	3-ketoacyl-CoA thiolase	593.8333
FTT_1532		conserved hypothetical protein	721.3435
FTT_1536c		conserved hypothetical protein	622.9351
FTT_1537c		conserved hypothetical protein	550.9291
FTT_1539c		conserved hypothetical protein	577.88
FTT_1540c		conserved hypothetical protein	602.2217
FTT_1541c		hypothetical protein	610.4764
FTT_1542c	omp26	outer membrane protein 26	796.0693
FTT_1543		two component response regulator	619.5496
FTT_1549		hypothetical protein	563.5103
FTT_1550		conserved hypothetical protein	623.7955
FTT_1551		Oxidoreductase	562.0231

FTT_1552	ole1	Delta 9 acyl-lipid fatty acid desaturase	572.7166
FTT_1553c	rnr	Ribonuclease R	637.3699
FTT_1554c	truB	tRNA pseudouridine synthetase B	598.7783
FTT_1555c	rnc	Ribonuclease III	546.0794
FTT_1561	kdtA	3-Deoxy-D-manno-octulosonic-acid transferase	544.3472
FTT_1566c		hypothetical protein	589.9006
FTT_1571c	lpxD	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	575.9385
FTT_1575c	gyrA	DNA gyrase, subunit A	555.552
FTT_1577		hypothetical protein	582.9261
FTT_1578c	ung	Uracil-DNA glycosylase	708.2011
FTT_1587c		amino acid transporter protein, fragment	624.8001
FTT_1589c		hypothetical protein	1444.3051
FTT_1591		Lipoprotein	637.279
FTT_1600c	fumA	fumerate hydratase	541.2134
FTT_1602		hypothetical lipoprotein	650.0192
FTT_1606	minD	septum site-determining protein MinD	642.7557
FTT_1608		ABC transporter, ATP-binding protein	557.8523
FTT_1609		ABC transporter, membrane protein	592.399
FTT_1610		ABC transporter, periplasmic protein,pseudogene	625.5598
FTT_1614c		hypothetical protein	597.6625
FTT_1616	cysS	CysteinyI-tRNA synthetase	678.1954
FTT_1617	hemK	Adenine-specific methylase, HemK family	711.9258
FTT_1621c		hypothetical membrane protein	551.1001
FTT_1622c		hypothetical membrane protein	568.1492
FTT_1623c		hypothetical protein	727.7279
FTT_1624c		hypothetical protein	654.9551
FTT_1629c		hypothetical membrane protein	606.2493
FTT_1630c	putP	Sodium/proline permease	601.9158
FTT_1631c	gplX	GlpX protein	570.3927
FTT_1632c		conserved hypothetical protein	581.2598
FTT_1640c		ProP osmoprotectant transporter, fragment	556.192
FTT_1641c	hsdR2	HsdR protein, fragment	556.7684
FTT_1642c	hsdR3	HsdR protein, fragment	606.0075
FTT_1645		conserved hypothetical membrane protein	564.5823
FTT_1647c	pyrD	diyrorotate dehydrogenase	556.6388
FTT_1649		Transglutaminase-like superfamily domain protein,pseudogene	589.5241
FTT_1652c		transcriptional regulator, LysR family	545.0682
FTT_1655		hypothetical membrane protein	607.581
FTT_1656c		conserved hypothetical protein	799.8283
FTT_1658c		conserved hypothetical membrane protein	540.4878
FTT_1660c	pyrC	Dihydroorotate	563.6244
FTT_1663	carA	Carbamoyl-phosphate synthase small chain	570.49
FTT_1664	carB	Carbamoyl-phosphate synthase large chain	634.3129
FTT_1665	pyrB	aspartate carbamoyltransferase	603.6586
FTT_1673	ribA	riboflavin biosynthesis protein ribA/GTP-cyclohydrolase II	587.8564
FTT_1676		hypothetical membrane protein	559.8888
FTT_1678c	lepA	GTP-binding protein LepA	566.6615
FTT_1679	rpsT	30S ribosomal protein S20	633.2032
FTT_1681c	lpcA	phosphoheptose isomerase	618.2396

FTT_1684		transcription regulator	631.2133
FTT_1686c		conserved hypothetical protein	544.719
FTT_1687c	gidB	methyltransferase glucose-inhibited cell division protein	551.8721
FTT_1690		NADH dehydrogenase	540.1577
FTT_1691		hypothetical protein	836.5128
FTT_1719c		modification methylase, pseudogene	574.9473
FTT_1720c	purL	phosphoribosylformylglycinamide synthase	569.3752
FTT_1721c	purF	Amidophosphoribosyltransferase	664.297
FTT_1724c	tolC	outer membrane protein tolC precursor	615.3011
FTT_1725c	pcm	Protein-L-isoaspartate O-methyltransferase	571.7761
FTT_1726	yegQ	protease yegQ	626.0918
FTT_1727c		multidrug resistance protein, membrane located	609.9899
FTT_1728	nhaD	Na <sup>+</sup> /H <sup>+</sup> antiporter	575.8223
FTT_1729c	abcZ	ABC transporter, ATP-binding protein,pseudogene	565.0882
FTT_1731c		GTP-binding protein	578.7718
FTT_1736c	kdpD	two component sensor protein kdpD	590.5341
FTT_1738c	kdpB	Potassium-transporting ATPase B chain	622.9351
FTT_1739c	kdpA	Potassium-transporting ATPase, A chain,pseudogene	572.3216
FTT_1743		NA <sup>+</sup> /H <sup>+</sup> antiporter NHAP, fragment	614.4917
FTT_1746		Peptidase	659.846
FTT_1749	secB1	preprotein translocase, subunit B, chaperone protein	628.1262
FTT_1752	ssb	Single-strand binding protein	602.3665
FTT_1753	tdcD	propionate kinase	669.4529
FTT_1754	pta	phosphate acetyltransferase	644.9918
FTT_1755	gabD2	Succinate-semialdehyde dehydrogenase,pseudogene	568.0801
FTT_1757c		major facilitator superfamily (MFS) transport protein, pseudogene	610.0399
FTT_1759c		Oxidase-like protein, pseudogene	637.8085
FTT_1760	nhaA	Na <sup>(+)</sup> /H <sup>(+)</sup> antiporter 1	588.0572
FTT_1762c		Acetyltransferase protein	542.2309
FTT_1765		hypothetical membrane protein	578.6438
FTT_1766		O-methyltransferase	572.446
FTT_1768c		Chitinase	649.1045
FTT_1769c	clpB	ClpB protein	545.0682
FTT_1772c	trpA	tryptophan synthase alpha chain	643.1228
FTT_1776c		hypothetical membrane protein	655.7211
FTT_1783		major facilitator superfamily (MFS) transport protein	1274.1854
FTT_1793c	pepN	Aminopeptidase N	642.7394
FTT_1796c		conserved hypothetical protein	569.8953
FTT_1797c	msrA2	peptide methionine sulfoxide reductase msrA	599.2365
FTT_1798c		hypothetical protein	557.0964
FTT_1801c	trpG1	anthranilate synthase component II, pseudogene	606.8314

## APPENDIX V

**Appendix V: Active *F. tularensis* transcripts 96 hours post infection in the in the lungs of infected mice.** Raw sequence reads from *F. tularensis* transcripts isolated lungs of mice 96 hours post infection were mapped to the *F. tularensis* Schu4 gene bank reference file and expression reports for each organ and time point were exported in text format. Global means for each expression report were calculated using RPKM values and genes that fell below the global mean were removed to remove background noise and potential DNA contamination.

Locus	Gene Symbol	Annotation	RPKM
FTT_0004c	<i>isftu1</i>	Transposase	10702.53
FTT_0005	<i>gabD1</i>	Succinate-semialdehyde dehydrogenase, fragment	626.46
FTT_0006		Proline/betaine transporter, major facilitator superfamily (MFS) transport protein	588.09
FTT_0007	<i>aspS</i>	Aspartyl-tRNA synthetase	605.84
FTT_0009	<i>isftu1</i>	Transposase, fragment	10901.20
FTT_0010		modification methylase, fragment	578.28
FTT_0011		restriction endonuclease, pseudogene	646.70
FTT_0012		conserved hypothetical protein, pseudogene	577.56
FTT_0013c		hypothetical lipoprotein	639.73
FTT_0014c		hypothetical protein	633.65
FTT_0015	<i>purB</i>	adenylosuccinate lyase	567.45
FTT_0018		Secretion protein	612.28
FTT_0019	<i>gatC</i>	Glu-tRNA <sup>Gln</sup> amidotransferase C subunit	639.79
FTT_0020	<i>gatA</i>	Glutamyl-tRNA(Gln) amidotransferase subunit A	574.61
FTT_0021	<i>gatB</i>	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B	563.44
FTT_0023c		Lipase/acyltransferase	654.05
FTT_0025c		hypothetical membrane protein	580.30
FTT_0026c		conserved membrane protein	581.04
FTT_0027c	<i>lysA</i>	diaminopimelate decarboxylase	632.30
FTT_0029c		conserved hypothetical protein	639.24
FTT_0030c	<i>fur</i>	ferric uptake regulation protein	774.49
FTT_0031	<i>nuoA</i>	NADH dehydrogenase I, A subunit	556.31

FTT_0032	<i>nuoB</i>	NADH dehydrogenase I, B subunit	582.30
FTT_0033	<i>nuoC</i>	NADH dehydrogenase I	598.05
FTT_0034	<i>nuoD</i>	NADH dehydrogenase I, D subunit	577.40
FTT_0037	<i>nuoG</i>	NADH dehydrogenase I, G subunit	570.68
FTT_0038	<i>nuoH</i>	NADH dehydrogenase I, H subunit	742.01
FTT_0039	<i>nuoI</i>	NADH dehydrogenase I, I subunit	699.08
FTT_0040	<i>nuoJ</i>	NADH dehydrogenase I, J subunit	683.59
FTT_0042	<i>nuoL</i>	NADH dehydrogenase I, L subunit	556.29
FTT_0043	<i>nuoM</i>	NADH dehydrogenase I, M subunit	664.41
FTT_0044	<i>nuoN</i>	NADH dehydrogenase I, N subunit	785.63
FTT_0046		chelataase family protein, pseudogene	575.56
FTT_0047	<i>hemE</i>	uroporphyrinogen decarboxylase	564.25
FTT_0048		conserved hypothetical protein	584.44
FTT_0050	<i>infB</i>	translation initiation factor IF-2	573.64
FTT_0051	<i>rbfA</i>	Ribosome-binding factor A	557.77
FTT_0054		ATPase	650.17
FTT_0056c		major facilitator superfamily (MFS) transport protein	686.72
FTT_0058	<i>atpB</i>	ATP synthase A chain	603.98
FTT_0059	<i>atpE</i>	ATP synthase C chain	589.61
FTT_0063	<i>atpG</i>	ATP synthase gamma chain	652.38
FTT_0064	<i>atpD</i>	ATP synthase beta chain	668.92
FTT_0067c		Glutaredoxin-related protein	582.70
FTT_0068	<i>sodB</i>	superoxide dismutase [Fe]	571.97
FTT_0070c	<i>ampG</i>	major facilitator superfamily (MFS) transport protein	571.93
FTT_0071c	<i>gltA</i>	citrate synthase	687.06
FTT_0072	<i>sdhC</i>	succinate dehydrogenase, cytochrome b556	545.91
FTT_0073	<i>sdhD</i>	succinate dehydrogenase hydrophobic membrane anchor protein	726.99
FTT_0074	<i>sdhA</i>	succinate dehydrogenase, catalytic and NAD/ flavoprotein subunit	575.63
FTT_0075	<i>sdhB</i>	succinate dehydrogenase iron-sulfur protein	554.60
FTT_0076	<i>sucA</i>	2-oxoglutarate dehydrogenase E1 component	606.93
FTT_0077	<i>sucB</i>	dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex	630.64
FTT_0078	<i>apt</i>	adenine phosphoribosyltransferase	636.21
FTT_0079	<i>mrsA</i>	phosphoglucosamine mutase	571.21
FTT_0080	<i>tpiA</i>	triosephosphate isomerase	598.17
FTT_0083		hypothetical membrane protein	627.09
FTT_0087	<i>acnA</i>	aconitate hydratase	600.66
FTT_0089c		conserved hypothetical protein, pseudogene	616.66
FTT_0092c	<i>appC</i>	cytochrome oxidase bd-II, subunit I, pseudogene	596.08
FTT_0095		hypothetical protein	677.21
FTT_0096		hypothetical protein	575.82
FTT_0097		hypothetical protein	600.01
FTT_0098c	<i>isftu1</i>	Transposase	1483.35
FTT_0099	<i>isftu2</i>	Transposase	9042.79
FTT_0104c		major facilitator superfamily (MFS) transport protein	569.34
FTT_0105c		Transporter AcrB/AcrD/AcrF family	654.10
FTT_0106c		Efflux protein, RND family, MFP subunit	659.15
FTT_0107c	<i>dsbB</i>	disulfide bond formation protein	579.02
FTT_0109	<i>valA</i>	Lipid A transport protein, ABC transporter, ATP-binding and membrane protein	612.95
FTT_0110	<i>valB</i>	Tetraacyldisaccharide 4-kinase	552.46



FTT_0111	<i>polA</i>	DNA polymerase I	660.46
FTT_0112		transcriptional regulator	545.37
FTT_0113	<i>deoB</i>	Phosphopentomutase	628.29
FTT_0115	<i>nupC1</i>	nucleoside permease NUP family protein	588.55
FTT_0116	<i>nupC</i>	nucleoside permease NUP family protein	546.63
FTT_0117	<i>tmk</i>	thymidylate kinase	565.23
FTT_0118	<i>prfC</i>	peptide chain release factor 3	553.63
FTT_0119		hypothetical membrane protein Similar to OPPA_HAEIN (P71370) Periplasmic oligopeptide-binding protein (precursor) from Haemophilus influenzae (541 aa). FASTA: opt: 924 Z-score: 1112.1 E(): 4.7e-54 Smith-Waterman score: 924; 34.490identity in 461 aa	548.88
FTT_0122	<i>oppA</i>	overlap oligopeptide transporter, su	621.99
FTT_0123	<i>oppB</i>	oligopeptide transporter, subunit B, ABC transporter, membrane protein, pseudogene	686.80
FTT_0124	<i>oppC</i>	oligopeptide transporter, subunit C, ABC transporter, membrane protein, pseudogene	636.95
FTT_0125	<i>oppD</i>	oligopeptide transporter, subunit D, ABC transporter, ATP-binding protein	602.68
FTT_0128		hypothetical protein	777.05
FTT_0129		major facilitator superfamily (MFS) transport protein	587.41
FTT_0130	<i>glpK</i>	glycerol kinase	577.37
FTT_0131c	<i>isftu1</i>	Transposase	1442.53
FTT_0133	<i>glpF</i>	glycerol uptake facilitator protein	692.02
FTT_0135		ion channel protein, fragment	588.73
FTT_0137	<i>tufA</i>	elongation factor Tu (EF-Tu)	586.98
FTT_0141	<i>rplA</i>	50S ribosomal protein L1	562.80
FTT_0142	<i>rplJ</i>	50S ribosomal protein L10	642.66
FTT_0144	<i>rpoB</i>	DNA-directed RNA polymerase beta chain	625.37
FTT_0145	<i>rpoC</i>	DNA-directed RNA polymerase, beta subunit	586.80
FTT_0147	<i>gcp</i>	O-sialoglycoprotein endopeptidase	577.64
FTT_0148		fatty acid desaturase	599.09
FTT_0149c	<i>metK</i>	S-adenosylmethionine synthetase	590.94
FTT_0152	<i>trmD</i>	tRNA (Guanine-N(1)-)-methyltransferase	570.99
FTT_0155		oxidoreductase iron/ascorbate family protein	674.30
FTT_0160	<i>nudH</i>	(Di)nucleoside polyphosphate hydrolase	550.38
FTT_0163c	<i>parE</i>	Topoisomerase IV, subunit B	577.74
FTT_0164c		Eflux protein	553.32
FTT_0165c		conserved hypothetical lipoprotein	740.24
FTT_0166c		conserved hypothetical membrane protein	592.59
FTT_0169		hemK protein homolog	567.81
FTT_0171	<i>isftu1</i>	Transposase	4655.71
FTT_0173		conserved hypothetical protein, pseudogene	588.23
FTT_0175c		ABC transporter, ATP-binding protein	639.73
FTT_0176c		ABC transporter, membrane protein, pseudogene	594.51
FTT_0180		Acetyltransferase	556.86
FTT_0181c		conserved membrane protein	596.81
FTT_0182c		Sua5/YciO/YrdC family protein	607.70
FTT_0183c	<i>rpsA</i>	30S ribosomal protein S1	622.97
FTT_0184		Zinc-binding domain protein	565.23
FTT_0185	<i>ddlB</i>	D-alanine--D-alanine ligase B	580.84
FTT_0187	<i>ftsA</i>	cell division protein FtsA	618.40
FTT_0189	<i>lpxC</i>	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase	738.94
FTT_0191	<i>prfB</i>	peptide chain release factor 2	576.50

FTT_0192	<i>lysU</i>	Lysyl-tRNA synthetase	548.58
FTT_0196c	<i>glnA</i>	glutamine synthetase	576.34
FTT_0197c	<i>holA</i>	DNA polymerase III, delta subunit	560.72
FTT_0199		hypothetical protein	710.20
FTT_0200		hypothetical protein	622.30
FTT_0201	<i>isftu2</i>	Transposase	3097.82
FTT_0202c		Transporter protein, pseudogene	6802.83
FTT_0203c	<i>purH</i>	bifunctional purine biosynthesis protein	567.42
FTT_0204	<i>purA</i>	adenylosuccinate synthetase	570.90
FTT_0205	<i>hpt</i>	Hypoxanthine-guanine phosphoribosyltransferase	557.93
FTT_0207c		permease of ABC transporter	611.09
FTT_0208c		ABC transporter, ATP-binding protein	568.98
FTT_0209c		periplasmic solute binding family protein	563.75
FTT_0210c		major facilitator superfamily (MFS) transport protein, pseudogene	558.41
FTT_0212c	<i>wrbA</i>	trp repressor binding protein	640.22
FTT_0214		Transport protein, pseudogene	550.95
FTT_0215	<i>priA</i>	Primosomal protein N	602.86
FTT_0216	<i>isftu1</i>	Transposase	985.88
FTT_0219c		phosphate transport protein	604.22
FTT_0221	<i>acpA</i>	acid phosphatase (precursor)	657.64
FTT_0222c	<i>ybgK</i>	hydrolase subunit	632.45
FTT_0223c	<i>ybgL</i>	lactam utilization protein	550.19
FTT_0225c		major facilitator superfamily (MFS) transport protein, fragment	590.04
FTT_0226c	<i>isftu1</i>	Transposase	1498.48
FTT_0227c		hypothetical protein	894.80
FTT_0232c	<i>ddg</i>	Acyltransferase	660.76
FTT_0233c	<i>yidC</i>	Inner-membrane protein	577.72
FTT_0234c		conserved hypothetical protein	763.46
FTT_0237c		hypothetical protein	633.58
FTT_0238	<i>aroE1</i>	Shikimate 5-dehydrogenase	552.09
FTT_0239	<i>murC</i>	UDP-N-acetylmuramate--alanine ligase	692.41
FTT_0240		tetrapyrrole methyltransferase family protein	557.46
FTT_0243		hypothetical membrane protein	581.32
FTT_0244		DNA/RNA helicase	567.95
FTT_0245	<i>usp</i>	universal stress protein	587.11
FTT_0247	<i>isftu1</i>	Transposase	1115.92
FTT_0251	<i>ilvE</i>	Branched-chain amino acid aminotransferase protein (class IV)	574.78
FTT_0253c	<i>isftu1</i>	Transposase	1413.80
FTT_0258		Carboxylesterase/phospholipase family protein	558.89
FTT_0259	<i>hemC</i>	hydroxymethylbilane synthase (porphobilinogen deaminase)	682.22
FTT_0261		hypothetical membrane protein	593.49
FTT_0265		ABC transporter, membrane protein	631.74
FTT_0266		ABC transporter, ATP-binding protein	644.42
FTT_0268		Sodium/hydrogen exchanger (antiporter) family protein	553.55
FTT_0269		carbonic anhydrase, family 3	644.05
FTT_0270	<i>lolB</i>	lipoprotein releasing system, subunit B, outer membrane lipoprotein	578.56
FTT_0273	<i>isftu1</i>	Transposase	987.39
FTT_0275c		major facilitator superfamily (MFS) transport protein, fragment	546.04
FTT_0278c	<i>cydB</i>	cytochrome d terminal oxidase, polypeptide subunit II	666.06

FTT_0279c	<i>cydA</i>	cytochrome d terminal oxidase, polypeptide subunit I	687.24
FTT_0281	<i>cyoA</i>	Cytochrome O ubiquinol oxidase subunit II	782.12
FTT_0282	<i>cyoB</i>	Cytochrome O ubiquinol oxidase subunit I	606.64
FTT_0283	<i>cyoC</i>	Cytochrome O ubiquinol oxidase, subunit III	645.66
FTT_0284	<i>cyoD</i>	Cytochrome O ubiquinol oxidase subunit IV	727.16
FTT_0286c	<i>lpxD1</i>	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	557.11
FTT_0288c	<i>pdxY</i>	Pyridoxal/pyridoxine/pyridoxamine kinase	652.01
FTT_0289c		hypothetical lipoprotein	693.09
FTT_0290	<i>moxR</i>	methanol dehydrogenase regulatory protein	600.31
FTT_0291		conserved hypothetical protein	633.84
FTT_0293		hypothetical membrane protein	603.97
FTT_0295		conserved hypothetical membrane protein	581.08
FTT_0296	<i>pcp</i>	Pyrrolidone-carboxylate peptidase	649.52
FTT_0297		hypothetical membrane protein	631.58
FTT_0299	<i>valS</i>	Valyl-tRNA synthetase	593.49
FTT_0303c	<i>lldD</i>	L-lactate dehydrogenase	596.57
FTT_0304c	<i>nfnB</i>	Oxygen-insensitive NAD(P)H nitroreductase	557.19
FTT_0305		MutT/nudix family protein	662.58
FTT_0308		hypothetical protein	612.91
FTT_0309c	<i>isftu2</i>	Transposase	858.33
FTT_0311c		conserved hypothetical protein	594.78
FTT_0313	<i>rpsB</i>	30S ribosomal protein S2	628.11
FTT_0315	<i>pyrH</i>	uridylate kinase	620.40
FTT_0317	<i>uppS</i>	undecaprenyl pyrophosphate synthetase	631.83
FTT_0318	<i>cdsA</i>	phosphatidate cytidyltransferase	604.69
FTT_0321	<i>rpsL</i>	30S ribosomal protein S12	645.72
FTT_0323	<i>fusA</i>	elongation factor G (EF-G)	592.09
FTT_0324	<i>rpsJ</i>	30S ribosomal protein S10	548.70
FTT_0325	<i>rpIC</i>	50S ribosomal protein L3	604.69
FTT_0326	<i>rpID</i>	50S ribosomal protein L4	566.86
FTT_0327	<i>rpIW</i>	50S ribosomal protein L23	589.54
FTT_0330	<i>rpIV</i>	50S ribosomal protein L22	579.36
FTT_0332	<i>rpIP</i>	50S ribosomal protein L16	573.42
FTT_0335	<i>rpIN</i>	50S ribosomal protein L14	617.62
FTT_0338	<i>rpsN</i>	30S ribosomal protein S14	694.35
FTT_0346	<i>rpmJ</i>	50S ribosomal protein L36	791.32
FTT_0347	<i>rpsM</i>	30S ribosomal protein S13	708.20
FTT_0350	<i>rpoA1</i>	DNA-directed RNA polymerase, alpha subunit	576.40
FTT_0352	<i>isftu1</i>	Transposase	1017.63
FTT_0353c	<i>isftu2</i>	Transposase, fragment	827.29
FTT_0354		hypothetical protein	611.37
FTT_0355c	<i>isftu1</i>	Transposase	1439.50
FTT_0357c	<i>isftu1</i>	Transposase	1428.92
FTT_0360		Short-chain dehydrogenase/reductase	546.73
FTT_0363	<i>isftu1</i>	Transposase	943.54
FTT_0369c		hypothetical protein	556.61
FTT_0370c	<i>yjeE</i>	Nucleotide-binding protein, yjeE	932.84
FTT_0371c	<i>folC</i>	FolC Bifunctional protein	626.63
FTT_0373c	<i>ndk</i>	nucleoside diphosphate kinase	569.64

FTT_0374c	<i>pyrG</i>	CTP synthase	661.85
FTT_0377	<i>isftu1</i>	Transposase	929.93
FTT_0378c		hypothetical protein	717.44
FTT_0379	<i>isftu2</i>	Transposase, fragment	776.30
FTT_0381	<i>isftu2</i>	Transposase	796.11
FTT_0387	<i>glmU</i>	UDP-N-acetylglucosamine pyrophosphorylase/glucosamine-1-phosphate N-acetyltransferase	596.96
FTT_0389		Acetyltransferase	562.97
FTT_0391c	<i>cspC</i>	cold shock protein	546.94
FTT_0392c		conserved hypothetical protein	633.06
FTT_0393	<i>map</i>	methionine aminopeptidase	598.88
FTT_0396	<i>parC</i>	DNA topoisomerase IV subunit A	572.16
FTT_0402	<i>dnaE</i>	DNA polymerase III alpha subunit	546.08
FTT_0403	<i>def1</i>	peptide deformylase	640.15
FTT_0406	<i>cadA</i>	lysine decarboxylase, inducible	617.88
FTT_0407	<i>gcvT</i>	glycine cleavage complex protein T (aminomethyltransferase)	578.61
FTT_0408	<i>gcvH</i>	glycine cleavage system H protein	627.50
FTT_0409	<i>gcvP1</i>	glycine cleavage system P protein, subunit 1	551.84
FTT_0410	<i>gcvP2</i>	glycine cleavage system P protein, subunit 2	666.55
FTT_0411c	<i>aroE2</i>	Shikimate 5-dehydrogenase	579.46
FTT_0412c	<i>pulB</i>	pullulanase	612.15
FTT_0413c	<i>glgB</i>	1,4-alpha-glucan branching enzyme	578.99
FTT_0414	<i>pgm</i>	Phosphoglucomutase	553.93
FTT_0423		hypothetical protein	593.49
FTT_0424		hypothetical protein	651.68
FTT_0426	<i>thrA</i>	bifunctional aspartokinase/homoserine dehydrogenase I (pseudogene)	574.83
FTT_0430	<i>speH</i>	S-adenosylmethionine decarboxylase	570.30
FTT_0431	<i>speE</i>	spermidine synthase	705.37
FTT_0433		hypothetical protein	596.63
FTT_0434		conserved hypothetical protein	602.51
FTT_0440c	<i>isftu1</i>	Transposase	1651.20
FTT_0442c		major facilitator superfamily (MFS) transport protein	642.21
FTT_0444	<i>tet</i>	multidrug transporter (tetracycline resistance protein)	608.34
FTT_0445	<i>uup</i>	ABC transporter, ATP-binding, pseudogene	586.08
FTT_0448c	<i>glnS</i>	Glutaminyl-tRNA synthetase	656.55
FTT_0462	<i>hemB</i>	Delta-aminolevulinic acid dehydratase	657.41
FTT_0465		hypothetical protein	565.23
FTT_0467	<i>ostA1</i>	organic solvent tolerance protein	617.40
FTT_0468	<i>surA</i>	Peptidyl-prolyl cis-trans isomerase (PPIase)	562.61
FTT_0476c	<i>poxA</i>	Lysyl-tRNA synthetase	579.36
FTT_0478c	<i>recJ</i>	Single-stranded-DNA-specific exonuclease	634.69
FTT_0480c	<i>xasA</i>	Glutamate:gamma-aminobutyric acid antiporter family protein (APC family protein)	668.42
FTT_0482c		hypothetical lipoprotein	660.41
FTT_0484		hypothetical protein	670.98
FTT_0485		hypothetical protein	589.02
FTT_0486	<i>mutL</i>	DNA mismatch repair protein	674.80
FTT_0489c	<i>trxB</i>	thioredoxin reductase	562.91
FTT_0490c		Phospholipase D family protein.	609.09
FTT_0491c	<i>gph</i>	phosphoglycolate phosphatase	587.34
FTT_0493		major facilitator superfamily (MFS) transport protein, pseudogene	620.84

FTT_0495		conserved hypothetical protein	555.81
FTT_0496		conserved hypothetical protein	654.78
FTT_0497c		Asparaginase 2 family protein, pseudogene	618.28
FTT_0500		hypothetical protein	582.12
FTT_0502c		hypothetical membrane protein	763.46
FTT_0503c	<i>sucD</i>	Succinyl-CoA synthetase, alpha subunit	595.53
FTT_0505		hypothetical membrane protein	605.28
FTT_0507		conserved hypothetical lipoprotein	768.14
FTT_0508c	<i>dusA</i>	RNA dihydrouridine synthase A	556.10
FTT_0509c		conserved hypothetical protein	653.51
FTT_0511		Pyridoxine/pyridoxal 5-phosphate biosynthesis protein	644.32
FTT_0513c	<i>isftu1</i>	Transposase	1421.36
FTT_0530c		DJ-1/PfpI family protein	557.08
FTT_0532c	<i>nrdB</i>	Biofunctional protein, glutaredoxin 3 protein/Ribonucleoside-diphosphate reductase, beta subunit	632.48
FTT_0533c	<i>grxA</i>	Glutaredoxin 1	554.84
FTT_0534c	<i>nrdA</i>	Ribonucleoside-diphosphate reductase, alpha subunit	560.35
FTT_0535c	<i>mdh</i>	lactate dehydrogenase	651.61
FTT_0537		ubiquinone biosynthesis protein	600.96
FTT_0538c		conserved hypothetical lipoprotein	570.59
FTT_0540c		hypothetical protein	583.54
FTT_0542		AhpC/Tsa family protein, pseudogene	570.70
FTT_0543		hypothetical protein	568.06
FTT_0544	<i>phnA</i>	phosphonoacetate hydrolase	616.66
FTT_0547		hypothetical protein	673.51
FTT_0549	<i>vanY</i>	D-alanyl-D-alanine carboxypeptidase	628.55
FTT_0550		conserved hypothetical protein	549.30
FTT_0552		aldehyde dehydrogenase	620.06
FTT_0554		conserved hypothetical protein	547.84
FTT_0555		conserved hypothetical membrane protein	687.54
FTT_0557		AhpC/TSA family protein	599.15
FTT_0558		conserved hypothetical protein	603.19
FTT_0561	<i>isftu1</i>	Transposase	1056.95
FTT_0562	<i>potG</i>	polyamine transporter, ABC transporter, ATP-binding protein	568.10
FTT_0563	<i>potH</i>	polyamine transporter, subunit H, ABC transporter, membrane protein	632.28
FTT_0564	<i>potI</i>	polyamine transporter, subunit I, ABC transporter, membrane protein	679.54
FTT_0565c	<i>isftu2</i>	Transposase	856.74
FTT_0569c		conserved hypothetical membrane protein	630.04
FTT_0570		hypothetical lipoprotein	583.08
FTT_0571		conserved hypothetical protein	918.74
FTT_0573	<i>alr</i>	alanine racemase	550.25
FTT_0578	<i>csdB</i>	selenocysteine lyase	684.65
FTT_0579		hesB family protein	558.58
FTT_0580		conserved hypothetical protein	647.25
FTT_0581	<i>coaD</i>	phosphopantetheine adenylyltransferase	691.80
FTT_0583	<i>fopA</i>	outer membrane associated protein	603.54
FTT_0586		conserved hypothetical protein	545.32
FTT_0587c	<i>isftu2</i>	Transposase	867.90
FTT_0591	<i>ansA</i>	L-asparaginase	675.83
FTT_0595c	<i>rubA</i>	Rubredoxin	548.37

FTT_0596c		hypothetical protein	568.52
FTT_0597		conserved hypothetical protein	576.05
FTT_0598c		Sodium-dicarboxylate symporter family protein	575.42
FTT_0600		major facilitator superfamily (MFS) transport protein, pseudogene	564.79
FTT_0601		hypothetical protein	623.17
FTT_0607	<i>ispG</i>	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase	645.14
FTT_0614c		Apolipoprotein N-acyltransferase	562.05
FTT_0615c		metal ion transporter protein	601.08
FTT_0616c		cconserved hypothetical protein, UPF0054 family	632.12
FTT_0618c	<i>yleA</i>	conserved hypothetical protein yleA	656.46
FTT_0619		o-methyltransferase family protein	580.30
FTT_0620		HAD superfamily protein	615.83
FTT_0621	<i>tdk</i>	thymidine kinase	565.52
FTT_0622c		hypothetical membrane protein	546.27
FTT_0624	<i>clpP</i>	ATP-dependent Clp protease subunit P	658.13
FTT_0625	<i>clpX</i>	ATP-dependent Clp protease subunit X	574.56
FTT_0630	<i>hfq</i>	host factor I for bacteriophage Q beta replication	546.73
FTT_0631	<i>hflX</i>	protease, GTP-binding subunit	593.49
FTT_0632c		monooxygenase family protein	654.79
FTT_0633	<i>hflK</i>	SPFH domain, band 7 family protein	550.15
FTT_0634	<i>hflC</i>	SPFH domain, band 7 family protein	550.60
FTT_0637	<i>thrC1</i>	threonine synthase, pseudogene	569.61
FTT_0638		hypothetical protein	554.60
FTT_0645c		conserved hypothetical membrane protein	661.74
FTT_0647c		conserved hypothetical protein	560.52
FTT_0648c	<i>nth</i>	Endonuclease III	598.14
FTT_0654	<i>elbB</i>	DJ-1/PfpI family protein	550.33
FTT_0655		conserved hypothetical protein	545.03
FTT_0656	<i>ruvC</i>	holliday junction endodeoxyribonuclease	599.02
FTT_0658	<i>ruvA</i>	holliday junction DNA helicase, subunit A	598.94
FTT_0674	<i>prsA</i>	Ribose-phosphate pyrophosphokinase	694.55
FTT_0679c		GTP-binding protein	675.02
FTT_0686c		Proton-dependent oligopeptide transport (POT) family protein	618.51
FTT_0687c	<i>hslU</i>	ATP-dependent protease, ATP-binding subunit	567.46
FTT_0689		hypothetical membrane protein	553.93
FTT_0691	<i>tyrS</i>	Tyrosyl-tRNA synthetase	578.05
FTT_0692c	<i>isftu1</i>	Transposase	1465.21
FTT_0693c	<i>mutM</i>	Formamidopyrimidine-DNA glycosylase	546.73
FTT_0694		conserved hypothetical protein	647.19
FTT_0695	<i>mraW</i>	S-adenosyl-methyltransferase	709.86
FTT_0697	<i>ftsI</i>	penicillin binding protein (peptidoglycan synthetase)	586.14
FTT_0698	<i>rpsO</i>	30S ribosomal protein S15	600.16
FTT_0699	<i>pnp</i>	polyribonucleotide nucleotidyltransferase	549.59
FTT_0700		conserved hypothetical protein	632.38
FTT_0701	<i>kdsA</i>	2-dehydro-3-deoxyphosphooctonate aldolase	648.72
FTT_0704		hypothetical protein	571.74
FTT_0705	<i>rumA</i>	23S rRNA (Uracil-5-)-methyltransferase	554.81
FTT_0709	<i>eno</i>	Enolase (2-phosphoglycerate dehydratase)	677.91
FTT_0710	<i>ftsB</i>	cell division protein	558.82

FTT_0711	<i>ispD</i>	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase	571.13
FTT_0713c	<i>tdh</i>	L-threonine 3-dehydrogenase	594.62
FTT_0715		chitinase family 18 protein	592.19
FTT_0719		major facilitator superfamily (MFS) transport protein	568.28
FTT_0722c	<i>isftu1</i>	Transposase	1318.54
FTT_0723c		Short-chain dehydrogenase/reductase family protein	600.26
FTT_0725c	<i>glpT</i>	Glycerol-3-phosphate transporter	589.44
FTT_0726c		glycerophosphoryl diester phosphodiesterase family protein	556.22
FTT_0728	<i>ybhF</i>	ABC transporter, ATP-binding protein	678.10
FTT_0729	<i>ybhR</i>	ABC transporter, membrane protein	605.69
FTT_0730	<i>isftu2</i>	Transposase	808.87
FTT_0733		glutathione peroxidase	546.87
FTT_0734		conserved hypothetical membrane protein,pseudogene	597.05
FTT_0735		mandelate racemase/muconate lactonizing enzyme family protein, pseudogene	641.70
FTT_0736		conserved hypothetical protein	575.18
FTT_0742		hypothetical lipoprotein	577.08
FTT_0745c		hypothetical protein	728.15
FTT_0750		conserved hypothetical protein	560.42
FTT_0751c	<i>cspA</i>	cold shock protein	680.77
FTT_0759		conserved hypothetical membrane protein	558.58
FTT_0765	<i>isftu1</i>	Transposase	932.96
FTT_0774		conserved hypothetical protein	612.33
FTT_0775c	<i>bcr2</i>	major facilitator superfamily (MFS) transport protein, pseudogene	608.69
FTT_0777	<i>uvrC</i>	DNA excision repair enzyme, subunit C (UvrABC system protein A)	607.37
FTT_0779	<i>isftu1</i>	Transposase	985.88
FTT_0780c		hypothetical membrane protein	685.81
FTT_0781c		conserved hypothetical protein	576.87
FTT_0782	<i>fabI</i>	Enoyl-[acyl-carrier-protein] reductase (NADH)	545.74
FTT_0784		hypothetical protein	550.33
FTT_0789	<i>rpe</i>	D-ribulose-phosphate 3-epimerase	622.77
FTT_0791	<i>galE</i>	UDP-glucose 4-epimerase	573.71
FTT_0792		glycosyl transferases group 1 family protein	568.40
FTT_0800		haloacid dehalogenase-like hydrolase family protein	726.87
FTT_0801c		Carbohydrate/purine kinase pfkB family protein	598.32
FTT_0802	<i>cphB</i>	Cyanophycinase	552.19
FTT_0804		major facilitator superfamily (MFS) transport protein	566.58
FTT_0805	<i>capB</i>	capsule biosynthesis protein capB	550.61
FTT_0806	<i>capC</i>	capsule biosynthesis protein CapC	620.30
FTT_0807		conserved hypothetical membrane protein	628.75
FTT_0808	<i>spoT</i>	Guanosine-3,5-bis(Diphosphate) 3-pyrophosphohydrolase/(p)ppGpp synthase	586.79
FTT_0812	<i>gcvH1</i>	glycine cleavage system protein H	579.47
FTT_0814c		hypothetical protein	644.93
FTT_0815c		hypothetical protein	567.27
FTT_0816c		chitin binding protein	650.59
FTT_0817	<i>thrS</i>	Threonyl-tRNA synthetase	609.38
FTT_0820	<i>rplT</i>	50S ribosomal protein L20	561.91
FTT_0822	<i>isftu1</i>	Transposase	1096.26
FTT_0825c		hypothetical protein	565.23
FTT_0829c		Aspartate:alanine antiporter	556.83

FTT_0831c		OmpA family protein	586.87
FTT_0834	<i>aroQ</i>	chorismate mutase	719.39
FTT_0837	<i>tolQ</i>	TolQ protein	703.95
FTT_0838	<i>tolR</i>	TolR protein	584.20
FTT_0840	<i>tolB</i>	TolB protein precursor	668.13
FTT_0841		hypothetical lipoprotein	772.48
FTT_0842		Peptidoglycan-associated lipoprotein	582.08
FTT_0843		conserved hypothetical protein, pseudogene	643.65
FTT_0844		rossman fold oxidoreductase, pseudogene	668.19
FTT_0847		conserved hypothetical protein	681.15
FTT_0848		conserved hypothetical protein	550.49
FTT_0857c		conserved hypothetical protein	606.37
FTT_0858	<i>rph</i>	Ribonuclease PH	559.96
FTT_0860c		hypothetical protein	758.35
FTT_0861c		Type IV pili fiber building block protein	701.40
FTT_0862c	<i>htpX</i>	heat shock protein HtpX	600.12
FTT_0863c		LemA-like protein	634.71
FTT_0865		conserved hypothetical protein, pseudogene	563.09
FTT_0866c	<i>isftu2</i>	Transposase	602.32
FTT_0867		Cadmium-transporting ATPase (pseudogene)	842.38
FTT_0868c		arsenical resistance operon repressor	583.76
FTT_0869		hypothetical protein	608.01
FTT_0870c		hypothetical protein	575.51
FTT_0871	<i>gpsA</i>	Glycerol-3-phosphate dehydrogenase [NAD(P)+]	589.33
FTT_0873c	<i>radA</i>	DNA repair protein radA	592.19
FTT_0874c		hypothetical protein	577.33
FTT_0875c		conserved hypothetical protein	637.02
FTT_0876c	<i>aroC</i>	chorismate synthase	626.56
FTT_0880		conserved hypothetical transmembrane protein, fragment	561.94
FTT_0881c		amino acid permease	590.51
FTT_0882		Mannose-6-phosphate isomerase, fragment	623.56
FTT_0884c	<i>aspC1</i>	aspartate transaminase	598.97
FTT_0885		cation transporter	585.88
FTT_0887c		hypothetical protein	617.23
FTT_0888c		Type IV pili fiber building block protein	683.96
FTT_0889c		Type IV pili fiber building block protein	589.46
FTT_0891		conserved hypothetical membrane protein	565.47
FTT_0892	<i>folD</i>	methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase putative bifunctional protein	685.07
FTT_0894	<i>purCD</i>	Fusion protein PurC/PurD	595.80
FTT_0895	<i>purN</i>	phosphoribosylglycinamide formyltransferase	642.95
FTT_0899c	<i>prlC</i>	Oligopeptidase A	599.95
FTT_0904	<i>lpnB</i>	conserved hypothetical lipoprotein	560.52
FTT_0906c	<i>topA</i>	DNA topoisomerase I	577.72
FTT_0907	<i>parA</i>	chromosome partition protein A	591.64
FTT_0910		hypothetical protein	612.33
FTT_0913		hypothetical protein	588.42
FTT_0915c	<i>ileS</i>	Isoleucyl-tRNA synthetase	590.96
FTT_0917	<i>maeA</i>	NAD-dependent malic enzyme	580.74
FTT_0918		hypothetical protein	779.98



FTT_0920	<i>isftu1</i>	Transposase	972.27
FTT_0924		hypothetical membrane protein	705.05
FTT_0927	<i>hemL</i>	Glutamate-1-semialdehyde-2,1-aminomutase	572.43
FTT_0930c		acetoacetate decarboxylase, fragment	599.99
FTT_0931		major facilitator superfamily (MFS) transport protein	563.35
FTT_0932		ROK family protein	660.37
FTT_0934c	<i>bioD</i>	dethiobiotin synthetase	561.98
FTT_0938	<i>bioA</i>	Adenosylmethionine-8-amino-7-oxononanoate aminotransferase	570.32
FTT_0941c		Lipase/esterase	661.16
FTT_0942c	<i>folK</i>	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase/dihydropteroate synthase	608.49
FTT_0946	<i>trpG</i>	anthranilate synthase component II	622.37
FTT_0948c		Aldo/keto reductase	611.88
FTT_0952	<i>rhIE</i>	ATP-dependent RNA helicase RhIE	549.63
FTT_0953c		Proton-dependent oligopeptide transport (POT) family protein	571.94
FTT_0954c		hypothetical protein	584.25
FTT_0955c	<i>gor</i>	Pyruvate/2-oxoglutarate dehydrogenase complex,dihydrolipoamide dehydrogenase component	565.60
FTT_0963c	<i>aroG</i>	Phospho-2-dehydro-3-deoxyheptonate aldolase	579.10
FTT_0965c		conserved hypothetical membrane protein	546.33
FTT_0968c		amino acid antiporter	562.48
FTT_0971		ABC transporter, membrane protein	642.75
FTT_0974		amidinotransferase family protein, pseudogene	589.70
FTT_0975		conserved hypothetical protein	600.37
FTT_0976	<i>trxA2</i>	Thioredoxin 1	635.24
FTT_0980		Aminotransferase, class II	625.03
FTT_0986		conserved hypothetical protein	690.24
FTT_0990	<i>leuS</i>	Leucyl-tRNA synthetase	618.77
FTT_0991		hypothetical lipoprotein	550.22
FTT_0993c	<i>dcd</i>	deoxycytidine triphosphate deaminase	619.66
FTT_0994c		MRP like protein	581.77
FTT_0998		hypothetical lipoprotein	573.11
FTT_0999c		ZIP metal transporter family protein,pseudogene	633.78
FTT_1003c	<i>pheS</i>	Phenylalanyl-tRNA synthetase, alpha subunit	580.62
FTT_1013c	<i>ruvB</i>	holliday junction DNA helicase, subunit B	671.15
FTT_1016c		GDSL-like Lipase/Acylhydrolase family protein	557.70
FTT_1019c	<i>guaA</i>	GMP synthase (glutamine-hydrolyzing)	564.03
FTT_1020c		amino acid permease	580.46
FTT_1021c	<i>truA</i>	tRNA pseudouridine synthase A	637.03
FTT_1022c		conserved hypothetical protein	554.32
FTT_1025c		hypothetical protein	546.53
FTT_1027c	<i>yrbl</i>	3-deoxy-D-manno-octulosonate 8-phosphate phosphatase	605.38
FTT_1028c	<i>ppa</i>	inorganic pyrophosphatase	598.04
FTT_1029	<i>dacD</i>	D-alanyl-D-alanine carboxypeptidase (Penicillin binding protein) family protein	566.37
FTT_1031	<i>lipB</i>	Lipoate-protein ligase B	640.32
FTT_1033	<i>yihQ</i>	glycosyl hydrolases family 31 protein,pseudogene	549.20
FTT_1038c	<i>rpsU3</i>	30S ribosomal protein S21	593.49
FTT_1039	<i>dacB</i>	D-alanyl-D-alanine carboxypeptidase (Penicillin binding protein) family protein	588.42
FTT_1040		conserved hypothetical lipoprotein	630.34
FTT_1041		conserved hypothetical protein	640.46
FTT_1050c	<i>cysN</i>	sulfate adenylate transferase subunit 1	619.11

FTT_1053c		Transposase, pseudogene	601.13
FTT_1058c		Radical SAM superfamily protein	648.42
FTT_1059c	<i>dnaB</i>	Replicative DNA helicase	678.40
FTT_1062c	<i>rpsF</i>	30S ribosomal protein S6	678.28
FTT_1064		hypothetical protein	650.73
FTT_1067c	<i>res</i>	Type III restriction-modification system restriction enzyme R, pseudogene	565.65
FTT_1071c		conserved hypothetical protein	585.30
FTT_1072		hypothetical protein	640.60
FTT_1073c		hypothetical protein	577.54
FTT_1075		transcriptional regulator	567.46
FTT_1076	<i>hipA</i>	transcription regulator	617.23
FTT_1078c		conserved hypothetical protein	557.72
FTT_1079c		hypothetical protein	609.41
FTT_1081c		hypothetical protein	757.37
FTT_1083c		hypothetical protein	644.10
FTT_1084c	<i>rdgC</i>	recombination associated protein	562.47
FTT_1085		conserved hypothetical protein	552.50
FTT_1093c	<i>talA</i>	Transaldolase	594.72
FTT_1094c		cytosol aminopeptidase family protein	565.83
FTT_1096c	<i>alaS</i>	Alanyl-tRNA synthetase	575.22
FTT_1100		conserved hypothetical protein	572.30
FTT_1101	<i>yjeS</i>	4Fe-4S ferredoxin (electron transport) family protein, pseudogene	576.44
FTT_1102		macrophage infectivity potentiator, fragment	546.58
FTT_1105c	<i>msrA1</i>	peptide methionine sulfoxide reductase	653.88
FTT_1106	<i>tspO</i>	Tryptophan-rich sensory protein	554.92
FTT_1109		choloylglycine hydrolase family protein	556.13
FTT_1111	<i>istu2</i>	Transposase	784.94
FTT_1112c	<i>rpoH</i>	RNA polymerase sigma-32 factor	607.67
FTT_1113c		hypothetical protein	565.55
FTT_1114c	<i>secF</i>	preprotein translocase, subunit F, membrane protein	695.86
FTT_1115c	<i>secD</i>	preprotein translocase, subunit D, membrane protein	604.52
FTT_1117c		isochorismatase hydrolase family protein	644.25
FTT_1119		LysR transcriptional regulator family protein	563.68
FTT_1120c	<i>tgt</i>	queuine tRNA-ribosyltransferase.	644.03
FTT_1123	<i>ygiH</i>	conserved hypothetical protein	550.07
FTT_1124	<i>metN</i>	D-methionine transport protein, ABC transporter,ATP-binding subunit	644.74
FTT_1125	<i>metIQ</i>	D-methionine binding transport protein, ABC transporter, membrane and periplasmic protein	621.29
FTT_1128	<i>ispF</i>	2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	638.00
FTT_1129c		conserved hypothetical protein	576.60
FTT_1130c	<i>cphA</i>	cyanophycin synthetase	587.40
FTT_1131		molybdopterin binding family protein, fragment	634.97
FTT_1133	<i>pilB</i>	Type IV pili nucleotide binding protein, ABC transporter, ATP-binding protein	585.15
FTT_1137c		hypothetical protein	641.25
FTT_1140		hypothetical protein	557.52
FTT_1143		hypothetical protein	641.74
FTT_1146c	<i>galM</i>	Aldose 1-epimerase (pseudogene)	648.66
FTT_1149c		amino acid transporter family protein	585.23
FTT_1150c	<i>putA</i>	Multifunctional protein, transcriptional repressor of proline utilization, proline dehydrogenase,pyrroline-5-carboxylate dehydrogenase	593.78
FTT_1156c	<i>pilQ</i>	Type IV pilin multimeric outer membrane protein	545.95

FTT_1157c		Type IV pili lipoprotein.	662.78
FTT_1161	<i>adk</i>	adenylate kinase	711.83
FTT_1163c		hypothetical membrane protein	597.76
FTT_1165c	<i>aspC2</i>	aspartate aminotransferase	589.52
FTT_1166c		glutamine amidotransferases class-II family protein	579.52
FTT_1167c		glycoprotease family protein	585.13
FTT_1168c	<i>nagA</i>	N-acetylglucosamine-6-phosphate deacetylase	653.16
FTT_1169		GTP-binding protein	595.53
FTT_1171c	<i>hsdM</i>	DNA-methyltransferase, type I restriction-modification enzyme subunit M	546.97
FTT_1176c	<i>hsdR1</i>	Type I restriction enzyme subunit R, pseudogene	618.77
FTT_1179	<i>bipA</i>	GTP binding translational elongation factor Tu and G family protein	569.99
FTT_1182c	<i>vacJ</i>	VacJ lipoprotein, pseudogene	549.03
FTT_1183c		conserved hypothetical lipoprotein	643.69
FTT_1184c		conserved hypothetical protein	756.41
FTT_1185c		conserved hypothetical protein	620.97
FTT_1187		conserved hypothetical protein	610.76
FTT_1189c		major facilitator superfamily (MFS) transport protein, pseudogene	697.25
FTT_1192c		conserved hypothetical protein, pseudogene	631.65
FTT_1195c		conserved hypothetical protein, pseudogene	607.35
FTT_1196c		major facilitator superfamily (MFS) transport protein	648.04
FTT_1199c	<i>uvrB</i>	DNA excision repair enzyme, subunit B (UvrABC system protein B)	637.55
FTT_1202		transcriptional regulator, LysR family	586.90
FTT_1204c		hypothetical membrane protein	587.46
FTT_1205	<i>gidA</i>	glucose inhibited division protein A	568.92
FTT_1208	<i>rpiA</i>	Ribose 5-phosphate isomerase A	578.55
FTT_1209c		metallopeptidase family M13 protein, pseudogene	617.26
FTT_1211c		hypothetical protein	649.37
FTT_1214c		haloacid dehalogenase-like hydrolase family protein	587.50
FTT_1215c	<i>queA</i>	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	578.99
FTT_1217c	<i>visC</i>	monooxygenase family protein	578.13
FTT_1218c	<i>ubiH</i>	2-octaprenyl-6-methoxyphenyl hydroxylase	564.11
FTT_1221		hypothetical protein	657.95
FTT_1225c		hypothetical protein	546.73
FTT_1226c	<i>iscS</i>	cysteine desulfurase	558.17
FTT_1228	<i>lgt</i>	prolipoprotein diacylglycerol transferase	563.34
FTT_1229	<i>thyA</i>	thymidylate synthase	669.03
FTT_1230	<i>serA</i>	D-3-phosphoglycerate dehydrogenase	595.88
FTT_1231	<i>mesJ</i>	PP-loop family protein	556.31
FTT_1233c	<i>yjdL</i>	Proton-dependent oligopeptide transport (POT) family protein	601.08
FTT_1243c	<i>mreA</i>	FAD binding family protein	567.88
FTT_1244c	<i>yfiO</i>	conserved hypothetical lipoprotein	572.63
FTT_1245	<i>rluD</i>	ribosomal large subunit pseudouridine synthase D	698.65
FTT_1247		ABC transporter, membrane protein	545.52
FTT_1248		ABC transporter, ATP-binding protein	593.49
FTT_1251c		conserved hypothetical membrane protein	601.27
FTT_1253		Proton-dependent oligopeptide transport (POT) family protein	596.68
FTT_1254	<i>fadD1</i>	Acyl-CoA synthetase (long-chain-fatty-acid-CoA ligase)	545.79
FTT_1255c		transcriptional regulator araC family protein	591.40
FTT_1256	<i>emrB</i>	major facilitator superfamily (MFS) transport protein	609.01

FTT_1257	<i>emrA1</i>	HlyD family secretion protein	647.45
FTT_1259	<i>nadE</i>	NH(3)-dependent NAD(+) synthetase	675.79
FTT_1264	<i>isftu2</i>	Transposase	703.40
FTT_1274	<i>rpsI</i>	30S ribosomal protein S9	618.78
FTT_1275	<i>mglA</i>	macrophage growth locus, subunit A	597.33
FTT_1276	<i>mglB</i>	macrophage growth locus, subunit B	546.94
FTT_1281c	<i>yhbH</i>	Sigma-54 modulation protein	575.51
FTT_1283	<i>trmE</i>	tRNA modification GTPase trmE family protein	557.09
FTT_1285c		LysR transcriptional regulator family protein	579.50
FTT_1286		choloylglycine hydrolase family protein, pseudogene	596.87
FTT_1287	<i>cbs</i>	cystathionine beta-synthase (cystein synthase)	615.33
FTT_1288		conserved hypothetical membrane protein	614.32
FTT_1289		conserved hypothetical protein	568.18
FTT_1290	<i>metG</i>	Methionyl-tRNA synthetase	547.48
FTT_1291		major facilitator superfamily (MFS) transport protein	657.26
FTT_1295c	<i>glk</i>	glucose kinase	599.91
FTT_1296	<i>ubiE</i>	menaquinone biosynthesis methyltransferase	706.20
FTT_1301c		Purine/pyrimidine phosphoribosyl transferase family protein, pseudogene	571.85
FTT_1304c	<i>murB</i>	UDP-N-acetylenolpyruvoylglucosamine reductase	859.83
FTT_1306c	<i>engA</i>	GTP-binding protein	646.98
FTT_1307c		hypothetical protein	652.07
FTT_1312c	<i>uvrA</i>	DNA excision repair enzyme, subunit A (UvrABC system protein A), ABC transporter, ATP-binding protein	572.26
FTT_1313c	<i>greA</i>	transcriptional elongation factor	587.35
FTT_1314c		Type IV pili fiber building block protein	631.03
FTT_1317c	<i>guaB</i>	Inosine-5-monophosphate dehydrogenase	594.71
FTT_1318c	<i>pepA</i>	cytosol aminopeptidase	611.63
FTT_1320		Permease YjgP/YjgQ family protein	551.02
FTT_1328c		FAD-binding family protein, pseudogene	576.65
FTT_1329	<i>gpml</i>	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	592.34
FTT_1330	<i>serS</i>	Seryl-tRNA synthetase	561.52
FTT_1335	<i>cydD</i>	ABC transporter, ATP-binding and membrane protein	601.49
FTT_1337c	<i>dctA</i>	C4-dicarboxylate transport protein	602.51
FTT_1338c		translation initiation inhibitor	560.78
FTT_1339c		sulfate permease family protein	578.51
FTT_1340c	<i>isftu2</i>	Transposase	858.33
FTT_1343c		hypothetical protein	590.56
FTT_1344	<i>pdpA</i>	conserved hypothetical protein	832.77
FTT_1345	<i>pdpB</i>	conserved hypothetical protein	686.44
FTT_1347		conserved hypothetical protein	995.15
FTT_1349		conserved hypothetical protein	1375.72
FTT_1350		conserved hypothetical protein	790.49
FTT_1351		conserved hypothetical protein	833.17
FTT_1352		conserved hypothetical protein	671.80
FTT_1354		conserved hypothetical protein	716.30
FTT_1355		conserved hypothetical protein	583.19
FTT_1356c	<i>iglD</i>	intracellular growth locus, subunit D	932.07
FTT_1357c	<i>iglC</i>	intracellular growth locus, subunit C	1069.41
FTT_1358c	<i>iglB</i>	intracellular growth locus, subunit B	1001.83
FTT_1359c	<i>iglA</i>	intracellular growth locus, subunit A	1162.88

FTT_1365c	<i>fbaB</i>	Fructose-1,6-bisphosphate aldolase	570.64
FTT_1366c	<i>pyk</i>	pyruvate kinase	579.86
FTT_1367c	<i>pgk</i>	phosphoglycerate kinase	560.77
FTT_1368c	<i>gapA</i>	Glyceraldehyde-3-phosphate dehydrogenase	596.33
FTT_1371	<i>rmpF</i>	50S ribosomal protein L32	570.79
FTT_1372	<i>plsX</i>	fatty acid/phospholipid synthesis protein IsX	553.25
FTT_1373	<i>fabH</i>	3-oxoacyl-[acyl carrier protein] synthase III	649.67
FTT_1374		malonyl coA-acyl carrier protein transacylase	672.75
FTT_1377	<i>fabF</i>	3-oxoacyl-[acyl-carrier-protein] synthase II	551.10
FTT_1379c		conserved hypothetical protein, pseudogene	564.38
FTT_1380		conserved hypothetical membrane protein,pseudogene	555.55
FTT_1382	<i>suhB</i>	Inositol-1-monophosphatase	609.29
FTT_1387c	<i>ligN</i>	DNA ligase	546.58
FTT_1390	<i>panC</i>	Pantoate-beta-alanine ligase	607.08
FTT_1392		transcriptional regulator	740.52
FTT_1396c		conserved hypothetical membrane protein	563.77
FTT_1402c		hypothetical protein	578.61
FTT_1405c	<i>gloB</i>	hydroxyacylglutathione hydrolase	603.66
FTT_1407c		hypothetical membrane protein	571.63
FTT_1412	<i>proS</i>	Prolyl-tRNA synthetase	644.52
FTT_1413		Aminotransferase	610.81
FTT_1417		Carbon-nitrogen hydrolase	578.39
FTT_1418c	<i>nusB</i>	N utilisation substance protein B	601.85
FTT_1419		hypothetical lipoprotein	715.10
FTT_1420		hypothetical protein	603.64
FTT_1423c		conserved hypothetical membrane protein	664.71
FTT_1424c		conserved hypothetical protein	624.00
FTT_1425c	<i>naoX</i>	NADH oxidase	623.96
FTT_1428c		Acetyltransferase	552.09
FTT_1430c		Methyltransferase, fragment	607.72
FTT_1432c	<i>ppnK</i>	inorganic phosphate/ATP-NAD kinase	686.08
FTT_1433	<i>gtrB</i>	glycosyl transferase	635.57
FTT_1436	<i>isftu2</i>	Transposase	784.94
FTT_1444c	<i>ppx</i>	Exopolyphosphatase	556.72
FTT_1448c	<i>manC</i>	Mannose-1-phosphate guanylyltransferase	582.95
FTT_1449c	<i>isftu1</i>	Transposase	1850.23
FTT_1450c	<i>wbtM</i>	dTDP-D-glucose 4,6-dehydratase	638.27
FTT_1451c	<i>wbtL</i>	Glucose-1-phosphate thymidyltransferase	545.88
FTT_1455c	<i>wbtI</i>	sugar transamine/perosamine synthetase	565.54
FTT_1457c	<i>wbtG</i>	glycosyl transferase	708.31
FTT_1459c	<i>wbtF</i>	NAD dependent epimerase	626.46
FTT_1460c	<i>wbtE</i>	UDP-glucose/GDP-mannose dehydrogenase	545.05
FTT_1461c	<i>wbtD</i>	galacturonosyl transferase	552.19
FTT_1465c	<i>isftu2</i>	Transposase	856.74
FTT_1466c	<i>add1</i>	adenosine deaminase, pseudogene	552.35
FTT_1468c	<i>nadC</i>	Nicotinate-nucleotide pyrophosphorylase	615.47
FTT_1471c	<i>deaD</i>	Cold-shock DEAD-box protein A	567.12
FTT_1474c	<i>galP1</i>	Galactose-proton symporter, major facilitator superfamily (MFS) transport protein	566.46
FTT_1475	<i>galT</i>	Galactose-1-phosphate uridylyltransferase	585.39

FTT_1479c		conserved hypothetical protein	596.63
FTT_1480c		hypothetical protein	580.30
FTT_1483c	<i>lpd</i>	dihydrolipoamide dehydrogenase	575.43
FTT_1485c	<i>aceE</i>	pyruvate dehydrogenase, E1 component	651.47
FTT_1488	<i>trpS</i>	Tryptophanyl-tRNA synthetase	630.70
FTT_1490		Na <sup>+</sup> /H <sup>+</sup> antiporter	656.09
FTT_1493c		hypothetical protein	548.53
FTT_1494c		glucokinase regulatory protein	600.87
FTT_1496c		hypothetical membrane protein	586.47
FTT_1498c	<i>accA</i>	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha	658.60
FTT_1500	<i>secB2</i>	preprotein translocase, subunit B, chaperone protein	596.17
FTT_1502		aromatic amino acid transporter of the HAAAP family	584.72
FTT_1503	<i>xerC</i>	Integrase/recombinase XerC	710.30
FTT_1507		hypothetical protein	598.18
FTT_1508c	<i>relA</i>	GTP pyrophosphokinase	628.30
FTT_1510c		aromatic amino acid transporter of the HAAAP family	567.21
FTT_1513		amino acid permease, fragment	566.18
FTT_1514c		hypothetical membrane protein	631.78
FTT_1515c		conserved hypothetical membrane protein	549.97
FTT_1520c	<i>gabP</i>	Glutamate/gamma-aminobutyrate anti-porter	642.29
FTT_1521c	<i>lysA1</i>	diaminopimelate decarboxylase, pseudogene	550.85
FTT_1522c		conserved hypothetical protein	580.44
FTT_1523c	<i>isfU2</i>	Transposase	855.14
FTT_1527c	<i>arsC2</i>	arsenate reductase	590.25
FTT_1529	<i>fadE</i>	Acyl-CoA dehydrogenase fusion product of 3-hydroxyacyl-CoA dehydrogenase and acyl-CoA-binding protein	579.85
FTT_1530	<i>fadB/acbP</i>		606.92
FTT_1531	<i>fadA</i>	3-ketoacyl-CoA thiolase	638.45
FTT_1532		conserved hypothetical protein	643.25
FTT_1533c		sugar transport protein, pseudogene	562.21
FTT_1535c		ornithine cyclodeaminase, pseudogene	644.58
FTT_1537c		conserved hypothetical protein	574.35
FTT_1538c		hypothetical protein	679.14
FTT_1539c		conserved hypothetical protein	587.27
FTT_1540c		conserved hypothetical protein	631.50
FTT_1542c	<i>omp26</i>	outer membrane protein 26	649.86
FTT_1543		two component response regulator	641.66
FTT_1550		conserved hypothetical protein	566.17
FTT_1553c	<i>rnr</i>	Ribonuclease R	653.93
FTT_1554c	<i>truB</i>	tRNA pseudouridine synthetase B	579.78
FTT_1559c	<i>proC</i>	Proline-5-carboxylate reductase	582.70
FTT_1568c	<i>lpxB</i>	Lipid-A-disaccharide synthase	548.32
FTT_1570c	<i>fabZ</i>	(3R)-hydroxymyristoyl-(acyl-carrier protein) dehydratase	545.24
FTT_1571c	<i>lpxD</i>	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	696.51
FTT_1573c		outer membrane protein	586.76
FTT_1575c	<i>gyrA</i>	DNA gyrase, subunit A	604.65
FTT_1578c	<i>ung</i>	Uracil-DNA glycosylase	563.95
FTT_1585		hypothetical membrane protein	561.12
FTT_1587c		amino acid transporter protein, fragment	648.38
FTT_1590c	<i>ubiG</i>	3-demethylubiquinone-9 3-methyltransferase	561.09

FTT_1591		Lipoprotein	682.00
FTT_1593c		conserved hypothetical protein, fragment	635.34
FTT_1600c	<i>fumA</i>	fumerate hydratase	592.32
FTT_1602		hypothetical lipoprotein	750.04
FTT_1606	<i>minD</i>	septum site-determining protein MinD	751.04
FTT_1607	<i>minE</i>	cell division topological specificity factor protein	595.67
FTT_1608		ABC transporter, ATP-binding protein	612.69
FTT_1609		ABC transporter, membrane protein	583.41
FTT_1614c		hypothetical protein	581.35
FTT_1616	<i>cysS</i>	Cysteinyl-tRNA synthetase	545.42
FTT_1617	<i>hemK</i>	Adenine-specific methylase, HemK family	723.50
FTT_1618		major facilitator superfamily (MSF) transport protein, pseudogene	567.03
FTT_1622c		hypothetical membrane protein	621.20
FTT_1623c		hypothetical protein	658.20
FTT_1624c		hypothetical protein	676.69
FTT_1629c		hypothetical membrane protein	604.80
FTT_1630c	<i>putP</i>	Sodium/proline permease	582.57
FTT_1631c	<i>gplX</i>	GlpX protein	626.57
FTT_1633c		amino acid transporter	575.14
FTT_1636	<i>lolA</i>	lipoprotein releasing system, subunit A, outer membrane lipoproteins carrier	547.40
FTT_1638	<i>trkH</i>	potassium uptake protein	565.35
FTT_1641c	<i>hsdR2</i>	HsdR protein, fragment	610.92
FTT_1642c	<i>hsdR3</i>	HsdR protein, fragment	608.98
FTT_1645		conserved hypothetical membrane protein	572.80
FTT_1646	<i>dtd</i>	D-tyrosyl-tRNA(Tyr) deacylase	687.01
FTT_1647c	<i>pyrD</i>	diyrorotate dehydrogenase	546.62
FTT_1648c	<i>pyrF</i>	Orotidine 5-phosphate decarboxylase	651.46
FTT_1649		Transglutaminase-like superfamily domain protein,pseudogene	589.63
FTT_1651		conserved hypothetical protein	571.72
FTT_1652c		transcriptional regulator, LysR family	575.76
FTT_1653		hypothetical membrane protein	573.13
FTT_1656c		conserved hypothetical protein	711.76
FTT_1657c		hypothetical protein	581.86
FTT_1660c	<i>pyrC</i>	Dihydroorotase	611.56
FTT_1661	<i>tmpT</i>	Thiopurine S-methyltransferase	625.74
FTT_1662c		acid phosphatase, pseudogene	593.49
FTT_1663	<i>carA</i>	Carbamoyl-phosphate synthase small chain	554.33
FTT_1664	<i>carB</i>	Carbamoyl-phosphate synthase large chain	646.79
FTT_1665	<i>pyrB</i>	aspartate carbamoyltransferase	576.09
FTT_1671	<i>ribD</i>	riboflavin biosynthesis protein ribD	547.93
FTT_1674	<i>ribH</i>	riboflavin synthase beta subunit (6,7-dimethyl-8-ribityllumazine synthase)	577.45
FTT_1675	<i>def2</i>	peptide deformylase	599.15
FTT_1676		hypothetical membrane protein	568.99
FTT_1678c	<i>lepA</i>	GTP-binding protein LepA	591.17
FTT_1679	<i>rpsT</i>	30S ribosomal protein S20	695.67
FTT_1681c	<i>lpcA</i>	phosphoheptose isomerase	608.40
FTT_1684		transcription regulator	592.84
FTT_1689c		conserved hypothetical membrane protein	561.81
FTT_1690		NADH dehydrogenase	568.54

FTT_1693c		conserved hypothetical protein	577.20
FTT_1719c		modification methylase, pseudogene	600.39
FTT_1720c	<i>purL</i>	phosphoribosylformylglycinamide synthase	568.21
FTT_1721c	<i>purF</i>	Amidophosphoribosyltransferase	632.90
FTT_1724c	<i>tolC</i>	outer membrane protein tolC precursor	654.78
FTT_1725c	<i>pcm</i>	Protein-L-isoaspartate O-methyltransferase	600.18
FTT_1726	<i>yegQ</i>	protease yegQ	653.20
FTT_1727c		multidrug resistance protein, membrane located	557.12
FTT_1728	<i>nhaD</i>	Na <sup>+</sup> /H <sup>+</sup> antiporter	634.22
FTT_1733		hypothetical protein	604.91
FTT_1736c	<i>kdpD</i>	two component sensor protein kdpD	554.55
FTT_1737c	<i>kdpC</i>	Potassium-transporting ATPase C chain	594.56
FTT_1738c	<i>kdpB</i>	Potassium-transporting ATPase B chain	623.75
FTT_1739c	<i>kdpA</i>	Potassium-transporting ATPase, A chain,pseudogene	573.46
FTT_1743		NA <sup>+</sup> /H <sup>+</sup> antiporter NHAP, fragment	583.96
FTT_1745c		conserved hypothetical protein, fragment	680.77
FTT_1746		Peptidase	680.85
FTT_1750	<i>recA</i>	Recombinase A protein	601.19
FTT_1752	<i>ssb</i>	Single-strand binding protein	562.39
FTT_1753	<i>tdcD</i>	propionate kinase	578.59
FTT_1754	<i>pta</i>	phosphate acetyltransferase	580.19
FTT_1755	<i>gabD2</i>	Succinate-semialdehyde dehydrogenase,pseudogene	555.31
FTT_1757c		major facilitator superfamily (MFS) transport protein, pseudogene	548.13
FTT_1762c		Acetyltransferase protein	599.10
FTT_1763c		Acetyltransferase protein	602.16
FTT_1765		hypothetical membrane protein	560.82
FTT_1766		O-methyltransferase	612.46
FTT_1767c	<i>purT</i>	phosphoribosylglycinamide formyltransferase 2	571.51
FTT_1768c		Chitinase	577.52
FTT_1769c	<i>clpB</i>	ClpB protein	582.45
FTT_1772c	<i>trpA</i>	tryptophan synthase alpha chain	596.42
FTT_1775c	<i>clcA</i>	Voltage-gated ClC-type chloride channel clcA	549.27
FTT_1776c		hypothetical membrane protein	660.43
FTT_1777c		hypothetical membrane protein	597.83
FTT_1783		major facilitator superfamily (MFS) transport protein	593.95
FTT_1793c	<i>pepN</i>	Aminopeptidase N	604.70



## APPENDIX VI

**Appendix VI: Active *F. tularensis* transcripts 96 hours post infection in the spleens of infected mice.** Raw sequence reads from *F. tularensis* transcripts isolated spleens of mice 96 hours post infection were mapped to the *F. tularensis* Schu4 gene bank reference file and expression reports for each organ and time point were exported in text format. Global means for each expression report were calculated using RPKM values and genes that fell below the global mean were removed to remove background noise and potential DNA contamination.

Locus	Gene Symbol	Annotation	RPKM
FTT_0001	<i>dnaA</i>	chromosomal replication initiator protein dnaA	542.49
FTT_0002	<i>dnaN</i>	DNA polymerase III, beta chain	728.82
FTT_0004c	<i>istu1</i>	Transposase	11020.32
FTT_0005	<i>gabD1</i>	Succinate-semialdehyde dehydrogenase, fragment	550.46
FTT_0007	<i>aspS</i>	Aspartyl-tRNA synthetase	694.28
FTT_0009	<i>istu1</i>	Transposase, fragment	10726.69
FTT_0010		modification methylase, fragment	687.37
FTT_0011		restriction endonuclease, pseudogene	877.73
FTT_0012		conserved hypothetical protein, pseudogene	711.64
FTT_0013c		hypothetical lipoprotein	791.98
FTT_0014c		hypothetical protein	552.32
FTT_0015	<i>purB</i>	adenylosuccinate lyase	635.20
FTT_0018		Secretion protein	625.11
FTT_0020	<i>gatA</i>	Glutamyl-tRNA(Gln) amidotransferase subunit A	542.27
FTT_0021	<i>gatB</i>	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B	558.63
FTT_0023c		Lipase/acyltransferase	656.60
FTT_0026c		conserved membrane protein	623.95
FTT_0031	<i>nuoA</i>	NADH dehydrogenase I, A subunit	642.23
FTT_0035	<i>nuoE</i>	NADH dehydrogenase I, E subunit	565.95
FTT_0036	<i>nuoF</i>	NADH dehydrogenase I, F subunit	590.88
FTT_0037	<i>nuoG</i>	NADH dehydrogenase I, G subunit	625.74
FTT_0038	<i>nuoH</i>	NADH dehydrogenase I, H subunit	740.10
FTT_0039	<i>nuoI</i>	NADH dehydrogenase I, I subunit	817.48
FTT_0042	<i>nuoL</i>	NADH dehydrogenase I, L subunit	650.18
FTT_0043	<i>nuoM</i>	NADH dehydrogenase I, M subunit	634.98
FTT_0044	<i>nuoN</i>	NADH dehydrogenase I, N subunit	671.38
FTT_0047	<i>hemE</i>	uroporphyrinogen decarboxylase	564.49
FTT_0049	<i>nusA</i>	N utilization substance protein A	613.60
FTT_0050	<i>infB</i>	translation initiation factor IF-2	572.80

FTT_0054		ATPase	561.44
FTT_0056c		major facilitator superfamily (MFS) transport protein	593.00
FTT_0057		hypothetical membrane protein	688.08
FTT_0058	<i>atpB</i>	ATP synthase A chain	698.86
FTT_0062	<i>atpA</i>	ATP synthase alpha chain	561.69
FTT_0064	<i>atpD</i>	ATP synthase beta chain	595.49
FTT_0068	<i>sodB</i>	superoxide dismutase [Fe]	566.49
FTT_0070c	<i>ampG</i>	major facilitator superfamily (MFS) transport protein	591.03
FTT_0071c	<i>gltA</i>	citrate synthase	598.92
FTT_0073	<i>sdhD</i>	succinate dehydrogenase hydrophobic membrane anchor protein	541.66
FTT_0074	<i>sdhA</i>	succinate dehydrogenase, catalytic and NAD/ flavoprotein subunit	574.20
FTT_0075	<i>sdhB</i>	succinate dehydrogenase iron-sulfur protein	678.95
FTT_0076	<i>sucA</i>	2-oxoglutarate dehydrogenase E1 component	603.90
		dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex	
FTT_0077	<i>sucB</i>		543.87
FTT_0078	<i>apt</i>	adenine phosphoribosyltransferase	660.03
FTT_0079	<i>mrsA</i>	phosphoglucosamine mutase	561.75
FTT_0080	<i>tpiA</i>	triosephosphate isomerase	706.20
FTT_0088	<i>pilT</i>	Type IV pili nucleotide-binding protein	547.86
FTT_0089c		conserved hypothetical protein, pseudogene	559.18
FTT_0091c	<i>appB</i>	cytochrome oxidase bd-II, subunit II	553.48
FTT_0092c	<i>appC</i>	cytochrome oxidase bd-II, subunit I, pseudogene	559.49
FTT_0093		conserved hypothetical protein	575.25
FTT_0095		hypothetical protein	589.08
FTT_0096		hypothetical protein	556.31
FTT_0097		hypothetical protein	553.80
FTT_0098c	<i>isftu1</i>	Transposase	1508.11
FTT_0099	<i>isftu2</i>	Transposase	9698.87
FTT_0103c		hypothetical protein	589.99
FTT_0104c		major facilitator superfamily (MFS) transport protein	585.48
FTT_0105c		Transporter AcrB/AcrD/AcrF family	613.88
FTT_0106c		Efflux protein, RND family, MFP subunit	548.30
FTT_0109	<i>valA</i>	Lipid A transport protein, ABC transporter, ATP-binding and membrane protein	585.31
FTT_0110	<i>valB</i>	Tetraacyldisaccharide 4-kinase	581.78
FTT_0111	<i>polA</i>	DNA polymerase I	644.90
FTT_0112		transcriptional regulator	712.35
FTT_0113	<i>deoB</i>	Phosphopentomutase	670.98
FTT_0114	<i>deoC</i>	Deoxyribose-phosphate aldolase	625.49
FTT_0115	<i>nupC1</i>	nucleoside permease NUP family protein	555.21
FTT_0121	<i>uvrD</i>	DNA helicase II	560.22
		Similar to OPPA_HAEIN (P71370) Periplasmic oligopeptide-binding protein (precursor) from Haemophilus influenzae (541 aa). FASTA: opt: 924 Z-score: 1112.1 E(): 4.7e-54 Smith-Waterman score: 924; 34.490 identity in 461 aa	
FTT_0122	<i>oppA</i>	overlap oligopeptide transporter, subunit A, ABC transporter, membrane protein, oligopeptide transporter, subunit B, ABC transporter, membrane protein, pseudogene	569.44
FTT_0123	<i>oppB</i>		696.12
FTT_0127c		major facilitator superfamily (MFS) transport protein	545.30
FTT_0128		hypothetical protein	598.79
FTT_0129		major facilitator superfamily (MFS) transport protein	714.83
FTT_0131c	<i>isftu1</i>	Transposase	1423.24
FTT_0132	<i>glpA</i>	anaerobic glycerol-3-phosphate dehydrogenase	568.33
FTT_0135		ion channel protein, fragment	720.38
FTT_0138	<i>secE</i>	preprotein translocase, subunit E, membrane protein	631.10
FTT_0139	<i>nusG</i>	transcription antitermination protein nusG	604.63
FTT_0140	<i>rplK</i>	50S ribosomal protein L11	624.42
FTT_0142	<i>rplJ</i>	50S ribosomal protein L10	622.11
FTT_0145	<i>rpoC</i>	DNA-directed RNA polymerase, beta subunit	546.95
FTT_0149c	<i>metK</i>	S-adenosylmethionine synthetase	565.03
FTT_0152	<i>trmD</i>	tRNA (Guanine-N(1)-)-methyltransferase	549.34
FTT_0154	<i>xerD</i>	Integrase/recombinase	641.35
FTT_0155		oxidoreductase iron/ascorbate family protein	613.55
FTT_0163c	<i>parE</i>	Topoisomerase IV, subunit B	552.21
FTT_0164c		Efflux protein	572.33
FTT_0165c		conserved hypothetical lipoprotein	571.93
FTT_0167	<i>hemA</i>	Glutamyl-tRNA reductase	577.63

FTT_0169		hemK protein homolog	539.47
FTT_0170c		conserved hypothetical protein	668.99
FTT_0171	<i>isftu1</i>	Transposase	4935.64
FTT_0173		conserved hypothetical protein, pseudogene	545.45
FTT_0174		YggT family protein	548.46
FTT_0175c		ABC transporter, ATP-binding protein	621.80
FTT_0185	<i>ddlB</i>	D-alanine--D-alanine ligase B	586.70
FTT_0186	<i>ftsQ</i>	cell division protein FtsQ	659.35
FTT_0187	<i>ftsA</i>	cell division protein FtsA	580.26
FTT_0188	<i>ftsZ</i>	cell division protein	563.48
FTT_0189	<i>lpxC</i>	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase	666.66
FTT_0191	<i>prfB</i>	peptide chain release factor 2	565.95
FTT_0192	<i>lysU</i>	Lysyl-tRNA synthetase	559.57
FTT_0195c		L-glutaminase	538.42
FTT_0196c	<i>glnA</i>	glutamine synthetase	562.86
FTT_0198	<i>b1c</i>	outer membrane lipoprotein	709.12
FTT_0199		hypothetical protein	645.23
FTT_0200		hypothetical protein	646.84
FTT_0201	<i>isftu2</i>	Transposase	3176.11
FTT_0202c		Transporter protein, pseudogene	7143.27
FTT_0203c	<i>purH</i>	bifunctional purine biosynthesis protein	556.20
FTT_0205	<i>hpt</i>	Hypoxanthine-guanine phosphoribosyltransferase	623.83
FTT_0207c		permease of ABC transporter	620.10
FTT_0209c		periplasmic solute binding family protein	569.44
FTT_0212c	<i>wrbA</i>	trp repressor binding protein	609.50
FTT_0214		Transport protein, pseudogene	606.18
FTT_0215	<i>priA</i>	Primosomal protein N	668.58
FTT_0216	<i>isftu1</i>	Transposase	1038.05
FTT_0219c		phosphate transport protein	684.36
FTT_0221	<i>acpA</i>	acid phosphatase (precursor)	547.33
FTT_0222c	<i>ybgK</i>	hydrolase subunit	600.22
FTT_0225c		major facilitator superfamily (MFS) transport protein, fragment	581.03
FTT_0226c	<i>isftu1</i>	Transposase	1423.24
FTT_0227c		hypothetical protein	946.15
FTT_0229c	<i>efp</i>	elongation factor P	737.28
FTT_0232c	<i>ddg</i>	Acyltransferase	671.94
FTT_0233c	<i>yidC</i>	Inner-membrane protein	711.80
FTT_0234c		conserved hypothetical protein	601.52
FTT_0237c		hypothetical protein	625.27
FTT_0238	<i>aroE1</i>	Shikimate 5-dehydrogenase	741.60
FTT_0239	<i>murC</i>	UDP-N-acetylmuramate--alanine ligase	582.04
FTT_0240		tetrapyrrole methyltransferase family protein	563.57
FTT_0241c		hypothetical protein	826.96
FTT_0244		DNA/RNA helicase	650.43
FTT_0245	<i>usp</i>	universal stress protein	557.20
FTT_0247	<i>isftu1</i>	Transposase	1201.27
FTT_0251	<i>ilvE</i>	Branched-chain amino acid aminotransferase protein (class IV)	554.05
FTT_0253c	<i>isftu1</i>	Transposase	1397.13
FTT_0259	<i>hemC</i>	hydroxymethylbilane synthase (porphobilinogen deaminase)	760.52
FTT_0265		ABC transporter, membrane protein	643.47
FTT_0266		ABC transporter, ATP-binding protein	669.32
FTT_0269		carbonic anhydrase, family 3	787.73
FTT_0270	<i>lolB</i>	lipoprotein releasing system, subunit B, outer membrane lipoprotein	701.06
FTT_0273	<i>isftu1</i>	Transposase	1070.69
FTT_0275c		major facilitator superfamily (MFS) transport protein, fragment	636.68
FTT_0277c		conserved hypothetical membrane protein	724.74
FTT_0278c	<i>cydB</i>	cytochrome d terminal oxidase, polypeptide subunit II	630.96
FTT_0279c	<i>cydA</i>	cytochrome d terminal oxidase, polypeptide subunit I	679.87
FTT_0280c	<i>yajR</i>	major facilitator superfamily (MFS) transport protein	610.65
FTT_0281	<i>cyoA</i>	Cytochrome O ubiquinol oxidase subunit II	885.38
FTT_0282	<i>cyoB</i>	Cytochrome O ubiquinol oxidase subunit I	645.98
FTT_0283	<i>cyoC</i>	Cytochrome O ubiquinol oxidase, subunit III	798.92
FTT_0285	<i>cyoE</i>	Protoheme IX farnesyltransferase	615.72
FTT_0286c	<i>lpxD1</i>	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	554.71

FTT_0287c		conserved hypothetical protein	611.17
FTT_0288c	<i>pdxY</i>	Pyridoxal/pyridoxine/pyridoxamine kinase	763.93
FTT_0289c		hypothetical lipoprotein	589.08
FTT_0290	<i>moxR</i>	methanol dehydrogenase regulatory protein	583.72
FTT_0291		conserved hypothetical protein	724.91
FTT_0295		conserved hypothetical membrane protein	589.40
FTT_0296	<i>pcp</i>	Pyrrolidone-carboxylate peptidase	634.95
FTT_0298	<i>hoIC</i>	DNA polymerase III (CHI subunit) protein	604.31
FTT_0307	<i>gltX</i>	Glutamyl-tRNA synthetase	630.15
FTT_0308		hypothetical protein	634.07
FTT_0309c	<i>isftu2</i>	Transposase	881.72
FTT_0311c		conserved hypothetical protein	610.12
FTT_0316	<i>frr</i>	ribosome recycling factor	698.02
FTT_0317	<i>uppS</i>	undecaprenyl pyrophosphate synthetase	754.84
FTT_0318	<i>cdsA</i>	phosphatidate cytidylyltransferase	618.86
FTT_0319	<i>dut</i>	dUTP pyrophosphatase (Deoxyuridine 5-triphosphate nucleotidohydrolase)	596.19
FTT_0323	<i>fusA</i>	elongation factor G (EF-G)	562.17
FTT_0324	<i>rpsJ</i>	30S ribosomal protein S10	580.19
FTT_0325	<i>rpIC</i>	50S ribosomal protein L3	741.35
FTT_0326	<i>rpID</i>	50S ribosomal protein L4	558.49
FTT_0328	<i>rpIB</i>	50S ribosomal protein L2	559.09
FTT_0329	<i>rpsS</i>	30S ribosomal protein S19	679.66
FTT_0330	<i>rpIV</i>	50S ribosomal protein L22	549.10
FTT_0332	<i>rpIP</i>	50S ribosomal protein L16	656.10
FTT_0333	<i>rpmC</i>	50S ribosomal protein L29	790.42
FTT_0335	<i>rpIN</i>	50S ribosomal protein L14	833.33
FTT_0338	<i>rpsN</i>	30S ribosomal protein S14	653.18
FTT_0341	<i>rpIR</i>	50S ribosomal protein L18	738.34
FTT_0342	<i>rpsE</i>	30S ribosomal protein S5	746.75
FTT_0343	<i>rpmD</i>	50S ribosomal protein L30	633.73
FTT_0344	<i>rpIO</i>	50S ribosomal protein L15	628.76
FTT_0347	<i>rpsM</i>	30S ribosomal protein S13	890.05
FTT_0349	<i>rpsD</i>	30S ribosomal protein S4	742.75
FTT_0352	<i>isftu1</i>	Transposase	1122.92
FTT_0353c	<i>isftu2</i>	Transposase, fragment	743.23
FTT_0354		hypothetical protein	607.18
FTT_0355c	<i>isftu1</i>	Transposase	1390.60
FTT_0357c	<i>isftu1</i>	Transposase	1377.54
FTT_0359		hypothetical protein	565.81
FTT_0361c		amino acid transporter	554.26
FTT_0363	<i>isftu1</i>	Transposase	1005.41
FTT_0368c	<i>mviN</i>	virulence factor MviN	553.96
FTT_0370c	<i>yjeE</i>	Nucleotide-binding protein, yjeE	573.60
FTT_0371c	<i>folC</i>	FolC Bifunctional protein	628.70
FTT_0372c	<i>accD</i>	Acetyl-CoA carboxylase beta subunit	591.99
FTT_0377	<i>isftu1</i>	Transposase	1051.11
FTT_0379	<i>isftu2</i>	Transposase, fragment	778.48
FTT_0380c	<i>gdh</i>	NAD(P)-specific glutamate dehydrogenase	550.46
FTT_0381	<i>isftu2</i>	Transposase	737.06
FTT_0383		hypothetical protein	549.10
FTT_0391c	<i>cspC</i>	cold shock protein	854.16
FTT_0393	<i>map</i>	methionine aminopeptidase	551.72
FTT_0396	<i>parC</i>	DNA topoisomerase IV subunit A	564.07
FTT_0399c		BNR/Asp-box repeat protein	567.91
FTT_0400	<i>slt</i>	soluble lytic murein transglycosylase	541.79
FTT_0402	<i>dnaE</i>	DNA polymerase III alpha subunit	566.99
FTT_0405	<i>lolD</i>	lipoprotein releasing system, subunit D, ABC transporter, ATP-binding protein	677.44
FTT_0406	<i>cadA</i>	lysine decarboxylase, inducible	583.80
FTT_0408	<i>gcvH</i>	glycine cleavage system H protein	787.43
FTT_0409	<i>gcvP1</i>	glycine cleavage system P protein, subunit 1	595.67
FTT_0410	<i>gcvP2</i>	glycine cleavage system P protein, subunit 2	616.70
FTT_0411c	<i>aroE2</i>	Shikimate 5-dehydrogenase	599.73
FTT_0413c	<i>glgB</i>	1,4-alpha-glucan branching enzyme	631.63
FTT_0414	<i>pgm</i>	Phosphoglucomutase	548.54

FTT_0415	<i>glgC</i>	Glucose-1-phosphate adenyltransferase,pseudogene	605.31
FTT_0422	<i>murF</i>	UDP-N--acetylmuramoylalanyl-D-glutamyl-2,6- diaminopimelate-D-alanyl-D-alanyl ligase	554.36
FTT_0424		hypothetical protein	572.79
FTT_0426	<i>thrA</i>	bifunctional aspartokinase/homoserine dehydrogenase I (pseudogene)	544.10
FTT_0428	<i>thrC</i>	threonine synthase	700.85
FTT_0430	<i>speH</i>	S-adenosylmethionine decarboxylase	718.67
FTT_0434		conserved hypothetical protein	571.17
FTT_0435		Carbon-nitrogen hydrolase family protein	577.38
FTT_0436c	<i>lpxH</i>	UDP-2,3-diacylglucosamine hydrolase UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-me so-diaminopimelate ligase	578.97
FTT_0438	<i>mpl</i>		620.53
FTT_0440c	<i>isftu1</i>	Transposase	1553.81
FTT_0442c		major facilitator superfamily (MFS) transport protein	583.75
FTT_0444	<i>tet</i>	multidrug transporter (tetracycline resistance protein)	628.73
FTT_0448c	<i>glnS</i>	Glutaminyl-tRNA synthetase	665.90
FTT_0452	<i>ftsW</i>	cell division protein FtsW	675.68
FTT_0456c		UPF0269 family protein	679.84
FTT_0457c	<i>yccK</i>	anaerobic sulfite reductase subunit	569.44
FTT_0458	<i>sspA</i>	stringent starvation protein A, regulator of transcription	558.65
FTT_0462	<i>hemB</i>	Delta-aminolevulinic acid hydratase	636.02
FTT_0464	<i>ansB</i>	Periplasmic L-asparaginase II precursor	582.27
FTT_0465		hypothetical protein	650.79
FTT_0467	<i>ostA1</i>	organic solvent tolerance protein	562.23
FTT_0468	<i>surA</i>	Peptidyl-prolyl cis-trans isomerase (PPIase)	562.23
FTT_0471	<i>aroD</i>	3-dehydroquinate dehydratase, type II	620.15
FTT_0475	<i>msc</i>	mechanosensitive ion channel protein	599.97
FTT_0478c	<i>recJ</i>	Single-stranded-DNA-specific exonuclease Glutamate:gamma-aminobutyric acid antiporter family protein (APC family protein)	552.78
FTT_0480c	<i>xasA</i>		577.92
FTT_0482c		hypothetical lipoprotein	590.38
FTT_0486	<i>mutL</i>	DNA mismatch repair protein	608.29
FTT_0487		hypothetical membrane protein	613.60
FTT_0489c	<i>trxB</i>	thioredoxin reductase	582.02
FTT_0490c		Phospholipase D family protein.	664.82
FTT_0491c	<i>gph</i>	phosphoglycolate phosphatase	637.77
FTT_0495		conserved hypothetical protein	762.64
FTT_0496		conserved hypothetical protein	743.62
FTT_0497c		Asparaginase 2 family protein, pseudogene Di-/tripeptide transporter, proton-dependent oligopeptide transport (POT) family protein, pseudogene	636.40
FTT_0498c			570.62
FTT_0501c		conserved hypothetical membrane protein	566.16
FTT_0502c		hypothetical membrane protein	685.74
FTT_0504c	<i>sucC</i>	Succinyl-CoA synthetase beta chain	713.27
FTT_0506c		hypothetical protein	846.03
FTT_0508c	<i>dusA</i>	RNA dihydrouridine synthase A	546.87
FTT_0509c		conserved hypothetical protein	761.39
FTT_0510	<i>gyrB</i>	DNA gyrase subunit B	570.15
FTT_0513c	<i>isftu1</i>	Transposase	1371.01
FTT_0514	<i>lldD1</i>	L-lactate dehydrogenase, pseudogene	568.43
FTT_0515		hypothetical membrane protein	579.09
FTT_0518	<i>prmA</i>	50S ribosomal protein L11, methyltransferase	539.15
FTT_0528		hypothetical protein Biofunctional protein, glutaredoxin 3 protein/Ribonucleoside-diphosphate reductase, beta subunit	623.67
FTT_0532c	<i>nrdB</i>		689.98
FTT_0534c	<i>nrDA</i>	Ribonucleoside-diphosphate reductase, alpha subunit	549.21
FTT_0535c	<i>mdh</i>	lactate dehydrogenase	592.57
FTT_0536		hypothetical membrane protein	595.93
FTT_0537		ubiquinone biosynthesis protein	564.07
FTT_0538c		conserved hypothetical lipoprotein	566.44
FTT_0540c		hypothetical protein	649.64
FTT_0543		hypothetical protein	562.00
FTT_0544	<i>phnA</i>	phosphonoacetate hydrolase	554.05
FTT_0546		hypothetical protein	778.79
FTT_0547		hypothetical protein	643.02

FTT_0548	<i>dnaQ</i>	DNA polymerase III, epsilon subunit	584.23
FTT_0549	<i>vanY</i>	D-alanyl-D-alanine carboxypeptidase	605.48
FTT_0552		aldehyde dehydrogenase	599.11
FTT_0553		conserved hypothetical protein	604.48
FTT_0555		conserved hypothetical membrane protein	665.13
FTT_0558		conserved hypothetical protein	561.07
FTT_0559c	<i>cmk</i>	cytidylate kinase	646.39
FTT_0561	<i>isftu1</i>	Transposase	1090.28
FTT_0562	<i>potG</i>	polyamine transporter, ABC transporter,ATP-binding protein	666.89
FTT_0564	<i>potI</i>	polyamine transporter, subunit I, ABC transporter, membrane protein	616.01
FTT_0565c	<i>isftu2</i>	Transposase	881.72
FTT_0568		conserved hypothetical protein	669.16
FTT_0569c		conserved hypothetical membrane protein	781.52
FTT_0570		hypothetical lipoprotein	693.61
FTT_0574		amino acid permease family protein, pseudogene	539.47
FTT_0576		conserved hypothetical protein	773.73
FTT_0577	<i>sdaA</i>	L-serine dehydratase 1	566.95
FTT_0580		conserved hypothetical protein	622.05
FTT_0581	<i>coaD</i>	phosphopantetheine adenylyltransferase	880.36
FTT_0583	<i>fopA</i>	outer membrane associated protein	624.36
FTT_0586		conserved hypothetical protein	593.05
FTT_0587c	<i>isftu2</i>	Transposase	881.72
FTT_0591	<i>ansA</i>	L-asparaginase	602.36
FTT_0592	<i>cynT</i>	carbonic anhydrase	731.07
FTT_0595c	<i>rubA</i>	Rubredoxin	569.44
FTT_0596c		hypothetical protein	588.79
FTT_0597		conserved hypothetical protein	562.09
FTT_0598c		Sodium-dicarboxylate symporter family protein	556.11
FTT_0601		hypothetical protein	726.04
FTT_0602c		hypothetical protein	682.64
FTT_0610		DNA/RNA endonuclease family protein	538.96
FTT_0614c		Apolipoprotein N-acyltransferase	732.14
FTT_0615c		metal ion transporter protein	613.09
FTT_0617c	<i>phoH</i>	phoH-like protein	546.87
FTT_0618c	<i>yleA</i>	conserved hypothetical protein yleA	551.45
FTT_0619		o-methyltransferase family protein	698.51
FTT_0622c		hypothetical membrane protein	606.18
FTT_0624	<i>clpP</i>	ATP-dependent Clp protease subunit P	558.17
FTT_0626	<i>lon</i>	DNA-binding, ATP-dependent protease La	542.26
FTT_0630	<i>hfq</i>	host factor I for bacteriophage Q beta replication	543.56
FTT_0633	<i>hflK</i>	SPFH domain, band 7 family protein	575.84
FTT_0636	<i>engB</i>	ATP/GTP-binding protein	569.44
FTT_0637	<i>thrC1</i>	threonine synthase, pseudogene	599.28
FTT_0639		hypothetical protein	554.05
FTT_0644c	<i>mfd</i>	Transcription-repair coupling factor,ATP-dependent	550.49
FTT_0647c		conserved hypothetical protein	545.71
FTT_0648c	<i>nth</i>	Endonuclease III	625.58
FTT_0652c	<i>ftnA</i>	Ferritin-like protein	555.72
FTT_0654	<i>elbB</i>	DJ-1/PfpI family protein	590.15
FTT_0655		conserved hypothetical protein	576.30
FTT_0658	<i>ruvA</i>	holliday junction DNA helicase, subunit A	838.49
FTT_0660		hypothetical membrane protein	758.29
FTT_0661c		conserved hypothetical protein	672.98
FTT_0665c		Aldolase/adducin class II family protein	761.13
FTT_0674	<i>prsA</i>	Ribose-phosphate pyrophosphokinase	576.49
FTT_0678c		hypothetical lipoprotein	631.34
FTT_0679c		GTP-binding protein	633.58
FTT_0682c		hypothetical protein	636.08
FTT_0683c	<i>pilD</i>	Type IV pili leader peptidase and methylase.	550.67
FTT_0684c	<i>sthA</i>	soluble pyridine nucleotide transhydrogenase	691.29
FTT_0686c		Proton-dependent oligopeptide transport (POT) family protein	600.86
FTT_0687c	<i>hslU</i>	ATP-dependent protease, ATP-binding subunit	561.95
FTT_0692c	<i>isftu1</i>	Transposase	1397.13
FTT_0693c	<i>mutM</i>	Formamidopyrimidine-DNA glycosylase	708.18

FTT_0694		conserved hypothetical protein	602.79
FTT_0695	<i>mraW</i>	S-adenosyl-methyltransferase	547.11
FTT_0696		hypothetical protein	584.04
FTT_0698	<i>rpsO</i>	30S ribosomal protein S15	633.42
FTT_0699	<i>pnp</i>	polyribonucleotide nucleotidyltransferase	600.62
FTT_0701	<i>kdsA</i>	2-dehydro-3-deoxyphosphooctonate aldolase	609.68
FTT_0704		hypothetical protein	679.75
FTT_0705	<i>rumA</i>	23S rRNA (Uracil-5-)-methyltransferase	565.65
FTT_0708		major facilitator superfamily (MFS) transport protein	702.95
FTT_0713c	<i>tdh</i>	L-threonine 3-dehydrogenase	621.21
FTT_0714c	<i>kbl</i>	2-amino-3-ketobutyrate coenzyme A ligase	753.55
FTT_0715		chitinase family 18 protein	606.11
FTT_0719		major facilitator superfamily (MFS) transport protein	602.94
FTT_0721c	<i>katG</i>	Peroxidase/catalase	559.46
FTT_0722c	<i>isftu1</i>	Transposase	1351.43
FTT_0723c		Short-chain dehydrogenase/reductase family protein	623.57
		D-alanyl-D-alanine carboxypeptidase (Penicillin binding protein) family protein, pseudogene	
FTT_0724c	<i>dacB1</i>		588.23
FTT_0725c	<i>glpT</i>	Glycerol-3-phosphate transporter	564.25
FTT_0726c		glycerophosphoryl diester phosphodiesterase family protein	683.33
FTT_0728	<i>ybhF</i>	ABC transporter, ATP-binding protein	664.65
FTT_0730	<i>isftu2</i>	Transposase	737.06
FTT_0733		glutathione peroxidase	554.93
FTT_0734		conserved hypothetical membrane protein, pseudogene	562.12
FTT_0735		mandelate racemase/muconate lactonizing enzyme family protein, pseudogene	588.58
FTT_0740c	<i>ostA2</i>	organic solvent tolerance protein	603.36
FTT_0742		hypothetical lipoprotein	569.44
FTT_0745c		hypothetical protein	602.94
FTT_0758	<i>acs</i>	Acetyl-coenzyme A synthetase, pseudogene	550.74
FTT_0759		conserved hypothetical membrane protein	776.00
FTT_0760c		hypothetical lipoprotein	594.20
FTT_0765	<i>isftu1</i>	Transposase	1011.94
FTT_0766	<i>deoD</i>	purine nucleoside phosphorylase	588.34
FTT_0770	<i>tag</i>	DNA-3-methyladenine glycosylase I (pseudogene)	641.75
FTT_0774		conserved hypothetical protein	555.88
FTT_0775c	<i>bcr2</i>	major facilitator superfamily (MFS) transport protein, pseudogene	592.48
FTT_0779	<i>isftu1</i>	Transposase	1005.41
FTT_0781c		conserved hypothetical protein	610.12
FTT_0782	<i>fabI</i>	Enoyl-[acyl-carrier-protein] reductase (NADH)	667.62
FTT_0784		hypothetical protein	543.56
FTT_0789	<i>rpe</i>	D-ribulose-phosphate 3-epimerase	658.82
FTT_0792		glycosyl transferases group 1 family protein	708.33
FTT_0799		glycosyl transferases group 1 family protein	566.07
FTT_0800		haloacid dehalogenase-like hydrolase family protein	641.59
FTT_0804		major facilitator superfamily (MFS) transport protein	566.72
FTT_0806	<i>capC</i>	capsule biosynthesis protein CapC	562.09
FTT_0807		conserved hypothetical membrane protein	608.91
FTT_0808	<i>spoT</i>	Guanosine-3,5-bis(Diphosphate) 3-pyrophosphohydrolase/(p)ppGpp synthase	697.32
FTT_0809c	<i>recR</i>	Recombination protein recR	645.93
FTT_0814c		hypothetical protein	615.00
FTT_0816c		chitin binding protein	682.18
FTT_0822	<i>isftu1</i>	Transposase	1024.99
FTT_0828c		L-aspartate-beta-decarboxylase, pseudogene	550.38
FTT_0831c		OmpA family protein	617.12
FTT_0832	<i>fkpB</i>	FKBP-type 16 kDa peptidyl-prolyl cis-transisomerase	573.12
FTT_0834	<i>aroQ</i>	chorismate mutase	720.04
FTT_0838	<i>tolR</i>	TolR protein	573.26
FTT_0840	<i>tolB</i>	TolB protein precursor	609.56
FTT_0841		hypothetical lipoprotein	671.13
FTT_0842		Peptidoglycan-associated lipoprotein	583.13
FTT_0843		conserved hypothetical protein, pseudogene	643.98
FTT_0844		rossman fold oxidoreductase, pseudogene	602.52
FTT_0846		deoxyribodipyrimidine photolyase	574.00
FTT_0847		conserved hypothetical protein	572.91

FTT_0848		conserved hypothetical protein	557.06
FTT_0854c		conserved hypothetical membrane protein	860.22
FTT_0857c		conserved hypothetical protein	697.48
FTT_0860c		hypothetical protein	589.78
FTT_0861c		Type IV pili fiber building block protein	681.60
FTT_0862c	<i>htpX</i>	heat shock protein HtpX	634.66
FTT_0864c		transcriptional regulator, LysR family	668.47
FTT_0865		conserved hypothetical protein, pseudogene	598.08
FTT_0866c	<i>isftu2</i>	Transposase	558.72
FTT_0867		Cadmium-transporting ATPase (pseudogene)	771.50
FTT_0868c		arsenical resistance operon repressor	700.13
FTT_0870c		hypothetical protein	892.99
FTT_0871	<i>gpsA</i>	Glycerol-3-phosphate dehydrogenase [NAD(P)+]	600.22
FTT_0873c	<i>radA</i>	DNA repair protein radA	635.48
FTT_0874c		hypothetical protein	565.01
FTT_0875c		conserved hypothetical protein	708.95
FTT_0877c		hypothetical protein	813.49
FTT_0879	<i>sodC</i>	superoxide dismutase (Cu-Zn) precursor	652.10
FTT_0880		conserved hypothetical transmembrane protein, fragment	862.81
FTT_0882		Mannose-6-phosphate isomerase, fragment	546.66
FTT_0884c	<i>aspC1</i>	aspartate transaminase	619.64
FTT_0885		cation transporter	683.33
FTT_0886		DNA repair protein recN	543.56
FTT_0888c		Type IV pili fiber building block protein	746.86
FTT_0889c		Type IV pili fiber building block protein	546.20
FTT_0890c		Type IV pili fiber building block protein	590.38
		methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate	
FTT_0892	<i>folD</i>	cyclohydrolase putative bifunctional protein	772.67
FTT_0893	<i>purM</i>	Phosphoribosylaminoimidazol (AIR) synthetase	603.80
FTT_0895	<i>purN</i>	phosphoribosylglycinamide formyltransferase	569.44
FTT_0904	<i>lpnB</i>	conserved hypothetical lipoprotein	635.15
FTT_0905		Type IV pili glycosylation protein	621.53
FTT_0906c	<i>topA</i>	DNA topoisomerase I	596.24
FTT_0908	<i>parB</i>	chromosome partition protein B	560.11
FTT_0910		hypothetical protein	563.63
FTT_0913		hypothetical protein	580.39
FTT_0915c	<i>ileS</i>	Isoleucyl-tRNA synthetase	722.75
FTT_0917	<i>maeA</i>	NAD-dependent malic enzyme	550.62
FTT_0918		hypothetical protein	915.39
FTT_0919		hypothetical protein	559.99
FTT_0920	<i>isftu1</i>	Transposase	842.19
FTT_0927	<i>hemL</i>	Glutamate-1-semialdehyde-2,1-aminomutase	597.12
FTT_0929c		D-Beta-hydroxybutyrate dehydrogenase, pseudogene	538.78
FTT_0932		ROK family protein	565.43
FTT_0936c	<i>bioF</i>	8-amino-7-oxononanoate synthase	754.21
FTT_0937c	<i>bioB</i>	biotin synthase	603.90
FTT_0939c	<i>add</i>	adenosine deaminase	558.59
FTT_0940c		conserved hypothetical protein	542.16
FTT_0941c		Lipase/esterase	812.43
		2-amino-4-hydroxy-6-hydroxymethyl dihydropteridine	
FTT_0942c	<i>folK</i>	pyrophosphokinase/dihydropteroate synthase	550.55
FTT_0947c		major facilitator superfamily (MFS) transport protein, pseudogene	615.16
FTT_0952	<i>rhIE</i>	ATP-dependent RNA helicase RhIE	572.02
FTT_0953c		Proton-dependent oligopeptide transport (POT) family protein	618.19
		Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide	
FTT_0955c	<i>gor</i>	dehydrogenase component	617.10
FTT_0958c		Short-chain dehydrogenase	752.82
FTT_0959c	<i>xthA</i>	Exodeoxyribonuclease III	591.09
FTT_0965c		conserved hypothetical membrane protein	548.70
FTT_0970		conserved hypothetical protein	573.60
FTT_0976	<i>trxA2</i>	Thioredoxin 1	767.96
FTT_0977c		conserved hypothetical protein	557.82
FTT_0986		conserved hypothetical protein	586.07
FTT_0993c	<i>dcd</i>	deoxycytidine triphosphate deaminase	632.71
FTT_0999c		ZIP metal transporter family protein, pseudogene	541.94



FTT_1002c	<i>pheT</i>	Phenylalanyl-tRNA synthetase, beta subunit	613.36
FTT_1003c	<i>pheS</i>	Phenylalanyl-tRNA synthetase, alpha subunit	768.24
FTT_1004c		conserved hypothetical membrane protein	567.53
FTT_1009		hypothetical membrane protein	582.17
FTT_1013c	<i>ruvB</i>	holliday junction DNA helicase, subunit B	680.39
FTT_1016c		GDSL-like Lipase/Acylhydrolase family protein	634.52
FTT_1019c	<i>guaA</i>	GMP synthase (glutamine-hydrolyzing)	650.95
FTT_1025c		hypothetical protein	626.80
FTT_1027c	<i>yrbl</i>	3-deoxy-D-manno-octulosonate 8-phosphate phosphatase	606.78
FTT_1028c	<i>ppa</i>	inorganic pyrophosphatase	677.44
FTT_1029	<i>dacD</i>	D-alanyl-D-alanine carboxypeptidase (Penicillin binding protein) family protein	587.36
FTT_1031	<i>lipB</i>	Lipoate-protein ligase B	759.26
FTT_1038c	<i>rpsU3</i>	30S ribosomal protein S21	672.98
FTT_1039	<i>dacB</i>	D-alanyl-D-alanine carboxypeptidase (Penicillin binding protein) family protein	547.54
FTT_1043		FKBP-type peptidyl-prolyl cis-trans isomerase family protein	542.13
FTT_1044c	<i>ispB</i>	Octaprenyl-diphosphate synthase	565.95
FTT_1050c	<i>cysN</i>	sulfate adenylate transferase subunit 1	612.97
FTT_1057c		Type IV pili lipoprotein	678.80
FTT_1058c		Radical SAM superfamily protein	538.74
FTT_1059c	<i>dnaB</i>	Replicative DNA helicase	579.22
FTT_1061c	<i>rpsR</i>	30S ribosomal protein S18	842.46
FTT_1062c	<i>rpsF</i>	30S ribosomal protein S6	915.17
FTT_1064		hypothetical protein	554.99
FTT_1075		transcriptional regulator	629.38
FTT_1086c		conserved hypothetical protein	635.23
FTT_1087c	<i>rep</i>	ATP-dependent DNA helicase	549.10
FTT_1092c		hypothetical protein	614.10
FTT_1094c		cytosol aminopeptidase family protein	593.57
FTT_1095c		conserved hypothetical protein	592.91
FTT_1097		hypothetical protein	550.33
FTT_1100		conserved hypothetical protein	823.66
FTT_1102		macrophage infectivity potentiator, fragment	616.41
FTT_1103		conserved hypothetical lipoprotein	648.79
FTT_1105c	<i>msrA1</i>	peptide methionine sulfoxide reductase	569.44
FTT_1108		rRNA methyltransferase	578.52
FTT_1110		hypothetical protein	608.05
FTT_1111	<i>isftu2</i>	Transposase	723.28
FTT_1114c	<i>secF</i>	preprotein translocase, subunit F, membrane protein	764.68
FTT_1115c	<i>secD</i>	preprotein translocase, subunit D, membrane protein	605.58
FTT_1116c	<i>yajC</i>	preprotein translocase family protein	646.00
FTT_1117c		isochorismatase hydrolase family protein	608.20
FTT_1122c		hypothetical lipoprotein	641.98
FTT_1124	<i>metN</i>	D-methionine transport protein, ABC transporter,ATP-binding subunit	775.65
FTT_1125	<i>metIQ</i>	D-methionine binding transport protein, ABC transporter, membrane and periplasmic protein	615.83
FTT_1126		aromatic amino acid transporter of the HAAAP family	575.08
FTT_1127		Rhodanese-like family protein	600.95
FTT_1128	<i>ispF</i>	2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	694.01
FTT_1129c		conserved hypothetical protein	595.79
FTT_1138	<i>hemH</i>	Ferrochelataase	629.11
FTT_1140		hypothetical protein	647.09
FTT_1143		hypothetical protein	708.33
FTT_1148c	<i>yjhB</i>	major facilitator superfamily (MFS) transport protein	1379.63
FTT_1150c	<i>putA</i>	Multifunctional protein, transcriptional repressor of proline utilization, proline dehydrogenase,pyrroline-5-carboxylate dehydrogenase	553.51
FTT_1159c		Type IV pili associated protein	663.34
FTT_1160c		hypothetical protein	606.84
FTT_1162c		FAD-binding family protein, pseudogene	547.89
FTT_1165c	<i>aspC2</i>	aspartate aminotransferase	545.12
FTT_1167c		glycoprotease family protein	705.79
FTT_1176c	<i>hsdR1</i>	Type I restriction enzyme subunit R, pseudogene	602.42
FTT_1179	<i>bipA</i>	GTP binding translational elongation factor Tu and G family protein	614.55
FTT_1180		conserved hypothetical protein, pseudogene	793.15
FTT_1182c	<i>vacJ</i>	VacJ lipoprotein, pseudogene	595.41
FTT_1183c		conserved hypothetical lipoprotein	569.44

FTT_1187		conserved hypothetical protein	691.46
FTT_1189c		major facilitator superfamily (MFS) transport protein, pseudogene	581.39
FTT_1190c	<i>xseA</i>	Exodeoxyribonuclease VII large subunit	658.19
FTT_1193c		conserved hypothetical protein	592.48
FTT_1195c		conserved hypothetical protein, pseudogene	580.78
FTT_1199c	<i>uvrB</i>	DNA excision repair enzyme, subunit B (UvrABC system protein B)	569.44
FTT_1202		transcriptional regulator, LysR family	558.05
FTT_1204c		hypothetical membrane protein	591.53
FTT_1205	<i>gidA</i>	glucose inhibited division protein A	587.58
FTT_1209c		metallopeptidase family M13 protein, pseudogene	746.23
FTT_1211c		hypothetical protein	665.07
FTT_1214c		haloacid dehalogenase-like hydrolase family protein	672.98
FTT_1215c	<i>queA</i>	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	596.16
FTT_1217c	<i>visC</i>	monooxygenase family protein	584.64
FTT_1221		hypothetical protein	556.64
FTT_1227	<i>rne</i>	Ribonuclease E	564.94
FTT_1228	<i>lgt</i>	prolipoprotein diacylglycerol transferase	558.86
FTT_1229	<i>thyA</i>	thymidylate synthase	608.78
FTT_1230	<i>serA</i>	D-3-phosphoglycerate dehydrogenase	613.35
FTT_1233c	<i>yjdL</i>	Proton-dependent oligopeptide transport (POT) family protein	555.30
FTT_1236		hypothetical protein	545.91
FTT_1245	<i>rluD</i>	ribosomal large subunit pseudouridine synthase D	713.08
FTT_1247		ABC transporter, membrane protein	609.78
FTT_1248		ABC transporter, ATP-binding protein	578.41
FTT_1253		Proton-dependent oligopeptide transport (POT) family protein	619.96
FTT_1254	<i>fadD1</i>	Acyl-CoA synthetase (long-chain-fatty-acid--CoA ligase)	560.35
FTT_1255c		transcriptional regulator araC family protein	579.50
FTT_1256	<i>emrB</i>	major facilitator superfamily (MFS) transport protein	572.79
FTT_1257	<i>emrA1</i>	HlyD family secretion protein	596.16
FTT_1259	<i>nadE</i>	NH(3)-dependent NAD(+) synthetase	669.66
FTT_1264	<i>isftu2</i>	Transposase	717.07
FTT_1268c	<i>dnaJ</i>	Chaperone protein dnaJ (heat shock protein 70 family cofactor)	687.89
FTT_1276	<i>mgIB</i>	macrophage growth locus, subunit B	577.82
FTT_1281c	<i>yhbH</i>	Sigma-54 modulation protein	638.46
FTT_1283	<i>trmE</i>	tRNA modification GTPase trmE family protein	553.03
FTT_1286		choloylglycine hydrolase family protein,pseudogene	596.94
FTT_1292c		conserved hypothetical protein	569.44
FTT_1295c	<i>glk</i>	glucose kinase	569.44
FTT_1296	<i>ubiE</i>	menaquinone biosynthesis methyltransferase	735.06
FTT_1297		hypothetical protein	583.54
FTT_1299	<i>hitA</i>	histidine triad (HIT) family protein	650.07
FTT_1301c		Purine/pyrimidine phosphoribosyl transferase family protein, pseudogene	623.10
FTT_1302		hypothetical protein	585.89
FTT_1304c	<i>murB</i>	UDP-N-acetylenolpyruvoylglucosamine reductase	2825.07
FTT_1305c	<i>murA</i>	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	541.29
FTT_1310c	<i>hflB</i>	ATP-dependent metalloprotease	588.16
		DNA excision repair enzyme, subunit A (UvrABC system protein A), ABC	
FTT_1312c	<i>uvrA</i>	transporter, ATP-binding protein	609.99
FTT_1313c	<i>greA</i>	transcriptional elongation factor	689.70
FTT_1315c	<i>pgi</i>	Glucose-6-phosphate isomerase	593.65
FTT_1317c	<i>guaB</i>	Inosine-5-monophosphate dehydrogenase	571.78
FTT_1318c	<i>pepA</i>	cytosol aminopeptidase	711.80
FTT_1319		Permease YjgP/YjgQ family protein	553.67
FTT_1321		Peptidase M16 family protein	555.82
FTT_1324		conserved hypothetical membrane protein	558.94
FTT_1326	<i>udp</i>	uridine phosphorylase	586.44
FTT_1329	<i>gpml</i>	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	639.37
FTT_1333c		hypothetical protein	815.92
FTT_1337c	<i>dctA</i>	C4-dicarboxylate transport protein	577.63
FTT_1338c		translation initiation inhibitor	578.41
FTT_1340c	<i>isftu2</i>	Transposase	909.27
FTT_1342		conserved hypothetical membrane protein	582.38
FTT_1343c		hypothetical protein	601.08
FTT_1344	<i>pdpA</i>	conserved hypothetical protein	819.83

FTT_1345	<i>pdpB</i>	conserved hypothetical protein	677.71
FTT_1346		hypothetical protein	555.88
FTT_1347		conserved hypothetical protein	1056.05
FTT_1349		conserved hypothetical protein	1138.88
FTT_1350		conserved hypothetical protein	866.70
FTT_1351		conserved hypothetical protein	615.98
FTT_1352		conserved hypothetical protein	578.34
FTT_1354		conserved hypothetical protein	830.38
FTT_1356c	<i>iglD</i>	intracellular growth locus, subunit D	926.40
FTT_1357c	<i>iglC</i>	intracellular growth locus, subunit C	1152.31
FTT_1358c	<i>iglB</i>	intracellular growth locus, subunit B	1101.29
FTT_1359c	<i>iglA</i>	intracellular growth locus, subunit A	858.50
FTT_1365c	<i>fabB</i>	Fructose-1,6-bisphosphate aldolase	577.46
FTT_1366c	<i>pyk</i>	pyruvate kinase	570.63
FTT_1368c	<i>gapA</i>	Glyceraldehyde-3-phosphate dehydrogenase	685.29
FTT_1369c	<i>tktA</i>	Transketolase	558.29
FTT_1372	<i>plsX</i>	fatty acid/phospholipid synthesis protein IsX	606.97
FTT_1373	<i>fabH</i>	3-oxoacyl-[acyl carrier protein] synthase III	637.99
FTT_1374		malonyl coA-acyl carrier protein transacylase	567.59
FTT_1377	<i>fabF</i>	3-oxoacyl-[acyl-carrier-protein] synthase II	577.58
FTT_1379c		conserved hypothetical protein, pseudogene	572.54
FTT_1383	<i>sun</i>	Sun protein	584.11
FTT_1387c	<i>ligN</i>	DNA ligase	636.53
FTT_1390	<i>panC</i>	Pantoate-beta-alanine ligase	723.76
FTT_1392		transcriptional regulator	830.90
FTT_1395c		ATP-dependent DNA helicase	598.09
FTT_1398c		conserved hypothetical membrane, pseudogene	647.50
FTT_1401		prophage repressor protein	561.75
FTT_1402c		hypothetical protein	557.95
FTT_1406c		hypothetical membrane protein	606.32
FTT_1409c		conserved hypothetical protein	626.80
FTT_1412	<i>proS</i>	Prolyl-tRNA synthetase	679.10
FTT_1417		Carbon-nitrogen hydrolase	612.91
FTT_1418c	<i>nusB</i>	N utilisation substance protein B	589.49
FTT_1419		hypothetical lipoprotein	736.62
FTT_1420		hypothetical protein	810.36
FTT_1423c		conserved hypothetical membrane protein	601.33
FTT_1424c		conserved hypothetical protein	669.78
FTT_1430c		Methyltransferase, fragment	569.44
FTT_1432c	<i>ppnK</i>	inorganic phosphate/ATP-NAD kinase	580.95
FTT_1433	<i>gtrB</i>	glycosyl transferase	558.59
FTT_1434c	<i>yadH</i>	ABC transporter, membrane protein	689.90
FTT_1436	<i>isftu2</i>	Transposase	723.28
FTT_1437c		conserved hypothetical membrane, pseudogene	540.16
FTT_1439c		Deoxyribonuclease	607.26
FTT_1442c	<i>rpoA2</i>	DNA-directed RNA polymerase, alpha subunit	551.59
FTT_1444c	<i>ppx</i>	Exopolyphosphatase	613.24
FTT_1445	<i>trxA1</i>	Thioredoxin	601.08
FTT_1449c	<i>isftu1</i>	Transposase	2261.33
FTT_1450c	<i>wbtM</i>	dTDP-D-glucose 4,6-dehydratase	543.34
FTT_1453c	<i>wzx</i>	O-antigen flippase	547.63
FTT_1461c	<i>wbtD</i>	galacturonosyl transferase	713.37
FTT_1465c	<i>isftu2</i>	Transposase	881.72
FTT_1466c	<i>add1</i>	adenosine deaminase, pseudogene	638.36
FTT_1467c	<i>nadB</i>	L-aspartate oxidase	544.18
FTT_1468c	<i>nadC</i>	Nicotinate-nucleotide pyrophosphorylase	794.85
FTT_1469c	<i>nadA</i>	quinolinate sythetase A	554.46
FTT_1470c	<i>gmk</i>	guanylate kinase	572.42
FTT_1471c	<i>deaD</i>	Cold-shock DEAD-box protein A	590.42
FTT_1473c	<i>galP2</i>	Galactose-proton symporter, major facilitator superfamily (MFS) transport protein	617.20
FTT_1474c	<i>galP1</i>	Galactose-proton symporter, major facilitator superfamily (MFS) transport protein	737.43
FTT_1475	<i>galT</i>	Galactose-1-phosphate uridylyltransferase	609.40
FTT_1477c		conserved hypothetical protein	595.33
FTT_1478c	<i>kdsB</i>	3-deoxy-D-manno-octulosonate cytidyltransferase	571.71

FTT_1479c		conserved hypothetical protein	569.44
FTT_1480c		hypothetical protein	740.27
FTT_1482		Transposase, fragmentation	585.04
FTT_1483c	<i>lpd</i>	dihydrolipoamide dehydrogenase	580.32
FTT_1485c	<i>aceE</i>	pyruvate dehydrogenase, E1 component	556.07
FTT_1490		Na <sup>+</sup> /H <sup>+</sup> antiporter	579.96
FTT_1493c		hypothetical protein	815.34
FTT_1494c		glucokinase regulatory protein	642.79
FTT_1495c		hypothetical membrane protein	552.92
FTT_1498c	<i>accA</i>	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha	686.57
FTT_1500	<i>secB2</i>	preprotein translocase, subunit B, chaperone protein	577.14
FTT_1502		aromatic amino acid transporter of the HAAAP family	639.57
FTT_1503	<i>xerC</i>	Integrase/recombinase XerC	583.05
FTT_1506		hypothetical protein	610.75
FTT_1507		hypothetical protein	655.80
FTT_1508c	<i>relA</i>	GTP pyrophosphokinase	614.26
FTT_1509c		hypothetical protein	545.52
FTT_1510c		aromatic amino acid transporter of the HAAAP family	616.54
FTT_1511		conserved hypothetical membrane protein	637.00
FTT_1515c		conserved hypothetical membrane protein	589.37
FTT_1518	<i>ogt</i>	Methylated-DNA--protein-cysteine methyltransferase	608.20
FTT_1520c	<i>gabP</i>	Glutamate/gamma-aminobutyrate anti-porter	727.76
FTT_1522c		conserved hypothetical protein	650.38
FTT_1523c	<i>isftu2</i>	Transposase	881.72
FTT_1526c	<i>idh</i>	isocitrate dehydrogenase	557.26
FTT_1528	<i>fadD2</i>	long chain fatty acid CoA ligase	555.28
FTT_1530	<i>fadB/acbP</i>	fusion product of 3-hydroxacyl-CoA dehydrogenase and acyl-CoA-binding protein	590.98
FTT_1531	<i>fadA</i>	3-ketoacyl-CoA thiolase	621.21
FTT_1533c		sugar transport protein, pseudogene	616.35
FTT_1535c		ornithine cyclodeaminase, pseudogene	626.33
FTT_1536c		conserved hypothetical protein	660.93
FTT_1537c		conserved hypothetical protein	576.79
FTT_1538c		hypothetical protein	614.58
FTT_1539c		conserved hypothetical protein	658.98
FTT_1540c		conserved hypothetical protein	908.86
FTT_1541c		hypothetical protein	656.00
FTT_1543		two component response regulator	609.05
FTT_1549		hypothetical protein	786.73
FTT_1550		conserved hypothetical protein	566.30
FTT_1551		Oxidoreductase	681.95
FTT_1553c	<i>rnr</i>	Ribonuclease R	608.84
FTT_1554c	<i>truB</i>	tRNA pseudouridine synthetase B	569.44
FTT_1555c	<i>rnc</i>	Ribonuclease III	569.44
FTT_1569c	<i>lpxA</i>	Acyl-(acyl-carrier-protein)--UDP-N-acetylglucosamine O-acyltransferase	584.77
FTT_1570c	<i>fabZ</i>	(3R)-hydroxymyristoyl-(acyl-carrier protein) dehydratase	541.66
FTT_1574c	<i>dxr</i>	1-deoxy-D-xylulose 5-phosphate reductoisomerase	659.43
FTT_1575c	<i>gyrA</i>	DNA gyrase, subunit A	615.31
FTT_1587c		amino acid transporter protein, fragment	634.23
FTT_1588c		conserved hypothetical protein, fragment	540.61
FTT_1589c		hypothetical protein	544.18
FTT_1591		Lipoprotein	543.97
FTT_1593c		conserved hypothetical protein, fragment	722.75
FTT_1594		transcriptional regulator, LysR family	583.20
FTT_1596		hypothetical protein	667.92
FTT_1600c	<i>fumA</i>	fumarate hydratase	571.70
FTT_1602		hypothetical lipoprotein	742.75
FTT_1604	<i>rpmG</i>	50S ribosomal protein L33	591.34
FTT_1606	<i>minD</i>	septum site-determining protein MinD	733.03
FTT_1608		ABC transporter, ATP-binding protein	720.30
FTT_1609		ABC transporter, membrane protein	683.33
FTT_1610		ABC transporter, periplasmic protein, pseudogene	738.99
FTT_1616	<i>cysS</i>	Cysteinyl-tRNA synthetase	540.05
FTT_1617	<i>hemK</i>	Adenine-specific methylase, HemK family	569.44

FTT_1621c		hypothetical membrane protein	541.37
FTT_1622c		hypothetical membrane protein	539.76
FTT_1624c		hypothetical protein	910.04
FTT_1632c		conserved hypothetical protein	593.50
FTT_1635	<i>ftsK</i>	cell division protein	546.91
FTT_1641c	<i>hsdR2</i>	HsdR protein, fragment	637.30
FTT_1645		conserved hypothetical membrane protein	739.86
FTT_1646	<i>dtD</i>	D-tyrosyl-tRNA(Tyr) deacylase	760.98
FTT_1647c	<i>pyrD</i>	diurootate dehydrogenase	548.86
FTT_1648c	<i>pyrF</i>	Orotidine 5-phosphate decarboxylase	548.25
FTT_1649		Transglutaminase-like superfamily domain protein,pseudogene	626.99
FTT_1651		conserved hypothetical protein	637.56
FTT_1656c		conserved hypothetical protein	584.92
FTT_1658c		conserved hypothetical membrane protein	703.43
FTT_1660c	<i>pyrC</i>	Dihydroorotase	555.49
FTT_1661	<i>tmpT</i>	Thiopurine S-methyltransferase	955.76
FTT_1663	<i>carA</i>	Carbamoyl-phosphate synthase small chain	566.51
FTT_1664	<i>carB</i>	Carbamoyl-phosphate synthase large chain	603.76
FTT_1668	<i>sdaC2</i>	serine transporter	640.62
		riboflavin synthase alpha subunit3,4-dihydroxy-2-butanone 4-phosphate synthetase	
FTT_1672	<i>ribB</i>		541.25
FTT_1673	<i>ribA</i>	riboflavin biosynthesis protein ribA/GTP-cyclohydrolase II	553.94
FTT_1674	<i>ribH</i>	riboflavin synthase beta subunit (6,7-dimethyl-8-ribityllumazine synthase)	634.85
FTT_1676		hypothetical membrane protein	567.72
FTT_1679	<i>rpsT</i>	30S ribosomal protein S20	581.96
FTT_1681c	<i>lpcA</i>	phosphoheptose isomerase	540.83
FTT_1683c		major facilitator superfamily (MFS) transport protein	542.75
FTT_1684		transcription regulator	584.58
FTT_1686c		conserved hypothetical protein	589.87
FTT_1687c	<i>gidB</i>	methyltransferase glucose-inhibited cell division protein	580.50
FTT_1695	<i>groS</i>	Chaperonin protein, groES	569.44
FTT_1719c		modification methylase, pseudogene	675.38
FTT_1721c	<i>purF</i>	Amidophosphoribosyltransferase	584.34
FTT_1724c	<i>tolC</i>	outer membrane protein tolC precursor	556.04
FTT_1726	<i>yegQ</i>	protease yegQ	546.36
FTT_1727c		multidrug resistance protein, membrane located	559.40
FTT_1730c		amino acid transporter	541.20
FTT_1731c		GTP-binding protein	606.84
FTT_1732c		aromatic amino acid transporter of the HAAAP family	732.14
FTT_1733		hypothetical protein	722.75
FTT_1734c	<i>fopA1</i>	outer membrane associated protein, fragment	556.20
FTT_1736c	<i>kdpD</i>	two component sensor protein kdpD	569.44
FTT_1738c	<i>kdpB</i>	Potassium-transporting ATPase B chain	630.57
FTT_1739c	<i>kdpA</i>	Potassium-transporting ATPase, A chain,pseudogene	624.61
FTT_1744c	<i>ipdC</i>	indolepyruvate decarboxylase	546.30
FTT_1745c		conserved hypothetical protein, fragment	602.94
FTT_1746		Peptidase	565.74
FTT_1750	<i>recA</i>	Recombinase A protein	597.91
FTT_1751	<i>recX</i>	Regulatory protein recX	633.55
FTT_1752	<i>ssb</i>	Single-strand binding protein	709.12
FTT_1753	<i>tdcD</i>	propionate kinase	732.14
FTT_1754	<i>pta</i>	phosphate acetyltransferase	559.67
FTT_1757c		major facilitator superfamily (MFS) transport protein, pseudogene	603.90
FTT_1758c		B-type cytochrome	655.72
FTT_1759c		Oxidase-like protein, pseudogene	737.07
FTT_1760	<i>nhaA</i>	Na(+)/H(+) antiporter 1	556.10
FTT_1766		O-methyltransferase	670.85
FTT_1768c		Chitinase	613.53
FTT_1770		conserved hypothetical membrane protein,pseudogene	680.43
FTT_1775c	<i>clcA</i>	Voltage-gated ClC-type chloride channel clcA	582.84
FTT_1776c		hypothetical membrane protein	706.45
FTT_1777c		hypothetical membrane protein	611.01
FTT_1778c		hypothetical membrane protein	612.91
FTT_1783		major facilitator superfamily (MFS) transport protein	800.40

FTT_1793c	<i>pepN</i>	Aminopeptidase N	610.26
FTT_1796c		conserved hypothetical protein	606.58
FTT_1797c	<i>msrA2</i>	peptide methionine sulfoxide reductase msrA	549.63