

Screening of Ancestral Polymorphisms for Immune Response Genes

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Abbreviations and Glossary

Allele	Allele is used for two or more alternative forms of a gene resulting in different gene products and thus different phenotypes. An organism is homozygous for a gene if the alleles are identical, and heterozygous if they are different.
Adenine (A)	A purine base (nitrogenous base) and constituent of nucleotides and as such one member of the base pair A-T (adenine-thymine) in DNA and A-U (adenine-uracil) in RNA.
Annotation	The process of attaching biological information to DNA sequences. It consists of two procedures: 1. identifying elements in a genome, and 2. attaching biological information (ORFs and their localization, gene structure, coding regions, location of regulatory motifs, etc) to these elements. Automatic annotation tools (e.g. Ensembl) try to perform every step of this by computer analysis, as opposed to manual annotation, which involves human expertise.
Alignment	The process of lining up two or more sequences to achieve maximal levels of identity (and conservation, in the case of amino acid sequences) for the purpose of assessing the degree of similarity and the presence of homology.

BAC clone	Bacterial artificial chromosome vector which carries a genomic DNA insert.
Base pair (bp)	Two nitrogenous (purine or pyrimidine) bases (adenine and thymine or guanine and cytosine) held together by weak hydrogen bonds. Two strands of DNA are held together in the shape of a double helix by the bonds between base pairs. The number of base pairs is often used as a measure of length of a DNA segment, e.g. 500 bp.
Breakpoint	Refers to sites of recombination when chromosomes undergo meiosis.
BLAST	Basic Local Alignment Search Tool. A sequence comparison algorithm, optimized for speed, used to search sequence databases for optimal local alignments to a query. The initial search is done for a word of length "W", which scores at least "T" when compared to the query using a substitution matrix. Word hits are then extended in either direction in an attempt to generate an alignment with a score exceeding a threshold of "S". The "T" parameter dictates the speed and sensitivity of the search.

BLAT	The BLAST-Like Alignment Tool is a bioinformatics software tool, which performs rapid mRNA/DNA and cross-species protein alignments. BLAT is more accurate and 500 times faster than other popular existing tools for mRNA/DNA alignments and 50 times faster for protein alignments at sensitivity settings typically used when comparing vertebrate sequences.
Consed	A tool for viewing, editing, and finishing sequence assemblies created with Phrap. Finishing capabilities include allowing the user to pick primers and templates, suggesting additional sequencing reactions to perform, and facilitating checking the accuracy of the assembly using digest and forward/reverse pair information.
Contig	The result of joining an overlapping collection of sequence or clones.
Chromosome	The individual threads of DNA within a cell nucleus. The self-replicating genetic structures of cells containing the cellular DNA that bears in its nucleotide sequence the linear array of genes.

Cytosine (C) Cytosine is a pyrimidine base (nitrogenous base) and constituent of nucleotides and as such one member of the base pair G-C (guanine and cytosine) in DNA.

Deoxyribonucleic acid

(DNA) The molecule that encodes genetic information. DNA is a double-stranded molecule, held together by weak bonds between base pairs of nucleotides. The four nucleotides in DNA are the bases adenine (A), guanine (G), cytosine (C), and thymine (T).

Draft genome

sequence A sequence produced by combining the information from the individual sequenced clones and positioning the sequence along. Compared to finished sequence, many gaps exist and the ordering and orientation of contigs is tentative.

Ensembl A genome browser developed by the European Bioinformatics Institute (EBI) and the The Wellcome Trust Sanger Institute. It is a software system which produces and maintains automatic annotation on selected eukaryotic genomes.

EST	Expressed sequence tag obtained by performing a single raw sequence read from a random complementary DNA clone.
Exon	The protein-coding DNA sequence and untranslated regions (UTR) of a gene, after the introns are spliced out of the mRNA.
Filtering (Masking)	The process of hiding regions of (nucleic acid or amino acid) sequence having characteristics such as repetitiveness or low complexity that frequently lead to spurious high scores. The most commonly used software is Repeat Masker.
Finished Sequence	Complete sequence of a clone or genome, with an accuracy of at least 99.99% and only intractable gaps.
Gene	An ordered sequence of nucleotides located in a particular position (locus) on a particular chromosome that encodes a specific functional product (the gene product, i.e. a protein or RNA molecule). It includes regions involved in regulation of expression, and regions that code for a specific functional product.

Genotype	The set of genes carried by an individual, referring to a particular pair of alleles.
Genomic DNA	DNA from the genome, containing all coding (exon) and noncoding (intron and other) sequences, in contrast to cDNA, which contains only coding sequences.
Guanine (G)	A purine base (nitrogenous base) and constituent of nucleotides and as such one member of the base pair G-C (guanine and cytosine).
Intron	The DNA base sequence interrupting the exon sequences of a gene; intron sequences are transcribed into RNA but are spliced out of the messenger mRNA before it is translated into protein.
LD	Linkage disequilibrium (LD) is the non-random association of alleles at two or more loci. LD describes a situation in which some combinations of alleles or genetic markers occur more or less frequently in a population than would be expected from a random formation of haplotypes from alleles based on their frequencies.

Megabase (Mb) Unit of length for DNA fragments equal to 1 million nucleotides and roughly equal to 1 centimorgan (cM).

Polymerase Chain Reaction

(PCR) A method for amplifying a DNA base sequence using a heat-stable polymerase and two approximately 20-base primers, one complementary to the (+)-strand at one end of the sequence to be amplified and the other complementary to the (-)-strand at the other end.

Primer3 Primer designing software.

Phrap A widely used computer program that assembles raw sequences into sequence contigs and assigns to each position in the sequence an associated 'quality score', on the basis of the Phred scores of the raw sequence reads. A Phrap quality score of X corresponds to an error probability of approximately $10^{-X/10}$. Thus, a Phrap quality score of 30 corresponds an accuracy of 99.9% for a base in the assembled sequence.

Phred A widely used computer program that analyses raw sequences to produce a base call with an associated quality score for each position in the sequence. A Phred quality

score of X corresponds to an error probability of approximately $10^{-x/10}$. Thus, a Phred quality score of 30 corresponds an accuracy of 99.9% for the base call in the raw read.

Raw sequence Individual sequence reads, produced by sequencing of clones containing DNA inserts.

sim2 A program for building local alignments of two sequences, each of which may be hundreds of kilobases long. Sim2 first constructs the n best non-intersecting chains of 'fragments', such as all occurrences of identical 5-tuples in each of two DNA sequences, for any specified $n \geq 1$. Each chain is then refined by delivering an optimal alignment in a region delimited by the chain.

SNP Single nucleotide polymorphism. A single nucleotide position in the genome sequence for which two or more alternative alleles are present.

STS Sequencing Tagged Sites. A site that corresponds to a short (usually less than 500 bp), specific locus, for which a unique PCR assay has been developed.

Perl	A programming language (Practical Extraction and Report Language) extensively used in areas such as bioinformatics and web programming.
Thymine (T)	A pyrimidine base (nitrogenous base) and constituent of nucleotides and as such one member of the base pair A-T (adenine-thymine) in DNA.

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2. Abstract / Zusammenfassung

The immune system is a network of interacting cellular and soluble components. Its function is to distinguish between objects within the body as "self" or "nonself" and to eliminate those that are nonself. The immune system has evolved two mechanisms to accomplish these tasks: nonspecific immunity and specific immunity. An increasing number of studies in human and livestock animals indicate, that single nucleotide polymorphisms (SNPs) affect the speed and quality of response to infection by affecting transcriptional and cytokine circuits of innate and adaptive immune response. Apart from comparative sequence and evolutionary studies of immunoglobulin, the major histocompatibility complex region and the T-cell receptor complex, we know very little about variations (SNPs) in cytokine and chemokine-related loci of humans and chimpanzees, that can be exploited in chimpanzee models of infectious human diseases (e.g. HCV) or can be used to improve rodent models.

The chimpanzee is our closest living evolutionary relative with an average identity of around 98% at the DNA level. The complete sequence of the chimpanzee genome and its variation data will provide great insight into genome evolution and organization. The sequence will also further facilitate research in biodiversity, ecology, and medicine.

To identify SNPs which may cause functional changes leading to different immune response quality in chimpanzees compared to humans, we selected 166 gene

candidates. The genes were selected due to their significant role in the immune response on the human side. The exons and promoters of these genes were sequenced in five unrelated chimpanzees in order to identify *Pan troglodytes* specific variations. By combining the chimpanzee and human variation data, human ancestral, identical and species-specific SNPs could be defined. These data may eventually play a major role for identifying SNPs associated with known human immune disease genotypes.

Das Immunsystem ist ein Netzwerk bestehend aus zellularen und löslichen Komponenten, die sich gegenseitig beeinflussen und regulieren. Die Funktion des Immunsystems besteht darin, Objekte als körpereigen oder nicht körpereigen zu klassifizieren. Dafür hat das Immunsystem zweierlei Mechanismen entwickelt: unspezifische (angeborene) und spezifische (erworbene) Abwehrmechanismen. Studien an Menschen und Tieren zeigen, dass Variationen (Punktmutationen) im Genom – sogenannte „Single Nucleotide Polymorphisms“ (SNPs) – die Geschwindigkeit der angeborenen und erworbenen Immunantwort auf Infektionen durch Wirkung auf transkriptionale und cytokinische Schaltkreise beeinflussen. Mit SNPs werden Variationen von einzelnen Basenpaaren in einem DNA-Strang bezeichnet, die bei mindestens 1% der jeweiligen Population vorkommen.

Abgesehen von Sequenzvergleichen und Evolutionstheorien zu Immunoglobulin, der „major histocompatibility complex“ (MHC) -Region und dem T-Zell-Rezeptorkomplex, liegen bisher wenige Daten über SNPs in Cytokinen und Chemokinen von Menschen und Schimpansen vor, mit Hilfe derer Infektionskrankheiten am Primatenmodell ausgewertet (e.g. HCV) oder am Nagetiermodell optimiert werden können.

Der Schimpanse ist auf der Evolutionsstufe der nächste Verwandte des Menschen mit einer genomischen Identität von 98%. Das Schimpansengenom und die Variationsdaten liefern tiefgreifende Erkenntnisse in Hinblick auf die Evolution. Die Sequenzen werden darüber hinaus Forschungen über Biodiversität und im Bereich der Medizin erleichtern.

166 Gene wurden ausgewählt, um SNPs zu bestimmen, die eine Funktionsänderung aufweisen und somit eine unterschiedliche Immunantwort

beim Schimpansen im Vergleich zum Menschen hervorrufen. Die Selektion beruht auf der Bedeutung dieser Gene für die Immunantwort beim Menschen. Die Exons und die Promoter von fünf nicht miteinander verwandten Schimpansen wurde sequenziert, um Variationsdaten von Pan Troglodytes zu generieren. Anhand der Variationsdaten von Mensch und Schimpanse können identische, artspezifische und Ur-SNPs definiert werden. Dies ermöglicht ein besseres Verständnis von Immunkrankheiten, die mit Punktmutationen (SNPs) assoziiert sind.

3. Introduction

3.1 Comparative Genomics

Sequencing of the genomes of a wide variety of organisms - from yeast to human - has driven the development of a new research field called comparative genomics. By comparing the human genome with other genomes, the structure and function of human genes can be better analyzed for developing new strategies against human disease. Comparative genomics provides new possibilities for evolutionary studies, e.g. changes among organisms, identification of conserved genes among species.

The perspective of evolution is a powerful tool for understanding disease susceptibility. For example, chimpanzees do not suffer from some diseases that strike humans, such as malaria and AIDS, and vice versa. DNA sequence comparison of genes involved in disease susceptibility may reveal the reasons for these species specific disease characteristics. In order to carry out comparative genomics studies, DNA sequence data is needed. As a result, sequence data of many organisms including *Mus musculus*, *Rattus norvegicus*, *Homo sapiens*, *Pan troglodytes*, *Gallus gallus*, *Canis familiaris*, *Drosophila melanogaster*, and so on have recently been generated. Comparative genomic approaches have shown that 60% of the genes are conserved between fly and human. Comparative genomics will also benefit the animal world, by identifying those regions of the genome that are related to species-specific animal health and disease resistance / susceptibility.

3.2 The Chimpanzee Genome and Positive Selection

A number of researchers have called for the deciphering of the chimpanzee genome as a complement to the human genome¹⁻⁶, their key point being that chimpanzees are the most closely related species to human. Since the divergence of humans and chimpanzees about 5 million years ago, both species have undergone a remarkable evolution resulting in drastic changes in their phenotypic features. However, recent studies have shown that the divergence between humans and chimpanzees is much more recent and more complicated than previously estimated. Analyses have showed that the two species split between 6.3 and 5.4 million years ago. The time from the beginning to the completion of divergence between the two species ranges over more than 4 million years, a span of time much larger than previously predicted. All great apes have 24 pairs of chromosomes as compared to the 23 pairs in human. Therefore, the common ancestor of human and all great apes had 24 pairs of chromosomes with the fusion of two of the ancestor's chromosomes resulting in the formation of human chromosome 2. The X chromosome is on average 1.2 million years "younger" than the 22 autosomal chromosomes, indicating that the separation of human and chimpanzee involved an initial split followed by later interbreeding before a final separation²⁰.

The sequence difference of 1.2% between human and chimpanzee was initially confirmed by BAC end sequencing⁷. New comparison data shows differences of 1.44% between chimpanzee chromosome 22 and its human counterpart, chromosome 21¹⁶. This difference corresponds to single base pair substitutions, insertions, deletions and various various rearrangements. Although the genome difference is very little, conspicuous differences exist in physiology, anatomy and pathology. Since the divergence of human and chimpanzee, remarkable differences have also developed with regard to cognitive abilities.

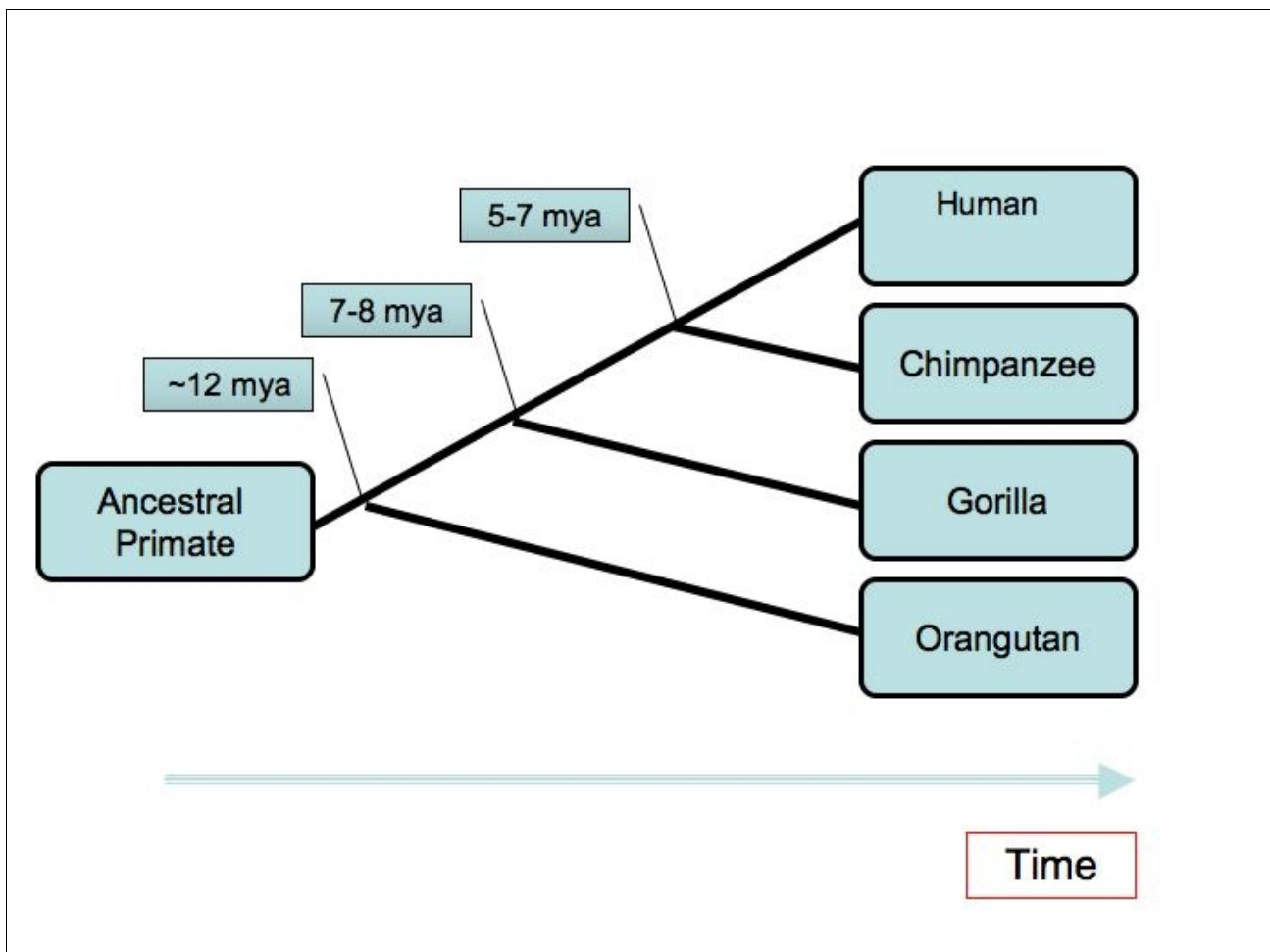


Figure 1: Primate relatives split from their common ancestors. The divergence of the split between human and chimpanzee was estimated to have occurred about 5 million years ago (mya).

Some examples are: differences in reproductive biology, unique vertebral column structure, high human susceptibility to *falciparum* malaria, suggestive evidence of different rates of epithelial cancers, Alzheimer's disease and HIV progression to AIDS^{8,9,10,11,12,13}. Through detailed comparative analysis genes involved in these processes might be identified. The chimpanzee data will also deliver important insights in evolutionary and population genetic studies in human, such as the detection of positive selection in early human evolution. Some genes may only change by a single base, while others may change dramatically compared to their chimpanzee counterpart. Identifying these genetic areas of natural selection is very interesting, because it will show which areas have been

selected for resistance to parasites or to epidemic diseases. This kind of effect is called functional molecular change and can be observed, for example, in the BRCA1 gene, which has been under positive selection in humans and chimpanzee¹⁴.

A comparison of human SNPs and chimpanzee sequence data shows regions of rapid evolution, particularly determination of the ancestral allele at the human site. 19,985 ancestral states from 21,435 human SNPs on the human chromosome 21 could be constructed. Transitional changes (G=>A, 19.6%; C=>T, 20.3%) , are more frequent than transversions. This change is compatible with the fact, that the G+C content of the human is lower than 50%.

The Ka/Ks test detects ancient selection by considering homologous regions from protein coding DNA sequences. It is a common method for detecting positive selection. If the ratio of synonymous (non protein-coding-change) to non-synonymous (protein-coding-change) is greater than 1, evidence for positive selection is given. A Ka/Ks value equal to 1 indicates neutral evolution and less than 1 indicates negative selection.

18 10kb DNA regions, including three known genes *KCNE1*, *DSCR2* and *B3GALT5* were detected as candidates of positive selections. These genes are rapidly evolving according to the ratio of non-synonymous to synonymous rates¹⁶. However, many other genes involved in sensory perception, immune defense, tumor suppression, apoptosis and spermatogenesis showed Ka/Ks values greater than 1¹⁷. Genes involved in olfaction (OR2W1, OR5I1, OR2B2, and C20orf185) and genes involved in host–pathogen interactions, such as CMRF35H, CD72 antigen, pre-T-cell antigen receptor α (PTCRA), APOBEC3F, and granzyme H (GZMH) showed particular evidence of positive selection¹⁷. APOBEC3F is an antiviral factor under positive selection and has been associated with anti-HIV activity¹⁸. The hypothesis for immune related genes is that most of the positive selection in the human genome may have been driven by a competition between the host of the immune system and pathogens.

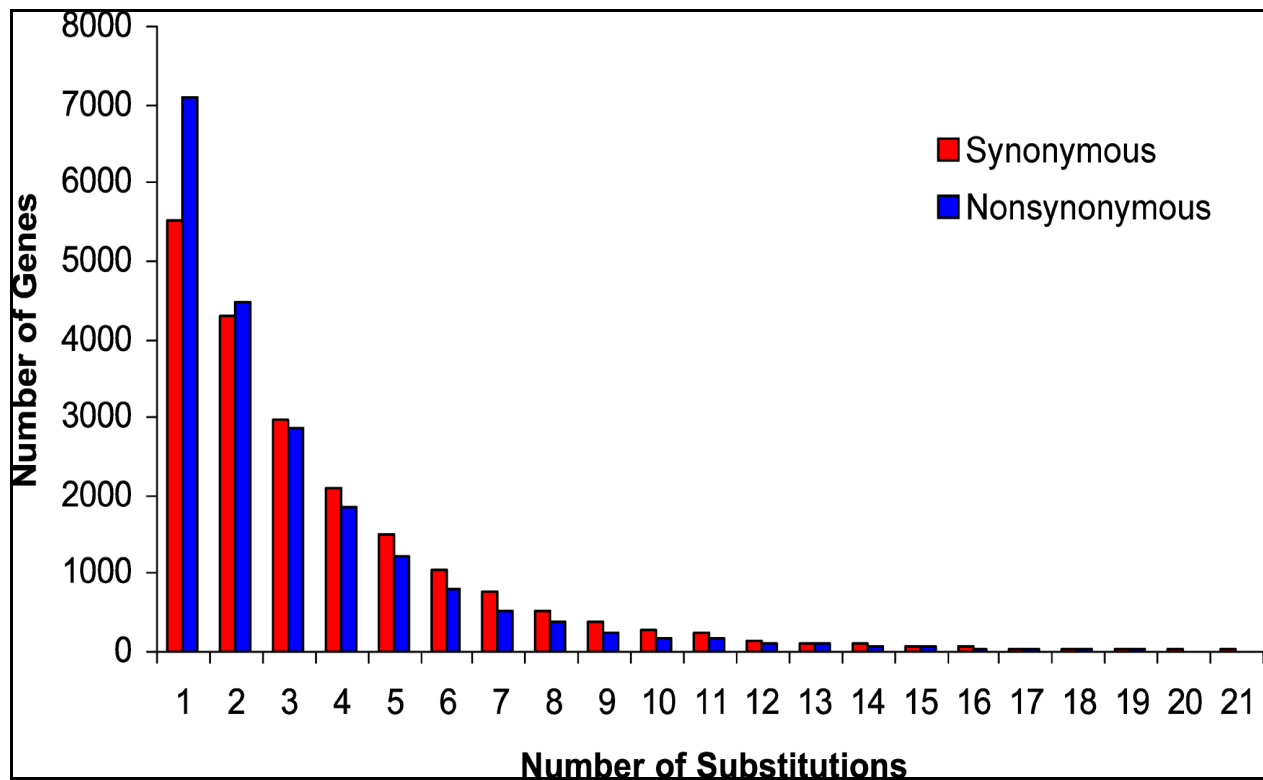


Figure 2 : Distribution of synonymous and nonsynonymous nucleotide differences. Red bars indicate synonymous, blue bars nonsynonymous nucleotide differences in human–chimpanzee orthologous gene pairs. This analysis shows data from 20,361 coding regions. The average numbers of mutations per nucleotide site are 0.002578 for nonsynonymous and 0.003281 for synonymous¹⁷.

Genes functionally related to testis, e.g. Protamine-1 (PRM1), USP26, C15orf2, PEPP-2, TCP11, HYAL3, and TSARG1, have also been under positive selection due to sperm competition, sexual conflict, selection for reproductive isolation, pathogen-driven selection in the reproductive organs, and selection related to the occurrence of mutations causing segregation distortion^{19,21}. Remarkably, cancer related genes involved in tumor suppression, apoptosis and cell cycle control show the strongest evidence for positive selection. These are four putative tumor suppressors: HYAL3, DFFA, PEPP-2, C16orf3 (HYAL3 and PEPP-2 also appearing in spermatogenesis) and in apoptosis: PPP1R15A, HSJ001348, TSARG1, and GZMH. However, the factors causing positive selection for all these genes are still unknown. In order to highlight regions, where chimpanzees have different polymorphism rates compared to human, SNP information for chimpanzee is needed. The data generated in this study will help to establish a SNP map for

chimpanzees, which will provide more precise data for haplotype and recombination studies of *PAN*. It will even give detailed information of the Ka/Ks tests if variation data of human and chimpanzee is taken into account.

HC Name ^a	Gene Name	Function	NDHC ^b	SD HC ^c	NP H ^d	SP H ^e	HC LR ^f
HC208	<i>PRM1</i>	Substitutes for histones in sperm	9	0	0	2	10.12208
HC15768	<i>CMRF35H</i>	Leukocyte membrane antigen	13	0	0	0	9.262642
HC12140	<i>DGAT2L1</i>	Fatty acid synthesis (presumed)	10	1	2	0	6.625498
HC1860	<i>FLJ46156</i>	Unknown	10	1	4	3	6.401844
HC2436	<i>USP26</i>	Testis-specific expression	11	0	1	0	6.217652
HC3085	<i>C15orf2</i>	Testis-specific expression	18	2	12	4	6.093642
HC13803	<i>ABHD1</i>	Unknown	6	0	4	1	5.778402
HC11239	<i>SCML1</i>	Transcriptional repressor, embryonic development (presumed)	15	1	0	0	5.748762
HC3472	<i>OR2W1</i>	Olfactory receptor	8	0	2	1	5.702798
HC10799	<i>LOC389458</i>	Unknown	8	0	1	0	5.493604
HC7761	<i>APOBEC3F</i>	Antiretroviral factor	11	0	2	1	5.476024
HC19072	<i>MS4A12</i>	Unknown	8	0	1	1	5.36116
HC4477	<i>HYAL3</i>	Testis-specific expression, putative tumor suppressor	5	0	2	2	5.266036
HC7681	<i>FLJ32965</i>	Similar to melanoma-associated antigens (function unknown)	7	0	2	0	5.24997
HC8130	<i>LOC151534</i>	Function unknown	7	0	0	1	5.13903
HC3434	<i>MMP26</i>	Zinc-binding endopeptidase, tumor progression (presumed)	7	0	2	1	4.869976
HC7508	<i>KIAA0495</i>	Component of the cell membrane (by similarity)	6	0	1	1	4.67452
HC4613	<i>CD72</i>	Signaling in the immune system	5	0	2	0	4.516886
HC14419	<i>DFFA</i>	Inhibition of apoptosis, putative tumor suppressor	6	0	1	0	4.448548
HC11263	<i>KRN1</i>	Hair keratin	2	0	2	0	4.4187
HC8067	<i>TNKS1BP1</i>	Tankyrase-binding, multifunctional (presumed)	6	0	2	3	4.323594
HC19953	<i>RNPC4</i>	RNA-binding, pre-mRNA-splicing process (presumed)	6	0	3	3	4.283004
HC1586	<i>KRTAP19-1</i>	Keratin-associated protein 19-1	4	0	1	0	3.923226
HC18280	<i>HSJ001348</i>	Apoptosis, p53-induced	10	0	0	0	3.904888
HC3104	<i>HSA404617</i>	Unknown	5	0	0	1	3.748416
HC15059	<i>FLJ20489</i>	Unknown	5	0	0	2	3.653678
HC13738	<i>RPP38</i>	Component of RNase P	4	0	5	2	3.638472
HC2758	<i>FLJ35725</i>	Unknown	4	0	3	0	3.637784
HC4426	<i>PEPP-2</i>	Testis-homeobox gene, putative tumor suppressor	11	0	3	1	3.602598
HC18485	<i>PGR</i>	Progesterone receptor	11	0	2	3	3.51589
HC738	<i>MGC57858</i>	Unknown	3	0	2	0	3.208712
HC973	<i>GZMH</i>	Cell lysis	12	1	1	0	3.131548
HC4889	<i>TCP11</i>	Germ-cell development (presumed)	3	0	2	1	3.122404
HC17263	<i>C20orf185</i>	Possible carrier molecule for odorants	4	1	2	3	3.047252
HC18160	<i>PPP1R15A</i>	Growth arrest, DNA-damage inducible, apoptosis	9	2	5	5	3.007004
HC14000	<i>SLC22A4</i>	Cation transporter, susceptibility to rheumatoid arthritis	4	0	2	3	2.979532
HC16621	<i>GREAT (LGR8)</i>	Receptor for relaxin. Mutations may cause cryptorchidism	4	0	1	0	2.951438
HC11003	<i>LR8</i>	Unknown (expressed by a lung fibroblast subpopulation)	3	0	7	0	2.948436
HC16489	<i>HHLA1</i>	Unknown	3	0	0	0	2.569134
HC3738	<i>C16orf3</i>	Putative tumor suppressor	2	0	1	1	2.56533
HC2610	<i>CYSLTR2</i>	Anaphylactic reactions	9	1	5	0	2.47886
HC9844	<i>ASB11</i>	Cytokine signaling	3	0	2	0	2.448126
HC8169	<i>FLJ32743</i>	Unknown	3	0	2	2	2.39831
HC12857	<i>GDF3</i>	Putative regulator of cell growth and differentiation	2	0	1	1	2.261462
HC6579	<i>FLJ32844</i>	Unknown	2	0	3	0	2.2473
HC2300	<i>OR2B2</i>	Olfactory receptor	3	0	3	0	2.246402
HC1723	<i>MGC41945</i>	Unknown	12	2	5	0	2.184832
HC3892	<i>OR5I1</i>	Olfactory receptor	5	1	7	4	2.152316
HC4879	<i>PTCRA</i>	Pre-T-cell antigen receptor α	8	1	2	0	2.075898
HC16795	<i>TSARG1</i>	Spermatogenesis cell apoptosis	6	1	3	2	1.671884

^aReference number used in Dataset S1.
^bNumber of nonsynonymous differences between humans and chimps.
^cNumber of synonymous differences between humans and chimps.
^dNumber of nonsynonymous polymorphism in humans.
^eNumber of synonymous polymorphism in humans.
^fLikelihood ratio from the likelihood ratio test of d_N/d_S equals one versus d_N/d_S is greater than one in the human-chimp alignment.
DOI: 10.1371/journal.pbio.0030170.t003

Figure 3: 50 genes, sequenced in 20 European-American and 19 African-American individuals, are summarized with mutations (nonsynonymous change) holding the strongest evidence for positive selection in the intra specific comparison. In total, 55 synonymous and 116 nonsynonymous polymorphisms were discovered. However, human and chimpanzee SNPs from public databases were not integrated. This result shows that the Ka/Ks ratio is relatively high in the polymorphism data¹⁷.

3.3 The Immune System

The immune system is the major defense organ against viruses, bacteria fungi and other non-self bodies. The primary objective is to distinguish between self and non-self bodies and eliminate non-self entities. This systemic organ is formed lymphocytes, monocytes and macrophages. The immune system has established two mechanisms: nonspecific immunity and specific immunity.

3.3.1 Nonspecific (Innate) Immunity

The innate immunity system is phylogenetically old, present at birth, provides rapid antimicrobial host defense, and does not develop memory. This innate system includes barriers such as the skin and chemical protection like gastric acid. The two cellular components are :

(1) the phagocytic system to ingest and digest invading microorganisms, and
(2) natural killer (NK) cells to kill some types of tumors, microorganisms, and virally infected cells. The soluble components consist of complement proteins, acute phase reactants, and cytokines. Phagocytes include neutrophils and monocytes in the blood and macrophages in the tissues. Widely distributed macrophages are strategically situated at the interface of tissue with blood or cavitary spaces. Cells have to interact with each other by transferring signal substances such as cytokines for an immune response. These molecules, in response, interact with a specific antigen, a nonspecific antigen, or a nonspecific soluble stimulus. The substances consist of nonimmunoglobulin polypeptides, hormone like proteins or glycoproteins secreted by monocytes and lymphocytes. Cytokines affect the magnitude of inflammatory or immune responses. Although cytokines

are not antigen specific, their secretion may be activated by the interaction of a lymphocyte with its specific antigen. This molecule acts as a bridge between the innate and the adaptive immune system. Cytokines involved in immune response are called interleukins. Interleukins created by lymphocytes are called lymphokines, and those produced by monocytes are called monokines.

3.3.2 Specific (Adaptive) Immunity

The specific immunity system has the ability to learn, adapt, and memorize. The cellular component is the lymphocyte, and the soluble component immunoglobulins are the soluble component.

Lymphocytes are divided into two subsets:

1. T (thymus) cells
2. B (bone marrow-derived) cells

An individual lymphocyte has specific receptors and only recognizes one single antigen.

The number of antigens, with which a body can react, is potentially limitless.

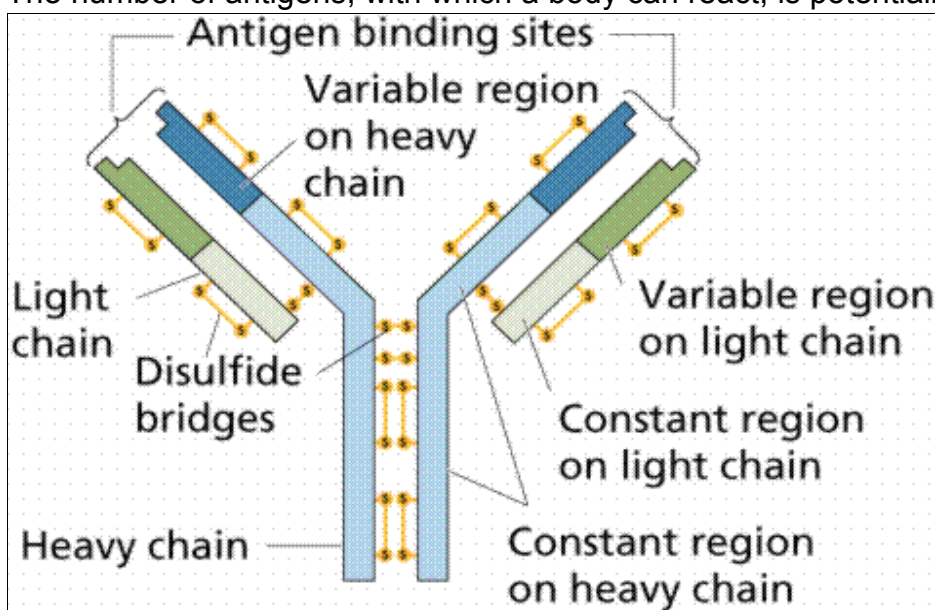


Figure 4: The antigen binding sites bind foreign molecules and microorganisms for inactivation.

(Source: www.emc.maricopa.edu/faculty/farabee/BIOBK/BioBookglossA.htm)

This specialization of providing an infinite number of unique cells is solved by the ability of the lymphocyte's antigen receptor genes to combine in potentially limitless arrangements. A look at the basic structure of the antibody helps to understand this specific mechanism underlying these arrangement variations. Antibodies are composed of two heavy (H), and two light chains (L), each with constant, and variable domains.

An antigen is bound with its antibody in the variable domain formed by the H and L chains. At the gene level, the C region is coded by the C-region, the V region by the V- and J-region for the light chains and by the V-, D-, and J-region genes for the heavy chains. These genes are not located on the same chromosome, but rather are discontinuous and must be juxtaposed during B-cell maturation. For the heavy chain of an antibody, one of several D segments (at least 12 have been identified) connects to one of six J segments. This construct then joins one of several hundred to thousands of V-region gene segments to form a complete transcriptional unit for the heavy chain. Depending on which particular segment of each gene region is used, a vast number of immunoglobulin molecules with varying specificities is possible. Since these arrangements occur at the genetic level, cells with a different specific receptor differ not only phenotypically but also genotypically.

The function of the receptor on B cells, which is anchored in the membrane, is mediated by surface immunoglobins. After B cells bind soluble antigen through their surface immunoglobins, a series of events (e.g. proliferation, differentiation) culminates in the secretion of immunoglobins that represent the specific antibody for that antigen (Ag). The current assumption is, that the antibody (Ab) repertoire of an organism before exposure to Ag is generated due to Ab during B-cell maturation through random rearrangements of immunoglobulin genes.

T cells carry many different antigen receptors for immunological reactions. They do not have surface immunoglobins, but recognize antigens by their principal recognition tool, the so-called T-cell receptor (TCR) and other accessory adhesion molecules. The antigen

binding portion of the TCR consists of two chains, namely α and β , which are linked by intermolecular disulfide bridges. Each chain has a constant and a variable segment. The N terminal domain is the variable portion responsible for antigen binding, and the C terminal domain is the constant portion. The diversity of antigen specificities of TCR is produced by recombination between each of several different V, D and J genes encoding the β chain (VDJ complex), and V and J genes encoding the α chain (VJ complex). The VDJ and its respective VJ complex are each transcribed together with a corresponding C gene to form a complete chain. The two resulting chains then again form the heterodimeric T cell receptor. The TCR is associated with the CD3 molecule. The whole unit is called the TCR/CD3 complex. Lymphocytes can be further divided into subsets, according to their function or by the surface markers they are carrying.

Lymphocyte subsets have been identified by the combination of certain molecules on their surfaces. These surface markers have been assigned clusters of differentiation (CD). So far, 166 CDs have been identified (<http://www.ncbi.nlm.nih.gov/prov>).

The ability of the immune system to differentiate self from non self is determined largely by products of the major histocompatibility complex (MHC). The responsible genes (namely DP, DQ and DR) are located on chromosome 6 for MHC class II. MHC class I consists of the genes HLA-A, -B, and -C. These gene products are widely distributed and present on the surfaces of all nucleated cells and on platelets. Class II MHC products HLA-D, -DR, -DP, and -DQ have a more limited distribution on B cells, macrophages, dendritic cells, Langerhans' cells, and activated T cells. B cells are able to respond to soluble antigens, but T cells recognize antigens only when embedded within the MHC. Thus, the MHC class I is relevant for cytotoxic T lymphocytes, and MHC class II for helper T-cells. Both classes physiologically serve for association with an antigen. The mechanism by which antigens are processed and associated with MHC before presenting to the T cells is accomplished by antigen-presenting cells (APCs), e.g. Langerhans cells, monocytes, macrophages,

follicular dendritic cells, and B cells. The antigen binding site of an immunoglobulin can accommodate only a small part of its determinant. Therefore, antigens must be unfolded, degraded, and fragmented into small pieces by exogenous processing. The internalized antigens are processed by proteolytic degradation and associated with MHC class II products. After this process, the antigenic product and MHC class II are transported to the cell surface by endogenous processing.

Antigens produced intra-cellularly by viral infection go through proteolytic degradation, in which newly created polypeptides are sized down to antigenic peptides. The resulting peptides are transported to the endoplasmic reticulum by transporter proteins. There, these peptides are associated with MHC class I products before being transported to the cell surface.

CD4⁺ and CD8⁺ act as accessory adhesion molecules by binding to MHC class I and II. After cellular interaction has first been initialized, the antigen representing cell induces additional activation signals such as interleukin-1, interleukin-6 for CD4⁺, and interleukin-6 for CD8⁺.

3.3.3 Gene Selection

Immune homeostasis and response is regulated by complex layers of networks at both gene and protein level. Despite the similarities of the immune system between various species, many differences still exist even within one single species. Prerequisites for gene network construction include knowledge of the gene structure, the transcriptional framework, transcription start sites and regulatory elements. Therefore, the genes in this study were chosen and compiled by searching for various keywords, Gene Ontology (GO) terms, InterPro motifs, Medical Subject Headings (MeSH <http://www.nlm.nih.gov/mesh>) terms and microarray probes from immuno-chips. MeSH showed the highest coverage

(52%) followed by gene ontology terms (49%) and InterPro motifs/domains (5%). Of the 529 control accessions (microarray), 317 (60%) were captured by the forementioned extraction methods. 212 entries were missed because the entry-associated GO terms were too broad (e.g. Nfkbib GO: nucleus) or the reference publications did not contain curated MeSH terms. 36% of the immune-related entries could be retrieved only by GO terms and 46% only by MeSH terms, indicating the importance of combining different data extraction methods. About 14% (571) of the sequences represented splice variants, while 19% (470) contained repeat elements. Of 288 cytokines and cytokine-related transcripts, 62 (21.5%) contained repeats with an additional poly(A) site, splice sites or sites that resided in the protein-coding region.

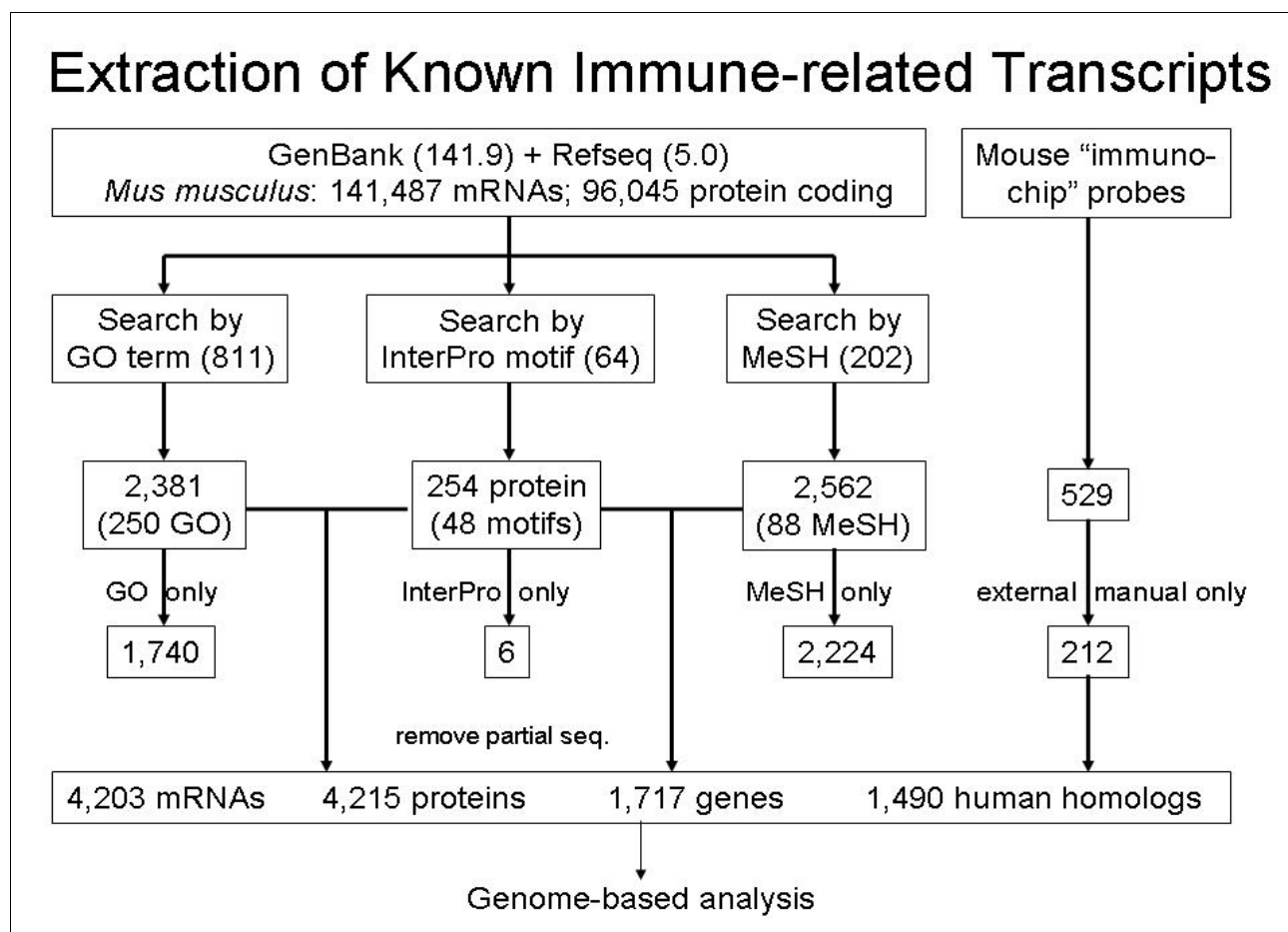


Figure 5: This figure describes the combination pattern of searches for the gene selection.

Due to budgeting constraints, the list of candidate genes was reduced to groups of genes such as cytokine, chemokines and receptor encoding genes as well as a few other innate immune response genes with human SNP information reported in the literature and documented disease associations to be used for comparison. A mouse equivalent of the list was used by the RIKEN Research Center for Allergy and Immunology (RCAI) and Dr. Yokoyama's Protein Research group for prioritizing and selecting targets for NMR analysis. Therefore, the immune-related gene extraction effort nicely contributed to the efforts of the RIKEN Structural Genomics project and of RCAI goal. In total, 166 genes were selected (see appendix table 1 and figure 6).

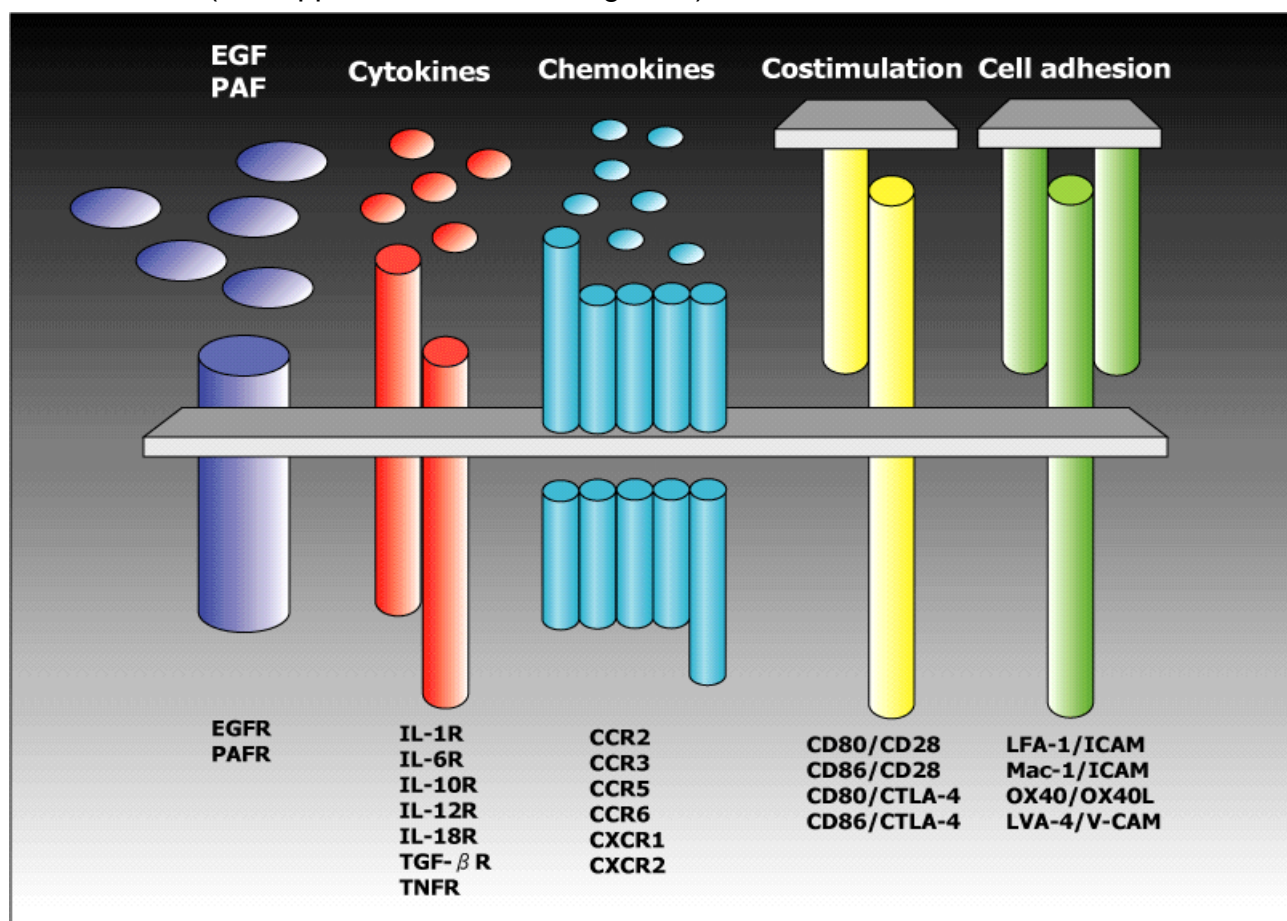


Figure 6: Cytokines are secreted in response interactions with specific antigens, nonspecific antigens, or a nonspecific soluble stimulus (e.g. endotoxin or other cytokines). The genes were selected by

- 1) functional categories : ligands, receptor, co-receptor and signaling molecules and by
- 2) data source: gene expression profiles, SWISS-PROT and LocusLink.

3.4 Single Nucleotide Polymorphisms (SNPs)

3.4.1 dbSNPs and HapMap

SNPs (single nucleotide polymorphisms) are polymorphisms within a DNA sequence. By comparing the same region of two or more sequences position-by-position, different nucleotides can be identified at millions of locations in the human genome. Sequence variations exist at defined positions within genomes and can be responsible for individual phenotypic characteristics. Sequence variations can be used for gene mapping, definition of population structure, and performance of functional studies, and therefore represent a powerful tool for understanding molecular genetics and evolution. Most human sequence variation is attributable to SNPs, with the remainder attributable to insertions or deletions of one or more bases, repeat length polymorphisms, and other rearrangements. SNPs are generally binary and hence well suited for automated, high-throughput genotyping. SNPs, in contrast to more mutable markers, have a low rate of recurrent mutation, making them stable indicators of human genomic evolutionary history. SNPs serve as excellent biological markers because they occur frequently throughout the genome.

Studies of genetic variation began inauspiciously with the study of ABO blood group frequencies²³, but these frequencies can be better explained by investigating single genes with single base changes²⁴. The SNP Consortium and the International Human Genome Sequencing Consortium (analysis of clone overlaps) discovered 95% of the currently known SNP information. Up to now, 1.42 million single nucleotide polymorphisms (SNPs) are distributed throughout the human genome. This demonstrates an average density on available sequence of one SNP in every 1 to 2 kilobases²⁶⁻³¹. 60,000 SNPs fall within exons (coding and untranslated regions), and 85% of the exons are within 5Kb of the nearest SNP. The SNP database, dbSNP, integrates all publicly available SNPs with

described genes and other genomic features. The data in dbSNP is integrated with other NCBI genomic data. The SNP database can be queried from the dbSNP homepage <http://www.ncbi.nlm.nih.gov/projects/SNP/>. Table 2 (see appendix) displays the currently available variation data of 35 organisms. The *Homo sapiens* data (dbSNP build 126 and NCBI build 36.1) comprises more than 10 million SNPs. 5 million have been validated and genotyped, with only 680,000 entries including allele frequencies. The new chimpanzee polymorphism data (see tables 3 and 4) has 1.5 million entries, with 550,000 SNPs being within genes, but of which only 112,549 are reliable.

Submitter	Batch ID	Submitted SNP's	Submission Date
TCAG	HSC-1001	3	06/14/2006
BROAD	DBSNP.2005.4.5.19.35.37011	1403709	04/06/2005
BROAD	DBSNP.2005.4.5.19.35.37012	108607	04/06/2005
BROAD	DBSNP.2005.4.5.19.35.9598	514	04/06/2005
PERLEGEN	CHIMP_23-FEB-2005	31538	02/28/2005
BROAD	CHIMP_ENCODE_020405	527	02/07/2005
OEFNER	chromosome19_Batch#2	2	08/31/1999

Table 3: *Pan troglodytes* whole genome shotgun data draft assembly (4x) was mainly released by the Broad Institute and the Genome Sequencing Center at the Washington University School of Medicine. The Chimpanzee Sequencing and Analysis Consortium produced a 6x Whole Genome Shotgun (WGS) draft assembly (build 2.1) in March 2006, including SNPs data.

SNP Count	Gene count	Functional classification
71,748	13,512	Locus region
5,144	3,831	Allele synonymous to contig nucleotide
6,587	4,470	Allele non-synonymous to contig nucleotide
36,400	3,743	Untranslated region
433,342	15,856	Intron
120	118	Splice site
11,717	6,691	Allele is same as contig nucleotide
546,997	20,995	Total

Table 4: SNP count is the number of RefSNPs having the noted functional relationship to at least one gene. GENE count is the number of distinct locus_id(s), having at least one variant of the noted functional class (see: ftp.ncbi.nih.gov/snp/chimpanzee/genome_reports).

Another public database, Hapmap (www.hapmap.org), reports over one million human SNPs, for which complete genotypes have been obtained in 269 DNA samples from four populations. In this database, the 500-kilobase regions display all information about common DNA variation, e.g. the generality of recombination hotspots, a block-like

structure of linkage disequilibrium and low haplotype (combination of alleles along a chromosome) diversity⁴¹.

For studies of diseases, there are two prevalent approaches: family-based linkage studies across the entire genome and population-based association studies of individual candidate genes. Recently, it is very common to test genetic variants for disease susceptibility through linkage disequilibrium (LD). Susceptible SNP alleles at one site are often associated with specific alleles at other variant sites nearby. These nearby variants are consequences of the historically small size and shared ancestry of the human population and thus provide information about genetic diversity in the human species. A partial list of validated susceptible SNP examples are HLA (autoimmunity and infection)⁴², APOE4 (Alzheimer's disease, lipids)⁴³, Factor V Leiden (deep vein thrombosis)⁴⁴, PPARG (encoding PPARgamma; type 2 diabetes)^{45, 46}, KCNJ11 (type 2 diabetes)⁴⁷, PTPN22 (rheumatoid arthritis and type 1 diabetes)^{48, 49}, insulin (type 1 diabetes)⁵⁰, CTLA4 (autoimmune thyroid disease, type 1 diabetes)⁵¹, NOD2 (inflammatory bowel disease)^{52, 53}, complement factor H (age-related macular degeneration)^{54, 55, 56} and RET (Hirschsprung disease)⁵⁷.

3.4.2 Chimpanzee SNPs

Recent publications on chimpanzee diversity are supported by analyses of the chimpanzee draft sequence^{32, 33, 34, 35}. However, recent data provided by the Chimpanzee Sequencing and Analysis Consortium, comprising sequence reads from eight chimpanzees (*Pan troglodytes troglodytes*), which were obtained with a whole-genome shotgun (WGS) approach, has led to the discovery of 1.66 million SNPs^{36,37}. This assembly at the chimpanzee genome covers 3.6-fold sequence redundancy for autosomes and 1.8-fold redundancy for both sex chromosomes. About one million SNPs are heterozygous

within the primary chimpanzee. The diversity in West African chimpanzees is similar to that seen for human populations, as compared to the diversity level for central African chimpanzees, which is twice as high²⁵.

The nucleotide divergence between human and chimpanzee was calculated as 1.23%⁷.

Although polymorphism accounts for 14-22% of the observed divergence rate between human and chimpanzee, the corrected divergence rate is approximately 1.06%. The total genomic difference between human and chimpanzee is defined as the sum of the differences between the human and the chimpanzee genomes, including the divergence between species and polymorphisms within each species³⁶.

3.4.3 SNPs in Cytokine and Chemokines Genes

Recently, there has been an increased focus on cytokine SNP function and association with human diseases. The database, www.nanea.dk/cytokinesnps/, describes SNP associations of cytokines in human diseases³⁸. This data was retrieved from articles published between 2002 and 2005. A file describing the investigated SNPs in cytokines and their association with human disease or expression patterns can be downloaded from their website.

Inflammatory cytokine genes encoding tumor necrosis factors (TNF)- α and TNF- β , and interleukin (IL)-1 β were examined in adult Japanese patients with chronic immune thrombocytopenic purpura (ITP) and controls. SNPs in TNF- β , with respect to the frequency of the G/G phenotype TNF- β (+252 G/A), were significantly higher in ITP patients than in the healthy control group. Circulating anti-glycoprotein IIb/IIIa, antibody-producing B cells were highly observed in ITP patients with the TNF- β (+252) G/G

phenotype. The polymorphisms at TNF- β (+252) contribute to susceptibility to chronic ITP by controlling the autoreactive B-cell responses to platelet membrane glycoproteins³⁹. Chemokines play an important role in intercellular signalling and immune response. These molecules bind to receptors expressed on the cell surface, e.g. leukocytes, natural killer cells, epithelial cells, endothelial cells and smooth muscle cells⁵⁸. These receptors also are important modulators of the human immunodeficiency virus (HIV)-1 infection due to their binding ability to the virus during infection of the host cell^{59, 60}. Resistance to the HIV-1 infection has been implicated by a mutation in the chemokine receptor gene CCR5⁶¹.

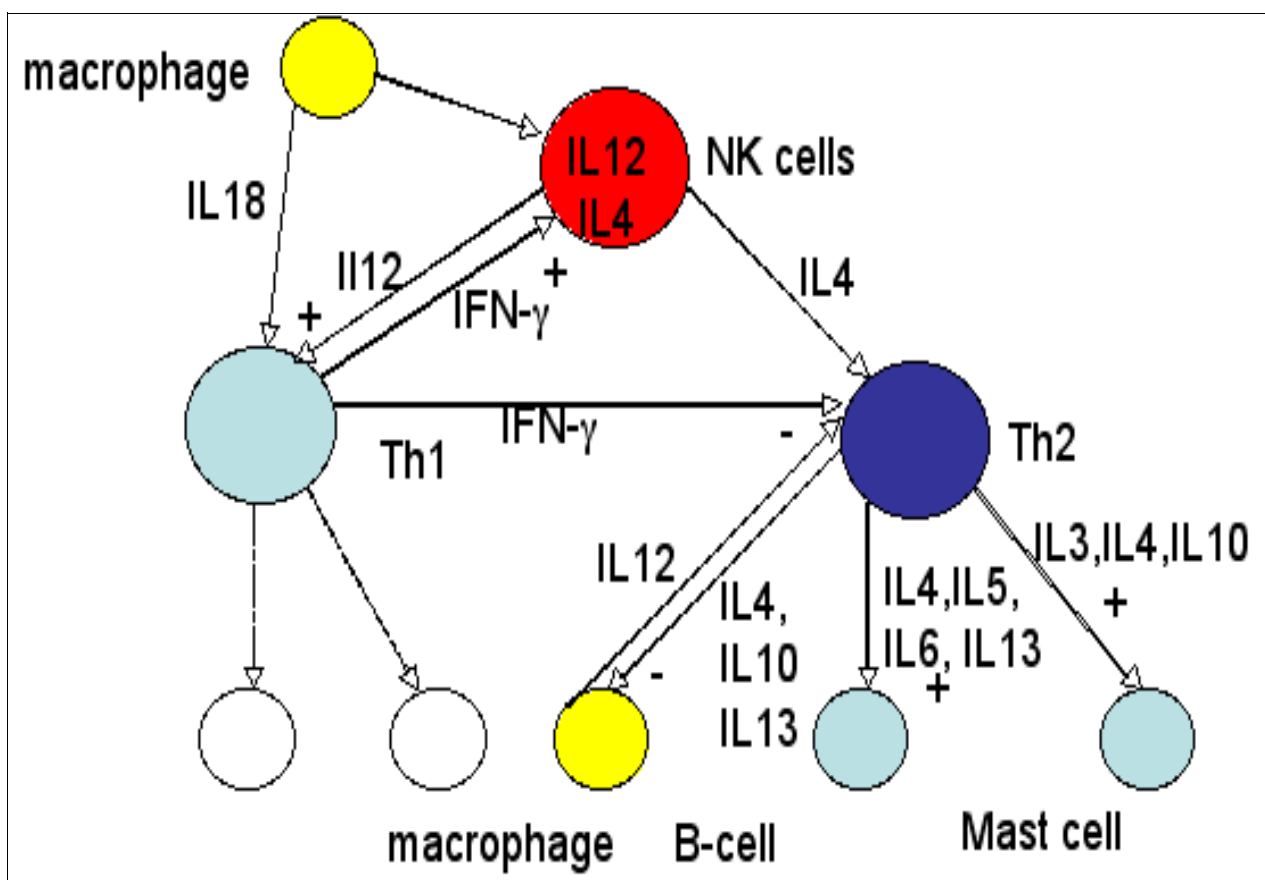


Figure 7: An example of immune cell cross-regulation by cytokines. Cytokines affect the magnitude of inflammatory or immune responses. This model describes human immune cell regulation by cytokines. Genetic variation or mutation affects biological function and dysfunction (in both coding and non-coding regions) in the immune network. Identification of species-specific and ancestral variation confer potential susceptibility to / protection against diseases.

A recent study presented haplotype structures and linkage disequilibrium data of chemokine (CCL) and chemokine receptor genes (CCR) containing two adjacent cysteine residues⁶². Haplotypes, inherited blocks in the genome, characterize the extent of LD in the genome. Thus, these blocks show evidence for historical recombination⁶³. The cluster (3p21.3) of four chemokine receptor genes, CCR3, CCR2, CCR5 and CCRL2, and three chemokine genes, CCL23, CCL18 and CCL3 (17q11), was genotyped in 11 geographically distinct population samples with a total sample size of $n = 278$.

87.5% of the 3p21 variation is attributed to 11 haplotypes, with a frequency of at least 1% for the total samples, while a SNP analysis of the 17q11-12 region indicated, that 97.5% of the variation is attributable to 15 haplotypes, representing at least 1% of the total sample. The ancestral haplotype was determined by direct sequencing of only four primates. However, the root haplotype differed from the common haplotypes.

4. Materials and Methods

4.1 Materials

4.1.1 DNA

For sequencing, DNA probes of unrelated chimpanzees from West Africa were used. All probes were kept in 10mMTris-1mMEDTA, pH 8.0 buffer. The DNA concentrations are summarized in the table below.

Species	Name	ID	Concentration
Chimpanzee	GMO3448	EC1	130 ng/μl
Chimpanzee	Izou	EC2	1900ng/μl
Chimpanzee	Takabou	EC3	540 ng/μl
Chimpanzee	Shirou	EC4	580 ng/μl
Chimpanzee	Dusit95C2	EC5	110 ng/μl
Gorilla	POPE6	ECG	1090ng/μl
Orangutan	AG05251	ECO	520 ng/μl

Table 5: DNA Concentrations for sequencing.

4.1.2 Oligonucleotides

Primers for exons and promoters were specially designed. Primers were produced according to the manufacturer's protocols (www.bioneer.com). The average primer size was approximately 20 bases.

4.1.3 Chemicals

Takara LA TaqTM DNA Polymerase, a thermostable polymerase, was used to obtain longer and more accurate PCR products. PCR products were purified using the Sap/Exo1

(shrimp alkaline phosphatase/exonuclease1) method prior to sequencing (Promega Shrimp Alkaline Phosphatase SAP). BigDye® Terminator v1.1 Cycle Sequencing Kits were used for sequencing PCR product templates.

4.1.4 Equipment

For PCR, Biometra, a 96-well thermocycler, was used. The 96-capillary 3730xl DNA and 3700 DNA Analyzer were utilized for high-throughput genetic analysis and traditional Sanger DNA sequencing.

4.2 Methods

4.2.1 Gene Annotation

Gene (exon) annotation was based on RefSeq genomic contigs Build31 and RefSeq

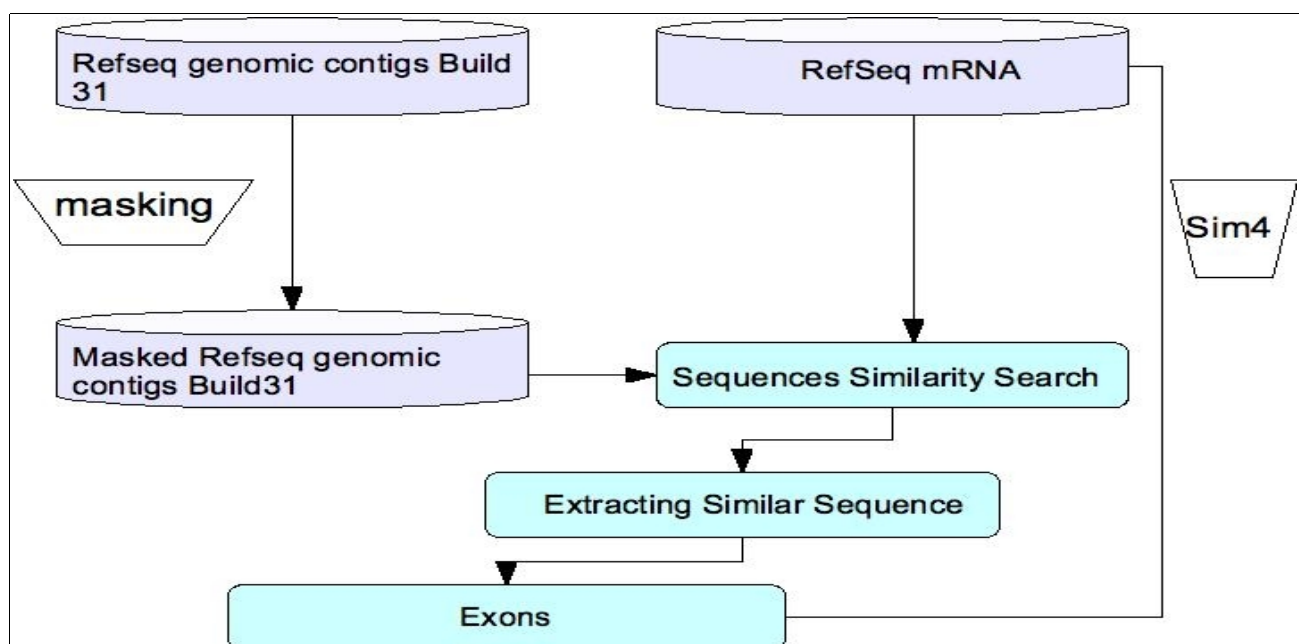


Figure 8: Schema of the gene annotation

mRNA (data release of 3.9.2002). The contigs were masked for repetitive elements. RefSeq mRNAs were blasted to the contigs using Megablast. Alignments with more than 95% identity were searched and extracted. These sequences were then aligned to RefSeq mRNAs with sim4. Alignments with more than 98% identity were extracted and defined as exons.

4.2.2 Promoter Annotation

Promoters normally are adjacent to the gene. Positions in the promoter are designed to be relative to the transcriptional start site (TSS), where DNA is transcribed to RNA for a particular gene. The upstream positions, negative numbers counting back from TSS, were defined as the area of 2500 bp prior to the first exon. The upstreams or the candidate promoters annotation were based on two methods:

1. DBTSS
2. Ensembl

DBTSS Annotation

DBTSS (Database of Transcriptional Start Sites: <http://dbtss.hgc.jp/>) is a database providing precise, experimentally determined, full-length cDNA sequences for human and mouse. Thus, DBTSS contains exact information of the genomic positions of the transcriptional start sites. cDNA libraries constructed using conventional methods contain a large number of non-full length cDNA clones. This is mainly due to reverse transcriptase having a tendency to stop and fall off during the first strand synthesis, leaving a non-fully

synthesized cDNA product. The polyA tail is used as a "sequence tag" for selecting the 3'-end of the mRNA, synthesizing the first strand from the oligo dT primer side. As a result, the largest part of the cDNA library contains cDNAs which are missing the 5'-end information. The 5'-end of the mRNA also has a so called cap structure, which is not a "sequence tag". Therefore, this tag cannot be used for the hybridization. "Oligo-Capping", a novel method employed for the construction of this database, allows enzymatic replacement of the cap structure with a synthetic oligo-nucleotide. Thus, each mRNA product of "Oligo-Capping" features "sequence tags" at both ends: polyA at the 3'-end and the cap-replaced oligo at the 5'-end. This procedure allows synthesis from both ends. The random sequenced cDNA libraries constructed by the oligo-capping method were compared to the human reference sequences (RefSeq) using BLAST. The cutoffs for the Homologous sequence were defined as 95% identity and an e-value of less than 10^{-100} . The sequences were then aligned to the human genome sequence using the sim4 program. Nearly half of the RefSeq sequences could be extended towards the 5'-ends.

Ensembl Annotation

Ensembl provides functions for automated genome annotation. The Ensembl analysis and annotation pipeline is based on a set of heuristic rules. The gene predictions in Ensembl are based on experimental evidence, obtained from the manually curated UniProt/Swiss-Prot database, the partly manually curated NCBI RefSeq database, and from automatically annotated UniProt/TrEMBL records.

4.2.3 Primer Design

Primers were designed for amplification and sequencing of chimpanzee exons and promoters regions from genomic DNA. The most important variable in the design of primer

pairs was the size of the amplicons. Primers for exons were designed so as to amplify a 1000bp region and to allow the sequencing of an area of 500 to 600 bp within this amplicon. Exons bigger than 400 bp multiple primers were designed e.g. until 800 pb 2 primer pairs.

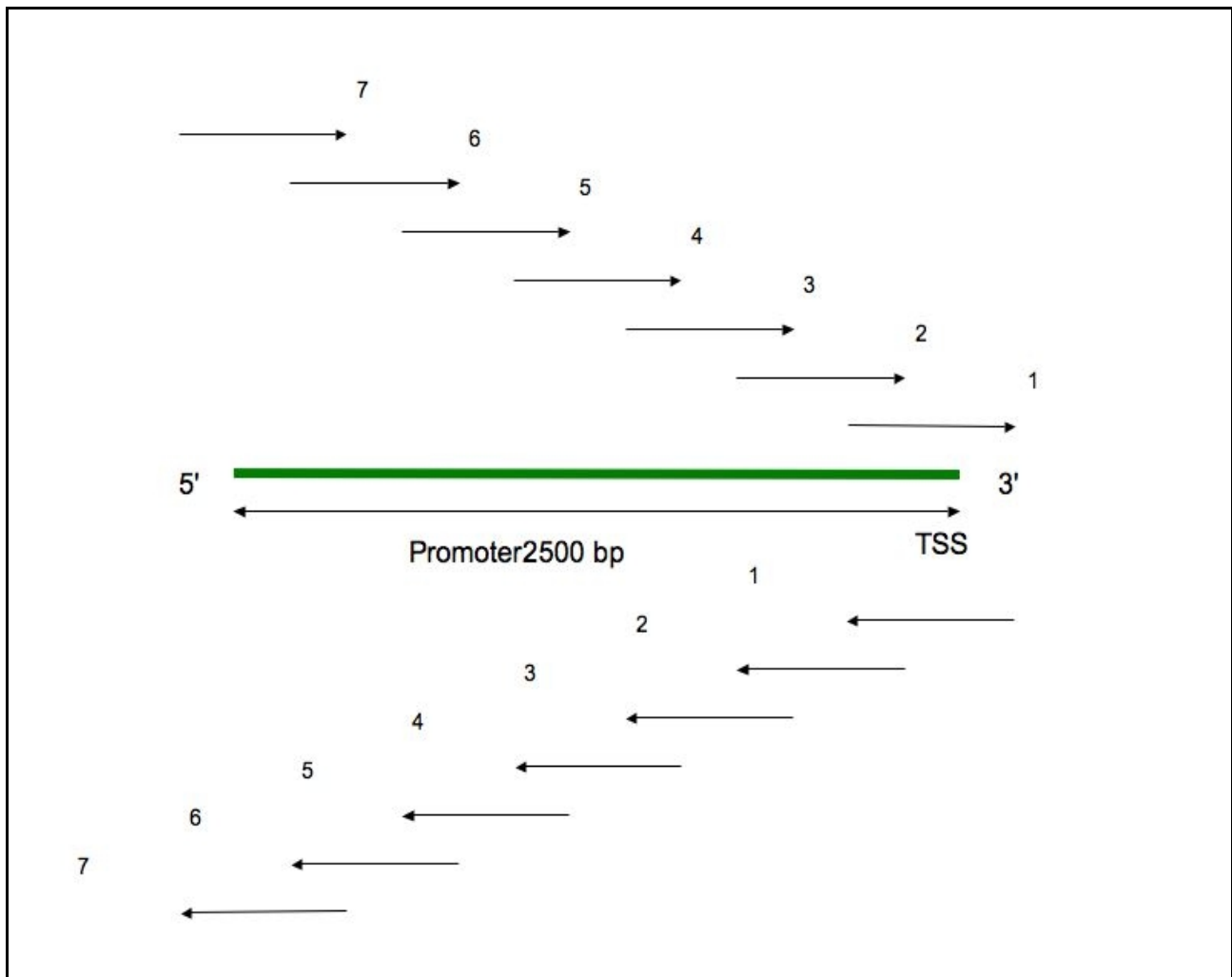


Figure 9: This figure illustrates the sequencing strategy of the promoter. The target region of 2500 bp is covered by 7 overlapping sequence pairs.

The promoter was defined as an area of 2500 bp prior the transcription start site (TSS) or the first exon, using either ENSEMBL or DBTSS annotation. Forward and reverse primers for PCR were designed in order to quantify the 4500 bp amplicon. The PCR products were verified by agarose gel electrophoresis. 7 primer pairs were created to determine the DNA of the target part.

Table 6 lists the conditions for PCR and sequence reaction:

Method	Reactants	Volume (μl)	Temperature (°C)	Time	Cycle
PCR Reaction	H ₂ O	0.35	96	15 sec	40
	Buffer	5.0	58	15 sec	
	dNTP	1.6	69	2.5min	
	Primer (pM)	2.0	4		
	LA Taq	0.05			
	DNA (5ng)	1.0			
	Total	10.0			
Purification	Sap	1.0	37	20 min	
	EXO I	1.0	80	20 min	
	H ₂ O	60			
	Total	62			
Sequencing	DNA	1.0			
	Primer	1.0			
	BigDye	0.8			
	5XBuffer	1.8			
	H ₂ O	5.4			
	Total	10.0			

Table 6: PCR and Sequencing reaction conditions.

4.2.4 Software

All programs for DNA sequence processing were written in Perl (see source code in the appendix). Primer3.0⁶⁴ was compiled in a Linux environment for PCR and sequencing primer design. Criteria such as oligonucleotide melting temperature, size, GC content, primer-dimer conditions, positional constraints within the source sequence were defined as follows:

- PRIMER_GC_CLAMP=2;
- PRIMER_OPT_SIZE=20;
- PRIMER_MIN_SIZE=18;

- PRIMER_MAX_SIZE=27;
- PRIMER_NUM_NS_ACCEPTED=1;
- PRIMER_PRODUCT_SIZE_RANGE=2500-3500;
- PRIMER_OPT_TM=60;
- PRIMER_MIN_TM=40;
- PRIMER_MAX_TM=65;
- PRIMER_MIN_GC=30;
- PRIMER_OPT_GC_PERCENT=40;
- PRIMER_MAX_GC=50;
- PRIMER_MAX_POLY_X=3;
- PRIMER_NUM_RETURN=4.

The programs Phred⁶⁶, Phrap, PolyPhred⁶⁷ and Consed⁶⁵ were used for sequence assembly, base quality calling, fast sequence comparisons, contig editing and automated finishing. Sequencher, a commercially available sequence assembly package, was used for analyzing the sequence. For similarity searching, the programs BLAST® (Basic Local Alignment Search Tool) and BLAT were used. The program ClustalW (<http://bioweb.pasteur.fr/seqanal/interfaces/clustalw.html>) was used for multiple sequence alignment. Scores of sequence traces were calculated and aligned by Phrap (<http://www.phrap.org/>). In Consed, polymorphic sites are highlighted in blue for homozygous, and in pink for heterozygous sites in (see figure 10). PolyPhred uses the base calls and peak information output of Phred and the sequence alignments produced by Phrap.

4.2.5 SNP Identification

SNP identification is done by sequencing. Five Chimpanzees were sequenced directly, in order to define the precise location of SNPs. This method ensures the highest reliability and quality regarding the detection of single nucleotide polymorphisms. The sequenced data is saved as ABI trace file format. This trace data, including a reference to chimpanzee trace data, was then assembled by the program Phred and SNP detected by PolyPhred. The method determines potential SNPs from aligned assemblies, regardless of their positions or the data origin.

Identified SNPs have to meet the so-called neighborhood quality standard (NQS) criteria²⁹. Specifically, a single base meets the standard, if its Phred quality score is at least 20, and five bases before and after the SNP display Phred scores greater than or equal to 15. All SNPs were further inspected visually using Sequencer or Consed.

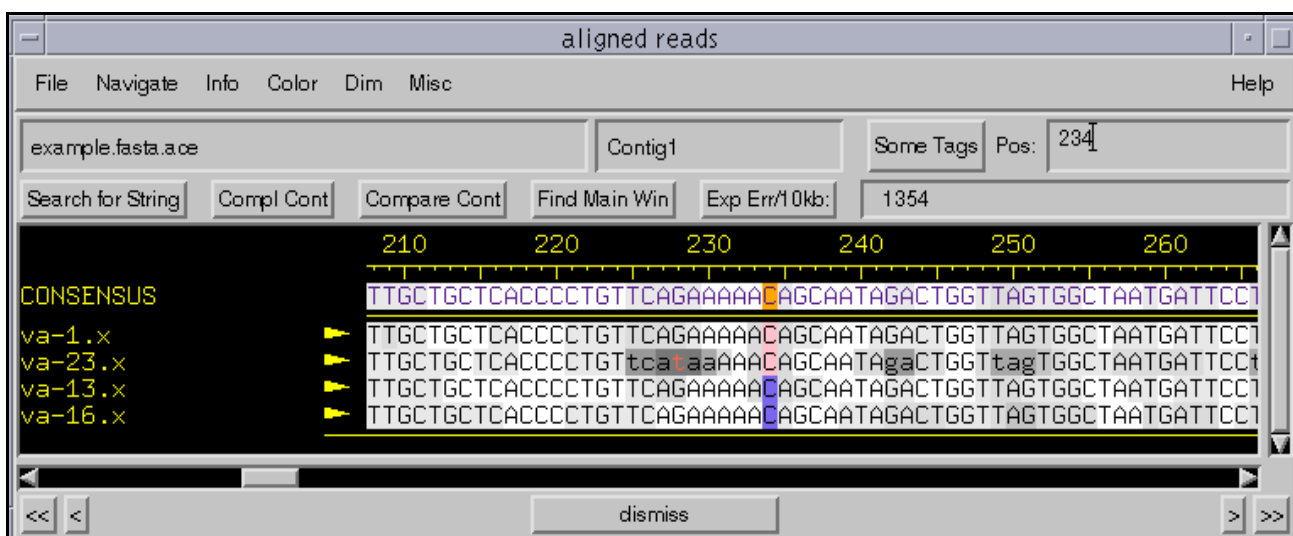


Figure 10: Screen shot of a Consed window. PolyPhred detects SNPs and marks them with a red rank. The top SNP tag ("Consensus") marks the consensus position of the SNP in the traces. Genotype homozygote tags are marked in blue, and heterozygote tags in pink, respectively.

4.2.6 Alignments

The finished sequences, obtained from direct sequencing, were analyzed and refined through additional comparison with the Chimpanzee Draft Genome (data version: panTro1, CGSC Build 1 Version 1 Arachne assembly) and the Human Genome (data version: Human May 2004 (hg17, NCBI build 35). First, the fragments were computationally explored using BLAST and BLAT to retrieve their positions in the genome. Exon and promoter sequences were excluded from alignments if they did not match the target gene annotation.

After this, the finished sequences obtained from direct sequencing are aligned with the corresponding part of *Pan troglodytes* from the Chimpanzee Draft Genome and *Homo Sapiens* from the Human Genome by ClustalW. A number of Perl-Scripts were written to extract the corresponding parts of the Human and Chimpanzee Draft Genome according to the annotation.

ClustalW is a multiple sequence alignment program for DNA. It produces biologically meaningful multiple sequence alignments of divergent sequences by calculating the best match for the selected sequences and lining them up. Evolutionary relationships can be determined by analyzing differences and similarities of sequences within the alignment.

5. Results

5.1 Annotation Results

5.1.1 Exons

For 166 redundant genes, 1087 exons were manually annotated based on RefSeq genomic contigs Build 31. Multiple primer pairs were designed for exons larger than 400 bp, to cover the sequence region. 1371 primer pairs were designed for PCR and sequencing. All primers are listed in the appendix, table 7 (for sequencing) and table 8 (for PCR). The average exon size was 597bp, and its amplicon size was 406 bp. In total, 81,802 bp per chimpanzee were sequenced for the detection of variation in exons.

5.1.2 Promoters

Promoters are extremely diverse and thus difficult to characterize. The upstream area was defined as 2500 bp prior the first exon, respectively transcription start site (TSS). 160 non redundant upstream regions of the selected genes (appendix, table 9) could be annotated. Out of these, 64 upstream regions could be extracted with both DBTSS and Ensembl. The remaining 96 upstream regions were identified by Ensembl only. All characteristics, i.e. RefSeq ID, Human Genome Organization (HUGO) ID, Gene Start, Gene End, Chromosome, Strand, selected Transcription start site (TSS) as well as start and end of the 2500 bp defined area are listed in table 9 (see appendix).

The Ensembl and DBTSS annotations differ in the position of the transcription start site within the genome. The maximum distance between two starting points of a gene between

the two annotation methods was 114,236 bp. The TSSs of 6 genes differed over 10,000 bp. On average, the position of TSSs differed about 691 bp.

5.2 Sequencing Results

5.2.1 Exons

For the 166 genes with 1087 exons, 1371 primers were designed. Exons were sequenced in the directions 5'-3' and 3'-5'. On average, 870 of 1371 data sets could be obtained per chimpanzee (figure 11, “Sequenced”), which corresponds to a sequence success rate of 63% for exons.

95 data sets, or 7%, contained no ABI trace files (figure 11, defined as “No trace file”). 28% of the chromatogram files could not be read, and 1% of the chromatograms could not be aligned to the reference sequence (figure 11, “Not aligned”).

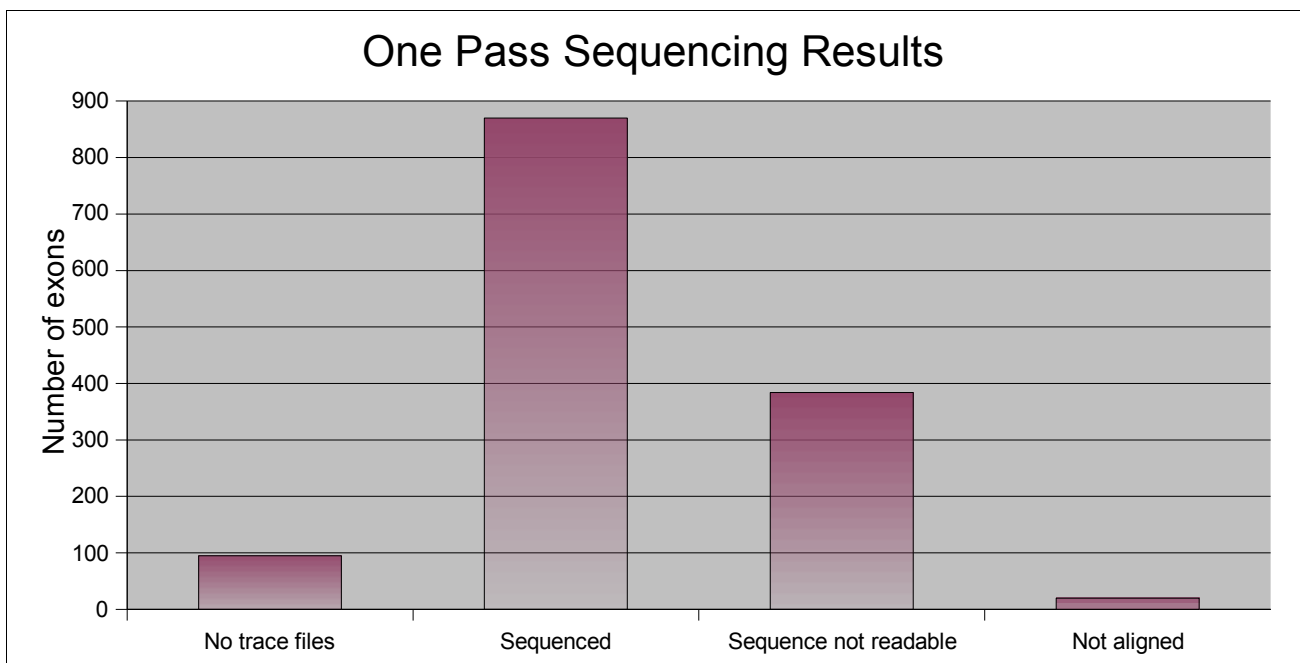


Figure 11: Results of chimpanzee exon sequencing

At last, all individual sequence reads were assembled. This way, 1049 of 1371 sequence data sets could be obtained.

5.2.2 Promoters

Out of 160 functional promoter regions, 82 potential cis-acting regions of chimpanzee could be determined by sequencing, which corresponds to a sequencing success rate of 51% for promoters. 1120 primers for sequencing and 320 primers for PCR were used to determine these regions of the selected genes. Upstream areas were also sequenced in the directions 5'-3' and vice versa.

The area for the detection of SNPs in the chimpanzee DNA was set to 2.5 kb. However, the average sequenced promoter length proximal to the transcription start site was 2.0 kb. Thus, 78% of the determined target length were covered by PCR amplification and direct sequencing with human primers.

5.3 Alignment Results

5.3.1 Exons

1049 obtained exon sequences based on five chimpanzees were blasted to the database. This database contains the exonic and cDNA information of the 166 target genes. 867 sequences matched the sequences of the database with a default E-value of 0.0. Those sequences were defined as putative chimpanzee sequences and further processed. 182 sequences had an e-value greater than 0.0. The 867 sequences were then aligned with the program BLAT, using the Human Genome as the database. In addition, this data was

compared to the Pan Troglodytes Genome database. This refinement process led to the determination of 254 out of 867 sequences, which could not be aligned by BLAT neither in the human nor the chimpanzee database. 613 out of 867 consensus sequences could be aligned to 109 genes. The resulting multiple sequences clustered to each gene were aligned to human and draft chimpanzee mRNAs using the program CLUSTAL W.

Gene Symbol	Gene Length [bp]	Exon Length [bp]	CDS Length [bp]	Exon Coverage [bp]	Exon Covered [%]	CDS Coverage [bp]	CDS Covered [%]
CCL1	2898	574	288	574	100%	288	100%
CCL19	1357	412	273	412	100%	273	100%
CCL21	1146	874	401	874	100%	401	100%
CSF2RB	456	292	292	292	100%	292	100%
CSF2RB	124	123	121	123	100%	121	100%
CXCR4	1071	1070	1070	1070	100%	1070	100%
CXCR6	5175	1952	1028	1952	100%	1028	100%
DEFB4	2013	334	192	334	100%	192	100%
IFNG	4973	1209	497	1209	100%	497	100%
IL13	1656	344	330	344	100%	330	100%
IL17B	4881	690	540	690	100%	540	100%
IL1B	6999	1490	803	1490	100%	803	100%
IL1F5	5757	2810	464	2810	100%	464	100%
IL2RG	418	161	161	161	100%	161	100%
IL4	9693	917	458	917	100%	458	100%
IL4	9693	870	411	870	100%	411	100%
IL5	2081	812	401	812	100%	401	100%
IL8	3150	1642	296	1642	100%	296	100%
IL9R	207	206	27	206	100%	27	100%
TNFRSF10B	13256	329	329	329	100%	329	100%
TNFRSF10B	14338	402	402	402	100%	402	100%
TNFRSF8	285	284	62	284	100%	62	100%

Table 10: This table describes 22 redundant and 19 non-redundant genes. The genes belong to the category A with 100% exon and 100% CDS coverage by the sequenced chimpanzee DNA. Only these genes were further processed with CLUSTAL W.

All in all, the target genes can be divided into 4 categories:

- A) 100% exon and 100% CDS coverage (table 10)
- B) >65% exon and 100% CDS coverage (table 11)
- C) partial coverage in exon and CDS (table 12)
- D) no coverage, data not shown

The average human-chimpanzee exon-CDS identity is $98\% \pm 1\%$, based on the 19 non-redundant genes in table 10. The average identity of the 8 genes described in table 11 with more than 65% exon and 100% CDS coverage is $98\% \pm 0.5\%$. This human chimpanzee genome comparison includes newly detected SNPs of the 5 chimpanzees. SNPs were converted into IUPAC and compared with the human genome only at the DNA level. Genes categorized as A were further processed. The multiple sequences clustered to one gene were then aligned to human and draft chimpanzee mRNAs using CLUSTAL W.

Gene Symbol	Gene Length [bp]	Exon Length [bp]	CDS Length [bp]	Exon Coverage [bp]	Exon Covered [%]	CDS Coverage [bp]	CDS Covered [%]
TNFRSF1B	7241	2673	484	1804	67,5%	484	100%
IRF1	7662	2014	969	1541	76,5%	969	100%
IL1RL1	27765	541	270	420	77,6%	270	100%
FGF2	21589	6117	288	4783	78,2%	288	100%
IL1RL1	1766	469	270	420	89,6%	270	100%
NKG7	546	473	302	443	93,6%	302	100%
IL1F5	6227	2782	464	2677	96,2%	464	100%
IL12A	7160	1425	751	1424	99,9%	751	100%

Table 11: This table shows 8 non-redundant genes, listing only genes categorized as B. The exon areas in this category are covered to at least 65%. The coding areas (CDS) could be fully determined (100%).

As a result, 384 multi-FASTA files were generated, containing an assembled RIKEN-sequence of *Pan Troglodytes* (five species with SNPs information), and the corresponding part of the Homo Sapiens and Chimpanzee Draft Genome. The output was

computationally and visually inspected in order to remove alignment errors. All genes shown in table 10 are aligned in 3'-5' direction. The alignment results can be viewed in a normal web browser (data source: media/websites/SNP.html on the included CD).

IL4_part1_RIKEN	TTCCAATGTAAACTCATTTTCCTCGGTTTCAGCAATTTTAAATCTATATATAGAGATAT	600
IL4_part1_CHIMP1A	-----	138372084
IL4_part1_HGP	-----	132037564
IL4_part1_RIKEN	CTTTGTCAGCATTGCATCGTTAGCTTCTCCTGATAAACTAATTGTCTCACATCATCACTG	660
IL4_part1_CHIMP1A	-----t-----ca-----	138372144
IL4_part1_HGP	-----cy-----tg-----	132037624
	-M--G--L--T--S--Q--L--L--P--P--L--F--F--L--	
IL4_part1_RIKEN	CAAATCGACACCTATTAATGGGTCTCACCTCCCAACTGCTTCCCCCTCTGTTCTTCTGTC	720
IL4_part1_CHIMP1A	-----	138372204
IL4_part1_HGP	-----	132037684
	L--A--C--A--G--N--F--V--H--G--H--K--C--D--I--T--L--Q--E--I--	
IL4_part1_RIKEN	TAGCATGTGCCGGCAACTTTGTCCACGGACACAAGTGGGATATCACCTTACAGGAGATCA	780
IL4_part1_CHIMP1A	-----	138372264
IL4_part1_HGP	--r-----y-----	132037744
	I--K--T--L--N--S--L--T--E--Q--K--	
IL4_part1_RIKEN	TCAAAACTTTGAACAGCCTCACAGAGCAGAAGgtgagtacctatctggcaccatctctcc	840
IL4_part1_CHIMP1A	-----	138372324
IL4_part1_HGP	-----	132037804

Figure 12: This is a snapshot of exon 1 and the boundary of the intron of the gene IL. Multiple alignments consist of the assembled five chimpanzee sequences (described as RIKEN), the draft chimpanzee genome (CHIMP1A), and the finished sequence of the Human Genome (HGP).

The web-interface displays the human-human-chimpanzee alignment in 3'-5' direction and includes SNPs of both species. SNPs of both species are displayed in the alignments as a IUPAC code. Chimpanzee SNPs are marked in green and human SNPs are marked in yellow. Identical segments (consensus sequences) are displayed as a sequence of dashes ("-"), missing areas are marked with asterisks ("*"), sequences with no corresponding part (missing data) with ("n"). On the top of the page for each gene, concise variation information, such as Reference ID, Allele, Chromosome Location, Location Information, Peptide Shift and Synonymous Status is displayed.

5.3.2 Promoters

160 of 166 functional promoter regions of the described genes could be annotated, and another 82 potential regions could be determined through sequencing.

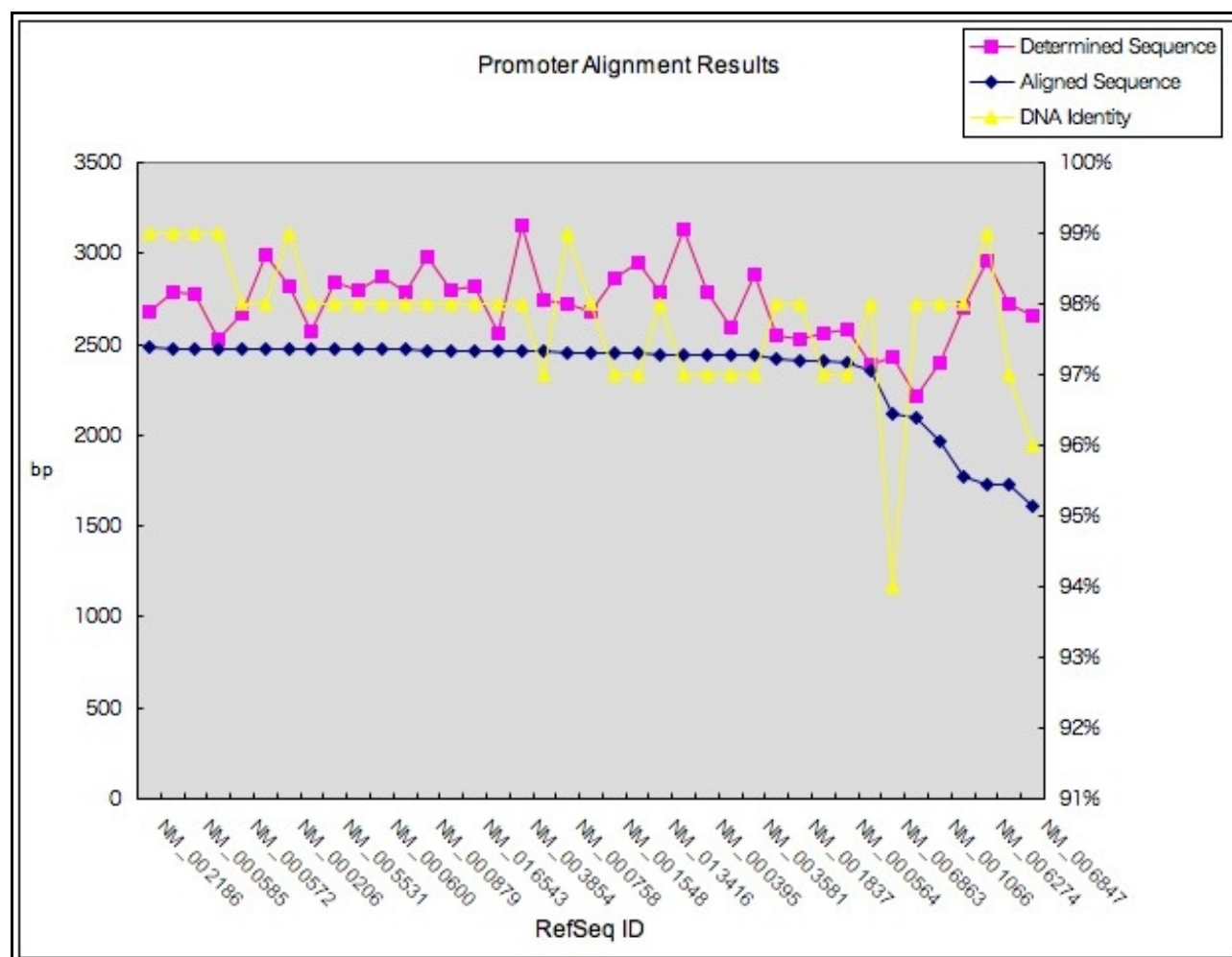


Figure 13: Only 39 of 82 functional promoters are presented in this figure. All alignments are greater than 1600 bp, which was set as threshold. The term “Determined Sequence” defines a sequence which is the direct result after the sequencing process. “Aligned Sequence” designates the DNA sequence which could be assembled with the corresponding human part (the corresponding reference sequence was set to 2500 bp). “DNA Identity” represents the calculated genome identity based on the human-chimpanzee comparison (including SNPs).

The 82 obtained sequences were compared using BLAST and a reference database describing the corresponding human upstream DNA sequences. The default E-value is 0.0. 2 out of 82 sequences could not be aligned. The comparison of the chimpanzee

promoter sequences inducing polymorphism with the corresponding human part showed an average DNA identity of 96,5% $\pm$ 2%.

To verify these results, the same sequences were furthermore aligned with BLAT, using the Homo Sapiens and Pan Troglodyte Genome as the database. The BLAT result shows the alignment of the several thousand bp long DNA upstream sequences to the genome with additional information such as match, mis-match and gaps of the alignments. The BLAT results are included in the enclosed CD and can be viewed in a common web browser (data source: media/BLATreport.htm). 13 regions did not yield any or only partial results in the alignment to the human and / or the chimpanzee genome. These genes with RefSeq accession number are listed in table 13.

Upstream area of the gene	Human BLAT	Chimpanzee BLAT
NM_000206	No result	
NM_002982	No result	
NM_000589		No result
NM_002163		No result
NM_003701		No result
NM_004590		No result
NM_005531		No result
NM_013431		No result
NM_000647	No result	No result
NM_012276	No result	No result
NM_024298	No result	No result

Table 13: Genes which could not be detected by BLAT in the Human and / or the Chimpanzee Draft Genome.

5.4 SNP Results

Chimpanzee SNPs provide important evidence for detecting ancestral and mutant alleles within both species, chimpanzee and human. In total, 1532 candidate SNPs in exons including intronic flanking regions and 346 SNPs in the upstream region could be unambiguously determined. However, for submitting potential SNP candidates to the *Pan*

Troglodytes SNP database (<http://www.ncbi.nlm.nih.gov/projects/SNP>), the following conditions were defined in order to reduce false positive data in the databases:

SNPs had to be detected in at least in two chimpanzees or confirmed in the same individual, but in both DNA sequencing directions (5'→3' as F and 3'→5' as R). 837 SNPs in exonic and upstream regions applied to this condition.

Categories	Amount of individual species	Direction
ECX_FR	1	Both
ECX,Y_FR	2	Both
ECX,Y,Z_FR	3	Both
ECX,Y_F	2	Forward
ECX,Y_R	2	Reverse
ECX,Y,Z_F	3	Forward
ECX,Y,Z_R	3	Reverse
ECX,Y,Z,W_F	4	Forward
ECX,Y,Z,W_R	4	Reverse
ECX,Y,Z,W,V_F	5	Forward
ECX,Y,Z,W,V_R	5	Reverse
ECX_FR, ECY_F	2	Both & Forward
ECX_FR, ECY_R	2	Both & Forward

Table 14: Overview of SNPs applying to the selection criterion

Out of 166 selected target genes, 837 SNPs in 147 chimpanzee genes, such as cytokine, chemokines and receptor encoding genes, as well as a few other innate immune response genes could be newly determined. The gene with the highest variation rate is NM_002995 with 37 SNPs in the upstream and exonic region (all genes with SNPs are shown in figure 14). As expected, transitional changes occurred at a higher frequency (32% C→T and 26% G→A), although there are more transversion possibilities. Transversion and transition patterns of the newly determined SNPs are categorized in detail in figure 15.

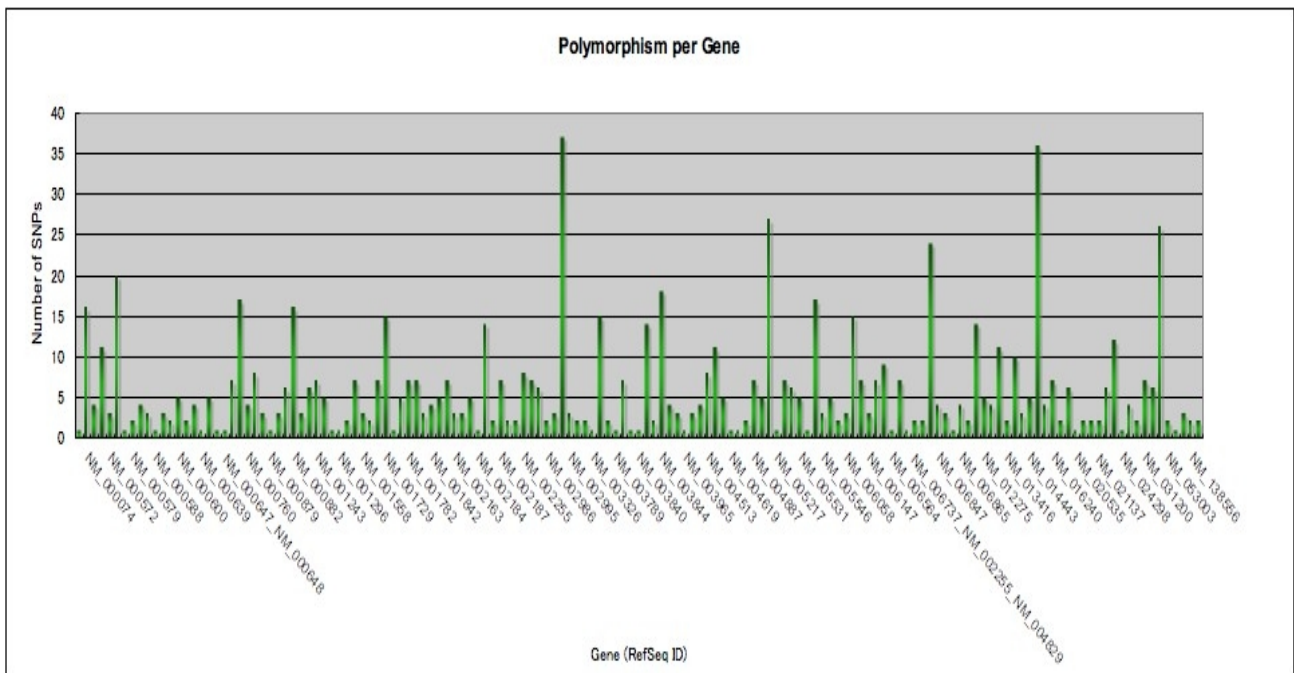


Figure 14: Reliable chimpanzee SNPs per gene

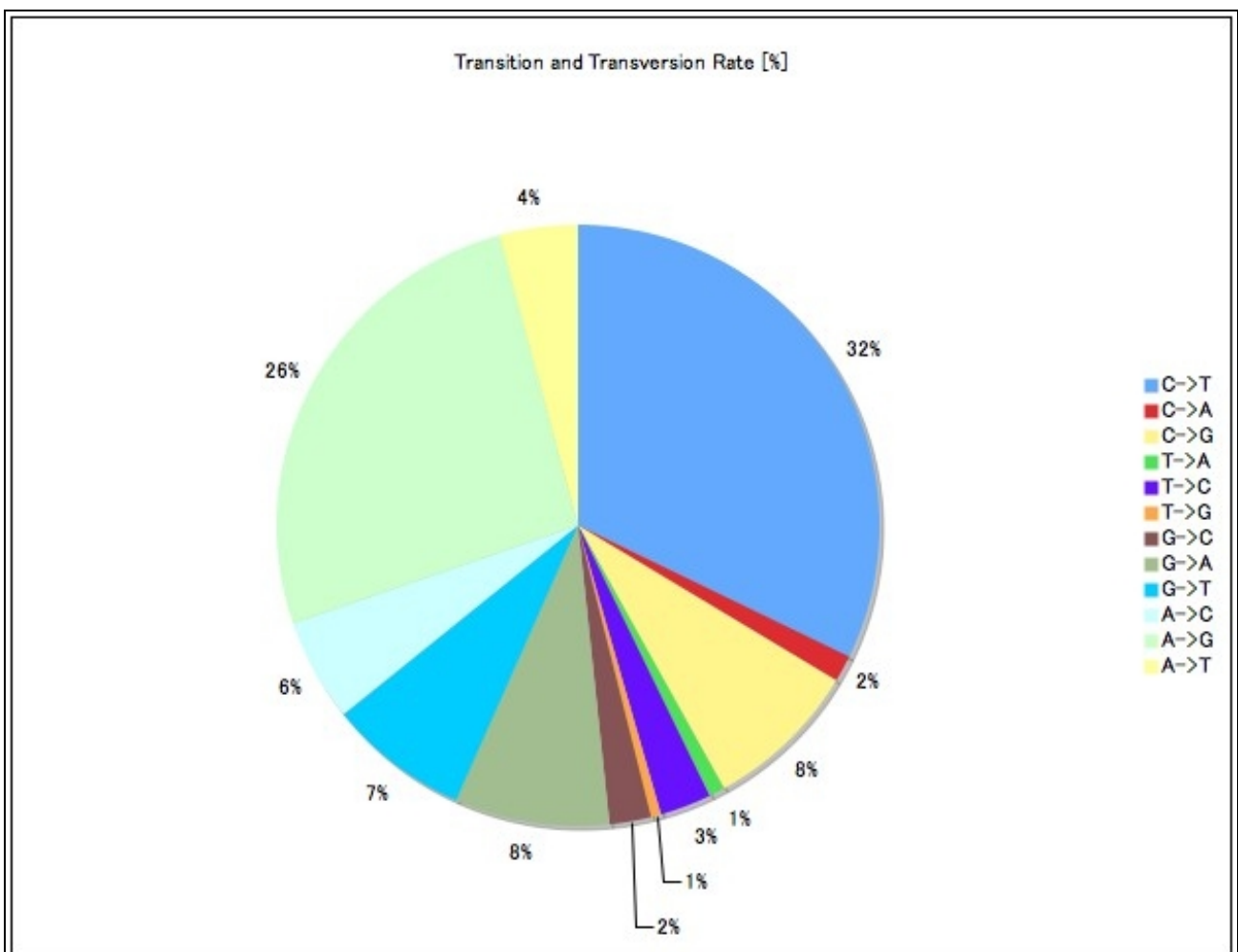


Figure 15: Transversion and transition patterns of the newly determined SNPs

6. Discussion

166 genes were selected due to their significant role in the immune response on the human side. The exons and promoters of these genes were sequenced by human primers in five unrelated chimpanzees in order to identify *Pan troglodytes* specific variations. 1087 exons and 160 upstream regions of the selected genes could be annotated either manually or by combining various databases. On average, the sequencing rate was 63% for exons and 51% for promoters. 27 corresponding human genes (coding regions) could be fully determined in chimpanzee. 82 of 166 potential promoter areas were identified. with 32 upstream regions sized greater than 1600 bp. The average human-chimpanzee exon-CDS identity is $98\% \pm 1\%$. However, based on the same genome comparison, the promoter region part showed an average DNA identity of only $96,5\% \pm 2\%$. 837 chimpanzee SNPs in 147 immune response related genes could be newly determined.

The exon sequencing rate was slightly better than the promoter sequencing rate. One of the reasons might be the fact that exonic areas are far more conserved between species than the defined 2500 bp upstream area. Therefore, primers designed based on the human sequence could anneal more easily. Another reason for the lower sequencing success rate of promoters is that the promoter amplicon size was 4 to 6 times larger than the exon amplicon size.

Previous publications calculated a difference of both genomes of 1.23%, resulting from nucleotide substitutions. The comparison of selected immune response related genes in this study, however, showed a nucleotide difference from 2 to 3.5%. This shows that the broad genome difference between the two species is about 1.23%, whereas nucleotide

differences differ between functional regions and conserved areas such as protein coding areas.



Figure 16: Reported non-synonymous amino acid change of CSF2RB⁶⁷.

837 of 1532 candidate chimpanzee SNPs in 147 immune response related genes were determined. However, a biological interpretation of all SNPs in this work is impossible without phenotypic information.

With CSF2RB, we could indeed detect an interesting case. This gene is a common beta chain of the high affinity receptor for IL-3, IL-5 and CSF. A chimpanzee specific SNP causes a non-synonymous change from Phenylalanine to Leucine. Amino acid comparison between 3 species, human, mouse and chimpanzee, showed a conserved character around the detected SNP in *Pan troglodytes*. Defective CSF2RB has been reported to be associated with protein alveolar proteinosis, a rare lung disorder of unknown etiology.

The chimpanzee SNPs here are sufficient for initial analyses, but they are still imperfect and incomplete. Currently, 837 *Pan troglodytes* specific SNPs are being submitted to the public database (<http://www.ncbi.nlm.nih.gov/projects/SNP>) for future definitive studies of gene and genome evolution by other researchers. It would also be advantageous to obtain an official ID (ss number) and the automatic mapping to the chimpanzee genome. This would make it easy to locate the variations on the genome map and correlate them with possible phenotypic and biological characters.

Genome analysis reveals our close biological relationship to chimpanzees. This kind of data allows unique insights into human and chimpanzee history, but it also creates ethical obligations.

7. Appendix

Nr.	Chr.	Start	End	Strand	HUGO ID	RefSeq ID
1	1	11832980	11913808	1	TNFRSF8	NM_001243
2	1	11936606	11978822	1	TNFRSF1B	NM_001066
3	1	36359306	36372782	-1	CSF3R	NM_000760
4	1	50276853	50795854	-1	FAF1	NM_007051
5	1	156196500	156241730	1	IFI16	NM_005531
6	1	165733233	165738692	1	XCL1	NM_002995
7	1	169867561	169875384	1	TNFSF6	NM_000639
8	1	170392247	170415847	-1	TNFSF4	NM_003326
9	1	204024647	204029538	-1	IL10	NM_000572
10	1	207040651	207058868	-1	IRF6	NM_006147
11	1	208579429	208627671	1	TRAF5	NM_004619
12	2	86986274	86992607	-1	CD8A	NM_001768
13	2	102391802	102417734	1	IL1R1	NM_000877
14	2	102424833	102477211	1	IL1RL2	NM_003854
15	2	102549362	102589781	1	IL1RL1	NM_003856
16	2	102549362	102589781	1	IL1RL1	NM_016232
17	2	102600497	102636618	1	IL18R1	NM_003855
18	2	106054430	106132124	1	NCK2	NM_003581
19	2	113626641	113638117	-1	IL1A	NM_000575
20	2	113682483	113689502	-1	IL1B	NM_000576
21	2	113911361	113917464	1	IL1F5	NM_012275
22	2	137083208	137084257	-1	CXCR4	NM_003467
23	2	152416650	152439104	1	TNFAIP6	NM_007115
24	3	3086421	3127031	-1	IL5RA	NM_000564
25	3	39265579	39282114	-1	CX3CR1	NM_001337
26	3	42821712	42869366	1	CCBP2	NM_001296
27	3	45888611	45905259	1	CCR9	NM_031200
28	3	45945565	45950437	1	CXCR6	NM_006564
29	3	46023030	46024031	-1	XCR1	NM_005283
30	3	46204320	46210412	-1	CCR1	NM_001295
31	3	46244280	46268754	1	CCR3	NM_001837
32	3	46356232	46363011	1	CCR2	NM_000647
33	3	46356232	46363011	1	CCR2	NM_000648
34	3	46372225	46378283	1	CCR5	NM_000579
35	3	46409271	46411605	1	CCRL2	NM_003965

36	3	49883452	49900082	-1	MST1R	NM_002447
37	3	50284186	50295911	-1	IFRD2	NM_006764
38	3	161027542	161034718	1	IL12A	NM_000882
39	4	75072526	75075682	1	IL8	NM_000584
40	4	75777104	75786978	1	AREG	NM_001657
41	4	76128372	76178082	-1	BTC	NM_001729
42	4	77413346	77415747	-1	CXCL11	NM_005409
43	4	122511388	122544297	-1	TNIP3	NM_024873
44	4	123992686	124001033	-1	IL21	NM_021803
45	4	124206684	124278211	1	FGF2	NM_002006
46	4	143135381	143232238	1	IL15	NM_000585
47	5	35902492	35922422	1	IL7R	NM_002185
48	5	43422251	43457973	-1	CCL28	NM_019846
49	5	55252580	55287992	-1	IL6ST	NM_002184
50	5	131472563	131475112	1	IL3	NM_000588
51	5	131485701	131488075	1	CSF2	NM_000758
52	5	131894996	131901386	-1	IRF1	NM_002198
53	5	131953352	131955430	-1	IL5	NM_000879
54	5	132070081	132073017	1	IL13	NM_002188
55	5	132085589	132094584	1	IL4	NM_000589
56	5	134982585	134991185	-1	CXCL14	NM_004887
57	5	135304151	135307732	-1	IL9	NM_000590
58	5	138284915	138286462	-1		NM_015564
59	5	140055885	140070565	1	IK	NM_006083
60	5	148782342	148787348	-1	IL17B	NM_014443
61	5	150438027	150495229	-1	TNIP1	NM_006058
62	5	156437332	156465867	-1	HAVCR1	NM_012206
63	5	156588802	156663004	1	ITK	NM_005546
64	5	158722686	158738376	-1	IL12B	NM_002187
65	5	159755672	159778526	-1	C1QTNF2	NM_031908
66	6	137499199	137521116	-1	IFNGR1	NM_000416
67	6	143053176	143076552	-1	HIVEP2	NM_006734
68	7	22509154	22513888	1	IL6	NM_000600
69	8	6715511	6722856	-1	DEFB1	NM_005218
70	8	6822585	6825017	-1	DEFA1	NM_004084
71	8	6860805	6863226	-1	DEFA3	NM_005217
72	8	6900239	6901669	-1	DEFA5	NM_021010
73	8	7259788	7261795	-1	DEFB4	NM_004942
74	8	22899591	22948630	-1	TNFRSF10B	NM_003842

75	8	22982372	22996884	1	TNFRSF10C	NM_003841
76	8	23016838	23043468	-1	TNFRSF10D	NM_003840
77	8	23070909	23104577	-1	TNFRSF10A	NM_003844
78	8	27513489	27556198	1	SCARA3	NM_016240
79	8	79694971	79760406	-1	IL7	NM_000880
80	9	21156042	21156611	-1	IFNA21	NM_002175
81	9	21191595	21192164	-1	IFNA7	NM_021057
82	9	21294686	21295255	-1	IFNA5	NM_002169
83	9	21340317	21340886	-1	IFNA6	NM_021002
84	9	21430440	21431315	1	IFNA1	NM_024013
85	9	34541432	34579722	-1	CNTFR	NM_001842
86	9	34541432	34579722	-1	CNTFR	NM_147164
87	9	34640699	34650935	1	IL11RA	NM_147162
88	9	34640699	34650935	1	IL11RA	NM_004512
89	9	34679567	34681274	-1	CCL19	NM_006274
90	9	34699002	34700147	-1	CCL21	NM_002989
91	9	35599976	35608408	-1	CD72	NM_001782
92	9	113041169	113068815	-1	TNFSF8	NM_001244
93	9	115842629	115854098	1	TLR4	NM_138554
94	9	115842629	115854098	1	TLR4	NM_138556
95	9	119091062	119188599	-1	C5	NM_001735
96	10	5998340	6023887	-1	IL15RA	NM_002189
97	10	44156588	44164551	-1	CXCL12	NM_000609
98	10	45236966	45314827	-1	03/08/07	NM_145021
99	10	90826613	90828046	1	IFIT1	NM_001548
100	11	111551625	111563425	-1	IL18	NM_001562
101	11	117394835	117409846	1	IL10RA	NM_001558
102	12	10451250	10453623	-1	KLRC4	NM_013431
103	12	66834816	66839770	-1	IFNG	NM_000619
104	13	40934872	40979054	1	TNFSF11	NM_003701
105	14	22620652	22625900	1	ISGF3G	NM_006084
106	14	101233857	101362669	1	TRAF3	NM_003300
107	15	79190912	79320920	1	IL16	NM_004513
108	16	57223242	57225170	1	CCL17	NM_002987
109	16	66964341	66970017	-1	TRADD	NM_003789
110	16	85718101	85736578	1	ICSBP1	NM_002163
111	17	7652940	7665483	1	TNFSF12	NM_003809
112	17	26808348	26819597	1	TNFAIP1	NM_021137
113	17	27216603	27222660	1	TRAF4	NM_004295

114	17	32727848	32729768	1	CCL2	NM_002982
115	17	32758237	32760749	1	CCL11	NM_002986
116	17	32832949	32835802	-1	CCL1	NM_002981
117	17	34449088	34454082	-1	CCL16	NM_004590
118	17	39083189	39094889	-1	CCR7	NM_001838
119	18	58141555	58201236	1	TNFRSF11A	NM_003839
120	19	4180495	4188506	1	EBI3	NM_005755
121	19	6536850	6542163	-1	TNFSF7	NM_001252
122	19	6615568	6621599	-1	TNFSF14	NM_003807
123	19	8023933	8033547	1	CCL25	NM_005624
124	19	10625988	10664095	1	ILF3	NM_004516
125	19	10804115	10807983	-1	TMED1	NM_006858
126	19	14003262	14025026	1	IL27RA	NM_004843
127	19	17374759	17377457	-1	BST2	NM_004335
128	19	18031701	18058702	-1	IL12RB1	NM_005535
129	19	18145579	18149927	1	IFI30	NM_006332
130	19	18362954	18369415	-1	LRRC25	NM_145256
131	19	55918417	55920776	1	SCGF	NM_002975
132	19	56337376	56348595	1	SIGLEC7	NM_016543
133	19	56566688	56567701	-1	NKG7	NM_005601
134	19	56606115	56612803	-1	SIGLEC10	NM_033130
135	19	56646064	56653509	-1	SIGLEC8	NM_014442
136	19	56686707	56696855	-1	SIGLECL1	NM_053003
137	19	59368921	59385478	-1	LENG4	NM_024298
138	19	59412565	59418660	-1	LILRB3	NM_006864
139	19	59446143	59452937	-1	LILRB5	NM_006840
140	19	59470349	59476163	-1	LILRB2	NM_005874
141	19	59491669	59495985	-1	LILRA3	NM_006865
142	19	59536505	59541992	-1	LILRA4	NM_012276
143	19	59557945	59568287	-1	LAIR1	NM_021708
144	19	59557945	59568287	-1	LAIR1	NM_021706
145	19	59705825	59713707	1	LAIR2	NM_002288
146	19	59705825	59713707	1	LAIR2	NM_021270
147	19	59736067	59987588	1	KIR2DS5	NM_012312
148	19	59736067	59987588	1	KIR2DL3	NM_012314
149	19	59777158	59790625	1	LILRA2	NM_006866
150	19	59796937	59805499	1	LILRA1	NM_006863
151	19	59866264	59873619	1	LILRB4	NM_006847
152	19	59911413	59916501	1	2007 deleted	NM_024317

153	19	60006878	60116153	1	KIR2DL4	NM_002255
154	19	60006878	60116153	1	NCR1	NM_004829
155	19	60006878	60116153	1	KIR3DL2	NM_006737
156	19	60567569	60573626	-1	IL11	NM_000641
157	21	33617679	33649252	1	IFNAR1	NM_000629
158	21	33695598	33730216	1	IFNGR2	NM_005534
159	22	35500069	35517096	1	NCF4	NM_013416
160	22	35561289	35577583	1	CSF2RB	NM_000395
161	22	35764924	35789001	-1	IL2RB	NM_000878
162	X	69194050	69198194	-1	IL2RG	NM_000206
163	X	69702558	69705151	-1	CXCR3	NM_001504
164	X	134435976	134448156	1	TNFSF5	NM_000074
165	X	151743864	151753246	-1	IRAK1	NM_001569
166	X	153659077	153672313	1	IL9R	NM_002186

Table1: The gene list based on the 3rd time reduction. The table shows chromosome number, gene start and end, strand position and gene name (HUGO & RefSEQ).

Organism	dbSNP Build	Genome Build	Number of Submission	Number of (rs #'s) in gene	Number of (ss #'s) with genotype	Number of (ss #'s) with frequency
Homo sapiens	126	36.1	27,846,394	4,116,991	5,546,513	682,608
Mus musculus	126	36.1	8,751,596	3,061,992	7,047,406	
Canis familiaris	125	1.1	3,526,873	1,170,325	2,551,456	17
Gallus gallus	125	1.1	3,641,959	1,446,038	3,624,831	
Pan troglodytes	125	1.1	1,544,897	546,997	1,544,895	2
Oryza sativa	125	2.1	3,931,108	1,028,130		
Anopheles gambiae	125	2.2	1,368,805			
Bos taurus	125	1.1	20,788	4,450	9,816	54
Rattus norvegicus	125	3.1	45,401	23,754	669	
Saccharum hybrid cultivar	125		42,853			
Apis mellifera	125	2.1	2,242	814		
Danio rerio	125	1.1	2,031	1,311	2,031	
Sus scrofa	125		6,441			
Bos indicus x Bos taurus	125	1.1	2,425	1,760		
Caenorhabditis elegans	125	4.1	1,065			
Pinus pinaster	125		1,439			
Cooperia oncophora	125		426			425
Ovis aries	125		681			
Glycine max	125		281		281	
Oncorhynchus tshawytscha	125		395			

Arabidopsis thaliana	125		186		184	
Plasmodium falciparum	125		203		199	
Oncorhynchus mykiss	125		139			124
Zea mays	125		148		90	
Macaca mulatta	125		29		29	29
Ficedula albicollis	125		37			37
Ficedula hypoleuca	125		28			28
Agelaius phoeniceus	125		47			
Bison bison	125	1.1	6	6		6
Salmo salar	125		17			10
Drosophila melanogaster	125		11			
Hydroides elegans	125		8			
Schistosoma mansoni	125		8			2
Gorilla gorilla gorilla	124		4			
Equus caballus	125		2			
Total: 35 Organisms		15 genomes	87,338,028	18,581,551	32,922,319	1,365,950

Table 2: This table describes the current status of the publicly available variation data NCBI dbSNP build 126; the build is a release of the dbSNP database. The ss number is the unique ID number assigned to each submitted SNP. Several ss numbers often map to one position in the genome. This cluster, a “reference SNP cluster” or a “refSNP”, has a unique ID number or so-called rs number. In total, 35 organisms are available.

Number	Forward PCR Primer	Rev PCR Primer	RefSEQ
P01201.G09	TCCATATACCAGGTTCCCGC	TGACGCTCTTCTTGCCTAGC	NM_000074.1
P01200.A03	GTTTGGCCTGATGTGCTCTG	AGCATCAAGGTTTGGATGGG	NM_000074.1
P01234.A06	GCTTTCTGGGTTGTTGGCTC	TTCCAAATCACAGGGACCAG	NM_000074.1
P01216.H01	GCCAGTTGCTTGACCAATTC	CATCCAGATTGCATTCCACC	NM_000074.1
P01021.D02	CAATCCATTCACTTGGGAGG	AACTGACTAGCAACGGCCTG	NM_000074.1
P01193.G11	GGCAAGCAAGGTATTCATGG	GAAAGTGTGCTGCCACCAAG	NM_000074.1
P01193.G10	GGCAAGCAAGGTATTCATGG	GAAAGTGTGCTGCCACCAAG	NM_000074.1
P00895.G07	TTGTTTCTTTGCGTGCAAGT	CTTCCAGAAAGTGTGCTGCC	NM_000074.1
P01193.G12	GGCAAGCAAGGTATTCATGG	GAAAGTGTGCTGCCACCAAG	NM_000074.1
P00983.F06	GATGGAAAGAGGAAGGGAGG	AATTCCCACCCTGAAGAACC	NM_000206.1
P00726.E03	GCCATCTGCCTCATTCAATC	TTGGAAGCCGTGGTTATCTC	NM_000206.1
P00987.B10	TGTGTTCTCTGTGCCTGTGG	CCGCTTTAACCCACTCTGTG	NM_000206.1
P01094.C12	CAAATCTCACCGTTCCAGCC	TCAGTGAAGGGAGCAGTGTG	NM_000206.1
P01310.G06	AGGATGAGGGAAAGTGGGTG	TCTGCAGTACCCAGATTGGC	NM_000206.1
P00793.H11	CTGCACCAAGTGCTCCAAAC	TGGTATGAGAAGGGACGAGG	NM_000206.1
P01158.E11	CCAATGTCCCACAGTATCCC	GGGAATGAAGACACCACAGC	NM_000206.1
P00985.H06	ATGAAGGCAGGGAGGGAAAG	AGAGGCATGGCATAGAACGG	NM_000206.1
P00785.D05	CTGCTGTCTAGCGCATTGTG	AGAAATGTGGGCAAGGAAGC	NM_000395.1
P00712.G07	TCTTGCTTCTGCCAGGAGAG	CCACCACCATTGTCACCAAC	NM_000395.1
P00784.E07	CTCCAATGAGTTTCCTCGCC	CTGGGCTCTGGCAACATTAC	NM_000395.1
P01153.D12	CTCCAATGAGTTTCCTCGCC	AATGTGGGTAAAGCCCTGAGC	NM_000395.1
P00965.E02	TCTTTCCAGTAGCGTCCCTG	GAGACGATGTATTGGCCGTG	NM_000395.1

P00718.A04	ATTCTACAAGCCCAGCCCAG	ATGGGAGAGGGAAGCAGAAG	NM_000395.1
P00740.A05	ATCTCAGCATCTCCCACGAG	CTTCTTCCCAGTGGCCTTTC	NM_000395.1
P00728.C02	TTCTGGGCCTCAGTGTTGTC	TCTTTCAACTTGCGGGTCTG	NM_000395.1
P00798.C04	TGGAAAGGATCTGACCCTCC	CACTCCCAAAGCTCCCAAAG	NM_000395.1
P01069.F07	AAGTGCTGCCTATGTGGGTG	ATTTCTCCTCCACACCAGCC	NM_000395.1
P00802.C03	CATGTTGGGAGGCTGAGATG	TCCCTCTTTCACCTCCGGTC	NM_000395.1
P01355.E03	TGTGAAGGGATCCAAGGGAG	TCCACATAGCCCTCAAACCC	NM_000395.1
P01357.D05	TGTTCCCTGTAGGATTCGGG	TGTGTGTGTCTGTGTGAGCG	NM_000395.1
P01392.F03	TGGAGTGGCCTCTGTTATG	CCTTTGTTTGGCAGTTTCCC	NM_000395.1
P00344.E12	ATCCATTTCCATGGCTCTGC	GCATAACGGGTAAATGCTGG	NM_000416.1
P00319.A04	CAAAGTCCTCATGGGCTCAG	TTGCAGAGCTGGGAAGAACC	NM_000416.1
P00322.G01	TTTCTTTCTGGGTCAAGGG	TCATTGGCGGTGACGTAAAG	NM_000416.1
P00333.D06	TTTACGTCACCGCCAATGAG	TTCTTTCTCTGCTCCTGCC	NM_000416.1
P00324.G12	AGCTAAGTGATGGCCACCTG	TGGAATGTGGCTTGCATAGG	NM_000416.1
P00345.C08	GCAAGCCACATTCCACATTC	TTGGCCATCCTCATTGTAGC	NM_000416.1
P00329.F10	ACGAAGTGAAGACCACGATGC	GGCTGTGGCCTAATGCAAAC	NM_000416.1
P00238.C06	GCGCTCTGAATGGTGAACAG	TTCCATTTGGTCTTCCCTGG	NM_000564.1
P00227.H06	TAGCTGAGGGCTGCATTGTG	AGCTCCAAGATCCAAGTGGC	NM_000564.1
P00221.E11	CACTGGCTTCATGGCAAATC	AGGGTGACTGCCAACACATC	NM_000564.1
P00249.B02	CAAGGCTGGGCAAGTATGTC	TCCTGTGGCTTGGAGATCAG	NM_000564.1
P00251.G06	TTGGAATGGAGAACCCTTGCC	CTGAGCAACCACCAACAAGG	NM_000564.1
P00250.H08	TTGCTGGAGCCGTTAACAAG	ACAAGGCCAGTGTTTCCCAC	NM_000564.1
P00228.E11	ACCAACTTTTCCACTGGAGGC	TGTCCGACATTGACCTCTGG	NM_000564.1
P00239.G12	AGCAGGTGCCTGAATGTAGC	AACACCTGGACATGGGCAAC	NM_000564.1
P00222.E06	CATTCCAAATGCGACCACTG	ACATTGGAAGGGCAAAGTCC	NM_000564.1
P00219.B01	TCCTTGACGCACACAACAGG	TGCCCAATTGTTCAAGGAC	NM_000564.1
P00253.H04	AAACAGCAGGAAAGGATCGG	AATCCGTGGCAAGGTGAGTC	NM_000564.1
P00226.F12	CACGGATTTGCACATCTCAC	ACAGCAGTTTGGTTGTTGGG	NM_000564.1
P01123.E08	TGGAAGCTTCTGTTGGCTCC	CTGATTTCCCAGAAACCGTG	NM_000572.1
P00162.E10	AGCTCAAAGAGGATTTGGCG	ACAGAGTGCCAACATCAGGG	NM_000572.1
P00100.E08	GGCAGCGAGCAGTCATTTAG	GCCTTGCAAACATCTTGGAG	NM_000572.1
P00117.G07	TACAAAGAGGCAGTGGAGGC	ATTGGGTTTGTTCCTTCGC	NM_000572.1
P01175.F12	TGAGTGAGAGATTGGCGGAG	TCCGCAGAAAGAAGACCAGG	NM_000572.1
P00099.F01	TGTAAACCCTCTGGCTGCTG	TCCGCAGAAAGAAGACCAGG	NM_000572.1
P00133.A02	TTTCAGGTCTGGAAACGCTC	GAACACGCGAATGAGAACCC	NM_000572.1
P01204.F01	TACGCACTGCGAACATCTCC	ATCTTGTCTCTGGGCTTGGG	NM_000572.2
P01217.A02	GGTCAGGCTTGGAAATGGAAG	ACAGAGTGCCAACATCAGGG	NM_000572.2
P01203.D06	ATCAGGTTTGGAGCCTTCCC	AACTGAGACATCAGGGTGGC	NM_000572.2
P01237.G04	GGCAGCGAGCAGTCATTTAG	GCCTTGCAAACATCTTGGAG	NM_000572.2
P01221.H05	TACAAAGAGGCAGTGGAGGC	ATTGGGTTTGTTCCTTCGC	NM_000572.2
P01234.G12	TGTAAACCCTCTGGCTGCTG	TCCGCAGAAAGAAGACCAGG	NM_000572.2
P01218.G10	TTTCAGGTCTGGAAACGCTC	GAACACGCGAATGAGAACCC	NM_000572.2
P01234.E09	GCCTCTGGAATCAATGGGAG	CCCGAAGGATTCAATCAACG	NM_000575.3
P01200.E01	AGTTGAACCTTCTGCCCTGG	CATGGTTTCTCCTCCATCCC	NM_000575.3
P01234.H08	TTCAGGCCACTGCTCATTTTC	TGGAAGGAGGAAGGAAGGTG	NM_000575.3
P01213.E04	TCAGGGATTTGGGATGTTTC	CAGGAACAGGAAATGGCTCC	NM_000575.3
P01216.G04	GGAGCCATTTCTGTTCTCTG	GCTTCTCATGGGAGGGAATC	NM_000575.3
P01193.D08	CCCATGCCCTCATAGGAAAC	GCTGGCATCACTGTTGCTTC	NM_000575.3
P01193.D07	CCCATGCCCTCATAGGAAAC	GCTGGCATCACTGTTGCTTC	NM_000575.3
P01193.D05	CCCATGCCCTCATAGGAAAC	GCTGGCATCACTGTTGCTTC	NM_000575.3
P00841.G10	CGGTTGCTCATCAGAATGTG	TATGCTCCTCAGCATTGGC	NM_000576.1
P00200.D09	CCTGTTCCAAATGTGCACTG	TATGCTCCTCAGCATTGGC	NM_000576.1
P00179.E12	TGCAGCAGGATTGAAGTTTG	CAAGTTGTTCCGCTCCTGTG	NM_000576.1
P00173.F01	CTGGCCAGTGCAATCAAATG	CTGAAGCTGGAACCCATGTC	NM_000576.1

P00204.E09	ACATGGGTTCCAGCTTCAGG	AAGGCAACCTCAGTGAAGCC	NM_000576.1
P00190.F02	AACTGGAGGTTGCAGGATGC	AGGCCTCAAGATCCAACAGG	NM_000576.1
P00171.H11	AGCCCTTGCAACAACACATC	TGTCAAAGCCTCTGCTCCAG	NM_000576.1
P00177.F02	TGGAGCAGAGGCTTTGACAC	TGGACATCAACTGCACAACG	NM_000576.1
P01203.E12	CCTGTTCCAAATGTGCACTG	TATGCTCCTCAGCATTTGGC	NM_000576.2
P01203.E11	CCTGTTCCAAATGTGCACTG	TATGCTCCTCAGCATTTGGC	NM_000576.2
P01236.D02	TGCAGCAGGATTGAAGTTG	CAAGTTGTTCCGCTCCTGTG	NM_000576.2
P01235.D02	CTGGCCAGTGCAATCAAATG	CTGAAGCTGGAACCCATGTC	NM_000576.2
P01204.D08	ACATGGGTTCCAGCTTCAGG	AAGGCAACCTCAGTGAAGCC	NM_000576.2
P01217.F01	AACTGGAGGTTGCAGGATGC	AGGCCTCAAGATCCAACAGG	NM_000576.2
P01235.G04	AGCCCTTGCAACAACACATC	TGTCAAAGCCTCTGCTCCAG	NM_000576.2
P01234.G09	TGGAGCAGAGGCTTTGACAC	TGGACATCAACTGCACAACG	NM_000576.2
P01234.H10	TAGAGCCAAGGTCACGGAAG	TTACATTAAACCCTGTGCC	NM_000579.1
P01214.E04	TTGGGTGGTGAGCATCTGTG	TGGGCACATATTCAGAAGGC	NM_000579.1
P01219.G05	TTCTGGGCTCACTATGCTGC	CAGAAGCGTTTGGCAATGTG	NM_000579.1
P00835.E10	TCAACCTGGCCATCTCTGAC	GCATTTGCAGAAGCGTTTGG	NM_000579.1
P01201.E05	AACTAAGATGCTGCCTGCCC	TAAGTGACCAGGCCATGACG	NM_000579.1
P01140.E06	AACCAGGCGAGAGACTTGTG	TTTCAGGCTTCCCTCACCTC	NM_000579.1
P01218.A04	TCAAGCACAGAAGGAGGAGG	TTTCCCTTCGTTGCTTCCTG	NM_000579.1
P00985.D09	TGTGACACGGACTCAAGTGG	TGGTCTCCTTGCCCTAAATG	NM_000579.1
P01217.A07	TTTACACCCGATCCACTGGG	ATGCTCATCCTTCCTGACCC	NM_000579.1
P01086.C11	TCCAGATGCCTTCTCCAGAC	ATGTGCCTACAACCTCAGGGC	NM_000579.1
P01217.F08	GCAGCAAACCTTCCCTTCAC	TCATTTGCACACCGAAGCAG	NM_000579.1
P01213.H06	ATCGTCTCTCCCTCCCTTTG	ATGTGCCTACAACCTCAGGGC	NM_000579.1
P01102.B04	TCAAGCACAGAAGGAGGAGG	TGCTGACAGCCACAATGCTC	NM_000579.1
P01220.G02	AACCAGGCGAGAGACTTGTG	TTTCAGGCTTCCCTCACCTC	NM_000579.1
P01203.A06	TGCTTCGGTGTCGAAATGAG	AGGCTTCTGTCTTTGCCAGC	NM_000579.1
P00269.G01	GATGACTCAGGTTTGCCCTG	ATTTCTGTGTTGGCGCAGTG	NM_000584.1
P00270.H07	GGCAGCCTTCTGATTTCTG	TTCTCCACAACCCTCTGCAC	NM_000584.1
P00273.C01	GGCAGCCTTCTGATTTCTG	CCAGAATTTCTGGGCAAAC	NM_000584.1
P00276.D08	TGCAGAGGGTTGTGGAGAAG	GCGCACAGACATACAAACCG	NM_000584.1
P01191.E04	TTGGCTGGCTTATCTTCACC	ATTTCTGTGTTGGCGCAGTG	NM_000584.2
P01199.D09	GGCAGCCTTCTGATTTCTG	TTCTCCACAACCCTCTGCAC	NM_000584.2
P01190.B04	TGCAGAGGGTTGTGGAGAAG	GCGCACAGACATACAAACCG	NM_000584.2
P01190.A11	TGCAGAGGGTTGTGGAGAAG	GCGCACAGACATACAAACCG	NM_000584.2
P01190.A12	TGCAGAGGGTTGTGGAGAAG	GCGCACAGACATACAAACCG	NM_000584.2
P01151.B09	CTCAGGAAGACTTGGATGCG	AGCTTGACTGGGTGCAGAAC	NM_000585.1
P00747.G08	GAACTGGCCTCAAATCCTGG	AATGATACCCACACCCTGCC	NM_000585.1
P00923.C11	ATGGAGAAAGCTGCTGCAAG	TAGAACTCATCCGTCTGGGC	NM_000585.1
P01230.D06	TTGTGCCTTCTCTGCAGGTG	TTCTTGAGCTTGACTGGGTG	NM_000585.2
P01184.E08	ATGGGTCTAAATGCCCATCC	ATGGAGCCCATACATTCCC	NM_000585.2
P01233.C11	GAACTGGCCTCAAATCCTGG	AATGATACCCACACCCTGCC	NM_000585.2
P01198.C07	GCAGGGTGTGGGTATCATTC	AGGCCCAATTTATTTGAGGG	NM_000585.2
P01233.B01	CTAATCCGGGTTGGTGAAGC	TAGAACTCATCCGTCTGGGC	NM_000585.2
P01184.D10	AGGCACACAGATTGGAAAGG	TGAGTTACCTGTTGCGTGGC	NM_000585.2
P01191.E09	CTGGGCACATGGGTGTATTC	TTTGCTCTCCTGGAACCCTC	NM_000585.2
P00290.E07	ATAAAGATCCTTCCGACGCC	TGCCCTACCAAACACTGACC	NM_000588.1
P00283.A01	ACGCCCTTGAAGACAAGCTG	TGCCCTACCAAACACTGACC	NM_000588.1
P00283.B02	AAATGGAGCCAGAGACTGGG	ATGGTGATGACCAGCTGAGG	NM_000588.1
P00284.A06	ACAGTGGGCTTGGGAAACTG	AGATCGCGAGGCTCAAAGTC	NM_000588.1
P00289.H08	AATCTCCTGCCATGTCTGCC	TTTGTGGCACACCAGTCTCC	NM_000588.1
P00291.C11	TGTGGCCTCTCCCTTCTATG	TTGGTCCAGGCAGAAATGAG	NM_000589.1
P00297.C11	GTTGGAAGTGGTGGTTGGTG	TGTGAAATTGAGGCTTTGGG	NM_000589.1
P00309.A04	TTATGTCTGTGGCAAGCAGC	TCCCATGACCTATCCCATTG	NM_000589.1

P01177.E12	TCAAGTTCCACCCTCTGAGC	TCCATAGCACTCTTGGACCC	NM_000589.1
P00291.F10	TCATGCAGAAGGCCCAGTAG	TCCATAGCACTCTTGGACCC	NM_000589.1
P01204.H02	TTGCCAAGGGCTTCCTTATG	TAGAGTTAATTTGGGCCCGC	NM_000589.2
P01215.H05	TCATGCAGAAGGCCCAGTAG	TCCATAGCACTCTTGGACCC	NM_000589.2
P00299.H11	TGCCTTCTCCTCTTTCAGGC	TGTTTAGCTGCATGCGTTTC	NM_000590.1
P00286.B02	TAAATGGCCTCGTCAGGAAC	AGAGCCGACTATTTTCAGGGC	NM_000590.1
P00294.E10	AGGGCAGCATTCAAACCAAC	TTCTGGCCATGGTCCTTACC	NM_000590.1
P00287.G03	TGTGCACATGGCCACCTATC	TTCTGGCCATGGTCCTTACC	NM_000590.1
P00284.B02	GAGGGAATGCCCAAACAGAG	TTTCTGGCACAGCATCATC	NM_000590.1
P00357.H07	TCTTGCCATGCTAAAGGACG	CCCGTTGGCCTCAAATCTAC	NM_000600.1
P01225.F10	TCTTGCCATGCTAAAGGACG	CCCGTTGGCCTCAAATCTAC	NM_000600.1
P00356.C10	TGTCTGAGGCTCATTCTGCC	CTCAGCTCATGCCAAAGGTG	NM_000600.1
P01227.D09	TGTCTGAGGCTCATTCTGCC	CTCAGCTCATGCCAAAGGTG	NM_000600.1
P01216.F03	TTCTCTCAAAGCCATTCCAGC	TCTGGCCATACCTGTCCAAG	NM_000600.1
P00363.H09	TTCTCTCAAAGCCATTCCAGC	TCTGGCCATACCTGTCCAAG	NM_000600.1
P01234.F08	TAGCATCTGTTGGGCTTTGG	TTTGCAGAAGAGAGCCAACC	NM_000600.1
P00350.B05	TAGCATCTGTTGGGCTTTGG	TTTGCAGAAGAGAGCCAACC	NM_000600.1
P01300.E04	AATTGGCCTTCTCCTGGACC	TCAAATTGGAGCTTCATGGC	NM_000609.1
P01308.A05	TTGTTGATGGGTTTGCCTTC	ACCAGTCAACCTGGGCAAAG	NM_000609.1
P01150.E02	CCAACACACAGCCAGTCAAC	CAAAGGCAAGCACTTGTGGG	NM_000609.1
P01010.G11	TCCCATCCACAGAGAGAAG	AGCCACGAAAGTGCCTCTTG	NM_000609.1
P00963.G01	TGGCCTTTCAGAAGCAATTC	AAAGGTTCCGCTTGGAGCAG	NM_000609.1
P01038.F05	GTCTTGTTTCATGGATTGGG	CCTTCAAAGTAGGGCCAAGC	NM_000609.1
P01330.A12	GAAATGTCCTGTGGGAAGGG	GGGAACCTGCCTTAATGGTG	NM_000609.1
P00833.D05	TGCAGGGTCTAAATGCTGGC	TCATGCCCATCCTTAAGTCG	NM_000609.1
P01061.E09	TTTCTTCCCGCATTTCTCCC	TCACTGTGTTGCCTGAGGAG	NM_000609.1
P01364.H10	TGCTGCAGCTCTCATTCTGG	GTTCTCATTAGTTCCCGCC	NM_000609.1
P01191.E03	ACTGGTGTTTGCCAGCATTG	ATGGCAGAGCCAAGAGGAAG	NM_000619.1
P01191.E01	ACTGGTGTTTGCCAGCATTG	ATGGCAGAGCCAAGAGGAAG	NM_000619.1
P00527.B02	ACTGGTGTTTGCCAGCATTG	ATGGCAGAGCCAAGAGGAAG	NM_000619.1
P01191.E02	ACTGGTGTTTGCCAGCATTG	ATGGCAGAGCCAAGAGGAAG	NM_000619.1
P01191.H10	TGGTCCCTCTCATTGAGCC	ACACACTCGCACATGTTTGG	NM_000619.1
P00525.C12	TGGTCCCTCTCATTGAGCC	ACACACTCGCACATGTTTGG	NM_000619.1
P01212.H11	AATGCTTTGCAAGACCCTCG	ACACACTCGCACATGTTTGG	NM_000619.1
P00512.F07	AATGCTTTGCAAGACCCTCG	ACACACTCGCACATGTTTGG	NM_000619.1
P00515.H12	CAGTGAGCAACGAAGTTCCG	AGGTGGGCATAATGGGTCTG	NM_000619.1
P01200.A05	CAGTGAGCAACGAAGTTCCG	AGGTGGGCATAATGGGTCTG	NM_000619.1
P00082.A11	CAATGGGAGCTTGGAGAAGG	TCGACACAAAGCTCTGGCAC	NM_000629.1
P00080.C07	TATCAGCATCCCTGTGCTGG	TGGCTATGGGTTAGAGACGC	NM_000629.1
P00672.B10	TTGGAGAGGGCAGAGGAAAC	TGGAGGACCAATCTGAGCTG	NM_000629.1
P00672.G01	TTGGAGAGGGCAGAGGAAAC	AAACAAATCCCAGCTCCTGC	NM_000629.1
P00088.H03	GTTATGTGGGCTTTGGATGG	AAACAAATCCCAGCTCCTGC	NM_000629.1
P00091.F05	TTAAGGTCAAGGGCAGGAGC	TCCAACCTTTCTTTCCACCG	NM_000629.1
P00091.D02	CTGGGCTTGAAGTGAAGTGC	TCACAGGCGTGTTTCCAGAC	NM_000629.1
P00091.H05	TCTCCGCGTACAAGCATCTG	GGAAGCAGCCAAATCAATGG	NM_000629.1
P00093.D03	GCCACTGAACGTTAAGGCAG	AAAGATTGGCGTGGGAAGTG	NM_000629.1
P00088.A03	TGCCTATGTTGCTGTGGAC	CGTTCTGACAAACGCATCAC	NM_000629.1
P00093.A01	TCCTGTCCTTTCCCGTGTTT	TTAGGTGCTCAGGCTTCCAG	NM_000629.1
P00842.D08	CCGGAAGTGCATTGGATGAG	TTAGGTGCTCAGGCTTCCAG	NM_000629.1
P01205.H11	TGTTTGGGTAGCACAGCGAC	AAACCAAGCCCTGGAAAGAG	NM_000639.1
P00915.G03	TGCAGCAGCCCTTCAATTAC	AAACCAAGCCCTGGAAAGAG	NM_000639.1
P01205.G08	TGTTTGGGTAGCACAGCGAC	AAACCAAGCCCTGGAAAGAG	NM_000639.1
P01215.B06	ACTGCCTGGCTTGCAAAGTG	TTCCAGGAGTTACAGCCAC	NM_000639.1
P01215.G07	TATACGACGGCATCTTCGGG	TGAGCTTCTTATGGGCAGGG	NM_000639.1

P01202.D02	CCCAGGATCTGGTGTATGATG	GGCCTAGCAAAGGCAGAAAG	NM_000639.1
P01201.C06	ATGAGCCAGACAAATGGAGG	TCAGTGGCCTCTGGAGAATG	NM_000639.1
P01203.A12	AAGGGAGACTCAATCCTGGC	TTCTCCATTTGTCTGGCTC	NM_000639.1
P01050.A12	TCTCATGTGTGTGCATGTGG	TGGGACAAAGCTGCAAGGTC	NM_000641.1
P01387.G05	CTCATGTGTGTGCATGTGGC	AGGGCGATTTGTCTGAGAGC	NM_000641.1
P00914.A06	AAACCCAGGCTTCCCTTTCC	TCACCTAGAACCGAGATGCC	NM_000641.1
P01342.B06	TTGCAGCTTTGTCCCATACG	TCCCGGCCCTAAACACTTCAC	NM_000641.1
P00741.F02	GTTTCTGGGCAGGATTTGGG	GGACAAATTCCCAGCTGACG	NM_000641.1
P00222.E12	CTGGAGACCTCAACCCAATG	TAACGTCCTTGGGTGCTCAG	NM_000647.3
P01237.E03	CTGGAGACCTCAACCCAATG	TAACGTCCTTGGGTGCTCAG	NM_000647.3
P01194.B09	AAGGCAAATCAGGAACTGGC	CCCTCACTCCCATTTCATCTG	NM_000647.3
P00970.D10	ATGGTCATCTGCTACTCGGG	TGCTCATGTCTCCCTCCTTC	NM_000647.3
P00247.F03	AAGGCAAATCAGGAACTGGC	CCCTCACTCCCATTTCATCTG	NM_000647.3
P01194.B11	AAGGCAAATCAGGAACTGGC	CCCTCACTCCCATTTCATCTG	NM_000647.3
P01194.B12	AAGGCAAATCAGGAACTGGC	CCCTCACTCCCATTTCATCTG	NM_000647.3
P00881.F11	ACATGCTGGTCGTCTCATC	GTGCTTTCGGAAGAACACCG	NM_000647.3
P00887.F10	CACGTCTGGCTTCACAGATG	AGCCCAGTGTTCCTTGCTTG	NM_000647.3
P01193.H04	TCCTTCACCAGGAGCAAAGG	CCGGGATGCTTGTCATATTG	NM_000647.3
P01193.H05	TCCTTCACCAGGAGCAAAGG	CCGGGATGCTTGTCATATTG	NM_000647.3
P00249.F07	TCCTTCACCAGGAGCAAAGG	CCGGGATGCTTGTCATATTG	NM_000647.3
P01193.F05	TCCTTCACCAGGAGCAAAGG	CCGGGATGCTTGTCATATTG	NM_000647.3
P00924.E02	ACGCATTACGCCAGGAGATG	AAGCCAGACGTGTGATTTC	NM_000648.1
P01203.B07	GCGCTTCTGCAAACAATGTC	TCCTTTGCTCCTGGTGAAGG	NM_000648.1
P01218.A10	GACAAAGGTGAGCAAAGGGC	CATCTGTGAAGCCAGACGTG	NM_000648.1
P01083.C01	CTTCAACAAACACGCCTTCC	TTTGCTCCTGGTGAAGGAAC	NM_000648.1
P00287.G10	GCTGTGCGTTCTTGAAAGG	TTGAGCACCCAGTTGCTACC	NM_000758.1
P00283.C02	TTCTCTGGAGGATGTGGCTG	TGGCCATTGAATGCTAGGTC	NM_000758.1
P00285.H12	TTTCAGGAACAACCCTTGCC	GGGATGAAATGGGCTGTCTG	NM_000758.1
P00301.C03	TTGTGGCCTTGACTCCACTC	AATACGCTGCACTGTGACCC	NM_000758.1
P01170.A05	TTACCCACTTGCCTGGACTC	AATACGCTGCACTGTGACCC	NM_000758.1
P00881.C04	CTTTAAGAGGCAGGCCCAAG	TGGACTGAAGCAGACCCAAC	NM_000760.1
P00144.D03	AGGAAGCAAGGGAAGGAAGG	CTGTCACTTCCGGCAACATC	NM_000760.1
P00106.B09	TTGAGATGGACAGAGGTGGG	TACACATCATCTGGGCCTG	NM_000760.1
P00100.G03	ACACACCCTCCGATCTTTCC	TCCTCACCTGATGACCTTG	NM_000760.1
P00105.G10	AACAGGCCCAGGATGATGTG	AAGCACATTGGCAAGACCTG	NM_000760.1
P00112.B04	ATGTGATACAGACTGGCGGG	AGGACCTGGCATAAATTCGG	NM_000760.1
P00108.G07	GCACCTGATTTCTGTCCAGC	TGCCCAAGAGACATGGATTC	NM_000760.1
P00149.F05	AGAGCTGAAAGGGCCTGATG	CCCTAAACATTGGTCCTCGC	NM_000760.1
P00136.F09	ATGGGCTGTGAGTGTGTGTG	TTTCTTCCTGCCCTCCTTCC	NM_000760.1
P00106.H06	TTCCCTCTGTTCCCTTGTC	TTCACTATGAGCTCTGCGGG	NM_000760.1
P01182.G09	GGAGGGCAGGAAGAAACAAG	ATGGTGAACCACAGACAGGG	NM_000760.1
P00116.G04	ATCTGTTTGGACTGCGGGAG	CTTGACGTGAACTGGAGCC	NM_000760.1
P00136.B11	TGGATACTGTTGGCTGCTCC	CATGCTTTCAGCGTGTTC	NM_000760.1
P00114.C07	TGGGTGCTTTAGGAAACACG	TCACAACCAGCAGCCTCATC	NM_000760.1
P00095.H09	AATAGTCCAGGCTTGGGTGC	GGTGCATGCCTGCAACTTAG	NM_000760.1
P00146.F02	TCAGATGGCTGAGGACTTGG	CACTGCTTGACCATCCTTG	NM_000760.1
P00105.G11	CGTCTCACCATTCTCTTGG	TTCTCACTGCTCCTTTCCC	NM_000760.1
P00129.H09	AGATTTAGCCTCCAAGGCC	AGAGGGAATGTGAAGGCAGC	NM_000760.1
P00121.G02	TTGGCTGTGAGTGACTTCCC	TTCCCTGGAACCTGGAACAC	NM_000760.1
P00189.G03	TATTCTTCCCTCCCTCCCTG	GGTGACCTGGGAAAGCAAAC	NM_000877.1
P00191.H02	AGGCATGACCTTTGAGCTGG	TGATGACTTCCAGCTGTGGG	NM_000877.1
P00218.F10	TCGTAAATGAAGACCCAGGC	TAAGGGCACACAAGTCCTCC	NM_000877.1
P00197.C08	TGTTCTGCTAAGGTGGAGG	CAATCTACCGCCAAAGGAGC	NM_000877.1
P00202.C01	GCAGAACTACCCGTTGCAG	AGCCATGCCAAAGAACAACC	NM_000877.1

P00172.G08	GATTCACAGTGTGCTGTGGC	TGACCTTGGTGTCTGGTTGG	NM_000877.1
P00212.H01	CTGATGCCTAGGCTGCATTG	TGTGAAGGAGAGGTCATGGG	NM_000877.1
P00206.B12	TCACAACACCTGCAAAGCAC	GACAAATATCCAGCTGGCCC	NM_000877.1
P00189.A04	AAGGAGGCCAGGAGAATGTG	AGGCCTACCAATGGCTTGTG	NM_000877.1
P00199.A07	TTCATGCATCAGGGAGGTTT	ACCGTATGGCTCCTAATGCC	NM_000877.1
P01325.F06	GCCATGACGTCAATAGCAGC	TGTGCTCACCACCATCTCTG	NM_000877.1
P01310.H10	AACATCAGGCTTCAGCTGGC	AGGGAGCTGTTCTCCAAAG	NM_000877.1
P01286.H09	TGTGTGAATTCCCAGGTTGG	TTCAACCCTTGAAGATGGG	NM_000877.1
P01299.D09	TGCTGCAGGCAAAGTGAGAC	CTTGTGTCCTGCAATCGGTG	NM_000877.1
P01355.D11	GGTTTGGAAATGGATGGACC	TGGATCGATTCCCACACTTG	NM_000878.1
P01348.D01	CAATCAGCTGTGAGCAAGGC	TCCTGCACACTTGGTCCATC	NM_000878.1
P01355.D10	TCTGGCAGATTAAGGGAGGC	TGACCAGCTGCTTCACCAAC	NM_000878.1
P01299.A03	CCTGAGGAATTATGCGGTCC	TGGGCCTGAACTAGCCAATC	NM_000878.1
P01339.E10	TAACCCTCCCAAGAAGTGGG	ACTGCCTCCCTTAATCTGCC	NM_000878.1
P01118.E08	TGGAGAAGAGACCCATGCAC	TCCTCCTTGTCGTTCTTGCG	NM_000878.1
P00755.E10	AAGCACGGGTGTATCAGAGC	TTTCGAGTTCAAGCCCAAGC	NM_000878.1
P01348.D02	ATCAGGCCGAGAGGTGAAAG	AACCCTCCACGTGTCAAAGC	NM_000878.1
P00845.B07	CAGAGGCAGAATGGCAGATG	TGGATTCCATAGGGTGTGGG	NM_000878.1
P01053.A12	CACCCTATGGAATCCACCTG	ACTTTCTGTCCCTGCCTTGC	NM_000878.1
P01328.H12	CGGAGAAGGGATTTCATGGAC	CTTCACACCATTGCCTCAGC	NM_000878.1
P00803.B02	CTGAATGGGTTGGGAAGGAG	AGGGACCTGCTTGTGTGAAG	NM_000878.1
P00305.A03	AAACCAGGTTACCTCCTGC	CCCAAAGAGCATCGTGTGAG	NM_000879.1
P00297.H11	CTTTGGCTGCAACAAACCAG	CAAAGAGCATCGTGTGAGGG	NM_000879.1
P00284.A04	CCCTGACACGATGCTCTTTG	CCCACAGAAATTCCCACAAG	NM_000879.1
P00296.G11	ACAGACATTCACAGCCACCC	GGCTTGGCAGTTTCCATTTC	NM_000879.1
P01190.H01	AAACCAGGTTACCTCCTGC	CCCAAAGAGCATCGTGTGAG	NM_000879.2
P01190.G12	AAACCAGGTTACCTCCTGC	CCCAAAGAGCATCGTGTGAG	NM_000879.2
P01233.B10	CCCTGACACGATGCTCTTTG	CCCACAGAAATTCCCACAAG	NM_000879.2
P01199.D10	ACAGACATTCACAGCCACCC	GGCTTGGCAGTTTCCATTTC	NM_000879.2
P00677.D02	GTGCAATGCAAACTGACAGC	GTGAAGCCCAACCAACAAAG	NM_000880.1
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P00395.C02	GTTTGGCAAATCCAGCACAC	GCCTCATGGCATCTCACAAAC	NM_000880.1
P00396.C02	GTTGTGAGATGCCATGAGGC	AGTCCAACCCGGTGCATAAG	NM_000880.1
P00677.C01	CACCCAAACCCAACATCACC	CAGTGTTGCCTCCAAGAAGC	NM_000880.1
P00386.F07	TCAAGTGGCTATGTGCCAGG	GTCGTCCGCTTCCAATAACC	NM_000880.1
P00221.G06	ACTGCGAACATTTGCTTTTC	TTTAGCACACGGTGAGACCC	NM_000882.1
P00230.B01	TGTTGGGTTCAACACCCTTG	TTGGCAGGCTACAGGAACAC	NM_000882.1
P00242.F06	TTTACCCAACGGTGCTTTCC	GGGTGACATGACAAGATGGG	NM_000882.1
P00223.F09	TTTCCTCCCAGAGCATGCAG	GGGTGACATGACAAGATGGG	NM_000882.1
P00233.C11	TTTCCTCCCAGAGCATGCAG	TTATCAAAGACCCTGGCTGG	NM_000882.1
P00236.E05	TTTCCTCCCAGAGCATGCAG	CTGCTCACATTTGTGCTCCC	NM_000882.1
P00242.C05	AATCCATCACCTCCCTGTGC	ACCATGACTCACTTGGCTGC	NM_000882.1
P01228.F04	ATTGCAGAGTCAGCCAGCTC	TTTAGCACACGGTGAGACCC	NM_000882.2
P01222.E02	TGTTGGGTTCAACACCCTTG	TTGGCAGGCTACAGGAACAC	NM_000882.2
P01201.F03	TTTACCCAACGGTGCTTTCC	GGGTGACATGACAAGATGGG	NM_000882.2
P01233.B04	TTTCCTCCCAGAGCATGCAG	GGGTGACATGACAAGATGGG	NM_000882.2
P01185.B12	AAGGTGAGCCTTTCTGTCC	AATCTGGCACATGCACACAC	NM_000882.2
P01185.C01	GTCCACATGGTTTCTCTGGC	TCACCAAAGCAGTCACCCTC	NM_000882.2
P01199.C12	CATTCTGCCTGGTGATCTGG	TTCTCTCAGAGCCCAAAGGG	NM_000882.2
P01356.D02	TCATCTGAGAAGACTGGGCG	ACCAACGGTGGAAGTCCAAG	NM_001065.1
P01391.E05	GGGCATGATCTTCCATCCTC	ATCCCTCCCTCTCTTGATGG	NM_001065.1
P01324.A10	ATGAGTCCTGCATCCTCCTG	GCTGCTTGTGGAAGAAGGG	NM_001065.1
P01349.G03	GATGATTCCCGGACCAAGAC	TAAAGAACGTTGGGCCTCC	NM_001065.1
P00139.E01	CAGGTGGAGATGGTGATTG	GACTTCATTTGCCTTGCTCG	NM_001066.1

P00126.B11	TGTCCCATGCAGTGTTAGGG	ATGGGAACATCAGAGGCCAG	NM_001066.1
P00104.C11	TCCAGTGGTGGAGGTTCAAG	GCTGTGAAGAGGCTTTGGTG	NM_001066.1
P00119.D10	AGCGAAACTGCTGGGAAGAG	GAATGAACGGTGGACAGGTG	NM_001066.1
P00118.A11	AACTCTACAGCCCAATCCCG	ATCCATGCTTGCATTCCAG	NM_001066.1
P00110.D07	TCCCAGGATAAATGGCATGG	AAAGCAGTCTCACTGCCACC	NM_001066.1
P00114.E06	TCAGGCCAGAGGTCTCAAAC	TCCCAACCATTCTCCAGTCC	NM_001066.1
P00099.F03	TTGATGGGTGGAGTCTGTGC	CCGGAGCATTTCACACTCAC	NM_001066.1
P00112.D09	TATTTGGTGAACAGGGCCAG	AAAGGCGGGAGGGAACCTAG	NM_001066.1
P00832.G04	TGTGGCCTGGGCAAGATAAC	GTCTCCATGGTAATGGCTGG	NM_001066.1
P00168.B02	ATTGGCTCCTCCCATCTCTG	CCAATACACAGGCCAAGGTC	NM_001066.1
P01169.E02	TGCCTGAGTCACCCATGAAG	TTCAACTTACCGACCTTGGC	NM_001066.1
P00885.G10	TGCCTTGAAGCCACTGAAGC	GAGCATGGACAAACCCAAGC	NM_001066.1
P01327.E02	TTAATCCCAAGTGCCCAAGG	ACGAGGAATGTTCTCTGGGAG	NM_001242.2
P01320.B09	TTCTGCCTTCAAAGGTTGGC	ACCCAGTGACACCAAACACG	NM_001242.2
P01344.C01	ATAATGGCAAAGGCATTGGG	GGCAGCTGTAATGACAAGGC	NM_001242.2
P01349.G01	AAACCCACCAGCTCCACTTC	GTTGGGCTTAGAAGGCGATG	NM_001242.2
P00123.E02	TCGTGTCTAGGGACAGGAAAC	GGTGCTAGCATATTCCGGTG	NM_001243.1
P00111.B05	ATGTTAATCCCAGGGCAAGG	GGTGGCAGCAAGAAACACAG	NM_001243.1
P01175.H09	ATGTTAATCCCAGGGCAAGG	GAGATGGACATTCTGGTGGC	NM_001243.1
P00161.H06	TCGTTTCTGATCTGCCAAGC	TCTGCACCTGGAACACAAGG	NM_001243.1
P00143.G04	CATAGCAGGCAAACCTGAGGG	TCTTACAGGCATGGTGCTGG	NM_001243.1
P00112.F03	CATGGTGTCTAGCACTTTGGG	CTCTGCACTGCTGGCAAATG	NM_001243.1
P01178.C10	CATGGTGTCTAGCACTTTGGG	TCAGATGGACACGTGCAGAG	NM_001243.1
P00106.G09	AGAGCCATGAGACAGGGTTG	TTGGAACAGGTGGGTGATTC	NM_001243.1
P00138.H09	TTGTCACCATTTCCTATCCC	CACACTGGTAAAGCCAACCG	NM_001243.1
P00129.B09	GCGTCACTGTTTCACCTTCC	TTCTCTGGAGACTGCGCAAC	NM_001243.1
P00126.B10	AAATGCCTGGCAGAGACTCG	AAGCCACGAGGATGAAGCTG	NM_001243.1
P00113.H11	TTGCCCTTCTCTCAGCCTTC	CCCACATTGCATCCCTACAG	NM_001243.1
P00095.D12	TCTGGGTGATCCTGGTGTTG	CCCACATTGCATCCCTACAG	NM_001243.1
P00103.C01	AAGTGAGCCTCCTTGCCTTG	CCAAATCCACTGTGTGCAGG	NM_001243.1
P00151.H06	ACCCAGAAAGCTGAGAAGCC	TTCCAGAAGCGACAGAGGTG	NM_001243.1
P00166.A04	GTTTGCTTTCTGTCCCACCC	CGCTGTTCTTGGAGAATCC	NM_001243.1
P00974.F02	ACAGCTGCCTCTGGAAAGTG	GTCCCTGGGCAAAGTAAAGC	NM_001243.1
P00900.H09	GCCTGTGGTTGTTTCTCCAG	CCCGATGAGTAAACAGCAGC	NM_001243.1
P00875.D03	ACGTGTTTCGTTTGCATTCC	TAATGGCGATTCTCCTGGAC	NM_001244.1
P00427.F03	GTTACACCATTCAGCAGGG	TAATGGCGATTCTCCTGGAC	NM_001244.1
P00410.F12	TTAAGTGCCTGCCTCCCTTG	TCCTTCCCTGATTTCACAG	NM_001244.1
P00417.E01	TCAGTCCTGAACAGCCCTTG	ATTGGGAGTTGAGTCCTGGC	NM_001244.1
P00419.D07	ACTCTTGGCAATGGGTGAGG	ACGCATGCACACACACACAC	NM_001244.1
P01205.A07	GTTACACCATTCAGCAGGG	AGCAATGTAGTGTGGTGGC	NM_001244.2
P01213.F09	ACGTGTTTCGTTTGCATTCC	TAATGGCGATTCTCCTGGAC	NM_001244.2
P01216.D07	TTAAGTGCCTGCCTCCCTTG	TCCTTCCCTGATTTCACAG	NM_001244.2
P01218.C06	TCAGTCCTGAACAGCCCTTG	ATTGGGAGTTGAGTCCTGGC	NM_001244.2
P01203.F05	ACTCTTGGCAATGGGTGAGG	ACGCATGCACACACACACAC	NM_001244.2
P00678.E03	GCTGCAGGGCTAGATTTGTG	TCATGCTCTCTGTGCGCACTC	NM_001252.1
P01207.H07	AATCAGCAGCAGTGGTCAGG	TCATGCTCTCTGTGCGCACTC	NM_001252.2
P01237.E09	TCCGTTTCCCTCCCTATCTC	CGATTGGGAAACGAAGAAG	NM_001252.2
P01209.B10	TGTGCCTACCTTTCCTATCC	GTGGTCTCCAAGAATGCAGG	NM_001252.2
P01218.D05	TCCTTGTTGGAGATGATGC	TGTGGGCTCCATTCAAAGTG	NM_001295.1
P01220.F12	CACAGCCAGGTCCAAATGTC	AGAAGCCGGGATGGAAACTC	NM_001295.1
P00995.D09	TTAGCCCACTCCCTGAATTG	AGTACCTGCGGCAGTTGTTC	NM_001295.1
P01143.F10	TGTCAATCGTCAGCAGGATG	AGTGCAAAGCTACTGCTCGG	NM_001295.1
P01219.E03	ACCTGTCAATCGTCAGCAGG	AGTGCAAAGCTACTGCTCGG	NM_001295.1
P01221.F08	TTCATATGGCCCGTGCTTAG	TGTGCACCTGGTTAAATGGC	NM_001295.1

P01016.G04	TGAGTCCAAGCCCTTCTCTG	ACCAGCATCATCATTTGGGC	NM_001295.1
P00952.F03	CCAGGTCCAAATGTCTGCTC	CCGGGATGGAACTCCAAAC	NM_001295.1
P01221.F10	TGCTTGAGTCCAAGCCCTTC	CACCAGCATCATCATTTGGG	NM_001295.1
P01236.E12	GAGATGCATCCATGGGCTAC	TCACCCAACCTCAGCTTCACC	NM_001295.1
P00254.B01	TGACCCAGTTTGAATGACGG	TTGCTTCTCTCCACCCAAAC	NM_001296.2
P01188.C03	TGACCCAGTTTGAATGACGG	TTGCTTCTCTCCACCCAAAC	NM_001296.2
P00222.D09	TGACCACAGGCAAACAGCTC	TGGGAGAGACAAAGTGAGGG	NM_001296.2
P01237.H01	TGTTTCCTGGCTCTTTCCAG	TGGGAGAGACAAAGTGAGGG	NM_001296.2
P01175.H01	TGACCACAGGCAAACAGCTC	GTTTGCAGTGCCATTGAGTG	NM_001296.2
P01223.C09	GAATCTGGCCATCTCCAACC	ATAATGAGGCCTGGGCAGTG	NM_001296.2
P01223.B02	TGGTTGTGTCTTGGTGAGGC	AAGGAGGAAGGGAAGAAGCG	NM_001296.2
P00832.H10	TTGTCAGCACCACAACCTTG	GGGACTGACACCCATGTTTC	NM_001337.2
P00856.F12	ACGAGGCTGGTGTAAATCAGG	CCACACGAGTGATGGAGATG	NM_001337.2
P00873.H02	GCCAGGCATTTCCCATACAG	TGGTAGTGTTTGCCCTCACC	NM_001337.2
P00254.F02	TGCCTTTGGAATAGCTCTGG	TGCTCATGGTTCTCCCTTTC	NM_001337.2
P00245.B11	TCCACCCACACAAACCTGAG	CTGTGCTGTGCTTTGCTGAC	NM_001337.2
P01228.A08	TTGATGTTGAAGAGGGCACC	CCTTGTGGGCAGCTAAATGG	NM_001504.1
P01029.D12	AAGGAGCAGCAATGGTGCAG	TCAACTTCTACGCAGGAGCC	NM_001504.1
P01226.D07	AATTATGCCAACCAGCTGCC	GGATGTGGATGCTGCTCTTG	NM_001504.1
P01230.B12	AGCAATGGTGCAGTCCTCAG	TCAGCTTTGACCGCTACCTG	NM_001504.1
P01121.B08	GATGTTGAAGAGGGCACCTG	CTTGTGGGCAGCTAAATGGC	NM_001504.1
P01229.H05	TCCATGAGGATGTCCACCAG	TTCTGCGCAGGCCTTTACAC	NM_001504.1
P00918.E11	ATGAGGATGTCCACCAGCAC	ACCAAGTGCTAAATGACGCC	NM_001504.1
P01242.F11	CAGCACGCCAAGAGTCAAAG	TCTTCTCAAAGGACCTGCCC	NM_001504.1
P00440.G03	CAACTGCCACAATAGGCAGC	CAAGCTGTCCATTCTTCCC	NM_001548.1
P00963.C10	ACACCTGAAAGGCCAGAATG	TTGCCAGGTCTAGATGAGCC	NM_001548.1
P00898.C03	AGGTTCTCCTTGCCCTGAAG	AGTGGCTGATATCTGGGTGC	NM_001548.1
P00457.H12	GCCAGCATATGAAGCCAAGC	ACTGCATGAGGTTTGGAAG	NM_001548.1
P00732.F07	CCACTTTGATCCGAAGGCAC	GGGTGGATGATGAGGTTTGC	NM_001558.1
P01333.E06	AGGCAGATGTCAGCAAGCAG	CCCGTACCAATTTCCATGTG	NM_001558.1
P00871.F07	AATTTCTGGAAGAGCTGGGC	TTCTGCCTACTGCTTGCTGC	NM_001558.1
P00782.C07	ACCACTGTTGATTCCAGCCC	ATGTTGTTGGGAAACACCGC	NM_001558.1
P00689.G11	TGGTTTGAAGGCCAGGTAG	CTGGGCTTCATGCTCACTTC	NM_001558.1
P00981.A06	GAGATGCCTGGTTGATGAGG	TCCAGTGACAAGCTTCCTGC	NM_001558.1
P01318.H12	TTCCAGCTCAGAACCCATCC	TGAGTCCTCAGCCCTGTTTC	NM_001558.1
P00813.E02	AGCAATAGCACAGACAGCGG	TGCCTCGTGCCTAACTTCTG	NM_001558.1
P01108.F04	CTCAGGGTTCCCTTGAAAGC	CAGATGGCTTCCGCACTTAG	NM_001558.1
P01340.F11	ATCTGACTGGAGCTTTGCCC	CTTGGCATGACACCATGGAC	NM_001558.1
P00851.E04	TGCATTAGGAGGAAAGCTGG	TCTGTCAAGGGCGATTCTTC	NM_001558.1
P00885.B06	TGCCAGAGGCTAACAGATCC	TGAGTCCTCAGCCCTGTTTC	NM_001558.1
P00995.C08	TTGGTGATTCAAAGGCAGGC	TTTGAACGCTTGCGCATTG	NM_001562.1
P00780.A05	TGGTGTGACAAGGTGCTGAG	TCACCCATAGGAACCCACTG	NM_001562.1
P01191.G03	TGCCAATTTGTAAGCATCCC	AAGTTGCAGCGTGTGTGTTG	NM_001562.2
P01214.B07	GGTGATTCAAAGGCAGGCTC	TAATGGCACCGATTTGAACG	NM_001562.2
P01212.G10	TGGTGTGACAAGGTGCTGAG	TCACCCATAGGAACCCACTG	NM_001562.2
P01202.C01	CCAAAGGTGTGGCAGATTTTC	TGTGCTGAAGTGTGACCAGG	NM_001562.2
P01343.B03	TGCTGCTCGACTTTCTGGAG	ATGCCTCCCTTAGCAAGACC	NM_001569.2
P01105.E05	TTCCACTCTGCCTGCCTATG	CCGCAGATTATCATCAACCC	NM_001569.2
P01052.E07	TGTTTCCCTTCCCTGTCTGC	ATCATCCAGTGAGGAGGCTG	NM_001569.2
P01090.D12	ATGCTCCCTTATCTCCTGGG	GGGCCAAATGTTTCAGCTCAC	NM_001569.2
P01357.F01	TGATGATAATCTGCGGTGGC	CACACATTTCTTGCTTGCCC	NM_001569.2
P00935.E09	TCAGAGAAGTCCAAGGGCAG	TCCCTGTGATGGGAACAGAG	NM_001569.2
P01134.H10	ATTTGGCCCTGTTCTCTTC	GCCCTTTGGTTCTGTTTGGG	NM_001569.2
P01345.H10	CCCAAACAGAACCAAAGGGC	AAGGCCAGTCCCTTATGTG	NM_001569.2

P01056.H08	TGCTTCTTCTCTACCACCGC	ATGAGAGGCTGACACCCAAG	NM_001569.2
P01098.E04	CGGCAAGGTAAACGAAGTTG	AAGGATGGGCCCTACTGATG	NM_001569.2
P00795.H10	TCAGCCTCTCATCCAGAAGG	AATGCCTTCAAGGACTTCCC	NM_001569.2
P01353.E04	TAGAATCTGCTGGGCTTCGG	TGCTGTGAAGAGGCTGAAGG	NM_001569.2
P01118.G05	AGGTGTGAGGAGTGCTTTGG	CCTTTGATGTAGCGCAGAGC	NM_001569.2
P00985.C09	TGCTTCACTGCAGTCCACTC	TAAGAGGGCCCGTTGTTAG	NM_001569.2
P00739.G03	TCCTTCAGCCTCTTCACAGC	AAGTTGCCATCCTCAGCCTC	NM_001569.2
P00925.C06	TTGTCTCGAATCTTCCCTGG	ACTTCTTGACGAGGTGCCG	NM_001569.2
P01365.F05	TCTTCTTTGGGTCCACCGAG	TAATCAAGGACGATGCCAG	NM_001569.2
P01080.B05	ACAGGCTGTGATGATGTCCC	AACGCATACACTCACGGCTG	NM_001569.2
P01080.D05	ACAGAAATGGGTGGGAAGGG	CACCTTGTCTGGACGTTTG	NM_001657.2
P01275.E05	CAGCTGAATTTGCTTGCTGG	GCTCTGAAACCATCTTGCCC	NM_001657.2
P01271.B05	ATCTGGGTGTTGGAGCATTG	ATGTGCTAGCTGCTTGTGGG	NM_001657.2
P01169.G07	TGACAAGGCGTGTCTTCTTG	TTGTCCTTGCTTGCTATGCC	NM_001657.2
P00952.B03	TCTCCAATTGTGCATGGCAG	ACGTTCACTTCCAAGGCCAC	NM_001657.2
P00906.E08	TGAAAGAGGAACTCAAGCCG	GTGATGGGCAGTGAGTTTGC	NM_001657.2
P01373.E07	ACCCAGGGCTTAAGGAATGC	CTCCAAGAAGGCACATGACG	NM_001729.1
P00757.D10	CTCATTCTGTGTGCCTGTGG	AGCTGCAAAGTGCCTTGCTC	NM_001729.1
P01126.B01	TCAGGAGGAAAGTGTGCGTC	AGCAGCTGGCTCAACAAATG	NM_001729.1
P00899.H08	TCCGGTGTCCAATAACCTTG	CGGTACAGAAGAGTTTGGCG	NM_001735.1
P00419.H07	TATGGAGAGGGCAATGGACG	AGAAGAGTTTGGCGGACAGC	NM_001735.1
P00422.G06	TATCAAGGGAGCTGGTGTGG	GGGCAGCCTAAGAAATCAGC	NM_001735.1
P00427.C08	GGGAACCATCCGATGCTATG	TTGGCCAGGGCTAATGATTC	NM_001735.1
P00421.C09	TGGGAAAGTATCCTGGCTGG	CACCATCGAGAGGGTTGTTG	NM_001735.1
P00401.B06	ATGGTGTTTCCCTGCCTCTG	CTTCCCAGGACAGCCAATTC	NM_001735.1
P00422.C06	TATGAATTGGCTGTCCTGGG	ATCACATCCCTGCATTGTGC	NM_001735.1
P00426.F01	AATTGGCTGTCCTGGGAAGG	ATCTGGATCCTCTCATGCGG	NM_001735.1
P00428.C11	CAATGCAGGGATGTGATCTG	GGGAGATGTTCCGGATGTCAC	NM_001735.1
P00415.C02	GGCCTCGGTATTTAGTTGGG	TCTTCCTCCCTCCAACATCC	NM_001735.1
P00410.H11	CAAGGTCCCAGATTGGAAGG	AGGTGCCCAGATTTGACTGC	NM_001735.1
P00424.H05	TGACACCAACCAGAAGTGGC	GGCACACAGGATGCTGATTC	NM_001735.1
P00413.D08	TCTGCATGTATGACCAGGGC	TTCTTCCACCTCCACAATGG	NM_001735.1
P00427.G10	CGTTGTGGAGAAGGAGCATC	TAGCATGGTTGGGCACTTTG	NM_001735.1
P00425.C11	AGGACTCCAAAGTGCCCAAC	CTCGGAGGGATTTGCTTCAC	NM_001735.1
P00415.F05	TTCTTCCATCCCAGTCCCAG	TGGAGGTAGATGGGCAAGTG	NM_001735.1
P00419.A01	TCCCACTCTTTCCCTTCCTG	GGGATGAACCCAATCCTCTC	NM_001735.1
P00419.F09	TAGAACTTCCCGCATGGAGC	AAGGCACCTGCATTCCAAAC	NM_001735.1
P00413.G07	CTCTGTGGCCAGCATTGAAC	TTGCCATGTTCTCTTGACGC	NM_001735.1
P00406.D06	AATCAGGCCGTTGGAAGAAG	TTCTGTCTTTGGGCAAGCTG	NM_001735.1
P00421.C10	AGGGAAGCAGGAGCAATGAG	TTTGTGCAAAGCACATTCCC	NM_001735.1
P00422.E11	ATGCATGGGAATGTGCTTTG	GTATTTGAGTCTGGGCACG	NM_001735.1
P00995.E12	TGGAATTCCACAGCACATGG	TCACTGACTGGGAGCTTGTG	NM_001735.1
P01252.A09	TACCTGCATCCCAGAAGTCC	CATGCATCACTTTGCTTCCC	NM_001735.1
P00425.C03	GCAAGTGCTCTTGATGACGC	ATAGGGAGGCTATTGCAGGG	NM_001735.1
P00416.D01	AAATAAAGGCCCAAAGGTGC	TGGAGAACGAATAAGCCTG	NM_001735.1
P00404.F04	GGATTGACCTGTGCTTTGGG	AACATGGTTCCCTTCATCCCG	NM_001735.1
P00421.B10	TCCACTGCTGCTAATGCCAC	TTTCTTTCCCTCCCTCCCTC	NM_001735.1
P00416.C05	GCTACGGAATTGGAACAGGC	TTCCGCCATAGCCCATATC	NM_001735.1
P00424.F02	TCTGGCCCAGTTTCATTGTG	TATTCCCAGAAGCGATTGCC	NM_001735.1
P00406.E06	TGAAGTCATTGCCAAGGCTG	TTCTTGGCATCCTTCCTCAG	NM_001735.1
P00412.A05	AATGGTCAAGGCAGAGAGCC	TTAAGGGCGGAAGTACGCTG	NM_001735.1
P00429.H06	AGCGCCCTAATCTCAGTTCC	AAAGTGTGCCATGATTTGGG	NM_001735.1
P00429.E10	CCTAAAGGCCAAAGGGAAGCC	TGGTGATGACGATGATGACG	NM_001735.1
P00426.H01	GCTGCCTCATCTTCATCTGG	TCTGCCCTCAGTTAATTCGC	NM_001735.1

P00419.C05	GCAAGGAACAAGACCACACC	GCCTCACTTATGTTGCCTGC	NM_001735.1
P00424.H01	GGAGTTCAATGCACAGCGTC	TTTGAGCATCAGCAACACCC	NM_001735.1
P00420.G12	TTTGATTGGCTATTCTGCC	GGTTTCACAAAGGGAATGGG	NM_001735.1
P00426.A09	CAATTGCTGCAGAGGAGCAG	TGGACCTGCCAGATGTATGC	NM_001735.1
P01017.C02	GCTGAAACTGGATGAGGCAG	ATGCTTGAGACGAAGGATGG	NM_001768.2
P00822.H10	GGCGTTTGTCTGTGTCCAG	ACGCTCTGTTGCTCTTGACG	NM_001768.2
P00897.D02	ACGCCGACATTTAGGAGAGG	TTCAAGCCTCTTAGCGCACC	NM_001768.2
P01359.B02	TTCCTGGGAGAAGGGATAGC	GAAGGCAAAGGAAGGGACAC	NM_001768.2
P01093.A07	AAGAGGCTTGAAAGCAGGGC	TTTGGTCTCCCTTCACCCAC	NM_001768.2
P00408.E12	TTGCTGGACAGTGCCAGTTC	CCAGTTGCTTGGTCTGCTTG	NM_001782.1
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P00408.D06	CTCGAAGGATGGAGAAACGC	CCAAAGGCTGGCAGAGATTC	NM_001782.1
P00419.H08	TCCAGGAACCTGTCAAGCAG	AAATTGGAGAGGGACGGAGG	NM_001782.1
P00411.A06	TGCAGCTTGGTCCTTCTCTC	CTTTGGGTTTGGTTTCCAGC	NM_001782.1
P00403.H07	TTGGCCACAGAGATTTGGTG	ACAGAAACCACCATGCTTGC	NM_001782.1
P00408.C02	GGGTGTTCCAGAATCAGTGC	TTGGAGCCGACAGATAAGGG	NM_001782.1
P00407.A09	TTTCTAAGAACCGCCCTCC	TGGATGACAGGGAAGACGAG	NM_001782.1
P00405.B05	GAAGAAGCCAAGCTTGAGGG	TGCATGGAGAGGAAGCACAG	NM_001782.1
P01204.A12	CTGCTCGTTATGGCCATCTG	TCTGCAATTTCAAGGATGGG	NM_001837.1
P01221.B11	CCATTTTCGGACCTGCTCTTC	ATGGGATGTATCTGCCCAGG	NM_001837.1
P00251.A09	GCCGGGTCATGCTAACTTTG	TCTGCAATTTCAAGGATGGG	NM_001837.1
P00854.F12	CTGCTCAACCTGGCCATTTT	GGAATGGGATGTATCTGCCC	NM_001837.1
P01219.C12	GCCGGGTCATGCTAACTTTG	CAGATGGCCATAACGAGCAG	NM_001837.1
P01196.A05	AGGATCAGCATGTCCGTTTC	TTTGCAAGCTCATCTTTGCC	NM_001838.1
P01188.H05	TTGAGGTAGCTGGGATTGGG	CCATGGAGAGGAAATGGTGC	NM_001838.1
P01195.D07	AACAGAAAGCTCATGGCCAGC	GTCCTGCTGATTGGGATCTG	NM_001838.1
P01189.A03	ACCTTTCAGCCTCTTGGTCC	CGGACGATTACATCGGAGAC	NM_001838.1
P01196.B12	TAAGAAACGAGGCCTGGGAG	TCCATCATTTGTTTCGTGGG	NM_001838.1
P01238.E03	AACATCTGTGGCTCTCCAGG	TGATGCTGCTTCTTTCCAGG	NM_001838.1
P00421.G11	TTTCCCTGGCAGCAACTCTG	TCCTGGTCCCTTGCTATCTGG	NM_001842.3
P00410.E04	TTTGGTGGGTGGGTAGCTG	TCCTGGTCCCTTGCTATCTGG	NM_001842.3
P00410.F03	GCAGATCCTGTTTCCAAGG	TGTAGGCACAGGGCAAAGAC	NM_001842.3
P00408.E03	TGTGTTCCCGCTGCACTAAC	TGGGATGATGGGATGATGAG	NM_001842.3
P00407.A06	ATGATCGAAAGAGCTGCTGG	CCCACCTACATTCCCAACAC	NM_001842.3
P00408.H06	TGATGGTGGAGAACAGGTGC	GATTGATGAGTTGAGGCCCG	NM_001842.3
P00407.A07	TGTGGGCAAATTGTCTAGGG	TTGCACAGGCATAGAGGAGC	NM_001842.3
P00407.E03	AGAGACACCGTCAGCATTCTG	GCAAACCACCATAGGTTGCC	NM_001842.3
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P01307.C10	AAGGGCAGAAGAACTGGGAG	CCGTTGCAAACCTGGAGACAG	NM_001926.2
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P00272.C01	TGTGACACAGGAGCGACAAG	TGGTGAAGTTGACAGGGAGC	NM_002006.2
P01186.C02	AGTGAGCAAATCTGCCCTGC	TGTGGAAGTTTCCAGGAGGC	NM_002006.2
P01186.A08	TGGCACCAGTGGATAGTGTG	GAAACTCTGGGAACCATGCC	NM_002006.2
P01186.G06	ATGCAAATTTGTGTGGCAGG	AAACTGCCGTTGGCATTAGC	NM_002006.2
P01187.B08	GCTCCAGGATTTGTGTGCTG	TCCATCTTGAGGTGGAAGGG	NM_002006.2
P01191.B03	GCTGAACCCAACATCACTGC	CACAGCACATGGGAATTGAG	NM_002006.2
P01191.C12	AAAGGCAAAGTCCCTCCCTC	CCTCCAAGTAGCAGCCAAAG	NM_002006.2
P01186.G12	CTCAATTCCCATGTGCTGTG	CAGTCTGCAGGTTTGCAAGG	NM_002006.2
P01191.D11	TCTGCTGGTGATGGGAGTTG	AGCAGGGCAGATTTGCTCAC	NM_002006.2
P01186.B07	TCACATGCTCTGCTCTCACG	GAAACTCTGGGAACCATGCC	NM_002006.2
P01186.B11	TCCTGGTGTTCCTCTGAC	TGTGGAAGTTTCCAGGAGGC	NM_002006.2
P00862.C03	CTGTAAACGACCTTCGCGTC	GACTTGGGCATTGAGATTGG	NM_002163.1
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P00746.B02	GGCTTGGGTCTTTCCACATC	AGGGAGGCCCTACAAATGTC	NM_002163.1
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P00772.G05	CATCTGCATGTGGCTCGTTG	CCTCATGTTGGGAAACCAGG	NM_002163.1
P00782.D08	GAGGTGGGAAGGAAATGTGG	CTGACCAAATGGTGAGGAGG	NM_002163.1
P01392.C03	TCGAAACATCGTTTGCCCTC	GGGATTCTCAGGGCTTATG	NM_002163.1
P00882.B11	TGGAGAGGCGTTCAAACGAG	TATTGAAGGTCTTGCCCAGG	NM_002163.1
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P00429.B10	TGCCTCTATCTGCGTTCTGC	TGTGAGTGAGATGGTGCTGG	NM_002169.1
P00429.C10	CCCAAGCTTTCACTTCATGG	TTCTCGGGATTTGATCCAGG	NM_002175.1
P00310.B02	TCGCAGCATCACTACCAATG	TACCACAACATGTGGCCTGG	NM_002184.1
P00304.C04	TGGACTGACGGAACCTTGGTG	TACCACAACATGTGGCCTGG	NM_002184.1
P00310.G08	TGTGGCCGAGTGTAACAACC	GCTATGCGGCCAGGTTAATG	NM_002184.1
P00299.C01	TTCAAGGATGGAAGGCCAAC	TATTGGCCTCAGGAGACACC	NM_002184.1
P00291.C08	TCTGTGTATGCTGCCATTCTG	ATGCTGATGGACCAGGAAGC	NM_002184.1
P00299.E08	TCTGTGTATGCTGCCATTCTG	TCGTCCTTGCTCCTTAGGCTG	NM_002184.1
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P00310.B03	TAAATAGGTGCGATGCACGG	ATGCAATTGGAGGGCAAGAG	NM_002184.1
P00304.C02	GCTGCATCTGATTTGCCAAC	CAGTGCCAGCACACAAACAG	NM_002184.1
P00306.C05	ATTCCAGGATCAACCGCTTC	AGCTGACCGGCTTCTTTCAG	NM_002184.1
P00306.H07	AGCCCAATTCCCTAACAAGC	GCCCTTGGGAAGGTTACATC	NM_002184.1
P00312.B04	AAATTATGTGGCGGATTGGG	GTGGTTTCGGGTGTTGTCAG	NM_002184.1
P00307.C10	AGGCTGACAACACCCGAAAC	TCCAACGAGTTTGGGAAAGC	NM_002184.1
P00302.F05	TTGCTTTCCCAAACCTCGTTG	TGGAGGGACAGGATACGTTG	NM_002184.1
P00302.G09	TGGTAGTGTGCCGAAAGGAG	TGCATTAGGTGTGGGTGAGC	NM_002184.1
P00291.G01	GTTCTTGAAGGGCGTTCTGC	TGGAACATTCCGCTCTTTCC	NM_002184.1
P00296.A11	TGCAGGGAATATCCAGGAGG	TTGGTGTGGAGGCAATTGAG	NM_002185.1
P00295.B01	AGGCAAGGGAAAGTGACCTC	TGAAGTTGGGAGGGATGTGG	NM_002185.1
P00674.C08	GTTCAACCAAGGGAAGCCAAC	ATGGATGACAGGAAGCCCAG	NM_002185.1
P00295.B09	TGAGACGAGGTGCAAGGTTCT	TGCATCAGGGAAGATCCAGG	NM_002185.1
P00285.G09	TGTGGAAAGGGAGATCCTGG	GCAAAGACAGCAGGCAAGTC	NM_002185.1
P00282.D12	CTGGTCACCCAAGTCAATGC	GGGACAGCGTTTGCCTAATG	NM_002185.1
P00286.H10	CAAGCCTTGGTGTTCCCTTCC	CAGAATTGCCAGCATGTTCC	NM_002185.1
P00962.G05	CAGGGAGAGTGGCAAGAATG	GTTTGGCACTCAAGAATGGG	NM_002185.1
P00303.D09	CATCCAGTGGCCAAGAATG	AGAAAGGCACATGGCTCAGG	NM_002185.1
P01331.D10	GAAAGCTGCAAACCAGAGGG	TGGCCGATGCCTTAGAGAAC	NM_002186.1
P00598.D12	AGCTGCCCTTATCTTCAGCC	TATGACCCACCATGTGGCAG	NM_002186.1
P00593.D03	GGTGTGTTGTTTCTCCCTGC	TGCCTGTGTGTGCCTATGTG	NM_002186.1
P00589.B09	AAACACAGGAGCACTACCCC	TTTCTGGACCAGTCTCCCAG	NM_002186.1
P00595.C03	TCCTGGTATGACCGAAGTGC	CTCAGGATCGATTGCCACTG	NM_002186.1
P00592.B08	CCAGACACGCATTTGGAAG	TCCCTTCCTTCACCCCTCTTG	NM_002186.1
P00589.G12	TCAAGAGGGTGAAGGAAGGG	GGTCAATCGGCCTTTCTGAG	NM_002186.1
P01000.F06	CAGGTTGCTTTAGCTGGTGG	CAACTGAGGCCCAAGTATGC	NM_002186.1
P01011.G02	AGTCTTCTCGGCAGATGTGG	AATGTTGTTGGTGAGGCAGG	NM_002186.1
P00700.C07	TCCTTCACTCTCTTGACGCC	TTGTCAGATGGCACGAGCAC	NM_002186.1
P00784.H11	CATTCTCAGGATCGATTGCC	TCACAGTCTGCTGCTGGAAG	NM_002186.1
P00772.B12	AGTCATTGCTGTCCTGTCCC	CACTCACACAAATGCAAGGC	NM_002186.1
P00698.A05	GTGTGTGCACGTGAATGTGG	TGGCAGGTGTTTCTGTCTCTC	NM_002186.1
P00755.G07	CTTGTGGCAGATGGGAAGAG	TTGATCTCGGTGACTCTGGG	NM_002186.1
P01336.D04	TTACAAGACAGGGTGCAGGG	GTGGTGCCATCATGTGATCC	NM_002186.1
P01393.E01	GGCACATGGAGGAAAGACAG	TCAGTTTCTTGAGCAAGGG	NM_002186.1
P00609.A12	TCCAGCCATCAACACTTTTG	TGTACCTTGGTTCAGGCTGC	NM_002186.1
P01147.A07	TATCTCTTGC GTTCCCATCC	AGCACCCAGTTGCCAGAATC	NM_002187.1
P01012.E07	GCTGTTAAGAAGCCACCTGC	TTTCCAGCTCTCAAGTTGCC	NM_002187.1
P00307.G01	CACAATGCAGTTCAGTGCCC	CACCCAGTTGCCAGAATCAG	NM_002187.1

P00291.D09	CATGCTTGCCAGAGGCTTTC	GGCCAAACGATTTCTCCCTC	NM_002187.1
P00296.B06	GGTTGGGCTACTGTCCAATG	CAGAGGTGCCTCACATTTGC	NM_002187.1
P00306.B11	TGGCAGCTGAATCAAAGTGC	ATCATCACCGAAGCAAACCC	NM_002187.1
P00281.E01	TAGACAAGGAAGGGCGGTTG	TCTGCCAGGCATGTTAGGTG	NM_002187.1
P00287.F07	ACCCAAAGGGTCCAGGAAAG	GTCAATGAGTCGATGGCAGC	NM_002187.1
P00295.D06	ATCACAGTGCCAACTGAGGG	ATTTGCTCCTAGGAAGCGGG	NM_002187.1
P01187.G02	CACAATGCAGTTCAGTGCCC	CACCCAGTTGCCAGAATCAG	NM_002187.2
P01187.G01	CACAATGCAGTTCAGTGCCC	CACCCAGTTGCCAGAATCAG	NM_002187.2
P01187.G03	CACAATGCAGTTCAGTGCCC	CACCCAGTTGCCAGAATCAG	NM_002187.2
P01221.E07	CATGCTTGCCAGAGGCTTTC	GGCCAAACGATTTCTCCCTC	NM_002187.2
P01216.B02	GGTTGGGCTACTGTCCAATG	CAGAGGTGCCTCACATTTGC	NM_002187.2
P01192.G11	TGGCAGCTGAATCAAAGTGC	ATCATCACCGAAGCAAACCC	NM_002187.2
P01234.D09	TAGACAAGGAAGGGCGGTTG	TCTGCCAGGCATGTTAGGTG	NM_002187.2
P01218.A01	ACCCAAAGGGTCCAGGAAAG	GTCAATGAGTCGATGGCAGC	NM_002187.2
P01216.C05	ATCACAGTGCCAACTGAGGG	ATTTGCTCCTAGGAAGCGGG	NM_002187.2
P01217.D11	TTAAGGAATGCACGAAAGGC	TCTGTGGAACCCAGGGAATC	NM_002187.2
P00289.C11	CCCACCCAGATCTTGGAAC	CAAATGCCACATGGTTCTGG	NM_002188.1
P00285.A11	GCATGCAGCTTGTCCCTTAC	GTTGATCAGGGATTCCAGGG	NM_002188.1
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P01049.D04	AAATGTCTTGGGTAGGCGGG	GGGAGCTAGCTTGCATTGAG	NM_002188.1
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P01091.H08	TAGAAGCCCAAACGCTGGTG	GGTGAGTCTTTGGTGGATGG	NM_002189.1
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P00433.C09	TGAAGAGCTGACCTTGAGCC	TCTGTGGAATGGAGGAGCTG	NM_002189.1
P00433.B05	GAAAGCCACGGAGAAAGAGG	TATGGCCCTTCCAGAGGAAC	NM_002189.1
P00445.G12	GGGATGTGCTGGTGTGTTAGG	TATCTTTGCATTGCGGTGGG	NM_002189.1
P00446.G01	TGCCAGCATCGTCTCAAATC	AAGGCTTCTGGGTGAGGATG	NM_002189.1
P00442.C05	TGTCTCCAAACTGCTGGACG	ACTTTGCCCACTCTCTTCGC	NM_002189.1
P00998.E11	TAAATGCAAAGGCCAAGAGC	CATGTCTATGGCCTTCAGGG	NM_002198.1
P00310.E02	TCACCTATGGCACATGCCTC	TGAGAGGAGCTGGCTCATTG	NM_002198.1
P00816.F09	TCACACTTGGCTGTTGAGGG	TGAGAGGAGCTGGCTCATTG	NM_002198.1
P00281.H09	AAACCTTAAGGCATGGCAGC	CCAACATGCATTTCTGCCTC	NM_002198.1
P00285.B05	GCATTTCCCGAACTAGCAGG	TGGCTTCAGGGTTTGAGAGG	NM_002198.1
P00288.F01	AGCCTCTCAAACCCTGAAGC	TTCCAGGCTACATGCAGGAC	NM_002198.1
P00283.H05	AGTTTGCAAGACATCGAGCG	TGCTTCCACCTCTCACCAAG	NM_002198.1
P00282.C08	TCCTGCATGTAGCCTGGAAC	TTTCGCTGTGCCATGAACTC	NM_002198.1
P00285.G10	CAGGCCACCTTAGCATTTTC	AAGCCTGGGCATTTGAGAAG	NM_002198.1
P00281.F07	AACACAAGTCTGCCACCAGC	ATGCTGCAGCTCATCCAAAC	NM_002198.1
P00285.E07	GCTGGAAAGTCTTGCTGCTG	TCACTTGCATGCCTGTCTCC	NM_002198.1
P00292.H11	TCTCCGTAGGTCACGATTCC	TTCCGCGCTAGCTCTACAAC	NM_002198.1
P01390.H06	TGCGCATGATGTGAAGTGAC	AAACCCACGACGACAGTGAC	NM_002255.2
P01317.B01	AATCCAGTCCAGTCTTCCC	TTCAACATCAGGCAACGGTC	NM_002255.2
P01313.D12	CAGACCGTTGCCTGATTGTG	CATGGAATGACTCTGCCAGC	NM_002255.2
P00765.B04	CAGACCGTTGCCTGATTGTG	GGTTTGAGACAGGGCTGTTG	NM_002255.2
P01319.B06	AATCCAGTCCAGTCTTCCC	CAATCAGGCAATGGTCTGTG	NM_002255.2
P01323.A10	CGTGGGTGCTTGTCTTAAAG	TCCTCAGTGTGATTGCAGCC	NM_002255.2
P01319.B07	TCCTCACTGGCAGGAAAGTC	ACAAATGAGGCTCCACCCTG	NM_002255.2
P00696.B07	CCAACCCATCTTCATGTCCC	GAACAAGGTTGCAATCACGG	NM_002288.2
P00972.F09	TGCCCAAGCATCTTGTCTCC	TCTACCCAGCATTCAGGAGC	NM_002447.1
P01004.E02	CTACGAGGGCGACAGAAATG	CCTTGCCAGTCACAAAGACC	NM_002447.1
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P00241.G03	TCTTGCGGAGCTGAGACTTC	TCTGTGATCCCACAACCCTG	NM_002447.1
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P00238.G08	ACACGCCTTGACAACGTCAC	AGAAGTTGGAGCCACACAGG	NM_002447.1
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P00226.A12	GAGCTTTCATGTGCCCTTCC	TCAGTCCCATTGACCAGCAC	NM_002447.1
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P00225.A03	TTCCCTCCTTACCCTCTTGG	TGCAGCTCAGGGAACATC	NM_002447.1
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P00221.H07	TATCAACGTGACCGTGGGTG	GAGAATCCTTGGTGGCTTGG	NM_002447.1
P00222.E05	TTGGTATCCTGCTGCCTTTG	AGCTGGATGGACTCTTTCCG	NM_002447.1
P00233.H07	CCAAGCCACCAAGGATTCTC	TCCAAGTGTCCCTTTAGCCC	NM_002447.1
P01183.F06	AGCTTGGAAGCCAAGCCAC	CAAACAGCAGCCACTTGATG	NM_002447.1
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P00223.D08	AGAAGATGGGAAGGCAGAGG	ACTCTCACATGCAGTTCCGC	NM_002447.1
P00233.G11	ATCATGTTGCCACCTGAGGG	TGAACCCACCTGTTCTAGGC	NM_002447.1
P00240.F02	GCAGAAGTTTGTGCACAGGG	CAGCTGGAATGGAAGACCC	NM_002447.1
P00230.E03	AATGATCTGAGCCCAGGGAG	ACCATGGCAACTGTGAGGTC	NM_002447.1
P00930.H07	TAGTTCTTGGGCTGGACCTG	CCTTGCTGCTGGCTTATCTC	NM_002447.1
P00245.B07	AGCACTTCACAGGCATCAGC	GGCTACAAGCGCAATCAATG	NM_002447.1
P00954.G03	AGATTCCTTGAGAGCCAGC	CAACAGTTCGCGCAGGATTC	NM_002975.1
P01042.H10	CTGGAACCTTGGGTGCCAAG	AGACAGGGATCATGCTGGAG	NM_002975.1
P01035.D11	ACTGCCAAGTGGCCTTTCAG	AGAGCAGGAAGCACTTGTGG	NM_002975.1
P00630.H04	AGCCAAATCTGGAGGCAGAG	TCCTGGTGGCTTTGGCTGTTC	NM_002981.1
P00636.B01	CAGGAAACACAAGCCACTGC	TGGAATCCTCGAACAATTCC	NM_002981.1
P00628.F04	TCACAGGTTCCCTTCCTTGG	TTTGCTTCCCACTCAACCAG	NM_002981.1
P00693.A12	TCCTGGAAATCCACAGGATG	AGAGCTGGAATCCTGGAAGG	NM_002982.1
P01082.C11	AGGGAAACTCATGACCAGGC	CCTGAACCCACTTCTGCTTG	NM_002982.1
P00624.B01	TCCAAGGCAAGATCCAGATG	GTATGGATGCACCCAGCAAC	NM_002986.1
P00620.H01	TGCTGAAGACACAGGACAGC	GTTGCTGCTCTTAAAGGCC	NM_002986.1
P00647.A01	TGCCTGGGAGATTGCTGTAG	CCCACCCAACTGGGTAAATG	NM_002986.1
P01166.A04	AACCAGAGCCTGAGTGTTGC	CCCAACTGGGTAAATGCAGC	NM_002986.1
P00590.C05	GTTGAGTGCCATTCTCTGG	AAGATGTGCTCGCCTTGGTC	NM_002987.1
P00607.C06	ATGCACACCCACAAACACAC	TCTTCTTCGTCCCTGGAAGG	NM_002987.1
P00608.A05	CAGGGATGCCATCGTGTAAG	AGTTTGTCTCAGCTCCACG	NM_002987.1
P00414.G11	ACCTCTCCATTGGCAGGATG	ATGTGCAGACCCAAAGGAGC	NM_002989.2
P00411.A11	CCTCCTTCTTGCATCTTGGG	ATCCTGGTTCTGGCCTTTGG	NM_002989.2
P00408.G04	ACCTCTTGCAGCCTTTGGAG	AAATAGCAGGCCAATCCCAG	NM_002989.2
P00405.G01	TCACAGGATAGCTGGGATGG	GCCTGCATGAAAGCAGTAGC	NM_002989.2
P00126.C11	AAAGGCCACAAGGCGTTAGG	TACATCCTCTGGTGCATCCC	NM_002995.1
P00132.G10	TGGCCATCTTTCCTTTCAGC	TAATCGCTATTTCGTTGGGC	NM_002995.1
P00159.D01	TGCACAACCTACATGGTCCC	AGCACTGCCCATATCCTTCC	NM_002995.1
P01104.E02	AGCCAGCCAGCTCATTTTAC	AAGGCAAGGTCAGGTCTTCC	NM_002995.1
P01035.G07	TTCCCATCTGAGGGTCCAC	CTGCCCATATCCTTCCACAC	NM_002995.1
P00558.F11	GCGGAAGTCAATGAGGAAGG	AAAGGATTACAAGCTGGGC	NM_003300.2
P00547.E11	TTCTCCCATGGCTTCCTATG	ATGACGGAAGTGACCCAACC	NM_003300.2
P00558.C04	ACCATAATGGCCACCTGCTC	TCAGGACGCACACATGGAAG	NM_003300.2
P00555.H05	AGCAAAGGGACACTGGAACC	GGCCTGTGGAACGGAATATC	NM_003300.2
P00556.H08	TGGAGATACCTGTGGCATCC	GTGAGACGTGCAACCTTTGG	NM_003300.2
P00556.G11	TGTGTGACCCAGTTGCATTC	TCACACTACATGTGCGGCAG	NM_003300.2
P00553.F02	TCCTTAGGCGCAGAGATTCC	TATGTGGAGAGCGCACCAAG	NM_003300.2
P00556.A10	TCTGAAATTCAATCAGCCGC	ATCAAAGGCATGGAAGAGGG	NM_003300.2
P00546.H01	GCACAAGCACTTGATCCCAG	GCGGGAAACGTTTGTCTTTG	NM_003300.2
P00139.D09	CATGGACCCAAACAATCCTC	AGTTTGGCAGAAATGCGGAC	NM_003326.1
P00127.A08	AAAGGAGAGACAGAAGGGCG	GATAAGAACCTTGGGCCAGC	NM_003326.1

P01202.G10	CATGGACCCAAACAATCCTC	AGTTTGGCAGAAATGCGGAC	NM_003326.2
P01217.E05	AAAGGAGAGACAGAAGGGCG	GATAAGAACCTTGGGCCAGC	NM_003326.2
P00937.A01	GGTAACCCATGACCAGGATG	ACACTCCCGCCCAATATACC	NM_003467.1
P01204.A11	TGCTGAAATCAACCCACTCC	GCAAGGCAGTCCATGTCATC	NM_003467.1
P00214.D10	ACAAATAGGTGCTGGCTGGC	ACACTCCCGCCCAATATACC	NM_003467.1
P01218.G08	TGCCACAATGCCAGTTAAG	ATGGCAAGAGACCCACACAC	NM_003467.1
P01219.H05	GGATGACAATACCAGGCAGG	TTCTCTTGTGCCCTTAGCCC	NM_003467.1
P00817.E10	CCATGATGTGCTGAAACTGG	TTGTGCCCTTAGCCCCTACTAC	NM_003467.1
P01213.A10	ACAAATAGGTGCTGGCTGGC	GGAAAGCGAGGTGGACATTC	NM_003467.1
P01227.D10	AAGATTCCAATCCTGCTCCC	TTACCTCCTGAATGGGCTGC	NM_003467.1
P00186.D06	AAGATTCCAATCCTGCTCCC	TTACCTCCTGAATGGGCTGC	NM_003467.1
P01348.E09	TTCGCAACTACAGGAGGCAG	AGGTGTCAGAAACCAGCCAC	NM_003581.1
P00996.B01	ACCGTCATGGAGAAGTGCAG	AATCACTCGGGCCTTCTACG	NM_003581.1
P01029.C03	TTCGCAACTACAGGAGGCAG	TCCCTAATGAGGAAGTCGCC	NM_003581.1
P01339.G11	TTGAGCAGTCAGGGCAACAC	CTTTATTGCAAGCACAGCCC	NM_003581.1
P00535.F12	AGACAGCTGAGGATGGCAAG	AGATTCAAACCCATCGTCCG	NM_003701.2
P01231.F01	AGACAGCTGAGGATGGCAAG	AGATTCAAACCCATCGTCCG	NM_003701.2
P01233.E07	AACTGTGCCTTGTCCTGTGG	TGCATGAACGTCCCTGATTG	NM_003701.2
P00532.D10	AACTGTGCCTTGTCCTGTGG	TGCATGAACGTCCCTGATTG	NM_003701.2
P00533.G11	TCGTTCTCTTTCCTGTGGGC	TACCAGATGGGATGTCGGTG	NM_003701.2
P01213.H04	TCGTTCTCTTTCCTGTGGGC	TACCAGATGGGATGTCGGTG	NM_003701.2
P00536.F06	TCGTTCTCTTTCCTGTGGGC	TGTCCTTCCAGGTTACAGGC	NM_003701.2
P01185.C12	GTTTCTGGCTTCTGCTCCAG	GTTACAGGCTTTCAGCTGGC	NM_003701.2
P00542.H12	TATAGACGCCTTGAGGGCAG	TTGGCCAATGATTGAGTTCC	NM_003701.2
P00875.G10	GCGTATTTACAGCCAGTGGG	AAAGGTACAATTTGCGGCAC	NM_003701.2
P01198.D02	TTCGCAGCTGAAGTGGAGAG	AACCAACCTGGGTCAGACAG	NM_003701.2
P01212.C12	CAAGTGCCGCAAATTGTACC	TTGGCCAATGATTGAGTTCC	NM_003701.2
P01213.B09	GCGTATTTACAGCCAGTGGG	AAAGGTACAATTTGCGGCAC	NM_003701.2
P01200.F09	CCCTGATGAAAGGAGGAAGC	TTGACAGATTTCAAGTGGCCC	NM_003701.2
P01215.G12	TATAGACGCCTTGAGGGCAG	CCCGTAATTGCTCCAATCTG	NM_003701.2
P01018.C12	CAAGTGCCGCAAATTGTACC	GGCCAATGATTGAGTTCCAC	NM_003701.2
P00826.D09	GGGAAGGCAATCAACTCTGC	ATGCGCTGCGAAATCTGAAG	NM_003789.1
P01393.C06	ACCCACAAGCCTTCCTCAAG	GAAATCTGAAGTGC GGCTCG	NM_003789.1
P01363.B01	CAATAGCCGCAGAAGGAACC	TCTGTGCTTCAAGTCCCTC	NM_003789.1
P00814.D06	AGGTCATGCCACAAGCAAAG	AGGATATGGGTCTGGTTGGC	NM_003789.1
P01107.C04	AAAGCCTGTGACTCCTTGCG	ATGTTCCCATATCTTCCGGG	NM_003789.1
P01196.E05	GTGGATGAAGTTTCCACCC	ACGCACACATGCACACACAC	NM_003807.2
P01196.E09	GTGGATGAAGTTTCCACCC	ACGCACACATGCACACACAC	NM_003807.2
P01220.B05	AAACCAAGAAACCAAAGCGG	TTTGCACAACCTGGCCAAATC	NM_003807.2
P01195.B10	AAAGCCAGCCTCCTAAAGGG	TCCATGTGTCCAGCCATCTC	NM_003807.2
P01208.F01	TGTTGGGCACACATAGACCC	ATCCAAGAAGGGAAAGCTGG	NM_003807.2
P01223.D05	ATTGCTCAACACTCCTGGGC	GCATGCAGACAAGCACACAC	NM_003807.2
P00643.F11	TGGTCCTCCTCAGATGCTTG	TTACACACACCCCTGCACAC	NM_003809.1
P00638.G09	TTTGATCACACACAGCGTCC	AGACCCTGCATTCAATTGGC	NM_003809.1
P00620.H02	CTGCGTTGGTTGTGTGTGTG	TCTAACTCATGGCCACCCTG	NM_003809.1
P00636.D08	TGGATGTGCTCCTCAGACC	GCTGGGACAGTGATTTGCTG	NM_003809.1
P00616.A05	TTTCCTTGATCCTCAGCACC	GCTGGGACAGTGATTTGCTG	NM_003809.1
P00625.A12	TCTGCCCTGAATGTCTCTGG	ACCAGCAAGTCCAGCTTCAG	NM_003809.1
P00648.C02	CATCTGGCTGCATGGGTAAC	GACGAAGAGACAAAGCAGCG	NM_003809.1
P01211.A09	TGGTCCTCCTCAGATGCTTG	TTACACACACCCCTGCACAC	NM_003809.2
P01231.E04	TTTGATCACACACAGCGTCC	AGACCCTGCATTCAATTGGC	NM_003809.2
P01239.H12	CTGCGTTGGTTGTGTGTGTG	TCTAACTCATGGCCACCCTG	NM_003809.2
P01225.E06	TGGATGTGCTCCTCAGACC	GCTGGGACAGTGATTTGCTG	NM_003809.2
P01241.D12	TTTCCTTGATCCTCAGCACC	GCTGGGACAGTGATTTGCTG	NM_003809.2

P01240.D09	TCTGCCCTGAATGTCTCTGG	ACCAGCAAGTCCAGCTTCAG	NM_003809.2
P01209.G09	CATCTGGCTGCATGGGTAAC	GACGAAGAGACAAAGCAGCG	NM_003809.2
P01209.F03	CATCTGGCTGCATGGGTAAC	GACGAAGAGACAAAGCAGCG	NM_003809.2
P00662.C04	TGCAGTCCTTCAGGCAACAG	GCAGCAACAATTCCAGTGTG	NM_003839.1
P00665.H10	CACTGCATTGTGGCCTCTTC	AATCTGCCAGCTGTCTCCAG	NM_003839.1
P00657.D08	AAGTGCGAGGAGGAACTTGG	CATTCTCAGGTCTTGCCTGG	NM_003839.1
P00658.H09	ACCTTTCTGAGCGTGGTTCC	AGTGATGTTGGGAAATCGGG	NM_003839.1
P00658.C12	AGAACACAGGCAGCGTTTGC	CACCATCATCCCACCATGTC	NM_003839.1
P00658.C06	GAAACACCGTAATGGCCCTG	ACGCCAGCGTATTCTGTTC	NM_003839.1
P00661.E03	ACTTGCGGTGGACTCTGTTG	CCTGGAAATGCCCTGTAAGC	NM_003839.1
P00665.G10	AGAGCAGCTCAAAGCCCAAG	ACGCCGATGTTGACTTTGTC	NM_003839.1
P01020.A05	ACAGCTTCAGACAGATGCCC	TGACGCCGATGTTGACTTTG	NM_003839.1
P00895.F02	TGCTAGGAACATGTGGTGGG	CCAGTGATCCACAGTCATGC	NM_003839.1
P00665.E01	TCCTCTTCCTCCACCCTTTC	AGTCATGCTCTTCAGCTGGG	NM_003839.1
P01204.A01	TGCAGTCCTTCAGGCAACAG	GCAGCAACAATTCCAGTGTG	NM_003839.2
P01187.H04	TTGTGGCCTCTTCTCCTGTG	GAATGTAAGCCTGGGTGGTG	NM_003839.2
P01245.B10	AAGTGCGAGGAGGAACTTGG	CATTCTCAGGTCTTGCCTGG	NM_003839.2
P01236.B04	ACCTTTCTGAGCGTGGTTCC	AGTGATGTTGGGAAATCGGG	NM_003839.2
P01234.H01	AGAACACAGGCAGCGTTTGC	CACCATCATCCCACCATGTC	NM_003839.2
P01234.F02	GAAACACCGTAATGGCCCTG	ACGCCAGCGTATTCTGTTC	NM_003839.2
P01203.G11	ACTTGCGGTGGACTCTGTTG	CCTGGAAATGCCCTGTAAGC	NM_003839.2
P01224.F01	TTCTCACTGAGCCTGGAAG	AATCTGAGGGAATGCCTTGG	NM_003839.2
P01209.A12	TGAACTTCAAGGGCGACATC	CACACACTGGGAAAGCCATC	NM_003839.2
P01215.F09	TGCTAGGAACATGTGGTGGG	AGTCATGCTCTTCAGCTGGG	NM_003839.2
P01230.D01	TCCTCTTCCTCCACCCTTTC	TGCTGCGAGTTTGAGGAGTG	NM_003839.2
P01204.B02	TCGCAGCAGTAATTTGTGGC	CAAGGCTAACCCACAGATGC	NM_003839.2
P01124.H01	AGGCAACCCATGTAAACAGC	TCGGCAACACTGGAAGAAGG	NM_003840.1
P01058.H04	AATGCTCCAAGGACGATCAG	TAGGGAAGGCAGGTGTTTGG	NM_003840.1
P01043.B02	GCTGTTTCAAGCAAGGGCTC	GAAGTGTTCCTCCATCCACTG	NM_003840.1
P00950.A04	TCCTGACCTTGATTTCTCTG	AGGATGAGAAGTGGTTCGTGG	NM_003840.1
P01159.C04	ACCCTTGTCACCCAGTTGAG	GTGTTTGCTGTGGTTGGGAG	NM_003840.1
P01174.F12	ACCACAGCAAACACTGGAGG	TCCCTTGCTACTGACCATGC	NM_003840.1
P00811.F07	GACAGGACCCGGAATCAAAC	CGATTCTGGAACCTCCCTCC	NM_003841.1
P00692.A09	AATAGCTGGCCCTAACAGGC	AGGGCAAAGAGGGCTTATCC	NM_003841.1
P01040.H01	GCCCTGAAGGAATGAGAACC	TGAAACCTAGCCCTGTCCAC	NM_003841.1
P00918.A03	TTTCAGTAGTGGCACGGGTC	ACAAGTTGGTCTGGCCAAGG	NM_003841.1
P00848.B11	TGAAATGCGCATGCTCAGAC	GATGGGACGATCACAAGGAG	NM_003841.1
P00898.A09	GAGACAATGATCACCAGCCC	CCCATGAGGCTTCCAGTTTC	NM_003841.1
P01316.A07	AACATTGGTGTCCCTGTCCC	CAGCCTCTTTCCAGCAAACC	NM_003842.2
P00931.G03	ACAGGGCAGAAGCATGAAAG	TTTGTTCGGGACTGGTTTG	NM_003842.2
P00993.G11	GGTGATGTTGGATGGGAGAG	TGTGCTTTCCACAGATGCAG	NM_003842.2
P01297.F06	GGTTTGCTGGAAAGAGGCTG	CCATCCAACATCACCCAGTG	NM_003842.2
P01301.E06	TCCAGTTCTCTTTGGTCCCG	TGGCTGTCTGTGGCTTTC	NM_003842.2
P01312.E02	TCACATGCTATTTGGCCTGG	CTGGGCAGTCTCATTTGCAC	NM_003842.2
P01002.C03	TAACCCATCTGCCTCTGTCC	CTGGATCATTCCGTTTGTGC	NM_003842.2
P01074.G07	AACCCAAAGACCGAGCAATG	TTGACTGCTGTATCGGCCTC	NM_003842.2
P01040.F03	ATCGATTCCGAAACTTCCCG	ACTGGGTACAGAAAGGCTG	NM_003844.2
P01295.F11	AGGGTGCAAGAAAGGATGAGG	TGTTTCAGTGCAAAGCGAGG	NM_003844.2
P00795.A12	TTTCTGAGGACATGGCAAGG	CCTGGATGCTGTGCATTGAC	NM_003844.2
P01031.B12	TCCAGGAAGTCCATGCTCAG	GTTCCACAGACAGAAACGC	NM_003844.2
P01099.F12	TCAACTCACCTGTCCATGC	TGGCTCCTCTTTCATCCAC	NM_003844.2
P00741.D10	TGAGCGTTTCTGTCTGTGGG	TGATTCCTCCTAACGCAGGC	NM_003844.2
P00901.F12	TCATGGGAAGTTGAAGGAGC	TGTTGGTGACAGCTGAAGGG	NM_003844.2
P01122.F07	GCCTGAGAACTGAAGGCTG	AGTTTCCAGGGATGCAGGTG	NM_003844.2

P00174.H03	CACATAGGCCAATGCAGAGC	AAGGAGAAAGGAAGGCAGGG	NM_003854.1
P00190.F10	GGGTTTCTGTTTAGACCGCC	ACGGTTTCCTTGCTTTCACC	NM_003854.1
P00188.C08	ATAACTGGGTGGCAGAGCAG	TGAGGTGCCATTTCCATAGG	NM_003854.1
P00207.G06	CTGGGAGCTGTGAAATGAGG	TGAGGAAGGTGTGATGAGCC	NM_003854.1
P00185.D03	TGCCTGTTCATGTCCTCCTG	CTAAGCTGCTCATGCCCTTC	NM_003854.1
P00178.E11	TAGCCACTGCCTGCAAAGTG	TGGGCCCATAGTCCTCATTG	NM_003854.1
P00177.B12	CAATGGTTGTCTGGAAGGC	TAAGCTTTGAAGGCCGATGG	NM_003854.1
P00197.D08	CGGGCATACAAAGCAAACAC	TTGAGTTGGAAGCCCTCCTG	NM_003854.1
P00184.H10	AGAAAGGGCAGCAGAACCAG	ACGAGCCTGCAAGCCTTATC	NM_003854.1
P00179.E07	ATTGCAGATGTGATGCAGCC	CTGCTGCAAGCAGGAATCTC	NM_003854.1
P00197.A06	CTCCAGGGAAAGCCACAAAG	CTGCAGAAGCCGTGTGTTTC	NM_003854.1
P00184.G07	CAATTCCACCCTCATCTCCC	TGACCATGTGGATGACCACC	NM_003854.1
P00181.C12	TGAACTTTGGCCTTGGAAGC	ATCTTTGCCTCCCTCTCAGG	NM_003855.1
P00192.D07	CGTGACTTCTGTGGCTTTCC	TATCGTGAAGTCCGAGCTGC	NM_003855.1
P00200.E04	CTTCTGAATCAAGCGGAGGC	TTCCCTGTGTTGTGGAGGTG	NM_003855.1
P00183.D07	AATCATGCCAACAGCAATGG	TACTTCCTTGCTTCCCTGCC	NM_003855.1
P00175.F05	AGTGGATGGGCATCTTCCTC	CAAGCCACACACAGCACAAC	NM_003855.1
P00185.E02	CATGGAATGAAATGGCCACC	TTCTGCATAATGCGTCCACC	NM_003855.1
P00171.G10	TCAGTTCTGATGCTCCACGG	TGGCATCATGAGACAGAGGG	NM_003855.1
P00175.H07	AGGCAGGAATGTGGAGTCAC	GCATCTCCAGGGCATTTAG	NM_003855.1
P00183.B12	GAATGAGGACACCTTTGGGC	GAAATGCCCTCTCCCTTTCC	NM_003855.1
P01079.H08	GCAGAATGGAGTGTGGTTCC	ACCAGACTTCCCGTGTGTTC	NM_003856.1
P00201.G10	CGTCCTGTGGCAGCTTAATG	ACCAGACTTCCCGTGTGTTC	NM_003856.1
P00250.H10	ATGGCCATGTTGATGCTGAG	GGGTGTGGCAAGTAAGCAAG	NM_003965.2
P00879.G06	TGACAAGTATGACGCCCAGG	GGTGGTGGCGATGAGTTTAG	NM_003965.2
P00764.H10	TCTGCACAAGGCACATCGAG	GGGTGTGGCAAGTAAGCAAG	NM_003965.2
P01090.H01	TGTCTGGCATGGGTAACAG	CCAGGGTTTGGAGTTTGATG	NM_003965.2
P01307.C12	AGCTGACACCGATTGTTTGC	TAAATCCAGGCTGGCTCCTC	NM_004084.2
P01000.A01	ATATCCTCAGGCTTGCTGC	TTCCCTGAGCCTGTTGAATC	NM_004084.2
P00724.H05	TTAGCTGGAAGCCATCGTCC	ATCCCAATCTCTTTGCAGGG	NM_004084.2
P00735.C12	TTCAATGTCATTCCCTGCC	GCAGCCGGAGTCTTTGAATG	NM_004295.2
P00956.F06	AGAGCCATGAGGGTATGTGC	AATCTTCCAGATGAGCACGC	NM_004295.2
P00892.D04	TTGCCCTTGAAGCCCTAGAC	CCTGGTGGGAGATGAACTTG	NM_004295.2
P00928.B11	AACACCTGGGAAACGGTGAG	ATCCAGTGAGAAGGATGCC	NM_004335.2
P00829.D05	AGGACGGACCTTCCAAGATG	ACCCAGGATCTCCTTTGCTC	NM_004335.2
P01047.H09	TGCGGTACAGATGGCAAATC	GCTCAGGCAATCTGGAAATG	NM_004335.2
P00855.E09	AATCAGGCATCTGCTCGTCC	GTGTGTGGTTGTGGCTGTTC	NM_004335.2
P01129.F05	ACATGCCCAGCGAGAGTTTC	AAAGCCCACCTCCTTTCTGG	NM_004335.2
P01042.F02	TGTCCACGTGTGTTCAAAGG	GAGCCAGCAGATGGAAATGG	NM_004512.3
P00748.D04	TGTGTGTGTGTGTGTGTGCG	ACAACACAGCTTCACGGACC	NM_004512.3
P00939.C06	ATGAGGGCACCTACATCTGC	AGGAACTGGGAAGCTCTGGG	NM_004512.3
P00679.H01	GGTGTGTGTGTGATTGGGTG	TGCAAGCTCACATCCAGCAG	NM_004512.3
P00794.E07	GGTATGCTGGTGCAATGTGG	CATGCACAGGTCAAGGAAGG	NM_004512.3
P00906.C01	TGCCTTTCACCTAGAGGCAC	CAGGGCTGTAGGCAAACAAG	NM_004512.3
P01139.D01	TGCCCCGGGACTTTCTAGATG	ATCTCAGTCTCCGCCAAAGG	NM_004512.3
P01139.C06	TGCCCCGGGACTTTCTAGATG	ATCTCAGTCTCCGCCAAAGG	NM_004512.3
P00898.C01	TTCTTTTCTGGGACTGGTGG	TGAGGGAGCCTCTTCAACAC	NM_004512.3
P01059.H08	TTGGATCAGTGCTAGGTCCC	TTTCATCTGGTCCTTGCTCC	NM_004512.3
P00572.F11	TTTCCTTGACCATTCTCTGGG	AATTTACCTGGTTGGGAGC	NM_004513.2
P00571.D08	CAAGGGATGCTCTGCATGTC	TGGGTGTGCTTTGGACCTC	NM_004513.2
P00868.B03	TTCTGGTCCTTCACTCCTGC	TTCTCATGCTTCCCAAGAG	NM_004513.2
P01136.E09	CTTTGGCTCCTCTCAACTGC	TGGCCTCATTCTGGTCTTTC	NM_004513.2
P00977.G02	AAGAAGAAGGGACACAGGGC	TTGCAGCTGAGTCTTCGTTG	NM_004513.2
P00579.B11	GCCTGTGGAGATTTGGAAGG	GGACAGCAGCACATGGAATG	NM_004513.2

P00572.G03	TGGCTGACTTCATGGCACTC	TGGCAGAACCAGAAACCATC	NM_004513.2
P00575.B10	GTTGGGATGGATTCTGAGGG	TGCCGACATCTTCTCCAGTG	NM_004513.2
P00578.B08	TGCAGCCAGTGATGTTTCTG	CAGGGAAATCCAAGTGACCC	NM_004513.2
P01035.C06	CACATGCGTCAAAGCCTCTC	TTTCTCCGCACAATGGAAG	NM_004516.1
P00756.A06	ATGCCTTGGCTTAGCAGTGG	TCACATGGCGGTCATCATT	NM_004516.1
P00936.A06	TAGGAACGAAGTCAGTGCCC	CCTCAATCAGCATGCCTACC	NM_004516.1
P00749.H02	AGAACATGGTGTCCCACACG	TTGGTGGTGTCTGTTGTC	NM_004516.1
P00778.H11	CACCGTTTGGAATCGCTTC	ACCATGGAATCACCAGGGAC	NM_004516.1
P00733.B03	ACAATTTCTCAGAGGGCAG	GGCACAAGTCAACATGAACG	NM_004516.1
P00721.F10	CACCTCAACAAATTCGACCC	ATCATTCCCACCTCCTGGTC	NM_004516.1
P00796.F01	GAATGATCCCTCTGGGAAGG	AGAAAGTCACGTGGGAGTGG	NM_004516.1
P00752.F03	CCTCTGGCACCATCATATCC	CAGCAAACACATCTCCCAGC	NM_004516.1
P01342.A08	AGCCACTGATGCTATTGGGC	TTCAGGGTGAGCCTTCACAG	NM_004516.1
P00941.D02	TTGCTGTCTGAAGGGAGACC	CAGCCATCCCATAGCTTCAG	NM_004516.1
P00806.E07	ACCCTGAAGCTATGGGATGG	GAGGAGGGCTGTTTCCTTTC	NM_004516.1
P00785.H01	TGGCCAGCATCACTGTCTTC	GATGCTGGGACAACATCCAC	NM_004516.1
P00786.G04	GTGGCCTTGGGTTGATAACG	AAGTGACATTCCCTTCGTGC	NM_004516.1
P00830.A05	GCAAGAACCCAGTCATGGAG	CCTGGAAAGGGAAAGACAGG	NM_004516.1
P00899.B07	ACAAGCGCTTCGTATGGAG	CTTTGCTAACTCAGGCCAG	NM_004516.1
P00751.C07	GTGAGCACGAAGGGAATGTC	AAGATTGGTGCTTCGCATGG	NM_004516.1
P01063.B08	GCTCGGAGTCCATCTCATTG	AAGTCACCTTGACGCCTCAC	NM_004516.1
P00795.A04	CTGCAGGAACAGATGGGAAG	ACCCTCGTTTCTGGGAGAAG	NM_004516.1
P00918.C03	AAACGAGGGTCACAGTGGTC	ACTGCCTGAATGACCCAGAC	NM_004516.1
P01320.H03	TTTAGCCGTGTTTGGGACTC	TGGTTACCCAAGCACAGGAG	NM_004516.1
P00651.D08	TTGAATCCAAGCGAGCTGAG	AAAGGCCCTCAACTGTCACC	NM_004590.1
P01148.C10	CCCTTTCTTTCCCTGTCCTG	GGCTTTAGTGGAAGCCCTTG	NM_004590.1
P00649.E10	TGGTTCACATGGAGCTCACC	AACCTCCGCTCTCCAATAC	NM_004590.1
P00621.F04	TCCTGAGGAAATGGTGACCC	TAGCTGACACACATTCGCCC	NM_004590.1
P00128.D01	AGCCAGATCTCAAGCAAGGC	GATTGGAAAGCCCTGCAAAG	NM_004619.2
P00112.H02	AAGACATTGCACCTTTGCCG	CCCATGCAAAGCAGGTACAG	NM_004619.2
P00096.E03	TGACTGCATCCCAGAGGTTG	ACAAGCCTCTCAAACAGGGC	NM_004619.2
P01175.B01	TGTGGCACAGCGTGATAAAC	ACAAGCCTCTCAAACAGGGC	NM_004619.2
P00103.B02	GGGCATTGTTACCTGGCTTG	AAGATGTCCTCCATGCGCTC	NM_004619.2
P00113.B08	CCAAGACTGGCTTTCCCATC	TGACTCAGCACCCAGCATTC	NM_004619.2
P00107.A05	ATGTCCCGAAGGAGCTATGC	CTTGGGAAGAAGGCAAGGAC	NM_004619.2
P00141.F08	GGGCCCAGGGCTTAAATTAC	CCAGAAGGTTCCCAAACCAG	NM_004619.2
P00156.E04	GGAGGCAGCATGGAAATGTG	TTCTTCCCTACCTGGGCTTG	NM_004619.2
P00153.G07	TGTGAATGGGTTTGAGGCTG	ATGCACACGCACACACACAC	NM_004619.2
P00117.F01	TTGGAGAACCAAGCAGAGGG	GAATTTGCTGGCCTGTTTCC	NM_004619.2
P00767.A09	GTTTCCTCTGGGCATGATTG	TCTGGAAGGGAATCAGAGGC	NM_004829.1
P00727.E01	ACCACGGCCTTTCTGTAAGC	TTCCCTGGCAACAGATGGTC	NM_004829.1
P00857.C09	TTCAAAGCCCAGGGTCACTC	GCAAAGTGTAAAGCCACTGCG	NM_004829.1
P01310.A04	GGGAGCAGAGAAAGGAATGG	CCCACCGTCATCTTCCAAAC	NM_004829.1
P00878.F09	TGGTGCAAAGACACATGCTC	CCATCCGAAGGAGATTCTGG	NM_004829.1
P01317.A12	ATGGGAACAAGAGGGTGTCC	GGTTGTTGCCACAATGCCTC	NM_004829.1
P00700.B06	AAACCCAGACTGTGGCAGTG	TGAACAAGAGGCACATGCAG	NM_004843.2
P00757.G06	CTGCCGGATGGAGAAAGAAG	GGGCAGCATGGTAAACTCTG	NM_004843.2
P01166.H12	TGAACCAAAGAAGCGAAGGC	ACTGATGGGTGGGTCTTGTG	NM_004843.2
P01342.A06	ATCCTCCGGCTTCATCTACC	TCATACCCAGAGTCAAGCGG	NM_004843.2
P00747.E09	TGAGGCTGTCTGGATACATGC	GTGCAACCTGCATGAGCATC	NM_004843.2
P00730.E11	TAAGGCACAAAGTGCTGCCC	CACCTTCCATCCGTGTCTTC	NM_004843.2
P01135.C08	GAAGACACGGATGGAAGGTG	TAAACCTGGGCTTCCAGACC	NM_004843.2
P00938.B01	CGGGCGCTTATAAAGCTCAG	AGTAAGGGAATGCCTCCAC	NM_004887.2
P01135.A05	GAAACCAGAGATGGGAAGCC	GAACCTTCCAAAGAGCCAGC	NM_004887.2

P01097.G09	TGAGTTGGCACAAGGGAACC	ATTAATGAGCTCGCTCGCTG	NM_004887.2
P01054.G08	TGTTTGTAGCCCGACCCAG	GTATGGGTGTGCAAGTGTGC	NM_004887.2
P00384.B10	TTTCTGGTCCCAAGAGCAGG	GTGAGGTGTCCATTGGGTTC	NM_004942.2
P00385.G02	GCAGTGCCAGTTTCCATGTC	GGTCTTTGAGTTGGGCTTGC	NM_004942.2
P00146.C04	CATAGTTGTTGCTGCCTGG	TTTGATTCACAGGCTCAGGG	NM_005217.2
P00385.H08	AGCTGACACCGACTGTTTGC	TCAGGTGTGTGTGTGATGGG	NM_005217.2
P00385.C10	AACATACCCTCAGGCTTGGC	ACAGGAGCATTGAGCAACC	NM_005217.2
P00388.H01	TTAGCTGGAAGCCATCGTCC	ATGCCTCAGACCAGTTCCTG	NM_005217.2
P00390.C06	AGTTCTGGGTCTGCCAAAG	GGCTTGATTTGGCCACAGC	NM_005218.2
P00383.E10	GGGAAGCAGCAATCTCATCC	AAAGCTAAATCCAGCGGCAG	NM_005218.2
P00802.G09	ACCACGATGGCGAAGATGAG	ATGCTCTAAACGTCCCTGCC	NM_005283.1
P00252.C05	ACTTTCCCGCAGATGAGAGG	TTCCATAGACAGCAGCAGCC	NM_005283.1
P00275.D06	GCATGGCTGAGTCCTTGTTG	AAGATGACAATGGTGCAGGC	NM_005409.3
P01190.G08	GCATGGCTGAGTCCTTGTTG	AAGATGACAATGGTGCAGGC	NM_005409.3
P01190.G09	GCATGGCTGAGTCCTTGTTG	AAGATGACAATGGTGCAGGC	NM_005409.3
P01191.B07	GCATGGCTGAGTCCTTGTTG	AAGATGACAATGGTGCAGGC	NM_005409.3
P01213.C01	GGTCCTTTACCCACCTTTC	CTGTCTTTGCATAGGCCCTG	NM_005409.3
P00260.B07	GGTCCTTTACCCACCTTTC	CTGTCTTTGCATAGGCCCTG	NM_005409.3
P00260.D07	TTGGGCTGTTCTTGTTTCCC	TCCTTCATGCTTCCCATTG	NM_005409.3
P01214.B10	TTGGGCTGTTCTTGTTTCCC	TCCTTCATGCTTCCCATTG	NM_005409.3
P00261.A12	GCAAAATCGCTAACAAATGGG	AAGGCTGGTTACCATCTGGG	NM_005409.3
P01214.C01	GCAAAATCGCTAACAAATGGG	AAGGCTGGTTACCATCTGGG	NM_005409.3
P00135.D01	GGGAGAAGAAGCCATGTTGC	TTCCAACACTTCTTCCAGCC	NM_005531.1
P00138.A06	TGCTTGTTCTCAGACCTCCC	AGCCAAAGGTTTCCATGAGG	NM_005531.1
P00098.B06	TCCTGTCTTGACTGCTGG	TTTGGTGCATTGCTTTGAGC	NM_005531.1
P00133.F12	ATCCCAAGTCAGCACATCCC	TCCACCACCATAGCCTTTC	NM_005531.1
P00124.F12	ATATCTTCTGCCCTGGCTCG	TCTGGGAAGGAGAACATGGG	NM_005531.1
P00124.D01	TGCCCTGTAGGTGAAAGCAG	ACACACACACACACACGACG	NM_005531.1
P00135.A11	AAAGCAGCCCTCCAACAAGC	TCAGCGAGAACTTGCCAGAG	NM_005531.1
P00141.D12	TGGGATGAGAGAAGGCTGAG	TGACACAAGGTGCACAGGAC	NM_005531.1
P00141.F01	TGGGAGTCACTTCATGGCAG	TCAGGATTCAGGCTTGGGAG	NM_005531.1
P00126.G12	CAAGGGAGGAGTTGAAAGGC	AATTCAGGGCTGCTGTGAGC	NM_005531.1
P00121.F11	TGTTCCCTGACATCTCCTGC	CTTGATCAGGGCTTTACCCG	NM_005531.1
P00087.C09	TGCACGTGTGCACGTATTTG	TTCCACCAAAGCAAGAACCC	NM_005534.1
P00090.G06	GTGGAAAGAACTCCGCACC	TAGCATCAGCCTCCAAGGTC	NM_005534.1
P00091.A10	AGAATCCAGCCCTGCTGTTG	AGGTCTCAGCAAACCGAGTG	NM_005534.1
P00082.E02	CTTTGGCCACACAACACACC	AATGGGCAAGTCCCTCTACC	NM_005534.1
P00086.G01	TATGAGGTCATGGGTGGTGG	CAAATCTCTGTGTCCACGGC	NM_005534.1
P00844.G07	CAAAGGATGACGTCTGGGAC	TTGCTGAGTTCCCATGAGGC	NM_005534.1
P00093.G12	CACTGAGGGTTGCAAGGAAG	TTGCTGAGTTCCCATGAGGC	NM_005534.1
P01073.D03	AATGAATTCCAAGGCTCGTG	TGTCCTTGAGGATGGAGAC	NM_005535.1
P01339.B03	TTCCATTTTCATGGCAGCATC	CTCTGATTGGAAGCAGGGTG	NM_005535.1
P01325.A02	AGGAAATGGACCTCTGCCTG	ATTGGCTCATCTTCTTCGCC	NM_005535.1
P01328.E08	TCCCTCCAGGGAACCTCAATG	TTTCTTGACAGCTACCGGGC	NM_005535.1
P00817.E08	AAGGCAATGGGAGCAGTTTG	TGGGCGCATTAAAGAGAAGAG	NM_005535.1
P01321.A08	TGCTGGTTGAGCACTTCCTG	TTCCATGGAGTAAGGGCTGG	NM_005535.1
P00901.E08	TTCAAGGAACAGGCTGAGGC	TGCTACCCACTTTGTGCCTG	NM_005535.1
P01313.E05	AACAGCCCATTAGGGACCTG	TAAACAGCTGCTGCCCTGAG	NM_005535.1
P00710.E06	GATGGATGGATGGTTGGATG	TTAGGAGGCTGAGGATTTCGG	NM_005535.1
P00717.D07	CGACCAATCTGAACGGACAC	GATGGATGGATGGATGGGTG	NM_005535.1
P00295.G08	ACGTCAGGACAGAAAGGCAG	CCTAGCACCACCATTTACC	NM_005546.3
P00296.F09	CCAATGCTGCCATTTGTCAC	AGGTTTCAGGCCGCTGATAG	NM_005546.3
P00282.F01	TGGAATCTGAGACGAGCAGC	CAGACAGCAGGCTGGATTTG	NM_005546.3
P00304.E03	CCATTTGCCCTCTGTGAAGG	AGATGGAAGCACCAACAGGC	NM_005546.3

P00298.A03	CAGCTTCTGACAAGGCCAAG	AAGACCACCACGCCAGAAAC	NM_005546.3
P00285.E04	TGGCTGCTTGGAATTCAGT	GTGCAGGGAACAAGCATAGC	NM_005546.3
P00297.G12	ACCGATGATCAGTCTGCCTC	CCAACATGTCAACCCACTGC	NM_005546.3
P00291.A10	TGAAAGGAGGCATCCTGGAG	TGAAAGAGGACCTGGCATCC	NM_005546.3
P00309.D06	TAAGGAGGTGACCTGCAACC	AAGCACAGATGGGCAAGTGG	NM_005546.3
P00306.C07	TGTGTTTCGATTCCATCCCTC	CAATGGCCACTGGTTTGACC	NM_005546.3
P00302.C08	CAAAGCAGTGGAATCTGGC	TACAGCTGCACCAGTTTGGG	NM_005546.3
P00291.E11	AAATGCCATTCAAACGCCAG	CCTCATGAAGCCCTTTCCAC	NM_005546.3
P00283.D06	TGGGAGATGCTTTCTTCCTG	ACTTCACCGGAATTTGGTG	NM_005546.3
P00282.D01	CTCCAGGCTGCCAGAAATTG	TAATCCCACCACCATGTCC	NM_005546.3
P00296.F02	CTGATTTGCAAGCAGCCTTC	TTAAGGTGCGCTTCAGCTCC	NM_005546.3
P01305.B04	ATTAGAAGCTGCCACCAGCC	TTCCCTCTGCAATCCGTTTC	NM_005546.3
P01372.A11	GATGGTGTTGCAATTGGCTC	ACACACACACACACAGCG	NM_005546.3
P01275.F08	GCACAGAATGCTTCCACCAG	GCACCAGGAGGTGAAGAATG	NM_005546.3
P01263.B09	TCCAAGAGGCATGAGAGTGC	TATGGAACCGAGGCCCTATG	NM_005546.3
P01151.G04	TGACTGAGTGCAAGGAAGGG	TACATCCACGTGACGCAGAC	NM_005601.2
P00795.B08	ACTCATCTTGCCGCTCTTGC	CACCGATTTCTGGTTTGAGG	NM_005601.2
P01104.D03	AGGTTTCATAGCCAGGACGG	AAGCTACCGGGAAGTGTGTG	NM_005601.2
P01344.F03	ATGGAGCTGGCAGACAGTTG	TGTTGAAGGTTCCATGGGTG	NM_005601.2
P01034.G04	TGTGCAGGTGAGGGAAACAG	CTGGCAGTAACTGGCTTTGC	NM_005624.1
P00719.H06	TCCGTTTCATTTGCTGGTTCC	CGTGTTGTGGTGGAGCTTTG	NM_005624.1
P00706.A02	TTCTCCCTTTTCACAGCCTCC	TCCCTATCACCCACAAGGTG	NM_005755.2
P00732.E05	ACCTTTAGAATCCCGGACCC	GGACTGGGCTGTCAATGATG	NM_005755.2
P01294.E10	TGATGCTCTGGGTGTGTTTG	GCAGAGCCCACATGATGAAG	NM_005874.1
P00734.A01	AGCGCTCTAACAACCAGACG	CCCTAAAGCTCCCATTCTC	NM_005874.1
P00973.H10	AGCGCTCTAACAACCAGACG	TTGGAACATGGAGGCAGGAG	NM_005874.1
P01173.E08	AGCGCTCTAACAACCAGACG	TTCCAGCATTTCTCACCAGG	NM_005874.1
P01105.H06	CTTCGGGCAGATTACCTCC	ACTCCAAGACTCGATTCCGC	NM_005874.1
P01042.G11	CAAGATGCCGATCACAACCC	TCAATCAAGGGCTTCTGTCC	NM_005874.1
P01062.A05	TCCTGGACACTCAAAGCTGC	TAGTGATGGCCAGGATGAGG	NM_005874.1
P01168.E09	TGGCTGCACTGAGATGAAGG	AAGAACACCCACAATGCCTG	NM_005874.1
P01158.E02	TGTGATCAGGATGTCCAGGG	TGCTGGTGATGACAGGTGAG	NM_005874.1
P00882.G06	CAGAAATGAAGCCGCCAAATG	GCAAATCCCTCACAGGGAAC	NM_005874.1
P00823.H06	CCGTTCTTCACAAGCTCTGG	GTGTGGCTGCAGATGACAAC	NM_005874.1
P00688.D05	GTTCCCTGTGAGGGATTTGC	TCGGTGAGACGAGGAGAAAC	NM_005874.1
P00764.C05	AGCCACACAAGAAGCGGAAC	CCAGGAATTGAGGTGCAGAG	NM_005874.1
P01031.F08	GACAAACCCACACTTCCCAC	GGAGGCTGCTTTGATGAGTG	NM_006058.2
P00885.D06	GAAACATGGTGAGGCTCTGG	TGCATGTGTACCCAGCCTTC	NM_006058.2
P00704.D04	TAGTCACATGGGCACGGAAG	TTAGCAGAGAAGCAGCGAGG	NM_006058.2
P01161.B10	TCAAGCCTCCTCACCTTTGC	TGCACTGGTTGATGGCTTTC	NM_006058.2
P01305.B08	TGAAAGCCATCAACCAGTGC	GCCACACATGTTCAAGGAAG	NM_006058.2
P00724.H04	TCTGGGAAGGCTTTGCTGAG	AATAATTGAGGGCAGGACCG	NM_006058.2
P00764.H11	TGCTTCCCTGTACAGTTCCC	AGCATTTCCGGTCCATGAAG	NM_006058.2
P00715.H12	AGGAGCTTGCGGTCAAAGTC	AATGCAGCAGTGGATGAAGG	NM_006058.2
P00740.D10	CTTCCTTCCATGATGGGTCC	TGGGATGGTTAGTGGTGTCC	NM_006058.2
P01068.H12	ATGGTAACGACTGGGCAAGG	ACCCTGCCATTGACAATCAG	NM_006058.2
P00877.F08	GCAAAGGAAGGAAGGGAAGG	TGGCTGATACTTGGTCAGGC	NM_006058.2
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P00845.D10	TGAACCTCCTTCTGTGTGC	ACAGTGCTGCTGGTTCAAGG	NM_006058.2
P01315.G12	ACAGGTCCTTCTTTCCCTGC	AGTTCTGATTGGTGCCAGG	NM_006058.2
P00914.G10	TCCAAATCTGACCTTCTGGG	CAGATCCTTGCTTGGGATGG	NM_006058.2
P00754.A01	GTGCTGAGGAATCAGGGTTG	TCCACATTGCACCCTACTG	NM_006058.2
P00787.H08	TTCCAGGTCTTCAGGCCAAG	ACAAGAAGCTGTGGGAGCAC	NM_006083.2
P01106.D12	GCGAGGTCAATTTCTTTGCG	ACCCTTATGCACTTGGCCTG	NM_006083.2

P01093.G11	TGGGTGATCCAACCTGTCTC	CCAACCTGGGACACTCCATC	NM_006083.2
P01315.C07	TTCAGGACCTGGTACTTGGC	CTGCAGCTGATTTGTCCCTG	NM_006083.2
P01315.C08	TCAGCATCCGAGAGTCATGC	TTTGCTGGCAATCTCAGCTC	NM_006083.2
P00785.C06	TGCTCTTGTATGGGTCTGGC	TCCCAGAGCATTAAATTCCG	NM_006083.2
P01279.C10	CCTAACCCCTGCTTGCTTTCC	TCCGCTCATATGCTTTGCTC	NM_006083.2
P00716.F09	CCATGACTTTGAGCCTCTGC	CCATCCCTCATGCTTCAGAC	NM_006083.2
P01315.C09	TCAGGTCTGAAGCATGAGGG	CCAACCTTGCTCACATTTCC	NM_006083.2
P01169.C12	AACGAGATCGGGAACGAGAG	TAAAGCTTCAGCCAGGAGGG	NM_006083.2
P01063.E08	CATGGACGTTGACAAAGGTG	TTGTTTCCCAATCATCCAG	NM_006083.2
P01091.E07	AAAGTTTGCTGGGTCTGCTG	GATGTTGCATACCCTGACCC	NM_006083.2
P00957.C05	TGATTGGGAAACAAGTTGGG	ACCATGGGAATCAAAGCCTG	NM_006083.2
P01056.A09	AAGTGCCAGGCTTTGATTCC	ATTGGTTTCCTTGAAGCGCC	NM_006083.2
P00691.D10	CCGTTGGGACTTTGATACCC	ACCAAGCTGCCCATCTAAGC	NM_006083.2
P00809.E11	TGCAGTAAGTAGGATGGCCC	AAGATGGGCCGGAATGAGTC	NM_006083.2
P00702.A05	TTGATCGCCAGTGGAAAGAAG	TCTTGGTGCTTCAAGGGCAC	NM_006083.2
P00808.B05	GATATGTGAGTTGCGGGAGG	TGGCAATCTCAGCTCGTACC	NM_006083.2
P00889.E07	TTATGCCAAGCTACGCCAAC	TCCCGTTCCCGATATCTCTC	NM_006083.2
P01315.D06	ACCATGAGATGCCAAGGGAG	TGGGCAAAGCTTCTTTGTTG	NM_006083.2
P00552.C02	GCCATTTGCCTTCTCATTGG	GGATTCACCTGCACAGCATC	NM_006084.2
P00552.D09	TTCTGTCTCGGCTAACCC	ATAATCGCAGCACATCTCGG	NM_006084.2
P00548.E02	AACCCTGTCTTTCGCAGCAC	TCTTCCAACAGCTGCTCCAG	NM_006084.2
P00545.E10	ATGGACTTATGCACCAGGGC	GAGGAGCATCCCAAATTTCC	NM_006084.2
P00553.B05	GAATGTAAAGGGACCAGGGC	CTGAATCTGCTGTGGATGGG	NM_006084.2
P00555.E11	GGAAATTTGGGATGCTCCTC	TGCTAACACATGGCCTGACC	NM_006084.2
P00553.H08	AGGTCAGGCCATGTGTTAGC	ATAACACACACCCAGCCAGG	NM_006084.2
P00552.E11	TTCAGGTAAGTGGCCTTCCC	AGTTCTGAGCGCAACCACTG	NM_006084.2
P00551.B03	GACAAGATGCGGGAAGAAGG	AACAATGCCTGGAGAGACCC	NM_006084.2
P00557.B10	TTAGTTCAGGCTGAGGGTGG	AAGCCTGTTCTGACTTCCC	NM_006084.2
P00669.C05	ATTGTTCCAGCACGGAGGTG	TTCAAGGCGATGGTGAAGTG	NM_006084.2
P00565.H12	CTTCTGCTCTTCAGTTGCC	TCAAAGGCCTGACCTGGAAC	NM_006084.2
P00549.C11	ATCACAGACATGGTGTGCC	CTTTCCTCCCGATTTCTC	NM_006084.2
P00547.E10	CACCGATGACACACAGTTGC	TCCCTCTGCTTCCCTTTCTC	NM_006084.2
P00551.A07	CACCACCAATCCTGTGGAAG	AAAGTGCATGCAGCCTCCTC	NM_006084.2
P00544.D09	GAAGTGGAAACGCATGAACG	ATTGGAGGAGCAAGCAAAGG	NM_006084.2
P00547.H11	TGCCATTGGCTTTGAGAGTC	CTTTACCCATCACACGGTGG	NM_006084.2
P00548.A05	TCTCCCATCTGGGTTTCTGC	TGATCATTTGGGAATGGGAG	NM_006084.2
P00544.C10	TCAGATGGTCTGCCGTTGAC	TTAACAACCCACCTGTGCC	NM_006084.2
P00550.E11	TTGGGCAGTGGGTAGAAGTG	AAGGACCACCAAGAAGCCTG	NM_006084.2
P00546.C12	AGCCTCATCAATGCCCACTC	TGACCATCCAGGGTGTCAAC	NM_006084.2
P00143.G11	TGAGCTTTCACTCCACAGGC	TCTAGGAAGTGGCAGCAAGG	NM_006147.1
P00141.E01	TGCTTGCCTTGCTACACAAC	TTAGGGAAAGCACCGTGATG	NM_006147.1
P00123.H07	TTGTTGCCTAGGTCACCTCC	ACTGTTTGCTTTCAGGCAGC	NM_006147.1
P00156.C10	ATCAGAGCATCCCTATGGGC	TTGCCACACGTTACATTCCC	NM_006147.1
P00136.A05	TCTATTGCCTGGAACCCACC	TTTGGGATTCAAGAGGCCAG	NM_006147.1
P00116.E06	TACCTGGCCTCTTGAATCCC	AAGGGCAGTGTTTCCTGCTG	NM_006147.1
P00132.F10	TACTGCGTGCCTGCTAACAC	CTCTTCCAAAGCCCTTGGTG	NM_006147.1
P00110.A03	CACCAAGGGCTTTGGAAGAG	ACTTTACCCATGCTGGCTCC	NM_006147.1
P00412.G04	GCAATGAGGCTGATCCTGAG	AATCCCTGAAACAGGTTCCC	NM_006274.2
P00405.E03	TTCTTCTGGTCCTCGGTTT	ATGCTGAAGACTGCTGCCTG	NM_006274.2
P00405.B12	CTGGATGATGCGTTTACCC	AGCCAGAGCCATATTGGTGC	NM_006274.2
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P00800.B09	ACACCACCATTCTCTCAGC	CAGTAGGCGCTCATTGAACC	NM_006332.1
P01006.B05	TAGGTGCCGCCTCTATTGAG	TGCACTCCTCTTCTCCATGC	NM_006332.1
P00701.H03	CAATGCACCGCTTGTCAATG	AAGTTCATCCAACACGCAGG	NM_006332.1

P01332.A09	AACATGGCTGTTGGTCATGG	AGATGGAGGCTTCAAGAGGG	NM_006332.1
P00860.B11	TCATCAAACATCCGGGTCAC	AATGCCCTCTTTCCCTATGC	NM_006332.1
P01103.F06	ACGAAACAGGCTTGGCTCAG	TTGGTAAGTAGCAGGTGCCG	NM_006332.1
P01236.A11	ACAAATGCCACCATCTTCGG	TACCATCAGCCTGCAAGCAC	NM_006564.1
P00226.F07	ACAAATGCCACCATCTTCGG	TACCATCAGCCTGCAAGCAC	NM_006564.1
P01220.D09	GTGTTTGGCCAGGTCATGTG	CTTGCAAATTCCAGAGCAGC	NM_006564.1
P00879.G05	AACACTCATGCTGAAAGCCC	TTCCGTGATAGAGCAATGCC	NM_006564.1
P01216.B07	AGTGGTCCATGGAATGCTTG	TATGCCACACACCTGGAAGG	NM_006564.1
P01220.G03	AGTGGGCTCAACCATCCATC	ATCTGGGTGGCAAGAACCAC	NM_006564.1
P01220.H09	GAAGTTCATCCGCAGCACAC	TGCCATTTCATAGTCCCTGG	NM_006564.1
P01031.E05	TGATGGCTGTGTTCTCTGCTG	CCCATTTCATAGTCCCTGGTG	NM_006564.1
P00860.A11	ATGTGCAAGAGCCTACTGGG	AGCCATGACTTGCAAATTCC	NM_006564.1
P01120.G06	AGTGGTCCATGGAATGCTTG	TGGAAGGCACGATACAAACC	NM_006564.1
P00253.E09	GGGCTCAACCATCCATCATC	GGAAGGCACGATACAAACCC	NM_006564.1
P01216.G08	ACTCATGCTGAAAGCCCAAG	TTCCGTGATAGAGCAATGCC	NM_006564.1
P01325.G06	CCTGATTTGCCTCCTGCTTC	AACAGGCCGAGAATTAGGGC	NM_006664.2
P01321.H02	TGACCATGTGTCTGTGAGGC	ACACAATTGGGTGGGAGAGG	NM_006664.2
P00336.D10	ATGCACTGCTGCTCTGATGC	TGCAGAGACAGGTTGTTGCC	NM_006734.2
P01095.G02	TGCAGCTTCCTTTCTTGGTG	CCATGCTCATTTGTTGAGGG	NM_006734.2
P00323.B06	AGGCAACAACCTGTCTCTGC	GCCAAAGCTCTCAGGGATTG	NM_006734.2
P00322.E11	TTTGGAGACAACCTGGCCTGG	CCCTTGATTGGAGGCCATAC	NM_006734.2
P00335.H04	CATCTCCAAACCGGTAATGC	GCATTGCACAGAGTGCTGAG	NM_006734.2
P01311.B09	AAGCCACAAGTTCGGCTGAC	ATCGCTCAACCTTCTGAGCC	NM_006734.2
P01325.G11	GAGGATTTGAAGGTGGCCTG	TTTCCCACATCCCTTTGCTC	NM_006734.2
P01314.E08	CTTTCAGCCTCCATTCCCTG	AAGCACCTCAGACTTTGCCC	NM_006734.2
P01299.G04	ATCGTCGGAACCAAGTCATCC	ACAGCACCAAGCCACATCAG	NM_006734.2
P01332.G09	TCTTTCCAGTGTGCTCTGCC	TGAGTCAGCCGAACCTTGTGG	NM_006734.2
P01325.G12	CGTCGCATCTCTTTCTGGTG	AAGGATGACTGGTTCCGACG	NM_006734.2
P01307.E02	TTTGCATTTGTGTTGGGAGG	GCAAGTTTGCAGACACCCTG	NM_006734.2
P01329.E02	AGCATTGCTTGGCTACCTCC	GCAGGATGAGTTTGGGAAGC	NM_006734.2
P00679.A01	CCAGGAAGTGTTGATCTGGG	AAAGGGAAAGAAAGGCCAGG	NM_006737.1
P00790.B07	TCTCAAGACAGTGGGCATCG	TCACTGAGTCGAAGTGTGCG	NM_006737.1
P00739.G06	TGACAGGCAGAAAGTGGGAG	TGCTGGTTCATTGGATCTGG	NM_006737.1
P00863.C09	TGAAATGAGGACCCAGAAGG	CATGAGGGAAGGTGGAACAG	NM_006737.1
P01139.G05	AGGCCCTCTGAGATCATGTG	AGTTATGGGAAGCTGCGTGG	NM_006764.2
P00989.G12	TCCCAAGCTCTAAGCCCTTC	TGTCCGGTGAGTTTGTCCAC	NM_006764.2
P00803.B10	CCAACCTTGCCAATGTCAGC	CCCAGGTCCAACCTTTCTTG	NM_006764.2
P00787.C04	ATTCCACCTTCTCCAGGTGC	TGTGAAACAGCTCCTCACCC	NM_006764.2
P00694.G09	CATGGGCTGAGGACAAGAAG	TGTGAAACAGCTCCTCACCC	NM_006764.2
P00894.G12	AGCGGGTGGAAGTTTGACAG	AGCACACTGTTGGGAGAAGG	NM_006764.2
P00760.F05	TGGGCTGACTGGAAAGCATC	ACCTGTCAAGGATGTGGCTG	NM_006764.2
P01143.G08	CCATGAAACCCTTCCTGCAC	ACAAACTCCTCCTGCAATGG	NM_006764.2
P00946.F10	TCCCAACAGTGTGCTTCTGC	ACAAACTCCTCCTGCAATGG	NM_006764.2
P01001.A11	ACTGCTCTTTGAGCTTGCCC	CAAACCTTCTCAAAGCGTGG	NM_006764.2
P00702.E11	CAATGCTCCCATTGCAGGAG	CAAACCTTCTCAAAGCGTGG	NM_006764.2
P00687.H09	AAGCCCAGTTGTGTTGGCAC	AGGCAGCAGCATTGTACAGG	NM_006764.2
P00995.F05	TGCAACAACCTGGTCTCCACC	AAAGTGGCTATGGGCAGGTC	NM_006764.2
P00743.G09	GCAAGGTTCCACGCTTTGAG	GCACACAAATCCATTCCAGG	NM_006764.2
P01337.E06	TGTGGTTGCTTCAGTCTGGC	AGATGCCATTTGGATCTGGG	NM_006764.2
P00810.B11	AACCAGACGGCCAAACAGAG	TCCAGCCCATTCTACCGTC	NM_006840.1
P00706.D02	TTGGGCTGTGTGTCCTTCAC	TCCAGGTTTCTTCTTTCCG	NM_006840.1
P01061.D12	TTGGGCTGTGTGTCCTTCAC	ACGTCATCACGCTCAAGGTC	NM_006840.1
P00836.H10	TCAAGCACTTCCACACATGC	TGGGAGTATGGGAACCTTGGC	NM_006840.1
P01012.B01	TGCATTGCTCTCACTCCAG	TCAAAGACTCAAGCGGGAGC	NM_006840.1

P01106.A03	CAGGGAAAGAGCCTGAATGC	GTCCAAGCTCAAAGGCTCAG	NM_006840.1
P01105.A04	CTCCCGCTTGAGTCTTTGAG	AATTAGTGATGGCCGGGATG	NM_006840.1
P01169.B08	GATGCCATGACTGACACAGC	TGTTGATGGATGGGCTGAAG	NM_006840.1
P00892.E01	TGAGGGACAGGAAATTGCAG	AGTTCCACATTCCATCCACG	NM_006840.1
P01060.D07	CAAACGTGAGAAGTCCGTCC	TCGGTGAGGTTTGAAGAGGG	NM_006840.1
P00725.H11	ATCGCCCTGCACTGTCATAC	TCGGTGAGGTTTGAAGAGGG	NM_006840.1
P00960.E03	ATCAGTCAGCCCAGAACAGC	GGCTCAAGCAAGCCACTTTG	NM_006840.1
P00898.F07	CGGGTTGATGTTTGGTCAAG	GTTCCCTGTGAGGGATTTGC	NM_006847.2
P00743.B04	AAATTTGCCTCACAGCCAGG	ATCAGAGGCTGGATCCCAAG	NM_006847.2
P00863.D04	GCAAATCCCTCACAGGGAAC	GAAAGTGTCCATTGGGCTCC	NM_006847.2
P00846.F11	AAGGCCAGATTCTCCATCCC	CATTTCTCTGTCCACCTGGC	NM_006847.2
P00972.H04	GTAAACCCACCCTTTCAGCC	ATCTCCTTCAGCCTTGACCC	NM_006847.2
P00768.G01	ACAAGGTCCGTCTCAACAGC	TGACTGTCTTGAACCACCGC	NM_006847.2
P00767.E04	TCTTTCCCTGCAACTCTGGG	TGCACATGCAAGTCAAGAGG	NM_006847.2
P00719.B07	TCTGCTCCAGAAATCCAG	CATTAGTGCCACTGCAACGC	NM_006847.2
P00683.F02	CAGGCTGATTTCCAACGTCC	TGTGTGTTCTTCACGGCAGC	NM_006847.2
P01011.B07	GGCTGATTTCCAACGTCCTC	TTTGCTCCCTGCTGTGTCTG	NM_006847.2
P00917.C08	ATCGTGTCCAGGAGTGCAAC	ATGGCCAGAGTGGCATAGAC	NM_006847.2
P01380.C01	TGAAGCCTTCTTCCTCCAG	AGGGACATTGGGTGGGTTAG	NM_006847.2
P01045.D05	CTTTCAGAGGAAGCCACTCG	GCAGGGTGTGTGCATATGAG	NM_006858.1
P00756.H04	AGCCTGGACACACCTTGATG	TTTGGTAGGTGCGTGGTCAG	NM_006858.1
P01145.G11	TATCAGCACTATCGCCACGC	AACACGACGCCACAGGTATC	NM_006858.1
P00733.D07	CAGATGTTTGTTCAGCGG	GTGTTGTCATCTGCAGCCAC	NM_006863.1
P00832.G02	TGAGCTACACAGCCAGATGC	TTCCCTGTGAGGAATTTGCC	NM_006863.1
P00858.H03	GACGCAGAAAGCACCAAGTTC	GGTCCCTGGAAGGAAATCAG	NM_006863.1
P00909.E09	TCACAAAGATCCAGGGAGG	CACAATGGAGGGTCACGTTT	NM_006863.1
P01057.C02	CTGGATTACACGGATCCAC	AAACACACTGGAGGGTCAGG	NM_006863.1
P00845.B05	CACAGCATTGCCTGGAGTTC	AAGAAGGATGGGTGAGAGGC	NM_006863.1
P01345.A01	ACATCCTGATCGCAGGTGAG	TGCTGCCCTGGAATCAGAC	NM_006863.1
P01264.D05	CCCAAACCAGTGGCTTTCTC	TTCTTCACACAGCCTCAGCC	NM_006863.1
P00680.A06	TTCCCTTGAGATCCTGAGC	ATGGTGGGCAAAGAGGTCAC	NM_006863.1
P01317.B02	TAACACCCTCAGCCCATCAC	GTCCTCTTGCTGTTTGCAC	NM_006863.1
P00946.D04	TGCCACCATGACTGACACAG	GGAAAGATCAGGCACAGTGG	NM_006864.1
P00878.F06	TGGGACCTCACAGCAAACAC	CTCCATCCCATCCATGACAG	NM_006864.1
P01355.A06	TTCTGTGAGCCACATCGGAG	TAACGCTGAGCTGATGGACG	NM_006864.1
P00762.F12	TTCCCTCTTTATGCAGTCGG	TGGGCTGAGGATGAGACAAC	NM_006864.1
P00938.H03	CTCTGTCATGGATGGGATGG	CTGAAATGCCTGCAGAGAGC	NM_006864.1
P00854.G06	AGAGGTCCCTGTGATTTCC	TGCATACAACCTCTCCTCCG	NM_006865.1
P00907.C03	AAAGTGTGCATCCCTCCCTG	CTCCAGGTGGGATGATGTTG	NM_006865.1
P00884.E06	CCCACAACTTTCCCTCTCC	GGATTACACGGATCCACAG	NM_006865.1
P00946.B10	GATGGTCACATTCCCTCCTG	CCACAGCCAACTCTTGTC	NM_006865.1
P00771.D12	CTGTGGGATCCGTGTAATCC	ATGAGAAGAAGGACCGAGCC	NM_006865.1
P00830.F04	ATCAGTCAGCCCAGAACTGC	CCCACAACGCTGAACTGATG	NM_006865.1
P00745.D03	ATTTGCTGCTACATCCAGG	ATCAGTCAGCCCAGAACTGC	NM_006866.1
P00731.C12	TGCACTTCCTGTGTGGTTGC	TGGATGATCACAGAGCCTGG	NM_006866.1
P01008.E02	TCACAAAGATCCAGGGAGG	GAATGGGAGTTCAGGCGTTG	NM_006866.1
P00941.A07	AAGAGCCTGGGAAGAATGGC	TGGCTGCACTGAGAGTGATG	NM_006866.1
P01079.H11	TGCTTGGAGTTCCTGAGTC	AATTCAGCCTGGTTCTGCTG	NM_006866.1
P01069.D02	TGTCTCTGATGTCGGCTACG	AGGTCCTGCCTATTTCCAC	NM_006866.1
P01065.H08	AAGAATGCAGAGCCCAGGAG	TGAGAAAGAGGGAAGGGCTC	NM_006866.1
P00823.F02	TCCAAAGATGGGTACCGTTG	TCATTTCCCGAAGGTTGGAG	NM_007051.2
P01080.C03	GTTGACCTGCTTGGCTTGTG	TGGGTGCCTGAAGTTTCTTG	NM_007051.2
P00914.G03	TGGTTGCCAATGCAAATGAG	TACTGCAAGCTGGCTTGGTC	NM_007115.1
P00816.G05	GGGCATCTCTGACAACTGG	AAGAGCCGGTGACAGAAAGG	NM_012206.1

P01078.D01	GCAGTCAGGCATTTGGATTC	GGAGCCGAAAGGTTTCAGAAG	NM_012206.1
P00735.G05	CCATCCCACATTACCCACTG	CAGCTTTCCCTGTCCTTTGG	NM_012206.1
P00679.D08	TTGCCAAGTTTGCCATTAGC	CGATTTAACGCATGTGGGTG	NM_012206.1
P00763.F10	GAAGGGAGGAAATGGGAAGG	ATCTTGAGCTCCACAGGGTG	NM_012275.1
P00938.D08	AAATCACGCTGGGAATCCTG	TGTAAAGCCCAGAACACGGC	NM_012275.1
P01116.A12	TCCACCTCATAGGATGCCAG	CAGGGAATGCAATGCTTGAC	NM_012275.1
P00707.H07	TTCCATGCCTTGATGTCCAC	CTCTTGATTCTTGGCACC	NM_012275.1
P01129.G02	AAGCCAGTGCCTGTCATGTG	TGGCAGGATTAAAGGGAAGG	NM_012275.1
P01106.H08	TGGCGGACAATCACTCTCTC	AACCAACCAGAGCAGCAGAG	NM_012275.1
P01239.G11	GCAGGGAGGAAAGAAAGTCG	ATCTTGAGCTCCACAGGGTG	NM_012275.2
P01224.G01	TCAGGTCTTGCCAGTTTCAG	TTGGTACATGCCAGTGGGTG	NM_012275.2
P01238.B07	AGGGTGAAGGAGCAAACCAC	TGCCTTTGCTTAGAGCCTGG	NM_012275.2
P01243.E03	TTCCATGCCTTGATGTCCAC	GCTCTTGATTCTTGGCAC	NM_012275.2
P01225.H09	AAGCCAGTGCCTGTCATGTG	TGGCAGGATTAAAGGGAAGG	NM_012275.2
P01203.E06	TGAATCGAGCTCTGCTGCTC	TCTGGCTTCTGCTCCCATTC	NM_012275.2
P01192.H12	CATCTTGTTGTGGGCATGAG	TCTGGCTTCTGCTCCCATTC	NM_012275.2
P01217.H04	CATGGCGGACAATCACTCTC	ACAACCAACCAGAGCAGCAG	NM_012275.2
P01203.A10	TGTGTGGCTGGAATCTCTGG	CACTGGAGTTCATTCTTGGC	NM_012275.2
P01310.A05	TCAGGAAGCCAGTCTATGCG	TGCTTGTGCTCCTGACTTCC	NM_012276.1
P00691.F02	TTTCTGCTGTTTGCCTCCTG	AACCCAATGACGTACCAGGG	NM_012276.1
P01347.G07	CATTGCTGCTCCCTTCTTCC	ACATCCTGATCGCAGGTGAG	NM_012276.1
P00965.A10	TCCCATGACTGACACAGCAG	TACAAAGTCAGGGCACCAGG	NM_012276.1
P01046.G06	TCACTAGGGTTTCCAGCGTC	ACCTACCCAAACCCATCCTG	NM_012276.1
P01111.E03	CAATCAGAGTGAACCTGCC	CCTCATTCTCACAAGCCTGC	NM_012276.1
P00818.F04	TGCCTCGACATTGAGTTTCC	AGGACAAGCCCTGGGAAATG	NM_012276.1
P00914.E11	AGTGAAGGACGCAAGGTGTC	GGCCCATATCTCCAATCCAG	NM_012312.1
P00679.C05	GGGTGGAAATATCAGCCTGG	AGGCAAGGTCAGAAATGTGG	NM_012312.1
P01319.B01	TAAGAGCCTGGATGTGCAGC	TTCTCTGGCCCATCTCTG	NM_012312.1
P01304.F02	TGGTGAGAATGATGGAAGGG	TTCTCCATCTGCCTGTGTGC	NM_012312.1
P00759.F08	AAGTCTCAAGACAGTGGGCG	GCAAGGCTCTTTCTCTGCTG	NM_012312.1
P01319.B02	TTGACTCAAGAATGCCGTGG	CAGAATCAGGCAACGGTCTG	NM_012312.1
P01386.A05	ATGGGATGGGAACCTCAGAGC	TTGCTTCTTGAACTTCGGG	NM_012312.1
P00857.C02	CACAGACCGTTGCCTGATTC	AGGCATGTTTCAATTCGTGG	NM_012312.1
P01165.D08	ATAGTGAAGGACGCGAGGTG	TCACTCCAGGCCATAACTC	NM_012312.1
P00719.E10	GGCCTGGATTGGAGATATGG	ACAACCCAGCTTTGAACACC	NM_012312.1
P01069.C10	AACCAAGCTGCTAAGAGCCG	AGTCAGCATGGAAGGACACC	NM_012312.1
P00727.A09	ACCAATCCAAGGAGAGCCAG	CTCCATCATCAGCAGGAAGC	NM_012312.1
P00816.C03	ACCAATCCAAGGAGAGCCAG	GTTTCTGGAGCCCTAATCGG	NM_012312.1
P00784.C02	GGCATCTCATGTTTGGGAGG	ACCTCCAGGCCATAACTTC	NM_012314.1
P00850.H07	TCACAAGACACCCTGATGGC	TTTGCGCAGAAGATGGAAAG	NM_013416.1
P00968.H08	TGGTCACCAGCTTCCCATTC	AAATGAGGAGCCATGCCTTG	NM_013416.1
P01092.E06	CTCCTCATTTCTTGGGCCTG	TTGCAAGCAGAGGCTTGAGG	NM_013416.1
P00777.C08	GTGTGCGCTTGGATGAACAG	TGATCCACCTGTTGGCATTTC	NM_013416.1
P00819.C04	TCATGAGATGGAGCAAGGGC	TGTGGCACCAAACCTCTCTGG	NM_013416.1
P00920.B07	ACCAATGTCTCCAAGGGTCC	CCAGGTAAACTGTCCGGATG	NM_013416.1
P00774.C12	TTCCATCCCTACGCTCATCC	TCACCTTCATCCTCACCTCC	NM_013416.1
P01087.G05	GAGACATTTTCAAGGCTGTGCC	AAGACACTCTTCCCGCAGC	NM_013416.1
P01332.D01	CGAGACATTTTCAAGGCTGTGC	AAGGAGATCCCGTTGCTTTG	NM_013416.1
P01051.G07	AAAGGTCCACCTCTCATCCC	TAATGATTGGAAGCGCCTTG	NM_013431.1
P01367.H08	TGGAGGTGGCAGTAAACCTG	ACAACCAAAGTGACCCTCGC	NM_013431.1
P01049.F03	TTTCCTTTGCTGCCTCTTTG	AACCAAAGTGACCCTCGCTG	NM_013431.1
P01204.D07	TGTTCCATCTCAGCCCTGC	AAGCCTGTCCGATTCTGAGG	NM_014442.1
P01195.E01	AGCAGGACCCAATCCATCTG	ACATCTGTAGCAACCTCGGG	NM_014442.1
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P01241.B06	ACAAGGACGCTCGTGAAATG	AAGCTGCATCCAGCACTCTC	NM_014442.1
P01205.F11	TGTCCCTCCAAACACACCTG	TGGCACAAATATCCTTCCGC	NM_014442.1
P01242.E12	ATGTCACCCTGTCCTTGCTG	TCATGGGTTGGGAGGTGTTC	NM_014442.1
P01244.E06	CAGGAGCTGCAAATACAGGG	TTGTGACAGGTAAGGCACGG	NM_014442.1
P01208.D03	TGAGGATGTCAGGCCTATGG	TTCGTTGCTGCTGAGAGAGG	NM_014442.1
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P00870.B02	TGCCTGCACTTCTCTGTCTG	TGTGTAAAGAGGAGGTGCCC	NM_014442.1
P00302.D09	CTGATGCACCTGCTCTTTGG	CGAAAGAAGGAAGCTGGGTG	NM_014443.1
P00293.H04	ACTGGAACACCGCATGGAAG	AGGAAGGAGCATGCTGAGTG	NM_014443.1
P00283.H10	CGATAACTGAGTTTGCCGGG	ACCAGACACACAGGGCATTG	NM_014443.1
P01286.G01	AGGCCAGAGCACATATTCGG	TAACAACCGCGACTGAATGC	NM_015564.1
P01252.A08	GGCATGTCGAGTTGTTCTGC	TGGACAGTGCAAGTGTCAGC	NM_015564.1
P01268.H01	CACCTGACAAATGGCAATGG	AATCCTGACATGCTCCCTCC	NM_015564.1
P01295.D03	AGCTGCTGACACTTGCACTG	CCCTGAGGCACAATCACATC	NM_015564.1
P01371.B12	ATTGGAGGGAGCATGTCAGG	TCCATGGATTTGAGCTCTGC	NM_015564.1
P00300.A03	CGTTTGCACTGAGTGGAAG	GGGTCTTCTTGAATGCAGCC	NM_015564.1
P00174.B10	TGATTCATTCTCCTGGGTGG	CCACAACACTTCCCATGTGC	NM_016232.2
P00191.E04	TGCACATGGGAAGTGTTGTG	TCTCATCAGCCTTCTGTGGC	NM_016232.2
P00200.A10	TGTGGCTGTATTTGGCACAC	AATCACCTGCGTCCTCAGTC	NM_016232.2
P00211.B07	TGTGGCTGTATTTGGCACAC	TCCAATATTGCTTTGCCCTG	NM_016232.2
P00173.C01	ATGGGTTGGATCTGCATTTG	ATTGCTGTGTCCCTGTTCCC	NM_016232.2
P00174.G03	AGGCAGAATCATTGGCCTTG	TCCTCTTCCTTCACGTCAGC	NM_016232.2
P00170.G04	CGTCCTGTGGCAGCTTAATG	CAGCAAACAACATCCCGAAG	NM_016232.2
P00189.G02	CTGGCCCTGACCAAACTTTC	AGATGGATCTCAGGACCGTG	NM_016232.2
P00193.D06	AGAAAGGTCCATCGGAATGC	CACCAGGACAATGATGGGAG	NM_016232.2
P00198.C08	AAATGCCAAATGGGAAAGGG	AGGATGGTGGAGGATTGAGG	NM_016232.2
P00388.E02	AAGATCAAGGAGCTCTCCCG	TGTGAGGTTAGAGCAACGGC	NM_016240.1
P00381.F01	TGTGTCTTTCCCAGCGTGTG	CGTGAACCTCTGCCCTTTCAC	NM_016240.1
P00389.F12	GCATTCCAGAAAGCACCAGC	TGTCAGCATCTGGAAGGCAG	NM_016240.1
P00381.B11	CTAACCGCCATGAAGAAGCC	TCTGTGGTCCACCCAGAATC	NM_016240.1
P01334.A02	TTCCATAGAGGTGGCAAGGC	CCGACTGCTGTAGGCATTTG	NM_016240.1
P00398.G01	ACAGGCAATCCTGGACAACC	TCTTCCGTAATCCGCAGACC	NM_016240.1
P01143.C06	AGGATTAGGCTGCAGAAGGG	TCCTCTTCCGTAATCCGCAG	NM_016240.1
P00982.H09	TGCATGCACACATACACAGG	TTCTGCAGCCTAATCCTCCC	NM_016240.1
P00858.F05	AAAGTGGACCTGGCAACCAC	CGTGTTGGGAAGGAGACAAC	NM_016240.1
P01035.E05	TGCAAGAGGGGCATGTGTGTC	ACCTCAGGGCATGAGAGATG	NM_016543.1
P01205.G05	TGAACGTGGGATAGAGGCAG	ATCAGAGCTATGCAGGCTGG	NM_016543.1
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P00874.E02	TTGTTTGAGGGTTCACGACC	TGGCCATTGGAAGCTCTATC	NM_016543.1
P01282.E08	AGATGGTGTGCTGGTATGGG	TGAGATGGGTGGATGAATGG	NM_019846.2
P00696.G04	ATGGAAGGACCTCATCTCC	CCAGGCAGGATGAACACAAG	NM_019846.2
P01346.E08	TCATAGTGAAGGACGCGAGG	CTACCGTCATGGAAACGCTG	NM_020535.1
P01330.D02	TGTGGTTCACACATTGGCTG	TGCACCCTTGCTGACCTTAG	NM_020535.1
P01337.C02	ACCAGGGTCCAATCATCCAG	ACTTTCTCCATCTGCCTGGG	NM_020535.1
P01385.C05	CGAAATCTCAGGACACTGGG	TATTCTGCCCTCCCATTTCG	NM_020535.1
P01387.E09	CATTTGTAGGGAGGGCTTGC	TCCTGGAGAGAGGGAAATGC	NM_020535.1
P01323.A09	GCTGGCAACCAAGAAATGAG	AACAGCATGAGGGAAGGTGG	NM_020535.1
P00427.G08	ATGTTGGAGAATCGGCTTGG	AGCGCTCAGGATTGGAGTTG	NM_021002.1
P00390.H11	TCCTTTGAGCCAACAACCAC	ATTGTTGGACCAGGGAGCAG	NM_021010.1
P00395.E05	AAGGCTCCCTAAAGCACCTG	GTGATGGTTTGCTGGGTGAG	NM_021010.1
P00428.F06	TTTCCCTCTCTGCTTGCTCC	TAGGGCCGAGGCAAACCTAAC	NM_021057.1
P00617.A08	GCTATGCATGCAGGGACTTG	TGGCGGATCTAGCAGAAACC	NM_021137.2
P00644.D07	AACTGGTTCCATGGGTTTGC	TGCCAGTCTTAAGGTGACG	NM_021137.2
P00626.G03	GCTGGTGGTTTCTGTGTTGG	TGGGTGGCATCTCACTTGTC	NM_021137.2

P00640.G07	TAGGCCCTGCTTCTGGTTTC	TTATATCCCAGCCAGGGCAC	NM_021137.2
P00616.C08	ACCAGCCTGTGTGCAACATC	TCGTGATACACGTTGAGGGC	NM_021137.2
P00631.D12	AAGGAATGCCTCCCACTGAC	CTGCGCTGTCAGGAACAAAG	NM_021137.2
P00820.E01	ATCTCCCATCCTGTGGAACC	TTAGCCATCCTTCCCTCCTC	NM_021137.2
P01018.H11	GAAAGGCAGTTCTGGTGCTG	TCTCCATGGCTGAGTTACCC	NM_021137.2
P00838.H06	CATGGGCCAGAAACATGAGC	TGGCCAAAGAAGTGGATTG	NM_021137.2
P00960.G03	CCACTGAGGTGTTGTGATGC	AATTGTGCTGCATCTTGCCC	NM_021137.2
P01055.H12	TTCTGCCAGCCTAACAAAGC	ATCCTTTAGGCCGACCTTGG	NM_021137.2
P00655.E09	TGGAGGATGTTGGTCTTCCC	GAATTGTGCTGCATCTTGCC	NM_021137.2
P01093.A10	CCAAGTCAGTTGGTTGCACG	AACCCTCCTCGACATCACTG	NM_021270.1
P00870.H04	AGGCCCAAGTTGTGAGCAAG	AACCCAATGCTGGGACTGAG	NM_021270.1
P01010.B10	CATGTCTGTGTGTGTGCGTG	ACCAGCATCCAGAAGGTTCCG	NM_021706.1
P01000.D03	TGACTGTGGCCTTGTCTTGG	GAAAGAGGTCAGGCTTTGGG	NM_021706.1
P00796.A04	CACATTGCATCTGGATTGGC	GAAAGAGGTCAGGCTTTGGG	NM_021706.1
P00824.G03	CACATTGCATCTGGATTGGC	GAGCATGAAGCTGGTGTGTG	NM_021706.1
P00948.C12	TCTGATTCTGGCGATGGAGG	GCAGAGGGCAGAAATTAGCG	NM_021706.1
P00960.A06	TAAGCGGGTATGAGGCAGAG	GTCCTTCACCAATGACCCTG	NM_021706.1
P00995.A11	TAAGACAGGTGGAGGATGCG	GGGAAGGGTGGAAAGAACAG	NM_021706.1
P01044.E06	TCAACATCACTCCCACCCAG	TTGCCCGACCTTTATTCTGC	NM_021706.1
P01120.D01	ACGAACCTTCTGGATGCTGG	ATTTGCCTTGCGACATCCTC	NM_021708.1
P00729.C03	TGACTGTGGCCTTGTCTTGG	AGGCCTGAAAGCTGAGCATC	NM_021708.1
P00961.C01	ATCACAGAGCCAACAGGAGC	CCAATCCACCTTCATGTCCC	NM_021708.1
P01146.A12	ACATATTCCAGCTGCCAAGG	TTGTCCACCACCCAGACATC	NM_021803.1
P00806.E06	ATTTCTCCATGCTGTCCCTG	TGGTCCACAAATCAAGCTCC	NM_021803.1
P00428.G11	CAATGGAACATCCAGGAGC	ACCCGCTGCTGAGAGAAATC	NM_024013.1
P01126.B12	ATGGCAACCAGTTCCAGAAG	TGTCTCAGTTTACCCGCTGC	NM_024013.1
P01356.H03	CCCTTTGTGAAATGGGAAGC	TGTGTATGGAAGGCTGCGAG	NM_024298.1
P00824.E11	TGATGCGAAAGGTCTCCTGG	AATTCTGTGAACCAGGCTGC	NM_024298.1
P00842.A04	TGCTAAGGAAGGGATCCTGG	AACTGCCATTCTGTTGTGGG	NM_024298.1
P00827.A10	CATCACTCATGTCGACAGCC	TGTTGCTGCAGATACGGCAC	NM_024298.1
P00735.A03	ACAAAGGATCCCTGGCAATC	TCATTCCCAGCTCAGGTCAC	NM_024317.1
P00770.H01	CGTGCATCTGTCTGTGATGG	TGGTGCTCTCTCATGGATGG	NM_024317.1
P00799.F02	GAAAGCCCAAGCACTTGCAG	GAACCTGTGAAATCCCACCC	NM_024317.1
P00949.G06	AGTCACCGGTGGATGTTTCA	AGAAGAAGGATGGGTGAGGG	NM_024317.1
P01166.G09	TGGCTCTGATGTCGGCTATG	TCTCATTTTCAGCCCTCCCTG	NM_024317.1
P00788.F11	AGGAATGCAGCAACTGAGGG	GACGTGCCCTTCACATCACAG	NM_024317.1
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P00784.A02	AGTTCCGAGCCTTTGGTTTC	TCTGGCCAAACACAGAGTGG	NM_024873.2
P00896.E07	TTGTCTGGGAAGACACAGCC	AACTTGACCTGTGAGCCTCG	NM_024873.2
P01133.B01	TGCTTGTGGGTCTAAGGAGC	CCCTTATGGGAATGTGGGAC	NM_024873.2
P01134.B12	TTACCCATCGTGGCAACTTC	TGGAAACTTGGGCATGTCAG	NM_024873.2
P01122.G05	CACCCAAAGGTTAATTGGCG	ATGAATCTGCATGGGCTTTC	NM_024873.2
P01269.C02	TGTTTCGAAACACCCACTTG	AATTGGAGGAGTGGTGGCAG	NM_024873.2
P00726.F09	ATGCAAAACCAGGAGGAAGCC	AGGAAGAGCTGGGTGGTTTG	NM_024873.2
P00798.H11	TGTGTTTGGATGCCCAGTTC	AAGCTGACTCATCCACCAGC	NM_024873.2
P00759.H07	AACCCACAGAACTGGAAGGC	TCCTCCAGTGGGAGAACTG	NM_024873.2
P01238.B03	ATGGGATCCTCCAATTTCCC	TCGCCCTACAAGAAACCTGG	NM_031200.1
P00225.G01	ATGGGATCCTCCAATTTCCC	TCGCCCTACAAGAAACCTGG	NM_031200.1
P00222.H09	AATGTAACAGCCACCTGCC	AACCCTCTGTGCTGGACAAC	NM_031200.1
P01234.F04	AATGTAACAGCCACCTGCC	AACCCTCTGTGCTGGACAAC	NM_031200.1
P01137.G02	AGTGAGCAGATATGGGCAGC	AACTACGGATGCAGTGCCAG	NM_031200.1
P01115.G08	CAACTGACCACACCCACAAG	CTAAAGCAAGTGGCAAAGCC	NM_031200.1
P00977.H06	GTCTTCCAAGCACAAAGCCC	GACCTGGCATGGGTTATCAG	NM_031200.1

P01153.A02	TCATGTGCAAGGTGGTCAAC	GAGAATTGCGGGCATCACAG	NM_031200.1
P00254.C12	ATGTGGGTGTATGCTGGTGC	ATGGTCAATGGATGGCTGTG	NM_031200.1
P01314.H08	GCCTTCGTGAATGGAACGAG	ATGGCACACCAGGCAAGAAG	NM_031908.2
P01388.G12	CTGCAGCCAACTTCGTAC	TGGCATTGTGGATTCCATT	NM_031908.2
P01134.F10	TTATCTTCCAGCCTCACGCC	GACCTTTGATGCCAACACCG	NM_031908.2
P01160.H03	CATTTGCGTGGGATCCATT	TGGACTTGGGCTTACAGAGC	NM_031908.2
P01048.B08	CTCTGCCTGCCGTTCAATAC	CGCGTGGGAAACAATCACTC	NM_031908.2
P01194.G07	TTGTCAGGCTGTTCCGAATG	AAACAGTCATCCCACCTCC	NM_033130.1
P01188.F01	AGCACCTTTAGAAGGCAGCG	GGAAGCCTTAATGCCGAGTG	NM_033130.1
P01221.D08	TGAGGAAATGAACCCACCTG	AGACCCGTGGCATCTGTATG	NM_033130.1
P01229.H03	CACTCGGCATTAAGGCTTCC	CGATTCTGCCTCTTCCTTCC	NM_033130.1
P01230.D04	CCTCCAAGAACCTTGGCATC	TGGTTCCCTTTACCCAGAGG	NM_033130.1
P01244.B04	TCTCCTTCGTGCTCCACTTG	TCATGCAGTTTGTGTCTGGG	NM_033130.1
P01244.G01	AAGGGAACCATCCTGGACAC	ATTTACGTGACAACACGCC	NM_033130.1
P01209.H05	TAGAAGGGCAGGGCAGAATC	TCCCAAGGAACCAACCAAC	NM_033130.1
P01227.C05	ATTGTGAGCTGGCTTCAGGG	TTTCGGGTGGAGAGAGGAAG	NM_033130.1
P01226.E05	GACATTCTCAAAGGCCAG	GCTCATTTTCATGCATCAGGC	NM_033130.1
P01243.G11	GTGCTCATTTCCACCTCTCG	AAGGACCAGCTCAACAAGCC	NM_033130.1
P01023.E12	TGGTTGTTCCACTCAGTGCC	ATGGAGGAAGGAACCTCCTGG	NM_053003.1
P00718.F03	AACGTGCAGAGGAAGCAGAC	TCTGTGGCAAACCTCAGACC	NM_053003.1
P00827.D01	GGTTTGCCACAGACATGGAG	TTGCTGCCAAGCAGTGAGTG	NM_053003.1
P00989.G06	CCCAAACACACTTGTCCAGG	TGAGACTGTTTGCACCCTCC	NM_053003.1
P00799.G01	ATGAGAAGGTGCTCAGGTGG	TCTCCCTTTCATCACCAGCC	NM_053003.1
P00906.E12	CCATCACTTTGAGGACTGGG	AGACCAACAACCTGCTCCCTG	NM_053003.1
P00922.G05	AGAAGGTGGGCATGTGAGTC	GCATGTGGGTTTGCAGTTTC	NM_053003.1
P01347.C08	GTCAGGGCTGGTGATGAAAG	TGACATCCTCATCCTGCCTC	NM_053003.1
P01341.G05	TCAGAGGCAGGATGAGGATG	TCCTGTGAACCTGGGCTCTTC	NM_053003.1
P01112.C12	AAAGCCCTCATCACATTTGC	TGTTGAACCTCACCTCACGG	NM_053003.1
P00423.A07	CTTGACCAATGCCTCAAAGC	TGAAAGGAGCAGGGTGACTG	NM_138554.1
P00420.G05	CCCGATTCCATTGCTTCTTG	CCATTATTCCCTGCCACAG	NM_138554.1
P00872.F10	AATGGCTGGCAATTCTTTCC	TGGGACACCACAACAATCAC	NM_138554.1
P00678.B04	GAGCCTATCATTGCAGCCAG	CCCAGGGATGTTCAATCACC	NM_138554.1
P00950.H08	ATTGGTGTGTCGGTCCTCAG	GAGTTGGTTGAAATGCCAC	NM_138554.1
P01213.G02	TGGACCTTTCCAGCAACAAG	CGAGACTGGACAAGCCATTG	NM_138554.1
P00990.D07	TGGACCTTTCCAGCAACAAG	GGACAAGCCATTGAAGATGC	NM_138554.1
P01139.B09	GTGGGCATTTCAACCAACTC	CAAGGAGCATTGCCCAACAG	NM_138554.1
P01219.F02	GACCATCATTGGTGTGTCGG	GAAATGCCACCTGGAAGAC	NM_138554.1
P00411.B10	TGGGCCATGACTAAGGAAGG	ACTGCATGGTCTCCCAACTC	NM_138556.1
P00894.D05	AGGCAGGAGTCTGTGTTTGG	CAGGAATCCTAGAATGGCCC	NM_145021.1
P00455.A05	TGTGAAGCCAACACCAACTG	TGCTGAGGAGATCAAGCAGG	NM_145021.1
P01171.D06	CAACCCGCACACAATCAGAC	GTGCTCAGTGACATTCCACG	NM_145021.1
P00435.A04	TTGCGGAGATTCTCATGCTC	GCATTATCTTTGATCCTGGC	NM_145021.1
P00436.C08	ACACCGACAAGCAAGCAGTC	TTCCATGTTGGTGCGGTAAG	NM_145021.1
P00436.G12	AACAGCAGACTGCACGGAAC	ATAAACGGCCACTGGACCTG	NM_145021.1
P00440.B11	TGCCTGAGATTTCTTCTGCC	TCACTCTTTCGCCGTGACTC	NM_145021.1
P00440.B03	ATTCCAGCCATCTGGTGTCC	ATCCACCTGCCTCTTTCAGG	NM_145021.1
P00438.H01	ACCAGGAATCACGAAATGGC	CTGTTGCTTTGTTGTGGTGG	NM_145021.1
P01071.E11	GGAGGGTGATGACAGGATTG	AGCGTTACCCACAGAACC	NM_145256.1
P00824.A06	AAACCCAGTTGAGGCATGAG	CCAATCCTGTCATCACCTC	NM_145256.1
P00964.G12	TGGCAAGTCCAAGAAGCAGG	ATTTGCATAGGGTCCCGTCC	NM_145256.1
P00689.B03	GCAATAAGCGGTTGCCCTTG	TTCTAGCAAGAGGGAAGCGG	NM_145256.1
P00411.B02	GGTCTTGCTTCTTTAGGG	GGGCAAACATCTCCAAGTCC	NM_147162.1
P00404.E02	TTCTTAACCTGGTGTTGCC	CTTCTGGCAACCTTTGTCCC	NM_147164.1

Table 7: PCR primers

Number	For	Rev	RefSEQ
S01201.G09	GGAGAGAAGACTACGAAGC	ACCATCATCCATCATTTG	NM_000074.1
S01200.A03	CCGTGGAAATGAATGTAG	ATTGGCATTGTCAAGTTTC	NM_000074.1
S01234.A06	TCCTCACCAGAAACAGAC	CACTGGGTTGTTCAATATG	NM_000074.1
S01216.H01	CAGTGGGAGAGATGTCAG	GGTAACATGACTTCGGC	NM_000074.1
S00895.G07	TGACTCTGGGTTCTATG	CAAATGCTTCCTCTTTCC	NM_000074.1
S01193.G11	AACAGTGTACCTTGCAG	AATAACTGTCCGAGAGGG	NM_000074.1
S01193.G10	TGACTCTGGGTTCTATG	CAAATGCTTCCTCTTTCC	NM_000074.1
S01193.G12	TCCATCCCTATACAAAGC	AAATAGGCAGTTAACAGGG	NM_000074.1
S01021.D02	AACAGTGTACCTTGCAG	AATAACTGTCCGAGAGGG	NM_000074.1
S00983.F06	ACTTAGGGCTACAGGACC	AGCATGCTGCAGTCTATC	NM_000206.1
S00726.E03	CTGACAGTTAGTGCAGGG	TTCATATGGGACAACTGG	NM_000206.1
S00987.B10	TTACTCCTAAAGACCCTGC	TATGTCTTTAGCGCGG	NM_000206.1
S01094.C12	TTAGTGACAGGGAAGTGG	TGGGTGTTTCAAGAGTATG	NM_000206.1
S01310.G06	ATCTGTCTGGTTGAATCC	AGGGAGGAGGTATTAGGG	NM_000206.1
S00793.H11	TAATACCTCCTCCCTTCC	TAGGCTCTGGATATCTGC	NM_000206.1
S01158.E11	AGAGCCTAGCCTCATCTC	TTACAGACATGAGCCACC	NM_000206.1
S00985.H06	GCACCAGATCTCTGTACG	GCTATGACAGAGGAAACG	NM_000206.1
S00785.D05	GCAGGAACACAGGACTTC	GAGAGACAGAGGGAGGG	NM_000395.1
S00712.G07	GGACATCCCAAAGCAG	CTGACAGGTCCCTCTCTAC	NM_000395.1
S00784.E07	GAGGCTCACAGAGGAGAC	AGGAGACAGTGGGTGC	NM_000395.1
S01153.D12	CTCTTGGGAGGTAGGAAC	CTACTGGAAGATGGCAG	NM_000395.1
S00965.E02	GCTCATGACCTCTGTGTG	ACAGGAGGAAGCTTGG	NM_000395.1
S00718.A04	CTCTCTCCAAGCTTCCTC	GATTCGGGTACACAATG	NM_000395.1
S00740.A05	GTCTAGCATGAGACACGG	CTCTGGTTGCTTTCCC	NM_000395.1
S00728.C02	GTATGGCAGGAGCTAGG	CTACAAGTTGTTGCAGGC	NM_000395.1
S00798.C04	CAAGGCAGTAAGTTCCAG	GTGACAGCCATCAGAGAC	NM_000395.1
S01069.F07	GGCATCTACGGGTACAG	ACCTACATCCCTACCACC	NM_000395.1
S00802.C03	GATTCTTCTCTTGTCTGGG	CTGATTTCCACAATGGAG	NM_000395.1
S01357.D05	GTGGAAGTGGAGAGAAGG	GGAAGAAGGTTTACTCCG	NM_000395.1
S01355.E03	TTCCAGAGAACCCTCTCC	TTTGGTCTGTCTCTCC	NM_000395.1
S01392.F03	CCTGTCCTGAACCCAG	GGGAGAGAAGTGATTTGC	NM_000395.1
S00344.E12	TAATGCATGGAACAAGC	CGTAAAGAGGATGTGTGG	NM_000416.1
S00319.A04	GACTGACTGATTGATGGC	AACTCTGGCCCTATTAC	NM_000416.1
S00322.G01	TGAGTTTGCTTCTCTCAC	CAGTTGTTTGACCAGGAC	NM_000416.1
S00333.D06	GATCTGTGAGTCTTGCTTG	GGTTGATTGATAGATTCTGG	NM_000416.1
S00324.G12	AAATTCCTCCAAGTGTTC	AAAGCAAAGCACAGACAG	NM_000416.1
S00345.C08	AGGCTGATGAAAGAACAC	ATATCTGGGCAATGTGG	NM_000416.1
S00329.F10	GAGTTCAAACCACGGAG	CAGAAGTCCAGGTCCC	NM_000416.1
S00238.C06	TAAGAACCGAATGACAGC	TTTGGAAGTCTTGGTACG	NM_000564.1
S00227.H06	AGAACCCTCTGCCTACC	CTGAGCTGTCTGATGACC	NM_000564.1
S00221.E11	TAAGACCCACGAGTGAAC	CATTCTGATAATCGGCAG	NM_000564.1
S00249.B02	AAGGCCAGTAAGATTTGG	GGGTGGATTGGAATTATC	NM_000564.1
S00251.G06	TTATAACCCTTCCTTCCAG	TTGTTGGCACAGATGC	NM_000564.1
S00250.H08	CTTTGCTGTATTCTTGGC	AATACGACGTTACATCAC	NM_000564.1
S00228.E11	GATAAGAAGTGGCAGCAG	CGTTCATGTGTATTGAG	NM_000564.1
S00239.G12	TGGTAACATAACATAGAGCC	CTGTGTCTGTGGTGCTG	NM_000564.1
S00222.E06	GCATCTGTCTTCTGATGG	TCTGTAAATGGCCAAAC	NM_000564.1
S00219.B01	GGAAACAAATAGGAAGGG	AAACAAATCAACAAACAAAC	NM_000564.1
S00253.H04	TTTGCTACAAATATCCAG	ATTCCTCTGTTAGGTTTAC	NM_000564.1
S00226.F12	AGGGTATTGTTACAGCCC	TGAAAGAGTGAAGAACCG	NM_000564.1

S00162.E10	CAGAATTCATTACCCAC	CCAACCACTTCATTCTTG	NM_000572.1
S01123.E08	TCGTTACAGAGAAGCTC	TCATGTGAATACGTGACC	NM_000572.1
S00100.E08	AGGTTCCCACACTCTCTC	GATAAATCTGGCCTCCTC	NM_000572.1
S00117.G07	CTCCAGGAGTCTTTCCTC	AAGGAGGATCGCTAGAAC	NM_000572.1
S00099.F01	CAATCAGGAAGCAGAGTC	TCCCATCACTGTTGAATC	NM_000572.1
S01175.F12	CAATCAGGAAGCAGAGTC	TCCCATCACTGTTGAATC	NM_000572.1
S00133.A02	GGGTTCTTATAGTTCCAGG	GAAACCTTGATTGTGGC	NM_000572.1
S01204.F01	CAGAATTCATTACCCAC	CCAACCACTTCATTCTTG	NM_000572.2
S01203.D06	GACCTCAAGTGATCCACC	CCCTTGAGAAACCTTATTG	NM_000572.2
S01217.A02	TCGTTACAGAGAAGCTC	TCATGTGAATACGTGACC	NM_000572.2
S01237.G04	AGGTTCCCACACTCTCTC	GATAAATCTGGCCTCCTC	NM_000572.2
S01221.H05	CTCCAGGAGTCTTTCCTC	AAGGAGGATCGCTAGAAC	NM_000572.2
S01234.G12	CAATCAGGAAGCAGAGTC	TCCCATCACTGTTGAATC	NM_000572.2
S01218.G10	GGGTTCTTATAGTTCCAGG	GAAACCTTGATTGTGGC	NM_000572.2
S01234.E09	TTGTTAGAGGTGTCTGCC	ACACACACCATGCACAC	NM_000575.3
S01200.E01	TTGCAAGCAGAAAGATTG	TCTTTGCTTCCTCATCTG	NM_000575.3
S01234.H08	CCCTAAATTCTACTGTCCC	AATGGAGATCCTCCTCAC	NM_000575.3
S01213.E04	CATTGCTGTTCTCTTTGG	GGTCATTAAAGTACATTGGC	NM_000575.3
S01216.G04	TTCTCTGAACCTGCTCTG	TTCAGGAAGCACAAAGAG	NM_000575.3
S01193.D07	GTGAAATCCGAAGTCAAG	TAGTAACCAGGCAACACC	NM_000575.3
S01193.D08	CCAGTGGCTAAGTTTGG	TTATTTCTGTGGCTCCTG	NM_000575.3
S01193.D05	GAGAAGGCAATGTGAGAG	GAGCTGCCAAGTATTCTG	NM_000575.3
S00200.D09	GAGGAGTGGGCTTTAGTC	CTGCCTTAGGGTAGTGC	NM_000576.1
S00841.G10	CGGGCTTTAAGTGAGTAG	ACCTGCTCGTCAGTTTC	NM_000576.1
S00179.E12	GAGAAGGTGGTTGTCTGG	GGGAAACCCTAAATCAAC	NM_000576.1
S00173.F01	ACTTGTGTTGATCATTTC	GTCATCAGACTTTGACCG	NM_000576.1
S00204.E09	TAAAGGGCTTTGGCTC	CCTCCTCTCTGAGCTTTC	NM_000576.1
S00190.F02	CCTGTGTCTCACTGGAAG	TCTTGACACAGGGAAGG	NM_000576.1
S00171.H11	TCAGATTTACTTGGCACC	ATTTCTTTGCATGACTGC	NM_000576.1
S00177.F02	GCATACACACAAAGAGGC	AAGAAGCTTCCACCAATAC	NM_000576.1
S01203.E12	GAGGAGTGGGCTTTAGTC	CTGCCTTAGGGTAGTGC	NM_000576.2
S01203.E11	CGGGCTTTAAGTGAGTAG	ACCTGCTCGTCAGTTTC	NM_000576.2
S01236.D02	GAGAAGGTGGTTGTCTGG	GGGAAACCCTAAATCAAC	NM_000576.2
S01235.D02	ACTTGTGTTGATCATTTC	GTCATCAGACTTTGACCG	NM_000576.2
S01204.D08	TAAAGGGCTTTGGCTC	CCTCCTCTCTGAGCTTTC	NM_000576.2
S01217.F01	CCTGTGTCTCACTGGAAG	TCTTGACACAGGGAAGG	NM_000576.2
S01235.G04	TCAGATTTACTTGGCACC	ATTTCTTTGCATGACTGC	NM_000576.2
S01234.G09	GCATACACACAAAGAGGC	AAGAAGCTTCCACCAATAC	NM_000576.2
S01234.H10	TTTCAGATGTCACCAACC	TTTAACTATGGGCTCACG	NM_000579.1
S01214.E04	AAATCATTTGCTTCTTGG	TGTTTGCCAAATGTCTTC	NM_000579.1
S01213.H06	TGACTTTCTCAGCCTCTG	CTTATGGCACCAATTCTC	NM_000579.1
S01203.A06	GTCTTCTCCTGAACACC	TAAGGAACTTTCGGAGTG	NM_000579.1
S01140.E06	CAAGCTTGGCTGTAGAAG	CTCAGTATTTAGCTGGG	NM_000579.1
S01086.C11	TGACTTTCTCAGCCTCTG	CTTATGGCACCAATTCTC	NM_000579.1
S01220.G02	CAAGCTTGGCTGTAGAAG	CTCAGTATTTAGCTGGG	NM_000579.1
S00985.D09	AGCCCATCAATTATAGAAAG	TCATGACTTAGACGGAGC	NM_000579.1
S01219.G05	CTTCATCATCCTCCTGAC	CTCTGTCACCTGCATAGC	NM_000579.1
S01217.F08	AACAGTTTGCATTCATGG	ATGATTCTGGGAGAGAC	NM_000579.1
S00835.E10	CTTCATCATCCTCCTGAC	CTCTGTCACCTGCATAGC	NM_000579.1
S01218.A04	TTGAACACAGTCTCACCC	TGTTGCTTCTGGTTTGTC	NM_000579.1
S01102.B04	TTGAACACAGTCTCACCC	TGTTGCTTCTGGTTTGTC	NM_000579.1
S01217.A07	AGCCCATCAATTATAGAAAG	TCATGACTTAGACGGAGC	NM_000579.1
S01201.E05	CATTTGGAAATAAGCTGC	GCTACTGTTGCACTCTCC	NM_000579.1
S00269.G01	AAGATGAGGGTGCATAAG	AGCATCAAGAATAGCTTTG	NM_000584.1

S00270.H07	AGAAAGGAAGTAGCTGGC	TCCTAAATATTTCCACCTTC	NM_000584.1
S00273.C01	TTGGACTTAGACTTTATGCC	GGCAGATACCTAATGACG	NM_000584.1
S00276.D08	AACACATGAATGTCAAAGAC	AGGGTTGCCAGATTTAAC	NM_000584.1
S01191.E04	GTGATGACTCAGGTTTGC	TGTTTGTACCAAAGCATC	NM_000584.2
S01199.D09	AGAAAGGAAGTAGCTGGC	TCCTAAATATTTCCACCTTC	NM_000584.2
S01190.A12	AACAAACAAACAATTGGG	TTCTGGAAAGGAGTTCTG	NM_000584.2
S01190.B04	TGGGTTTGCTAGAATGTG	ACTGGGAGTATCAAAGTAGG	NM_000584.2
S01190.A11	AACACATGAATGTCAAAGAC	AGGGTTGCCAGATTTAAC	NM_000584.2
S01151.B09	CGGCTCTTTCTCTTTCAC	GTAACGCTGGAGCTGG	NM_000585.1
S00747.G08	ATTAATTCCTCCCTTTC	CCATGTAACCTATTGCAAAG	NM_000585.1
S00923.C11	AGAAGCAAGGATAAACTG	GGTTTCCTTAAGACAGACAG	NM_000585.1
S01230.D06	CAGTCAGTCATCCAGGAG	GATAGACCGGAGGGTAAC	NM_000585.2
S01184.E08	AATCTGAGGAAGGGAGG	AGCATGCAATAACAAAGG	NM_000585.2
S01233.C11	ATTAATTCCTCCCTTTC	CCATGTAACCTATTGCAAAG	NM_000585.2
S01198.C07	GAGGTGGGAGAGAAAGTG	AAGCAAACCTGAACGTAAAC	NM_000585.2
S01233.B01	AGAAGCAAGGATAAACTG	GGTTTCCTTAAGACAGACAG	NM_000585.2
S01184.D10	TGTTGAAGGGTACACAGG	CAAGTCCCCTCTCAATAATC	NM_000585.2
S01191.E09	AATTAAGCTGCCTCCTATG	ACAGGACTCCTTCTCCTG	NM_000585.2
S00290.E07	GCTGCTGCACATATAAGG	CCATTGAGGTTGTTGAAG	NM_000588.1
S00283.A01	GGATAAGACTGGCCTGC	GTAAGATGGAATGACATGG	NM_000588.1
S00283.B02	GGGTGACTTCCACCTG	AGATGGTCAGAGATTCCC	NM_000588.1
S00284.A06	CAGCAATTGAGAGCATTC	AAGAAACCAAGAAGGTGG	NM_000588.1
S00289.H08	CTCCTCAGCTGGTCATC	CAGTTCACACTCCAGGC	NM_000588.1
S00291.C11	CAAGTGACTGACAATCTGG	TCCAACCTCTCTAGCAGC	NM_000589.1
S00297.C11	AGTTGGAGGGAGTGAGAG	CCTTAGAGTTAATTTGGGC	NM_000589.1
S00309.A04	ATTTGTCCTCCTGGAAAG	GAATGAATGAATGGGTTG	NM_000589.1
S00291.F10	GACAAGTGCCACAGTAGG	GCTCCCATAGCATTTATAG	NM_000589.1
S01177.E12	GACAAGTGCCACAGTAGG	GCTCCCATAGCATTTATAG	NM_000589.1
S01204.H02	AGATGCCACCTGTACTTG	ATAGGTGTGATTTGCAG	NM_000589.2
S01215.H05	GACAAGTGCCACAGTAGG	GCTCCCATAGCATTTATAG	NM_000589.2
S00299.H11	TTCTTTGTTCTGAGCAGC	CCACCTATTTGCTCTGTG	NM_000590.1
S00286.B02	AAACAGGGTTGGCATC	ATACGGGAGATCACTTCC	NM_000590.1
S00294.E10	TCAAACCTTCTCAAGAGGC	ACTGCAGTGCTAATGTGAG	NM_000590.1
S00287.G03	TTCAGAGTGAAGATTCCAG	CATGGGAAAGACAGCTAC	NM_000590.1
S00284.B02	AGAACCTTTAGTCAGCCC	AAGTGGGCTCTTGGTATC	NM_000590.1
S00357.H07	AAAGATTTATCAAATGTGGG	ACAGCACAGCTGGGAG	NM_000600.1
S01225.F10	AAAGATTTATCAAATGTGGG	ACAGCACAGCTGGGAG	NM_000600.1
S00356.C10	TCCACAAGTAAGTGCAGG	TTGGCCTCAAATCTACAG	NM_000600.1
S01227.D09	TCCACAAGTAAGTGCAGG	TTGGCCTCAAATCTACAG	NM_000600.1
S01216.F03	GCTGTGGTTGAACAATG	GCTGCCTGGATCTATATG	NM_000600.1
S00363.H09	GCTGTGGTTGAACAATG	GCTGCCTGGATCTATATG	NM_000600.1
S00350.B05	CTCTAGAGGAGCAGAGGG	ATTGCATCCCTGAGTTG	NM_000600.1
S01234.F08	CTCTAGAGGAGCAGAGGG	ATTGCATCCCTGAGTTG	NM_000600.1
S00963.G01	CAGGATTACACAACCCTC	GTGATCGTCTGACTGGTG	NM_000609.1
S01038.F05	AGTAAAGATCCCTCAGGC	CTTCTTCACCATTTGGC	NM_000609.1
S01010.G11	CCTCTTGGTGGCTCTC	CCTCCCGTCTGTTGTC	NM_000609.1
S01150.E02	GACGCACTTGACTAGCAG	AAATTGGAGCTTCATGG	NM_000609.1
S01300.E04	CTCAAATTCTCATCCAGC	CCCAGCTAAAGCAATATG	NM_000609.1
S01330.A12	TGCATCAAGACATTGGTC	GAGCCACTCCTCTGACTC	NM_000609.1
S01308.A05	TCAGGCAGGTTGACTTAC	ACATCTGTGTCTTGTGTTGG	NM_000609.1
S00833.D05	TTGCCCTTTCATCTCTC	GAGCGTACCAAGTGGAG	NM_000609.1
S01061.E09	ACCTTTAATAAGACTCGGG	ATCCTTAATCGCTGCAC	NM_000609.1
S01364.H10	TCTCTGCAGGTCACAAAC	AGCCTGAGAAGGTCAAAG	NM_000609.1
S01191.E03	TTTAATGGAACCAAATGC	ATTAGGCAAGGCTATGTG	NM_000619.1

S01191.E01	GAAACAGCATCTGACTCC	ACAGTGAGAATCATTGACC	NM_000619.1
S00527.B02	TTTAATGGAACCAAATGC	ATTAGGCAAGGCTATGTG	NM_000619.1
S01191.E02	TGAAATAAACACACAACCC	TTTCCCGATAGGTAAGT	NM_000619.1
S01191.H10	CAGCCATGAGTTGAGTTC	GCTGAATATTCCCATTG	NM_000619.1
S00525.C12	CAGCCATGAGTTGAGTTC	GCTGAATATTCCCATTG	NM_000619.1
S01212.H11	GAGCACAAACAGAGGATG	TCTGAGTTCAATGAACTTG	NM_000619.1
S00512.F07	GAGCACAAACAGAGGATG	TCTGAGTTCAATGAACTTG	NM_000619.1
S01200.A05	AGATGCTACAGCAAGTCG	CGTAATCCTCAGGAGACTTC	NM_000619.1
S00515.H12	AGATGCTACAGCAAGTCG	CGTAATCCTCAGGAGACTTC	NM_000619.1
S00082.A11	GTGTGTGTCAGAAGAGGC	GTCGGGTTTAATCTTTGG	NM_000629.1
S00080.C07	CAGGGATGTGAGGGATAG	CCAAACACTTTCCAAATC	NM_000629.1
S00672.B10	AAGAGTGGAAGGGTGTATG	GAATGGCTTGGAAGTG	NM_000629.1
S00672.G01	TAACCTCCAGAAAGTGGC	TCCATGACGTAAGTAGTGC	NM_000629.1
S00088.H03	CCTCTGTTTAATCGATGTG	AAACTTCAGCAATATGGG	NM_000629.1
S00091.F05	AGCCTTTATCTTCTTGCC	AGTCGGTCATTCTGTGTG	NM_000629.1
S00091.D02	CCCTAACATAGTGTCTGGC	TGGAGGAAGTAGGAAAGC	NM_000629.1
S00091.H05	TGTAATTCTCTGGTGCAAG	CTGAAGTGCTGGGATTAC	NM_000629.1
S00093.D03	GAGGCCAATGTTAGACTG	CGACTTGAGAGTTAAGCG	NM_000629.1
S00088.A03	CACACAGCTGTCAGCAC	AGCTTTGAAGAAGATACCC	NM_000629.1
S00842.D08	TCTGTGTTCTGTCCATC	CAGTCTCCTATCATTGCC	NM_000629.1
S00093.A01	ATGCATGCCAGAAGATAG	TCAGCCTCCCAAAGTG	NM_000629.1
S00915.G03	AGTTCTTCCCTGTCCAAC	GAACAAATTTACTTCCAAGC	NM_000639.1
S01205.H11	AGCTTCTTGAGGCTTCTC	TGGTTCCCTCTCTTCTTC	NM_000639.1
S01205.G08	AGTTCTTCCCTGTCCAAC	GAACAAATTTACTTCCAAGC	NM_000639.1
S01215.B06	TTATTTGACGATTCTGCC	AAGGCATTCCATTAACATAG	NM_000639.1
S01215.G07	AGACTGTTGCCATTTACG	GGGTTCAAATACTGTCTCC	NM_000639.1
S01202.D02	TAAGAGAAGCACTTTGGG	AGGAATGAAATGAGTCCC	NM_000639.1
S01201.C06	GGCAGCATCTTCACTTC	TGGTAATGGAACTCTGG	NM_000639.1
S01203.A12	TGTCATTCTGGGTGAAAC	ATGCATGTAAGAAGACCC	NM_000639.1
S01342.B06	AGGAGAATTGCTTGAACC	TTATTTGAGGAGCAGGG	NM_000641.1
S01387.G05	CCCACACTTAGTGACACAG	CATCTGTGGATAGAACGC	NM_000641.1
S00914.A06	TGTGGACAGACTTCTTGG	CGGCCTAAACACTTCAC	NM_000641.1
S01050.A12	CCCACACTTAGTGACACAG	CATCTGTGGATAGAACGC	NM_000641.1
S00741.F02	GTCTCAGGCTTCAAGGAC	TCTACAGGTAAGGGCAAG	NM_000641.1
S00222.E12	CTCCGCCTTCACTTTC	CATTTCCAGCTTTGAGG	NM_000647.3
S01237.E03	CTCCGCCTTCACTTTC	CATTTCCAGCTTTGAGG	NM_000647.3
S01194.B09	TGCCAGACTATTTGGAAG	CACAGCATGGACAATAGC	NM_000647.3
S00970.D10	TTTCTCTTCTGGACTCCC	AAAGAGGATTAGCACAAGG	NM_000647.3
S00881.F11	CAAATGAGTGGGTCTTTG	ATGCAGCAGTGAGTCATC	NM_000647.3
S01194.B12	TTTCTCTTCTGGACTCCC	AAAGAGGATTAGCACAAGG	NM_000647.3
S00247.F03	TGCCAGACTATTTGGAAG	CACAGCATGGACAATAGC	NM_000647.3
S01194.B11	CAAATGAGTGGGTCTTTG	ATGCAGCAGTGAGTCATC	NM_000647.3
S00887.F10	TTCCAAACTACCTTCCAG	TCTTTGCTTACTTCAGGG	NM_000647.3
S00249.F07	TCTTGTCTGGATCTGAGC	TTTCACGTTTGACATGATAG	NM_000647.3
S01193.F05	TCTTGTCTGGATCTGAGC	TTTCACGTTTGACATGATAG	NM_000647.3
S01193.H05	TTCCAAACTACCTTCCAG	TCTTTGCTTACTTCAGGG	NM_000647.3
S01193.H04	CAGTGGGAACCTCTAAATC	GGTTGTGTGGCCTGTAG	NM_000647.3
S01218.A10	GTGGAGTCCGATGATTC	CGAGGAGTCCTTGTGTAG	NM_000648.1
S01083.C01	GACTATGTCACCCAATGC	GCCTAAGAAGCATCTGAAC	NM_000648.1
S00924.E02	GTGGAGTCCGATGATTC	CGAGGAGTCCTTGTGTAG	NM_000648.1
S01203.B07	GACTATGTCACCCAATGC	GCCTAAGAAGCATCTGAAC	NM_000648.1
S00287.G10	CATGTGTGGCTGATAAGG	GTTATCAAGCTGACAGGC	NM_000758.1
S00283.C02	AGAGACACTGCTGCTGAG	AGAGAAAGTGGACAACCC	NM_000758.1
S00285.H12	AGGAGTGGTGGAGAGTTC	AACAGCCACAGCCATAG	NM_000758.1

S00301.C03	GGCAGTAGAGAAACATGC	AATATTCCCATTCTTCTGC	NM_000758.1
S01170.A05	AGGATGGTCATCTTGGAG	GTGGTGCCCTTCTCTG	NM_000758.1
S00881.C04	ACACAGTCGTCCTCCTG	ACCATGCTGAGTCTGAAC	NM_000760.1
S00144.D03	CCAACTCTGAGAAGTTTCC	CACTATCTCCGCTGTGAC	NM_000760.1
S00106.B09	GGAAGGCCTGAGTACTTG	TTCTCTCTGCACTAAGGG	NM_000760.1
S00100.G03	AAGGGACTTAGATGGGC	GGACTGACTTTGAATCCC	NM_000760.1
S00105.G10	GGATTCAAAGTCAGTCCC	TACACCATCTTCTGGACC	NM_000760.1
S00112.B04	GATGGTAAAGCTGCCTC	GCCACAAGAAGTCCAAC	NM_000760.1
S00108.G07	TATGGTAGGAAGGCAATG	GCCCTCACTAGAGGTCTG	NM_000760.1
S00149.F05	AAGAAAGGCTGGAGAATC	GTAAATAGCAAAGCCAGG	NM_000760.1
S00136.F09	TAGATTTAACCAGGCAG	TTGTATGATCCATCCACC	NM_000760.1
S00106.H06	CGGTTTGTAGGGATCTG	GGGTAAGGAGGTGATGAG	NM_000760.1
S01182.G09	TGTGGATGGAACAAGAAG	ACTGGTGAGGCAGAGG	NM_000760.1
S00116.G04	TGTGGATGGAACAAGAAG	ACTGGTGAGGCAGAGG	NM_000760.1
S00136.B11	TGGACAGGACTCTGAGC	ATGGTGAACCACAGACAG	NM_000760.1
S00114.C07	TGTGCCTCTGTCTCTAGG	ATGGGTAGGATGCTGG	NM_000760.1
S00095.H09	AGCATCCTACCCATGC	GACAACAGAGGAACCAAG	NM_000760.1
S00146.F02	AAAGTGCTGGAATACAG	GAGGCCTCTGAGTCTAGG	NM_000760.1
S00105.G11	GTGGCTCAGACTTGAATC	TGCACAGTGACAGACAAG	NM_000760.1
S00129.H09	GCATGGTCTCACTCTCTG	ACCTATGGTTGCTGAGTG	NM_000760.1
S00121.G02	GACATGAACACTTGGCAG	CTCACCAGCTTCCCTC	NM_000760.1
S00189.G03	ACATGCCTCTTGAGATCC	AATGGGAGATAGTCCAGG	NM_000877.1
S00191.H02	ATCAGTGTGACTTGTGGG	TGACTCTGTTAGGGAAGG	NM_000877.1
S00218.F10	ATAATCAATGTGTTTCTTCG	AGTTAGGCTCATTCTCCAC	NM_000877.1
S00197.C08	TTCCTGCAGTTGTTAAGG	TTCCCTATCAAGTTTCACC	NM_000877.1
S00202.C01	TTTGGCGGTAGATTGG	GTGGTATCATTGAGGTCTG	NM_000877.1
S00172.G08	TGGCCAGAAGTCATTTAG	TCACTTTCCCTCCATTG	NM_000877.1
S00212.H01	CTGCACATGTTACAGAG	TAACTGAACCGACAAGG	NM_000877.1
S00206.B12	GTTGTGACTGTGATTGGG	GAAGCGTGTTCTAAGCAG	NM_000877.1
S00189.A04	TCCCAGATATGGGCTC	AAACCTCTTAGTCATCTTC	NM_000877.1
S00199.A07	GGTATTGCTGCTTCAGTC	CCTATGCCACGATCTTC	NM_000877.1
S01310.H10	CAGTTACTGTCACCAGCC	CAGAGAGGGCATTATTG	NM_000877.1
S01286.H09	TTCAGGTCAATAACGGTC	TTTCAAGACGTGACATCC	NM_000877.1
S01299.D09	TCCTTTGCCTAGGAGG	TTGGAATTTGGTGTCTTG	NM_000877.1
S01325.F06	AACAAAGGGATTCTCCAG	GAGGAAGTCGCCTCTTAG	NM_000877.1
S01355.D11	CCTGGCCATCTGTCTAC	ACCAACCAGGGTTACTTC	NM_000878.1
S01355.D10	GAAGAGGTCAGGGCAG	AGGGCCCTTAATGCTC	NM_000878.1
S01348.D01	AGGAAAGATACGTGGAGG	AACTTCTAGCGTCAGTGC	NM_000878.1
S01299.A03	ATGTCTTCGACAGCTCC	ACCATTTGGTCAGGATTC	NM_000878.1
S01339.E10	TTTCAAGGCATAGACCC	ATTCACACAGAGAGGCAG	NM_000878.1
S01118.E08	AGCTACTAACCTGCCACC	GAACACTTAGTATCGGCG	NM_000878.1
S00755.E10	GTATGTGTGCTTGTGTGC	TTTAGCATGAAATCTGGC	NM_000878.1
S01348.D02	ACTGCTATACCCTCACCC	TCTGTGATGCTCAGCC	NM_000878.1
S00845.B07	ATCCTGCTTAGCCACAG	GCAGCAGAGAGATCTGAG	NM_000878.1
S01053.A12	TAAACGTTGACTCCTTGG	GTCCATGAATCCCTTCTC	NM_000878.1
S01328.H12	TCTGGGAAGAGGCTTTAG	GACCATGCACACTGAGG	NM_000878.1
S00803.B02	TCTGTGACTTTCACTCCC	GGAGTTTCAGGCTTTCTC	NM_000878.1
S00305.A03	AGACCCTTCCTCCAAAC	GGTGTAATGAACACCGAG	NM_000879.1
S00297.H11	GGAAACTGTCAATTCCATAG	ATTGCAGAATGGACAATG	NM_000879.1
S00284.A04	ACAGACATTCACAGCCAC	CATCACCAGCAAACATTC	NM_000879.1
S00296.G11	CCATGTACTAATGTGCTCAG	TGCCATTATTAGGCATTC	NM_000879.1
S01190.H01	ACTCTTTCTTGGCCCTC	CAAAGCCTAACTTTGTGG	NM_000879.2
S01190.G12	AGACCCTTCCTCCAAAC	GGTGTAATGAACACCGAG	NM_000879.2
S01233.B10	ACAGACATTCACAGCCAC	CATCACCAGCAAACATTC	NM_000879.2

S01199.D10	CCATGTACTAATGTGCTCAG	TGCCATTATTAGGCATTC	NM_000879.2
S00677.D02	ATCTCCCAAATTGCAAAC	CTGAATGCTCCAGTCAAC	NM_000880.1
S00399.C01	AAATGCAATTTAAAGGAATC	AGCAATTACAAACAACCTGG	NM_000880.1
S00395.C02	TGATCATCAGAGAATAGTGG	CTCAAGCTCTAGGCTCC	NM_000880.1
S00396.C02	ATTATGTGATCAGGCTGC	TAGTCAGCTGAGCCAGG	NM_000880.1
S00677.C01	GGGAAATAGGACTGAAATG	TAGTGGTCCAGTCCATTG	NM_000880.1
S00386.F07	GACTTGCCTAGGAGCAG	CGTTGAGAGATCATCTGG	NM_000880.1
S00221.G06	GAGTTAATCCGAAAGCG	TTTCTACCCACTCTTCCC	NM_000882.1
S00230.B01	TCTCTCAGGTGTTGAAGG	TTTCTCTGCAGTTCCATC	NM_000882.1
S00242.F06	GACAGAGGTCAAGGGC	AGAAGCAGGTGAGATTG	NM_000882.1
S00223.F09	TTTGCAACAATGTGAATAC	CAACTCCCATTCTAGAGG	NM_000882.1
S00233.C11	TGCCTAAATTCCAGAGAG	GTGACATGACAAGATGGG	NM_000882.1
S00236.E05	CAGCTCTTTCCTCAAATG	TTATCAAAGACCCTGGC	NM_000882.1
S00242.C05	TAAGGGACTGAGTTGCAG	TTTCCACAAACACTTTGG	NM_000882.1
S01228.F04	GGCACTCCTCTCTCTACG	TTTCTACCCACTCTTCCC	NM_000882.2
S01222.E02	TCTCTCAGGTGTTGAAGG	TTTCTCTGCAGTTCCATC	NM_000882.2
S01201.F03	GACAGAGGTCAAGGGC	AGAAGCAGGTGAGATTG	NM_000882.2
S01233.B04	TTTGCAACAATGTGAATAC	CAACTCCCATTCTAGAGG	NM_000882.2
S01185.B12	TGCCTAAATTCCAGAGAG	GTGACATGACAAGATGGG	NM_000882.2
S01185.C01	CAGCTCTTTCCTCAAATG	TTATCAAAGACCCTGGC	NM_000882.2
S01199.C12	ACATGTACTGGCTTCACTC	TGCTTTCATGATTACCAAG	NM_000882.2
S01356.D02	ACGAATTCCTTCCAGC	GTAGAATAAAGAGGGCCG	NM_001065.1
S01391.E05	TGTCTCCTACTCAGCCAG	CACTTCCTCTGTCCTGTG	NM_001065.1
S01324.A10	CAACTGGAAGAAGCAGAG	AACCTAGTGAGTGCGTG	NM_001065.1
S01349.G03	AGTGGCTGAGGTTAGGAC	CACTGCCTCACTCTTCC	NM_001065.1
S00139.E01	GTGACGCTGGAGGTATC	GTGTCTGATGCGGATG	NM_001066.1
S00126.B11	CCAAACATTTGCAGGG	AAGAATCAAGGGCTATGC	NM_001066.1
S00104.C11	AACTCTGGACTTTGTGGG	CAAAGAGGCTGGAGTTG	NM_001066.1
S00119.D10	AGTGCTGGGCTGTCTG	GTGACACTGCAAGGATG	NM_001066.1
S00118.A11	GACCTCTCCTAGGGCTC	AAAGCAGTCTGGACAATG	NM_001066.1
S00110.D07	CCTATCCTGCCTGCTG	GGAGAGGAAGAAAGAGAGAC	NM_001066.1
S00114.E06	ATCTCCGGCCTAGACTC	AGTGCTGGACTCACAGG	NM_001066.1
S00099.F03	CCATACTGCCCTCCTAC	CACTGCTTCTCTGTGAC	NM_001066.1
S00112.D09	ACTGAGAAGTGCTGATGG	GGAGGAGATGGCTAAGAC	NM_001066.1
S00168.B02	TTCCCATGTGTCTGAATC	AGAGGCTTTCACAACCTC	NM_001066.1
S01169.E02	GGAAAGCATCACCTCAG	TAGGACAGCAAGGAAGG	NM_001066.1
S00885.G10	GAAACCAGTGTAGCCTTG	GTCTTGGGATCAACACAC	NM_001066.1
S00832.G04	ACAAAGCCAAACTCTGC	ATGCCTTCTCCTTTATCC	NM_001066.1
S01327.E02	ATGTTTGAAGAGCAGCAG	CTTGAGCTCAGTCTCACC	NM_001242.2
S01320.B09	GAAATCCTGCAGCTGTG	GTCACCAGCCTTGCTC	NM_001242.2
S01344.C01	GGATGAAGCAAGTGGAC	GAAACAGGCTGACCTTATC	NM_001242.2
S01349.G01	CTACCCATCTCCTTCTCC	CAGATCCTGACCTGAGC	NM_001242.2
S00123.E02	CCTGAGTCATCTCTGCAC	AGGAGTGTCTCCTCTTG	NM_001243.1
S01175.H09	TACAAAGCTCCGTCTCAG	CCAATTATGACGATGACG	NM_001243.1
S00111.B05	TACAAAGCTCCGTCTCAG	CCAATTATGACGATGACG	NM_001243.1
S00161.H06	TTTAGTGGTCACCAGGG	AGGTCGGAAGTCAACAG	NM_001243.1
S00143.G04	GCCTGTGGTAGTGAAGG	CTGAATCCCGCTTACAC	NM_001243.1
S01178.C10	CCATCTCTGTGGAAACTG	TCATACCTTACCACCGTC	NM_001243.1
S00112.F03	CCATCTCTGTGGAAACTG	TCATACCTTACCACCGTC	NM_001243.1
S00106.G09	ATGAGTACCCTCCTCTCG	GTTACTGGAAGTTCACGG	NM_001243.1
S00138.H09	TGCTTCTCTGTCTTCTG	ATAACCAGAACCCAAACC	NM_001243.1
S00129.B09	TGGTTAACTCTTTCCTGG	GATGGGCACACATTTAAC	NM_001243.1
S00126.B10	GAATTATTCCTGAAGACCC	CAGACCATACCACAAAG	NM_001243.1
S00113.H11	CAGGAGAAGGAGGAAGTC	TCAGAGAGCAGGAGCAG	NM_001243.1

S00095.D12	GCAGAGTAAGTGGCTGTG	GAAGTTCAGTCTCTGGAGC	NM_001243.1
S00103.C01	CCAGGAGGACCATTG	TCAGATCTGTTAGGGAAGG	NM_001243.1
S00151.H06	GCCTCCCAAGTTCAGAG	TTTCAACTCCAGGGTCTC	NM_001243.1
S00974.F02	CTGGTGGTCTCTGCTTG	TGAGTGACTTGATCCTGG	NM_001243.1
S00166.A04	TCTCTGCCTCTTTGCTC	CCCTTGGACTGTCTCTTC	NM_001243.1
S00900.H09	ACACTGTACTCTGCACTGG	GGCCCTAGGGAGTCAG	NM_001243.1
S00875.D03	AGTTGGCAAATGATGAAG	CTTTCTGCAATGCCTATC	NM_001244.1
S00427.F03	TTTGAAGCAATTCAAACC	TCACTCTGGCACTAGGAG	NM_001244.1
S00410.F12	GTACACATCTGCAGGTCAC	AACGGTAATTGTCTCCATC	NM_001244.1
S00417.E01	GGTTTCACACTTTATGGC	AAGCCCATTTGGAACTAC	NM_001244.1
S00419.D07	CGAATATCATTGTGTTCC	CTTAATCCCTGGCAATG	NM_001244.1
S01205.A07	TTTGAAGCAATTCAAACC	TCACTCTGGCACTAGGAG	NM_001244.2
S01213.F09	AGTTGGCAAATGATGAAG	CTTTCTGCAATGCCTATC	NM_001244.2
S01216.D07	GTACACATCTGCAGGTCAC	AACGGTAATTGTCTCCATC	NM_001244.2
S01218.C06	GGTTTCACACTTTATGGC	AAGCCCATTTGGAACTAC	NM_001244.2
S01203.F05	GCTCTTAACCAACAAACG	CAGCCACCTTCTCTGTAG	NM_001244.2
S00678.E03	GATTCTCCTGCCTCAGTC	AGCTACGTATCCATCGTG	NM_001252.1
S01207.H07	GTACAACCTTGGTGGAAG	ACTGCAGTCTCAGCCTC	NM_001252.2
S01237.E09	CCCACTTGTCTTTCTACC	AGAGAGCTCCTGGCAC	NM_001252.2
S01209.B10	CCCTACCAGATCTTCCTC	TAGGATCTTCAGACTGGC	NM_001252.2
S01220.F12	TCATTTGGTCGTCTTAGC	TTGGTATTTGTCATTGGC	NM_001295.1
S01016.G04	TGTGCCAAGAGTCAGAAC	CTACGAGAGTGGAAGCTG	NM_001295.1
S01221.F08	CAGGATTCCAAGAGCC	ACTCAGACCATAGGAGGC	NM_001295.1
S01219.E03	AGGAGGTAGATGCTGGTC	GTGCTTAGGAAGTGTTGG	NM_001295.1
S00952.F03	TCATTTGGTCGTCTTAGC	TTGGTATTTGTCATTGGC	NM_001295.1
S01218.D05	AGACACTTTCTCCCAAC	TCCACAGTGACTCCACTC	NM_001295.1
S01143.F10	AGGAGGTAGATGCTGGTC	GTGCTTAGGAAGTGTTGG	NM_001295.1
S01221.F10	TGTGCCAAGAGTCAGAAC	CTACGAGAGTGGAAGCTG	NM_001295.1
S00995.D09	CAGGATTCCAAGAGCC	ACTCAGACCATAGGAGGC	NM_001295.1
S01236.E12	GCATGCATGTCTTTGAAC	ATCACACAGGAAGCTGAG	NM_001295.1
S01188.C03	GATTCTTGAACCTTTCTTTCCG	TAGGATTACAGGCGTGAG	NM_001296.2
S00254.B01	GATTCTTGAACCTTTCTTTCCG	TAGGATTACAGGCGTGAG	NM_001296.2
S01237.H01	TTATGCATGTACCTTGGG	GTGTAAATGGTGGGTGAG	NM_001296.2
S01175.H01	TTATGCATGTACCTTGGG	GTGTAAATGGTGGGTGAG	NM_001296.2
S00222.D09	TTATGCATGTACCTTGGG	GTGTAAATGGTGGGTGAG	NM_001296.2
S01223.B02	TTCTTCGTGCTATGGTTC	AAAGAAAGCGTGGTATCC	NM_001296.2
S01223.C09	GTTTCTTGTGCAAGATGG	GCGTAGTCTAGATGCTGG	NM_001296.2
S00254.F02	GATAATGTGTTCCCATGC	GAAACGTTTGAACAATC	NM_001337.2
S00832.H10	TGAGACCTGCAAGAGTTG	CTGGAAGGTGCTGTTATC	NM_001337.2
S00856.F12	AATAGTACCCACCCATCC	AAATGATGGACCCAATG	NM_001337.2
S00873.H02	CCTTCCTCATGTCACAAC	GATCTGCTGTTTGTAGCC	NM_001337.2
S00245.B11	AATGGTTTCCATTGTCTG	TGGAGTATCTGAGCTTGC	NM_001337.2
S01229.H05	ATGTGGGCATAGCAGTAG	TCAGCCTGAACTTCGAC	NM_001504.1
S00918.E11	ATGTGGGCATAGCAGTAG	TCAGCCTGAACTTCGAC	NM_001504.1
S01029.D12	GGAGCGAGGATATTGG	AATACAACCTCCACAGG	NM_001504.1
S01230.B12	GGAGCGAGGATATTGG	AATACAACCTCCACAGG	NM_001504.1
S01226.D07	AGACATTGATGAAGGCAG	CTCAGAGGCCTCCTACTC	NM_001504.1
S01121.B08	TACAGCTAGGTGGAGCAG	AAGGGAGAGCAGGGAG	NM_001504.1
S01228.A08	TACAGCTAGGTGGAGCAG	AAGGGAGAGCAGGGAG	NM_001504.1
S01242.F11	CCAGCTACTCACCCAAC	GAGGTTTAGGGAGGTCTG	NM_001504.1
S00440.G03	GACACACCCACAGCTTAC	GCAGATACTCAAATCGAGG	NM_001548.1
S00457.H12	CCTTTCAAGGATAAGCAC	TTCTTGCAAATGTTCTCC	NM_001548.1
S00898.C03	TGTCTTTCGATATGCAGC	TTTGTAGACGAACCCAAG	NM_001548.1
S00963.C10	TGTGAGGAGTCTGGTGAC	ACAGAAGTGGGTGTTCC	NM_001548.1

S00732.F07	CTGTGGGACAGTGGTTC	CAGGTTTGCCAGAGTAAG	NM_001558.1
S01333.E06	CTGAACCTCCCTTTCTTC	ATCTTCCCATGCTAGGAG	NM_001558.1
S00871.F07	AATGTGGGAGCTCTCTTC	AGACATGGTGAGCTATGG	NM_001558.1
S00782.C07	GACAAAGGATACTGAAGGG	AAGCAGCACCTAACACAG	NM_001558.1
S00689.G11	CCAGAGTCCTATGTCCAG	GCTAAGGCAATGGACTG	NM_001558.1
S00981.A06	CTGGGAATATCTGACTGG	AGCTTCCATTCTACAGC	NM_001558.1
S01108.F04	AAATGGGTATGAATGTGC	GGTTTCCAGGTTCTTCTC	NM_001558.1
S00851.E04	GAGCTCTCCTCCTGGG	GCTGGGTCTTCTTCCC	NM_001558.1
S00885.B06	TTCAAACAAAGGCAGTTC	ACACGATTCTGTGGTC	NM_001558.1
S00813.E02	GACAGTGGCATTGACTTAG	CTGAGTTAAAGCTGCCC	NM_001558.1
S01318.H12	CTTGCTGACAACTTCCAG	GAATGCTCCAGAGAAAGG	NM_001558.1
S01340.F11	CTGAAGTCAGCTCAGACC	TGGACATTAGCAGCAAAC	NM_001558.1
S00995.C08	AGCACGGAACAATGTAAG	TGTGCCTTTGAGAGTAGG	NM_001562.1
S00780.A05	TTACAGTGAAATTTGGTGAC	GACCACTGAACTTGAAGG	NM_001562.1
S01191.G03	ATGGTTCTCTGCTTCTTG	GGGAACAGGTGTATTAAGG	NM_001562.2
S01214.B07	AGCACGGAACAATGTAAG	TGTGCCTTTGAGAGTAGG	NM_001562.2
S01212.G10	TTACAGTGAAATTTGGTGAC	GACCACTGAACTTGAAGG	NM_001562.2
S01202.C01	TTCTCTCAATTGCTTTC	TATTTGCACTTCCATTGC	NM_001562.2
S01052.E07	AGGCCACCACATTAGG	CATCTCTTTGGACAGTGG	NM_001569.2
S01105.E05	TGAGAACTTTGACTTCCG	ACCTCTAGAAGCCCAGC	NM_001569.2
S01343.B03	AAGTGCTGGGATTACAGG	CCTCTTCCTTCTGTAGGC	NM_001569.2
S01090.D12	AGACACTCTGCTCTTTGG	TCTGTCTGGTAGCCTGAG	NM_001569.2
S00935.E09	GGCCCTGGTTCTCTTC	GAACCTCCTACGTGTCCAG	NM_001569.2
S01357.F01	GGCCCTGGTTCTCTTC	GAACCTCCTACGTGTCCAG	NM_001569.2
S01134.H10	CTCGTCACTCTCCACG	TGTGATGGGAACAGAGG	NM_001569.2
S01345.H10	GTCACACAGAGCAAGGC	CGATTGAGTGACAAGGAC	NM_001569.2
S01056.H08	AAACGAAGTTGTTTGGAG	ATCCATGTCCACACCAG	NM_001569.2
S01098.E04	AGTGCACCTCTGCAGCC	CTCGAGTCCAGCCTTATC	NM_001569.2
S00795.H10	CCCACATTGATAGGACG	CACGGTGACAGGTAGAAG	NM_001569.2
S01353.E04	ACTCACACAGGCTGAAAG	AGCTGTCCAGGTGAGG	NM_001569.2
S01118.G05	GAGCACTTTCCATCAGG	CTTCAGCCCTCATTCTG	NM_001569.2
S00985.C09	GAAAGGCTGGAGAAGTG	TTCAGCCTTTGATGTAGC	NM_001569.2
S00739.G03	CTCTGCGCTACATCAAAG	CAAAGAAGAGCCCACC	NM_001569.2
S00925.C06	AGCAGCAGGGTCTACAG	TCGTGCACATCCTCAC	NM_001569.2
S01365.F05	AAGGAAAGGAAGGTTGAG	CTACAAAGTGATGGACGC	NM_001569.2
S01080.B05	GTTGCGGTTGATCCAG	GTTGCTCCTCCAGAGC	NM_001569.2
S01080.D05	GGTAGCACCTTCTGGG	AGAGCCAAACTCAAGAGG	NM_001657.2
S01275.E05	CCTAACACAGCTGACTCG	GCTTTACTTCTGAAGCAGC	NM_001657.2
S01271.B05	GTTAGGTAATGAGGCACG	GTTTCCTGCAGTTAGGG	NM_001657.2
S01169.G07	TGTTGGAATTAAATGGTTC	TAAACCAAAGATCAAGTGAC	NM_001657.2
S00952.B03	ACTCATGAAGTGGAACCC	CATAGCCATTGTTCATAGTG	NM_001657.2
S00906.E08	AAGCTCTGCTGGAATTG	GATCAACCAACTGTTAGGAG	NM_001657.2
S01373.E07	TCTACCAATCTCCAACCTCTC	ATTTGCAACTTTAGTTTGTG	NM_001729.1
S00757.D10	TCTACCAATCTCCAACCTCTC	ATTTGCAACTTTAGTTTGTG	NM_001729.1
S01126.B01	GATGGCATGGTTAGCTC	AACTGGCAGCAAGATAAG	NM_001729.1
S00899.H08	AGCAAGTGCCACTAATTC	AGATCACAAGGTCAGGAG	NM_001735.1
S00419.H07	TCTCTCTCAATTTGCCTG	TGCACTTATGGACTCCTG	NM_001735.1
S00422.G06	TTGTTGGTTAAGAGCAGG	ATATCACGGCTGTCCAC	NM_001735.1
S00427.C08	ATGCCTGGCACATAGTC	TTGACAAATTCTGGCTTC	NM_001735.1
S00421.C09	GGATCACATGGAATGTTG	CTGGGCTCATGAGAAAC	NM_001735.1
S00401.B06	TTTACCAAACAGTGTCCC	CCATGTAAGACACTTGCC	NM_001735.1
S00422.C06	TGGATTTCTAAATGTTCTGG	GAATTCGGTAAGCTCCAC	NM_001735.1
S00426.F01	AAATCACTGGAGGGAATC	CCTGCATTGTGCTATCTC	NM_001735.1
S00428.C11	AAGACTGCATCACACTCC	GCAAATAAATGGAGACCC	NM_001735.1

S00415.C02	TCACATTTCTATCCCTCTG	GACAGGTTCCAAAGCAG	NM_001735.1
S00410.H11	TTACTTGGATGTCAACCTG	TGTTGCCATAATACCTTTG	NM_001735.1
S00424.H05	TTTCTGTGACTTTGTGGC	GAGCTCTGAGAGAGGAGG	NM_001735.1
S00413.D08	TCAGTGCCCAAGGATATAG	GGGCATTTGTAAATAGGG	NM_001735.1
S00427.G10	CTCATTTGGTGGACAAAG	TGGAAGGCCATAATACAC	NM_001735.1
S00425.C11	AGTTCACATGTCACCACC	AGTGGGATCTGAGGGTAG	NM_001735.1
S00415.F05	AGGTCTTCTGATTGGTGG	TGGGTGACAGAGTGAGAC	NM_001735.1
S00419.A01	CTTCTTCTTCATCCTCCC	AAATCTTCCCTTCCTTTG	NM_001735.1
S00419.F09	CTGGAGGAATGGAGTTTC	AGCTTACCATTCTCAGGG	NM_001735.1
S00413.G07	CTTGCCTCTCATTGAGG	TGGTTGTTCTTCTCTCTTG	NM_001735.1
S00406.D06	CGGAAGTGGAGAAACAG	TTACAGCCAAATTTAATGC	NM_001735.1
S00421.C10	GGCCAGAAGTGGATACTAC	TAAGCATTTGCTCTGGTC	NM_001735.1
S00422.E11	GGAATAACCTCCATCCAG	GGAGAATTGCTTGAATCC	NM_001735.1
S00995.E12	TGTTTGGTTTCTATTGCTG	CCTTGAAGTAAAGCAAATG	NM_001735.1
S01252.A09	CTACCATTAAAGTCCTGGG	TCTGTTAATGGATGTCTCTG	NM_001735.1
S00425.C03	TTAAGGCTATGGCAAATG	TCCTAATCCAAAGCAGC	NM_001735.1
S00416.D01	TGGCATTCTAAGATCAGG	TCACTGGTTTGTGATAACC	NM_001735.1
S00404.F04	GGCCTAGTCTTCCCTTAG	TTCAATGAAGGAGGCTG	NM_001735.1
S00421.B10	ATATGCATCTGCATCAGG	TAATTTCTGCTCCAGCTC	NM_001735.1
S00416.C05	CCTCTCTAGAGGCCAAAGG	CCCTTTAGCATTTGTTATTG	NM_001735.1
S00424.F02	CTGTTCTGCACACTAGCC	TGAGGCCAATAGTTCAAG	NM_001735.1
S00406.E06	GACTTCATGGCAACATTC	GCAAGAATGGAGTGAGTG	NM_001735.1
S00412.A05	ATGGCTTGTCCAATGAC	ATCGTGGACTCGGTTATC	NM_001735.1
S00429.H06	TTACCCTAAAGGCCAAAGG	TTAAAGTGCCTCAAGTGC	NM_001735.1
S00429.E10	CACAGATCTCACTTTGGG	TCTAGCTGTTTGCTAGGC	NM_001735.1
S00426.H01	CAGTGAGCTGAGATCGTG	TCTTTGTGTATTCTTCCCTC	NM_001735.1
S00419.C05	CCTTTAACTGGTTACCTGC	TTGAAGACATGGGTATTTG	NM_001735.1
S00424.H01	TGTGAGGACAGGGTTATG	CTTTAAAGGAATCCCTGAG	NM_001735.1
S00420.G12	TCTCCACTCAATTTGAGG	CTTCTTGCTCCTGTATCAC	NM_001735.1
S00426.A09	CTGTTCTCAGAAGTAGCAAG	TTAGAGGTTACCTTTCTG	NM_001735.1
S01017.C02	CTCTTTGCTCAGGAAGT	AGCAACAACAACAGCAAC	NM_001768.2
S00822.H10	TGGAGCTAGCAGAGCC	GATCTGAGGCGGAGAG	NM_001768.2
S00897.D02	ACAGCCCTTGACTCTACC	CTCTGCTATCCCTTCTCC	NM_001768.2
S01359.B02	TAAGAGGCTTGAAAGCAG	ATGGCCTTACCAGTGAC	NM_001768.2
S01093.A07	CACTTCAGCTCCACTGTC	CATCACATCCTCCAAATG	NM_001768.2
S00408.E12	GGACAGAGCACTTCCAG	AGAGCTGAGGAGGAGATG	NM_001782.1
S00415.G12	TTTCATCCCAGGTACAAG	CAGGCAGGGTGAGTTAG	NM_001782.1
S00408.D06	GGTGGGAAGGAAATCTG	CCTTGCCAAAGCTGAG	NM_001782.1
S00419.H08	CTGCCATTCTGACTTG	CAGGTATGGTGTTCAG	NM_001782.1
S00411.A06	GGTGATAGACTCCTGCC	GATGCTGCAGTCTCAGG	NM_001782.1
S00403.H07	TGAGGAAGATCAGCTTTG	ACCTGTCCCTTCTCTC	NM_001782.1
S00408.C02	GTTTATCCCGGAAGGAG	GACTGGAGTTTCCCAGTG	NM_001782.1
S00407.A09	AAACATTGTGGACTCCC	GGTTAGGACAGGGTAAGG	NM_001782.1
S00405.B05	ACCAAGGTGGGATTTG	GAGCCCATCTGTTTGAG	NM_001782.1
S00251.A09	AATCCCTAGGCTGCTATC	AAAGTGACAGTCCGGG	NM_001837.1
S01219.C12	AATCCCTAGGCTGCTATC	AAAGTGACAGTCCGGG	NM_001837.1
S00854.F12	GTGTAAGCTCCTCTCAGG	CAAAGGCGTAGATCACC	NM_001837.1
S01221.B11	GTGTAAGCTCCTCTCAGG	CAAAGGCGTAGATCACC	NM_001837.1
S01204.A12	TTGGAAATGACTGTGAGC	TTGTAGCGGCATATAGTAAC	NM_001837.1
S01195.D07	TAGTATCCAGATGCCCAC	TGCTCTAGGCTAAATCCC	NM_001838.1
S01188.H05	AGGTCCTTGAAGAGCTTG	TCTTTGCATCAGCATTG	NM_001838.1
S01196.A05	GTCTCTAAGAAACGAGGC	GCGTGATCAAAGCCAC	NM_001838.1
S01196.B12	GACATTTCCCTTGTCTCTC	CAACACTGGGAAACAGAG	NM_001838.1
S01189.A03	TTCAGAGGACTCTTCAGG	CAACTCAACATCGCCTAC	NM_001838.1

S01238.E03	CAGCTCCTCCACTAAACC	GTGTTCAAAGGCACAATC	NM_001838.1
S00421.G11	ACAATTTCTTTCCTCCG	ACAATTTGTGGAGACCC	NM_001842.3
S00410.E04	TCTGTAGAGACAGGCAGG	GTACCAGTCTGATGCAGG	NM_001842.3
S00410.F03	CAGGCCACAGGTTCTAC	CAGAGCCCTTTACTCTCC	NM_001842.3
S00408.E03	ATGCATCAGGTCTCACAC	AATGGTTGGCAATATGAG	NM_001842.3
S00407.A06	TGTGCACTGTACATACCTG	ACCTTTCCTCAACCTCTG	NM_001842.3
S00408.H06	GGCACTGTTACGAACATC	ATCAATGATGGGTTGAGG	NM_001842.3
S00407.A07	GACTTGATCTGGGCTAGG	CTCACAGGCTCTTGTCTG	NM_001842.3
S00407.E03	GGTAGTGTGAGGATGCAG	AGTCTTGCCTGAGAACAG	NM_001842.3
S00417.H11	TTCTCGTGAACCTTTCCTG	AGAAGGAGGGAGGGAG	NM_001842.3
S01307.C10	TCTGAGATACGACTTGGG	AAGATTCTCTTTACTGCCC	NM_001926.2
S01303.E03	TCACCTAAGAGAAAGAGCC	CTCACCGCAACATCTG	NM_001926.2
S00272.C01	TCCTCCAAAGTGGATTAG	TGATAAACAACAATGCTGG	NM_002006.2
S01202.D09	TCCTCCAAAGTGGATTAG	TGATAAACAACAATGCTGG	NM_002006.2
S01186.B07	TCTTTCAGCATTCACACC	GCTCAGTATTTAAGACAAGG	NM_002006.2
S01187.B08	GGCTGCAGTTCCTTTG	CAAGAGCATATCCAGGG	NM_002006.2
S01186.C02	TTGTCTCCAGAGTATGCG	AATAGAATGCAATCCTCAAG	NM_002006.2
S01186.G12	AGGAGTTCAAGACCAACC	AGTGCTTCCACGACATAG	NM_002006.2
S01191.B03	TGCTGTTACCCAGTGAAG	CTGAGTATTCGGCAACAG	NM_002006.2
S01191.C12	GCTGGTTGAGCAGAATAG	TTTGTTCCTAAACATGCAC	NM_002006.2
S01186.A08	ACACATTGAATTTGATCC	TTCAGAAATTACCTCAGAGC	NM_002006.2
S01186.G06	CATGCAAAGAAGAGGAAG	CTCAGCCTCCCAAGTATC	NM_002006.2
S01191.D11	ATGGTGAATGAATATGGC	CTGATCAAACACCTCCAG	NM_002006.2
S01186.B11	GCAGATACTCTTCCTGCC	CAACTCACCTACCCAGAG	NM_002006.2
S00862.C03	AGAGCACTTCGAAGAAGG	GGGACATTACGGTAGGTAG	NM_002163.1
S00839.G04	TGAATCTGTGGGTTTCC	TGTCACTCAACATCTCCAC	NM_002163.1
S00746.B02	TGAATGAGAGTTGATGGC	CAAGTCTGTGGTGAAGG	NM_002163.1
S00711.G03	ATTATGGCTTCAGCAAAG	CTGTACAGGTGGAGATGC	NM_002163.1
S00772.G05	TTTACAAACACTGGAGCC	ATGATAGCAACAACCACC	NM_002163.1
S00782.D08	GAGAAGGAGCGATTGG	CTGCTTGGGTTATCTGG	NM_002163.1
S01392.C03	GTTACCCGTGTAGGTGTG	CCTCCATGAGACCACAG	NM_002163.1
S00882.B11	TAAATGCTACAAGCCCTG	GGAGAATCACTTGAACCC	NM_002163.1
S01090.F01	TAGGGTCAAAGACAGTGC	TGACAAGTCTTTGGAAATG	NM_002163.1
S00429.B10	TATTTGAAACGGCAGAAC	CTGTGATCTGCCTCAGAC	NM_002169.1
S00429.C10	AAACCTCGCTTAGAGAAAG	GGAGGTTGTCAGAGCAG	NM_002175.1
S00310.B02	CCAGATATTCTGGAATGG	AGATCCGAGTCTACCCAG	NM_002184.1
S00304.C04	TTTGATTCAGCTTGAATATC	GGTAATTGGTTTGGTTTG	NM_002184.1
S00310.G08	AAAGGAGAACAAGGAAGC	AGTCTGGTTGGAAGTTG	NM_002184.1
S00299.C01	GAAACCACCAACCAAAG	TTAACACTTTCACAATGCC	NM_002184.1
S00291.C08	TCTCCTGAGGCCAATATAC	TTAGGGCTTTGTATTAACAG	NM_002184.1
S00299.E08	TTTGGAAGGTGCTGTAAC	TAAGCTTGAATCCAGTACAC	NM_002184.1
S00304.C12	GATAAATTGGAAGTCGTTTC	ACAGGAATGAGCCACAG	NM_002184.1
S00310.B03	TTATGGGAGCCCTGTC	CATAATGGCATGATTTGTG	NM_002184.1
S00304.C02	GATCACGCCACTACACTC	GGAGGGCAAGAGTATTAAG	NM_002184.1
S00306.C05	AACTAAGAAGCAATGAGGC	CAAGATCGCACCCTG	NM_002184.1
S00306.H07	CAACCCAGAAGAGGTTATC	TTTGACATATGAACCTGAAG	NM_002184.1
S00312.B04	GCTGTTAAGTGTGGTTGG	TTTGTTAGTGACCAGCAG	NM_002184.1
S00307.C10	GGATTACAGGCATGAGC	CAAATGCCTTGGGTAG	NM_002184.1
S00302.F05	TCCAAGTCACTAAGTCCAC	ACATTGAGTGCTACCAGC	NM_002184.1
S00302.G09	GAATCAGGTGAGTAGGGC	AAGCCTAAGAGCAGATGG	NM_002184.1
S00291.G01	CCTCGAGTGCCAGATAG	CTAGGTCCCGGTAGGG	NM_002184.1
S00296.A11	GCTTCTCTGTCTTCCTCC	TGGGAAATTCTCAAACCTG	NM_002185.1
S00295.B01	ATTTTCATGTCTGCCACAG	ACAAGGAGTTTCAGGAGG	NM_002185.1
S00674.C08	CTCACCCACCCACATAC	CTATTGCCAGTTGTTTCC	NM_002185.1

S00295.B09	GGTCAAAGTGACTTGCAG	ATGCACTACTAGGCCAAC	NM_002185.1
S00285.G09	CAATTGAAATGATTTGGG	CTCTCACTTGCTCCCAC	NM_002185.1
S00282.D12	AAGTAAATGCAAAGCACC	TCGTGAAATGCCTTAATC	NM_002185.1
S00286.H10	TTCTGATTCCAAGCTCAG	CAACTGTTCTTGTCTG	NM_002185.1
S00303.D09	TCTGTGACATTCCCTGTC	TAGAAGCTGGACATGGTG	NM_002185.1
S00962.G05	TCTGGAATCCTGACATTG	GTAATTGCACACACCTCC	NM_002185.1
S01331.D10	CTCATGAAAGCCAACATC	TGTGATGAGATGGGAGAG	NM_002186.1
S00598.D12	CACATCTGCACACATACAC	CACAAACCTTCCACTTTG	NM_002186.1
S00593.D03	GGTGAGGTGATCAGGG	CTGTGTGTTATGTGAGCG	NM_002186.1
S00589.B09	CTCTCCTTATTTAGAGTGGG	TTGGATGTGCTGACTGAC	NM_002186.1
S00595.C03	CTGAGAACTCACTGGG	GACAGGGATGAGGGTG	NM_002186.1
S00592.B08	CTGCTACACTATCCTGGC	GTGTCAGCTGTCAGATCC	NM_002186.1
S00589.G12	AACATCGGACAAACCAG	GTGAGTGCAGATGGAGAC	NM_002186.1
S01000.F06	CTGGCAGTTCTCAATGTC	CCACATGTCCCTCTCTG	NM_002186.1
S01011.G02	ATGGAGCACTCTGCTG	TTTCCCTAGAGGCTTGAC	NM_002186.1
S00700.C07	CATTTACTGGTGACTION	ATAGCTGCTTCAATCCTG	NM_002186.1
S00784.H11	GACAGGGATGAGGGTG	CTGAGAACTCACTGGG	NM_002186.1
S00772.B12	TTGGGAGTCTTTCAGACC	GCTCTAGTTCCTCCCTTC	NM_002186.1
S00698.A05	TGCATGTGTGATTCTCG	TTACAGGAGGGTGAAAGG	NM_002186.1
S00755.G07	CACAAACCTTCCACTTTG	CACATCTGCACACATACAC	NM_002186.1
S01336.D04	CTGCTGATGGAAGGAAG	TCAGTGAAAGCCAACATC	NM_002186.1
S01393.E01	CTTCTGGAGGAGGAG	ACTCCTTGCTGGGTCTC	NM_002186.1
S00609.A12	CCTTTAAGGGTATGAGGG	AGACTCAGAGGGCAGC	NM_002186.1
S00307.G01	ATCACTTCAAGAAAGGGC	GATTGTGCCACTGCATAC	NM_002187.1
S01147.A07	ACTGATGTACTTGCAGCC	CTTCTGGCATGAAATCC	NM_002187.1
S01012.E07	TGCCATGGAAGCTAAAG	ATCCATCAGGATCAGTCC	NM_002187.1
S00291.D09	CAATCATATCCCTGCATC	TATGCATTGCAGAAACAG	NM_002187.1
S00296.B06	TCAGAATGTATCCCTGTTG	ATCAAAGGTGCAAGTGAG	NM_002187.1
S00306.B11	TGCTTGTCAACCACCTAC	ACCTGCCTTACTGGCTAC	NM_002187.1
S00281.E01	GAGGTTGCCCTTAATTTT	ACCATCTGGTGATCTGTG	NM_002187.1
S00287.F07	ACTCACCATGACTTGGC	GTTGTGTTTAGGCAATGG	NM_002187.1
S00295.D06	TTCAGTTTGATTTCCCAC	GGTTCACAAAGGTAACAAG	NM_002187.1
S01187.G03	ATCACTTCAAGAAAGGGC	GATTGTGCCACTGCATAC	NM_002187.2
S01187.G02	TGCCATGGAAGCTAAAG	ATCCATCAGGATCAGTCC	NM_002187.2
S01187.G01	ACTGATGTACTTGCAGCC	CTTCTGGCATGAAATCC	NM_002187.2
S01221.E07	CAATCATATCCCTGCATC	TATGCATTGCAGAAACAG	NM_002187.2
S01216.B02	TCAGAATGTATCCCTGTTG	ATCAAAGGTGCAAGTGAG	NM_002187.2
S01192.G11	TGCTTGTCAACCACCTAC	ACCTGCCTTACTGGCTAC	NM_002187.2
S01234.D09	GAGGTTGCCCTTAATTTT	ACCATCTGGTGATCTGTG	NM_002187.2
S01218.A01	ACTCACCATGACTTGGC	GTTGTGTTTAGGCAATGG	NM_002187.2
S01216.C05	TTCAGTTTGATTTCCCAC	GGTTCACAAAGGTAACAAG	NM_002187.2
S01217.D11	GGGTAGCACACTAACGG	TTAAGTTTCCATCAGAAAGG	NM_002187.2
S00289.C11	TGTGGTTTCTAGATAGTGCC	GCTCATGACCTCATCTTG	NM_002188.1
S00285.A11	AACGAAGCTCAGGAATG	AGGGAGGCTCAGAGAAG	NM_002188.1
S00287.E05	ATCTTCTGCAGACTCAC	ACACCATGGATATTCAGC	NM_002188.1
S00301.C12	TGAATGAGACAGTCCCTG	CAAGAAGAAGTGTGCCTG	NM_002188.1
S01049.D04	TAGCATTACAGTGGGTGC	CTTCAGACCACAGACCAG	NM_002188.1
S00451.C09	CAGTCACCTTGGACTCTG	AGACCAAAGGCTTCTGAG	NM_002189.1
S01091.H08	AAGTTAGGATGAGGGACG	AGTGCTGGACATACATGC	NM_002189.1
S00440.B06	TGACCTCAAGTGATCTGC	CATGGTAAAGAATTTGTGG	NM_002189.1
S00433.C09	TTCTGAGTGTGGAAGGG	AAATGAGTCTGGTTACGC	NM_002189.1
S00433.B05	TGATGGTATAAAGCTGCC	AGGGTGACTCACTATGGC	NM_002189.1
S00445.G12	CGCTATTGCCTAAGTCTG	TTGTATCCCGTTCTGAAG	NM_002189.1
S00446.G01	AGACCTCAGCACAGATCC	CCCTAGGATAAGCTGGAC	NM_002189.1

S00442.C05	CCCTTACGTGGGTGAC	GATCTGTCACCGCTTTG	NM_002189.1
S00998.E11	TCCTTCACATTTCACTGG	TCTGAAGAACATGGATGC	NM_002198.1
S00310.E02	GGATGCCAATAATAAGTCC	CTGGCTCTGCACTAAGAG	NM_002198.1
S00816.F09	GCTTGCCTAGAGGAATAAG	CAGCTCTTGGAGCAGTC	NM_002198.1
S00281.H09	CAAGCTTTCTCCATCCC	ATACTGGCTGAGAGGAGC	NM_002198.1
S00285.B05	GTGACAACAGCAGCTACC	GAGAGACAGAGAAAGGGC	NM_002198.1
S00288.F01	TTTCTCTCTCAGGAAGCC	CATGGTGGCCCATTAG	NM_002198.1
S00283.H05	ATGCCTCCAAGAGAAAG	GTGGTCCTAAGCAGCC	NM_002198.1
S00282.C08	TAGCATTTCTTCCACTGC	GGAGGGTAGAAGGAGGTC	NM_002198.1
S00285.G10	TCGACTTTCTTTCTGTGG	GTACCTTGCCTTCCTCC	NM_002198.1
S00281.F07	AGCCTCTGTGTTAACGTG	AGACCTGTCTGGCTGG	NM_002198.1
S00285.E07	GGAGAAACACCTGCTTG	CTAAGTGACCTCGGGTG	NM_002198.1
S00292.H11	GATCTGCGAAAGCTGC	GCTAAGTGTGGATTGC	NM_002198.1
S01390.H06	GAAGCCTACCTATGTCCC	ACTTGCTTCAGAACATGG	NM_002255.2
S01317.B01	GCAACCAAGAAATGAGAG	CAGTGAGGAACACACACC	NM_002255.2
S00765.B04	GTCTGAGTCTGGCTGTTG	AGAGGGAAATCCTGAGTG	NM_002255.2
S01313.D12	GTCTGAGTCTGGCTGTTG	AGAGGGAAATCCTGAGTG	NM_002255.2
S01319.B06	GCAACCAAGAAATGAGAG	CAGTGAGGAACACACACC	NM_002255.2
S01323.A10	GTCTGAGTCTGGCTGTTG	AGAGGGAAATCCTGAGTG	NM_002255.2
S01319.B07	AGTGAACAGGGAGGTAGG	TTGCAGCCTCAAGTAGAC	NM_002255.2
S00696.B07	ACATTGTCTGGGATTGC	TCCCTAGACCTTGACTCC	NM_002288.2
S00250.F02	CTTAAATTTGGCCCAGTC	TCTAGGTCATGCAGGAAG	NM_002447.1
S00972.F09	AGCGTGACAGATGATCC	AGGAACTGGGTGAGAGAG	NM_002447.1
S01004.E02	ACACAGACACAAAGGTGC	GGAGCAAATCTGCAGTC	NM_002447.1
S00241.G03	GGGTGAGAGTGTGTTGGG	TTTAGTGACCTGACCAGC	NM_002447.1
S00224.B04	CAGGTGGGTCCCTCATC	CCTGTATGTCAATGCCTC	NM_002447.1
S00238.G08	GAGGCATTGACATACAGG	TCAAGACTTGCTGACCAC	NM_002447.1
S00233.G02	GTATGGCAGGAGACTTTG	AAGCAGTCAGAACCACTG	NM_002447.1
S00226.A12	GAAATGCCATTCTCTGG	ACTGGCTCCTAAGAGGAC	NM_002447.1
S00220.H02	CCTGTCTGTGCCCTTG	CCATCCTGACAGAATCC	NM_002447.1
S00225.A03	TAACAGACGAACTGGGAG	GCTGAAGTTAGATGCTGG	NM_002447.1
S00224.C11	GTAAGCACTGCCTCTTTG	ACCTGTGATTGCTCCTC	NM_002447.1
S00235.G03	TGGATGAGTTCCTGAG	ATGAGGACCAGCCAGTAG	NM_002447.1
S00225.H07	TAGTTCCACTGAAGCCTG	GACATTCACCATCTACGC	NM_002447.1
S00221.H07	CATTGCAGGTAGGCAG	GAGAGGATGTAGGGACTTG	NM_002447.1
S00222.E05	AGGGATCTAAGTCCTCCC	GACACAAGTGGTGGAATC	NM_002447.1
S01183.F06	TTGGTGAGATAGTGGAGG	TGGGATTACAGGAGTGAG	NM_002447.1
S00233.H07	TTGGTGAGATAGTGGAGG	TGGGATTACAGGAGTGAG	NM_002447.1
S00253.H08	TAGTGCTCTGAGGTCTGG	ATGGGAAATGAAGGTCTC	NM_002447.1
S00223.D08	ACCTTCATTTCCCATTTT	AAGCTGATGAGGTCCTTC	NM_002447.1
S00233.G11	AGTGTTTCATCTGGCTCTG	GAGGACAAGGCTGGAG	NM_002447.1
S00240.F02	GTAAGGGCCTAGAACAGG	TTCCATCTTACATCTGCC	NM_002447.1
S00230.E03	ACTCTGGGAGGTAGAAGC	GGAGCTCTGTCTCCTGTC	NM_002447.1
S00930.H07	ACAGAGTGAGCCAGTGAG	ATCCTGGATGGTGTGAC	NM_002447.1
S00245.B07	TTTAACAGCAAGTGGGTG	GTCAGTGTTGGTGTGGTC	NM_002447.1
S00954.G03	GGATCTAGGCTTTGGAAC	CCTAACCTTGCAATACCC	NM_002975.1
S01042.H10	TCAGAGACAGGACTCAGG	CAATGGACAAGTGAAGG	NM_002975.1
S01035.D11	CCTAGATCCCAGTTCTCC	ACACCTAGGGTCACCTTC	NM_002975.1
S00630.H04	GTCTCCCTCCTCCTGAC	AGCAAGAGCAGTTTAGGG	NM_002981.1
S00636.B01	CAAGTGTGGCTTGCAC	GTCTGGATGTGGTCCC	NM_002981.1
S00628.F04	AGTTCAAGGAGAAGCCTG	GAGTTTACCACATGGTCG	NM_002981.1
S00693.A12	CCTCCTGCTTGACTCC	ACTGTGGGTACCACGTC	NM_002982.1
S01082.C11	TTGTCTTCTCCTGCCTG	GTTTATGAGGCTTGTCCC	NM_002982.1
S00624.B01	GGAATCTCCCACACTGTC	TTCAAATGGAGAATTGTC	NM_002986.1

S00620.H01	AAGTCATGCTTGGAATG	TCTATGACTCCCAGCAAC	NM_002986.1
S00647.A01	CTCATCCTTCCTCCTCTC	GGGTTCACAAGAACAATG	NM_002986.1
S01166.A04	GTGTGGGCAATGTTCC	AAAGGTCACCTAGCCTTC	NM_002986.1
S00590.C05	TGTGAGGAGGTGACAGAG	CAAACGTGTGTATTGCTG	NM_002987.1
S00607.C06	TCTTCCACGAACACCC	GTCTCTTCCCTGCTCC	NM_002987.1
S00608.A05	AATCCTGGTCAGCACAG	AACCCTCCCAGAGTGAC	NM_002987.1
S00414.G11	TTTCAGCCTGAGCTTTC	CAAGAGGTGAGGAATCTG	NM_002989.2
S00411.A11	CTGTGAGGGCAGAAGAG	CCAGCTATCCTGTGAGTG	NM_002989.2
S00408.G04	AGCCTTCTTAGTCTTGCC	GTACCAAGGCAGGGAG	NM_002989.2
S00405.G01	TTCTTTGGCTGTACTTG	GCAAATCCAGCTTTCAG	NM_002989.2
S00126.C11	CTCTCACCACAGGAAGTG	ATGGGAAGTTTAAGGCTC	NM_002995.1
S00132.G10	GGCCTTAAATTCTCACAAC	GGCAGCATTTCTACAGAG	NM_002995.1
S00159.D01	TGATCTTAACTCCTGACCC	CCATTACAAGCTGGACTC	NM_002995.1
S01035.G07	TTAATGCTCCAAATGCTG	CAAACCATTCCATTCATC	NM_002995.1
S01104.E02	TTGTACCTCTCTTTGATGG	GGTGTTGAGTTACCAGATG	NM_002995.1
S00558.F11	TGAAAGACAGCAGGTCTC	AAACGAATGAAGGAGAGG	NM_003300.2
S00547.E11	TAAAGTGAATGCTCCAG	GAGAGAATGTGTTGTGCC	NM_003300.2
S00558.C04	TTGCCTTGTCCAAAGTAG	TCTTAAAGTGCCACATCC	NM_003300.2
S00555.H05	GGGTTTCATTGCATAGAG	TGGAACGGATTATCTACG	NM_003300.2
S00556.H08	GATGGTGAGCAGAGCC	ATGACTCTCACGAAGTGG	NM_003300.2
S00556.G11	TCAGATGCTATCTGTGCC	AACAGGGTGTTTCAGTTTC	NM_003300.2
S00553.F02	GTATGTTAGCCGTTCTGC	AAAGCACTTCACACTTGC	NM_003300.2
S00556.A10	AACAGAAGGCCTATATTGTG	TCAGCTCAAAGAGTTTGC	NM_003300.2
S00546.H01	ACTGTTCTGCTCCTAGCC	TAACATAGCCCTCATCCC	NM_003300.2
S00139.D09	TGCAGGCTACAACAATTC	ACTGCATTTCTGCTTCAC	NM_003326.1
S00127.A08	ATTATTTCCAAGCGACTG	TTCTGATTGATAGGCTTTG	NM_003326.1
S01202.G10	TGCAGGCTACAACAATTC	ACTGCATTTCTGCTTCAC	NM_003326.2
S01217.E05	ATTATTTCCAAGCGACTG	TTAGTCACAAAGAAGTTCCC	NM_003326.2
S00937.A01	TCATGGAGTCATAGTCCC	GCGCTTTAGGAGAATGAG	NM_003467.1
S00817.E10	GTCATCTGCCTCACTGAC	CTTGCTGAATTGGAAGTG	NM_003467.1
S01218.G08	TCATGGAGTCATAGTCCC	GCGCTTTAGGAGAATGAG	NM_003467.1
S01204.A11	CAGATGAATGTCCACCTC	GCCACCAACAGTCAGAG	NM_003467.1
S00214.D10	ACCTAGGATAGTGCTTTGC	ACATTCCAGAGCGTGTAG	NM_003467.1
S01213.A10	ACCTAGGATAGTGCTTTGC	ACATTCCAGAGCGTGTAG	NM_003467.1
S01219.H05	GTCATCTGCCTCACTGAC	CTTGCTGAATTGGAAGTG	NM_003467.1
S00186.D06	TACCTCCAATGTCCTGG	TCACTACCGACCACCC	NM_003467.1
S01227.D10	TACCTCCAATGTCCTGG	TCACTACCGACCACCC	NM_003467.1
S01348.E09	TGTATTTAACCGCCAGAG	TTGCATTTCCACCACTC	NM_003581.1
S01029.C03	TGTATTTAACCGCCAGAG	TTGCATTTCCACCACTC	NM_003581.1
S00996.B01	CCTTCAGCTCAGTCACC	GAATCTTGGGAGAGAAGC	NM_003581.1
S01339.G11	GTTTGGATTTAGACGCAC	CCTCCTCTAAAGCTGGC	NM_003581.1
S00535.F12	GATTGAGAGAGAGGGAGG	CCAGACTCAGTTTCCAAG	NM_003701.2
S01231.F01	GATTGAGAGAGAGGGAGG	CCAGACTCAGTTTCCAAG	NM_003701.2
S01233.E07	GGGACATAAAGACTCTTGC	GAGCAGAGTCAACAGCAC	NM_003701.2
S00532.D10	GGGACATAAAGACTCTTGC	GAGCAGAGTCAACAGCAC	NM_003701.2
S01213.H04	TTACTATGGCACCTTTGG	CAGATCTAACCATGAGCC	NM_003701.2
S00533.G11	TTACTATGGCACCTTTGG	CAGATCTAACCATGAGCC	NM_003701.2
S00536.F06	ATCACAGCACATCAGAGC	TTCAGTATTGAAATGGGC	NM_003701.2
S01185.C12	ATCACAGCACATCAGAGC	TTCAGTATTGAAATGGGC	NM_003701.2
S00542.H12	TCCCTAACCTCATAGAATTG	GTTTCCAAACATCCAGG	NM_003701.2
S01215.G12	TCCCTAACCTCATAGAATTG	GTTTCCAAACATCCAGG	NM_003701.2
S01198.D02	TGCCTTGAATAATAAGCAG	AAAGAGACATGAAGGTGAAG	NM_003701.2
S01018.C12	AAACATTGCCTTTGAATG	AAGTAACCAACCTGGGTC	NM_003701.2
S01212.C12	AAACATTGCCTTTGAATG	AAGTAACCAACCTGGGTC	NM_003701.2

S01213.B09	ATGAGAAACTGCATGTGG	TGGCCCATTATGTATCC	NM_003701.2
S00875.G10	ATGAGAAACTGCATGTGG	TGGCCCATTATGTATCC	NM_003701.2
S01200.F09	GATGCAACATACTTTGGG	CCAGCATGATGTAACAATTC	NM_003701.2
S00826.D09	AGAAGGAACCCTAAGGC	CTCTGTCTGGAGGTGAAG	NM_003789.1
S01393.C06	AGCAATCCTCCTATCTCTG	GAGAACGAGCTCACCAG	NM_003789.1
S01363.B01	AACGTCTGTTGGTCCTTC	TTTGAGTTGCATCCTAGC	NM_003789.1
S00814.D06	TTAAAGGTGGCTAAACCC	CTTGAGGCTACTGTGGTG	NM_003789.1
S01107.C04	CGAACAGCTCAGTAGACC	GTCTTCCTGCCGTCTAAC	NM_003789.1
S01196.E09	CTTCATCTCGCCTTGG	GTGGTGTGGTACACCTG	NM_003807.2
S01196.E05	GTAAGACCGGGTACCATC	AGGAGACTGAAGCAGGAC	NM_003807.2
S01220.B05	TATGGCGTTTATCTGGTC	AGGTGTACACGGTGGC	NM_003807.2
S01195.B10	TGTGCAAATCATATTGGG	GTGTGAGCAATGCGAG	NM_003807.2
S01208.F01	AGTGACCCACAATGACAC	GTACCGGAAGAAGAGGAG	NM_003807.2
S01223.D05	CTCACCTCCTCTTCTTC	AGGAGAATTGCTTGAACC	NM_003807.2
S00643.F11	TGATCACACACAGCGTC	ACCTGACATCTCACCTC	NM_003809.1
S00638.G09	CACATCAGGAGCTGAGAC	TGTTACACACACACCCTG	NM_003809.1
S00620.H02	CTGTCCCTGACTTCTGTG	AGCTGCATGACTCTGAAC	NM_003809.1
S00636.D08	AGATTCTAAGGCCAGGAG	AGGTCGTGGATGAACTG	NM_003809.1
S00616.A05	ATACCCAGGAGGAGAGG	GAGTGGGAGGTCAAAGG	NM_003809.1
S00625.A12	TGTTTCATATGCTCAATGG	CAGCCCTGTAGCTTGTC	NM_003809.1
S00648.C02	CTGGGAGGGTGAGTTG	TAGTGAGGTGGAGAGTGG	NM_003809.1
S01211.A09	TGATCACACACAGCGTC	ACCTGACATCTCACCTC	NM_003809.2
S01231.E04	CACATCAGGAGCTGAGAC	TGTTACACACACACCCTG	NM_003809.2
S01239.H12	CTGTCCCTGACTTCTGTG	AGCTGCATGACTCTGAAC	NM_003809.2
S01225.E06	AGATTCTAAGGCCAGGAG	AGGTCGTGGATGAACTG	NM_003809.2
S01241.D12	ATACCCAGGAGGAGAGG	GAGTGGGAGGTCAAAGG	NM_003809.2
S01240.D09	TGTTTCATATGCTCAATGG	CAGCCCTGTAGCTTGTC	NM_003809.2
S01209.G09	CTGGGAGGGTGAGTTG	TAGTGAGGTGGAGAGTGG	NM_003809.2
S01209.F03	TCTAGAGGCTGCCTGG	AGTGTGCCTTCTACCTC	NM_003809.2
S00662.C04	AAGTAATTTGGTGATTCCC	ACATTACCACCTGCCAC	NM_003839.1
S00665.H10	TTTGCTTTGTGTTGCTG	GAAACGAAACATCATTGG	NM_003839.1
S00657.D08	GCTGGATGTTGGATAGC	CAAGACTGTCTCAAAGCTG	NM_003839.1
S00658.H09	CTCCAGTCCTCTGGAGTC	GCCTAACCCAACAGAATC	NM_003839.1
S00658.C12	TTCAAATGTCCAAGAAGG	TCTGGGAGGGATCTAAAC	NM_003839.1
S00658.C06	CTGAGGTTTGATTTACCG	GGCAGCAAGTAGACAATC	NM_003839.1
S00661.E03	GATGGGTATGTTAATTTGC	ACTAGGATGGCTCTACCAG	NM_003839.1
S00665.G10	ATGGTGGAATAATCAGTG	TTCAGAGGACATGGGAG	NM_003839.1
S01020.A05	TTTAAGCCAGTGCTTCAC	ATAACCAAACACGTGGAC	NM_003839.1
S00895.F02	TCGTTCTTAAGCAGAAC	ATAACCTCCCAGATGTGC	NM_003839.1
S00665.E01	CTTCCTCTCGGCAGAC	GGACAGTCCTCATCAATTC	NM_003839.1
S01204.A01	AAGTAATTTGGTGATTCCC	ACATTACCACCTGCCAC	NM_003839.2
S01187.H04	TTTGCTTTGTGTTGCTG	GAAACGAAACATCATTGG	NM_003839.2
S01245.B10	GCTGGATGTTGGATAGC	CAAGACTGTCTCAAAGCTG	NM_003839.2
S01236.B04	CTCCAGTCCTCTGGAGTC	GCCTAACCCAACAGAATC	NM_003839.2
S01234.H01	TTCAAATGTCCAAGAAGG	TCTGGGAGGGATCTAAAC	NM_003839.2
S01234.F02	CTGAGGTTTGATTTACCG	GGCAGCAAGTAGACAATC	NM_003839.2
S01203.G11	GATGGGTATGTTAATTTGC	ACTAGGATGGCTCTACCAG	NM_003839.2
S01224.F01	TTTAAGCCAGTGCTTCAC	ATAACCAAACACGTGGAC	NM_003839.2
S01204.B02	CCTCAACCTTCGGAGTAG	AGAAGAATGCCAAGCTG	NM_003839.2
S01209.A12	CGGTACAGTCGAGGAAG	AGACCAGGCTGGGTAAC	NM_003839.2
S01230.D01	CTTCCTCTCGGCAGAC	GGACAGTCCTCATCAATTC	NM_003839.2
S01215.F09	TCGTTCTTAAGCAGAAC	ATAACCTCCCAGATGTGC	NM_003839.2
S01124.H01	AAGATAATCCCGTTCTAAAG	TGCCTGTGAAAGAATCTC	NM_003840.1
S01058.H04	CAGCTATAGGGACAGCAG	AGGTTTGTCTCCATCTCC	NM_003840.1

S01043.B02	CCATGTCCCACTGTCTAC	AGGTCCAGCTGTGTACTG	NM_003840.1
S00950.A04	GAGGACAAGGGATTGTG	GTCCTCTGGGAGGGAG	NM_003840.1
S01159.C04	TTACTGTCTGTGGGAACG	ACTGCTGACACGAGGAG	NM_003840.1
S01174.F12	GTCAGCGGAGAGATAGAG	CTGAGTTGAGCTGAGTGG	NM_003840.1
S00811.F07	AAGTGACAAGTGACCACG	GGACCCAGTTCTTCCC	NM_003841.1
S00692.A09	AGGGAATGTGAGATGGAG	TTGATTTAGCCATTCCAC	NM_003841.1
S01040.H01	GTCTCAATTCCAGTGAGG	ATATCGGCTACAACCTCCC	NM_003841.1
S00918.A03	GAAACTGGCCCTTAGAAC	GGGTACCAGGTGACTCAG	NM_003841.1
S00898.A09	GAAATTCCTTCCTTACCTG	AGTCTCCTTAGCAGGTGG	NM_003841.1
S00848.B11	TCAGGGACATTGGAGAG	GAACACAGCAGAGGGAG	NM_003841.1
S01316.A07	TTTCTGTCACTCAGAGC	ATTACAGGCGTGAGCC	NM_003842.2
S01312.E02	GACTGGCACCTTCTGAG	TGGTTATCTGTCACCCTG	NM_003842.2
S01002.C03	TTGTAAGGTTGTCCAGTTC	GTTGTCCGACTTCACTTG	NM_003842.2
S01297.F06	ATTCTAGGTCCTGTTGCC	AAGATGTCACTGTCTGGG	NM_003842.2
S00931.G03	GGATATAGCAAAGCCTAATG	ACTTCTGGAAGGCACAG	NM_003842.2
S00993.G11	AAAGGTAAACCAGGGAAG	GAGGGCTGATTCTCTGAC	NM_003842.2
S01301.E06	ATAGTGAGCCAAGATTGC	AGAGACTTGCCAAGCAG	NM_003842.2
S01074.G07	CAGCATGGAATACTCTGG	AATGTTCTGGAAGTGACG	NM_003842.2
S01040.F03	GTTCTTCCTCCGACTCC	AGGAAGTTCAGGGTTAGC	NM_003844.2
S01295.F11	AGAGCACTCTCAGCAATG	CTGATGGTCAGGGTCAG	NM_003844.2
S00795.A12	CTCAGGCTCCACTTCC	ACTTCCTGGAGTGACCTC	NM_003844.2
S01031.B12	GACTACACTGTGGGCAAG	AAGGATCTCCCGAGTTAG	NM_003844.2
S01099.F12	GGCCAGAGACACTAGGAC	GAATCAGGTACAAAGCCC	NM_003844.2
S00741.D10	TTATGTCCATTGCCTGAG	CGAGGAGACTATCCTTCC	NM_003844.2
S00901.F12	TCAGGGCTGATAGATACG	GGTGGTGAGGAAAGGTC	NM_003844.2
S01122.F07	AACTTGTTCCCTGACTC	AAGAGTTTCCTAGCCACC	NM_003844.2
S00174.H03	CAAAGACTTTCAAGCCAC	TGCACACCTCTCCTACTG	NM_003854.1
S00190.F10	TGTCTTTGAGATTCCGAG	ATTTGCCTAACTCCTTCC	NM_003854.1
S00188.C08	AGGGAACGGAGTAAATTC	TTCACTGGAAATTGTCTTG	NM_003854.1
S00207.G06	TTTGTGGATGCTTAGTGC	TTCTTTACCAATTCTGCC	NM_003854.1
S00185.D03	AGCTATCTGTTGTCTTCCAG	ACTAGCCTTCAGGGAAAC	NM_003854.1
S00178.E11	TGGGCTTCATGCTATTAC	ACGTATATCCAAAGCTGG	NM_003854.1
S00177.B12	ACGATGCACTTGTAATCC	GAAGGCAGTAGTGATACCAG	NM_003854.1
S00197.D08	TCTACAAACCTCACTGGG	TCCTTCAGATGTGTTTCC	NM_003854.1
S00184.H10	AAATGTTTAAGCAGTGCC	CCTAAATTTGCCAACAAC	NM_003854.1
S00179.E07	AGGAGATGATGTCCCTTG	AAAGTGGAGGAACAGAGG	NM_003854.1
S00197.A06	TCTCCTGGCCTGTTTC	AACTGCCAGCTTCAGAG	NM_003854.1
S00184.G07	TTGCAAAGATAACCCAAG	CTCTCACCCACCATGAC	NM_003854.1
S00181.C12	AAATCTGTGTGCCAGAAG	TCAGCATCTTCAGTAGCC	NM_003855.1
S00192.D07	GTGTTGGAAAGATTGACG	TGCATATTTGAGTTGCTG	NM_003855.1
S00200.E04	CTAAAGGGAAGATGGGTG	GATCAGGCAGCTTATTTG	NM_003855.1
S00183.D07	CAGGAATTGCTACTTTCC	CCCAACTAAGTGGACTCTC	NM_003855.1
S00175.F05	TCAAGTGAACGTAAACCAG	ATATTTACGCTTGGAAGG	NM_003855.1
S00185.E02	ATTCTCTTTCTGGGATGG	AAATACACATCAGCCACC	NM_003855.1
S00171.G10	ACAGCTGCCTTCAAGC	GCCATCTTTGAAATGTCTC	NM_003855.1
S00175.H07	CACGTGATGATGGACAAC	GGCAGAACAATATTTCCC	NM_003855.1
S00183.B12	CTTGTTAGCATGGGAG	AATGGGATAGCTCTCTGG	NM_003855.1
S01079.H08	GACTGTTCTGTTTGCTG	GATCTGGCTGTTTCAGTG	NM_003856.1
S00201.G10	AGAGAACCATCCTCTTCC	AAGGATGACCAAAGAAGC	NM_003856.1
S00879.G06	CTGGTTGTGCTTATCCTG	CCACATCAGAAGGAAGAC	NM_003965.2
S01090.H01	ATTTCGGTTCTTGTCCTC	CGTTTGTAAGAGCCTTG	NM_003965.2
S00764.H10	TCATCTTTCTGCATTATTTT	CTAGTTCTTCTCATCACCG	NM_003965.2
S00250.H10	TCATGCCAGCTTTATTTT	GCAGGGTAAGCAAGAAAC	NM_003965.2
S01307.C12	TGGTACGTGTATCCCAAG	AGCTAGCATGTGACTTCC	NM_004084.2

S01000.A01	TAAGTGAAGCCACCTCAG	GGAAGGTTTCTTGTCTCC	NM_004084.2
S00724.H05	TCAGAGGTCAGATTGGAG	CTTTAACCTCACCTTCCC	NM_004084.2
S00735.C12	GTGGCTGTGACTTCAGTG	ACAGAAAGTAGAGAGGCAGG	NM_004295.2
S00956.F06	GTCTTTGACACCATCCAG	TACATCAGAAGCTGAGCC	NM_004295.2
S00892.D04	ACACCCTCTGTCTTCCTC	ATTCTTCCAGTTTGGGTC	NM_004295.2
S00928.B11	AAGGGAGGTGTCATCG	CTTATGGATGGGTGGG	NM_004335.2
S00829.D05	TCTCTCTAGACTTCGGAGC	GTGGGCTTACAGGGAG	NM_004335.2
S01047.H09	TCAAACCTTTATCCCTTGG	AGGTTCTGTCCCAGAGTG	NM_004335.2
S00855.E09	ACTCTGGGACAGAACCTC	CAGGACCTAGGGAGGAG	NM_004335.2
S01129.F05	ACCCTGGGTCAGATTTC	TCCTGGAACCTTGCTATTG	NM_004335.2
S01042.F02	AGAGCTCCAGGGCTTAG	GACCAGAAGAGGAAGAGC	NM_004512.3
S00748.D04	TCTCCTAGGAAGCCTCAG	GTCACAAGTTAGGCATGG	NM_004512.3
S00939.C06	ATGGGACCTAAGTAAGCC	TCCTCAGAACCTACCTCC	NM_004512.3
S00679.H01	GAGGAAAGCCTCAGAGAG	CTCCTAGAAGGGAGGATG	NM_004512.3
S00794.E07	ATAGCCAGAGGTAGGACG	AATGGAGTCTAGGTTGGG	NM_004512.3
S00906.C01	GCTCTTTGTAGATGGTGG	TTTGGAACCTGGTTCAGC	NM_004512.3
S01139.D01	TTGAGCACAGGACGTG	ATGTCACTGAGAGCAAGC	NM_004512.3
S01139.C06	GGGCAAGACTTGTAAGG	GTGGAGATGAATGTGGTC	NM_004512.3
S00898.C01	CCTCTCCTGACCCTTTAC	CAGCCAGCTCTTAATCTG	NM_004512.3
S01059.H08	TCATTCTCAGGGTGTCTG	ACCAAGAGAGAAAGCTCC	NM_004512.3
S00572.F11	AACCAATATGAACCTTGGG	TTTCCTGGAACCATGC	NM_004513.2
S00571.D08	TCTCACTGAAAGCAGCTC	GCAGAGCACTCTGATCC	NM_004513.2
S00977.G02	GAAAGGTTTGAGGAATCG	ACACTTGCTGCTGATAG	NM_004513.2
S01136.E09	AGGCTGAGGAATCTCAAG	ATGAGCAATTCACCAGG	NM_004513.2
S00868.B03	CCTCCTCTTGAATCCTTC	CTGATTCTCTGCCTGATG	NM_004513.2
S00579.B11	CCACACCTGGGACATAG	CTACAGTGTCCCACCATC	NM_004513.2
S00572.G03	TCTGATGTCAGTCCGATG	CATGCATTCTTCATTTCC	NM_004513.2
S00575.B10	CTAACCGGTTCAATCCTC	TCAGGCAGTGTACTAGGC	NM_004513.2
S00578.B08	TCACTTGAAGCCCAGG	ACAACATAGCCCAGAAAG	NM_004513.2
S01035.C06	ATTGTCACATGATGGAGC	GGGATCTCACTGAGGG	NM_004516.1
S00756.A06	CACACATGTCATTCTTGC	TGGTAATGGAAGCAAATG	NM_004516.1
S00936.A06	TCATTCTGAATTGTGCAG	AACAGGTGCCAACCTC	NM_004516.1
S00749.H02	GTAGGGTAGCCAGGGTAG	AGCCTAGCAGGACACTTC	NM_004516.1
S00778.H11	CGGGTCATCATACTCAAG	CACCGTATACCAAAGCAG	NM_004516.1
S00733.B03	TTAGAAAGCTGCCACATC	TGGTGACAGTTAGCCAAG	NM_004516.1
S00721.F10	TTGACTGTTTACCCTTGG	GACCATCAAGTGTTCTCTG	NM_004516.1
S00796.F01	CTCATGCAGTGACAGCTC	CTGTCTTAACCCAGTCAG	NM_004516.1
S00752.F03	ACACCTAGTTCCTCAGC	GTAATGGAACCTGGAAGCC	NM_004516.1
S01342.A08	CAGAAGGCAGTAGTGAGC	TCTGAACTGCAAGGAGAG	NM_004516.1
S00941.D02	AACCCAGTGGACTACACC	GAGCTCAAGCGATTCTC	NM_004516.1
S00806.E07	TGTGTTACGCCACAGAG	TGAGAGACAATGGCTCAG	NM_004516.1
S00785.H01	CAGGAGCTGAAAGGAAAC	AGGACCAGTAACCACCTC	NM_004516.1
S00786.G04	AGTCCTGCCACTCCTC	AGATGACTCAGTGCCTCC	NM_004516.1
S00830.A05	CTTCGTCATGGAGGTG	AGGGTTATGTGGCTAGAAG	NM_004516.1
S00899.B07	AAATTTGCTGCTAAGGTG	AGGGAAAGACAGGGTTAC	NM_004516.1
S00751.C07	CTCATACTGCACTGTCCC	CACCCTTTGCTAACTCAG	NM_004516.1
S01063.B08	TCTCCCTCCTTGTCTAC	GAGCTTCTGCCACTCC	NM_004516.1
S00795.A04	GGCAGGGAGAAGAGTTAG	GAGTGCCTGTTCTCACAG	NM_004516.1
S00918.C03	AGGAGCCCATAAGTCTTG	CAAATGACGTATCCCTTC	NM_004516.1
S01320.H03	TTTGCAGTTCAGTATCCC	GAACCTACACCAGAATCGG	NM_004516.1
S00651.D08	AAGAAATGTGGAGAAGCC	TTTCACATCCTTCTCCTG	NM_004590.1
S01148.C10	AAAGATCATCTGGAAGGC	AGCCAGTCACATTGAGAG	NM_004590.1
S00649.E10	ATGGAGACCTCTTGATCC	GGAGTGAAACACAAATGG	NM_004590.1
S00621.F04	AAGCTATGCATGAAGGTG	TTTCAGCAAACACTGAGG	NM_004590.1

S00128.D01	TGAGGGAAATCAGATGAC	TTCAAAGTAACTGGGACG	NM_004619.2
S00112.H02	TGAGACAAATAACCAAAGC	TGAGTGGCCACAGTTG	NM_004619.2
S01175.B01	CTTCTGGGTAGAGGGAAC	CCTGCTCCTATCTCAATG	NM_004619.2
S00096.E03	CTTCTGGGTAGAGGGAAC	CCTGCTCCTATCTCAATG	NM_004619.2
S00103.B02	CTGAGATACACTCGAAGACC	TCCCTGTACCATGCTTAG	NM_004619.2
S00113.B08	ACCCTGTTCTCTCTCCC	ATTCCACCTGATTCACTG	NM_004619.2
S00107.A05	CTGTAGAGAGTAAGCCACG	CGTGTAAATTTAAGCCCTG	NM_004619.2
S00141.F08	TCATAGCTCTTTCTTGCC	ATCCTCGATGGAACAGAG	NM_004619.2
S00156.E04	AGCAGAATATCCTACCACC	ATACCAGCATAGAGCAGG	NM_004619.2
S00153.G07	ACTTTCTTAGCTGCAAGTG	ACAAGTGTTCTTTGCACC	NM_004619.2
S00117.F01	GTGGCTCATCTCTCTGTG	CAGGTGTTTGTTGTTTC	NM_004619.2
S00767.A09	AAGCAGTCAACGTGAAAG	GCTTTGAAGGAAGGACTC	NM_004829.1
S00727.E01	CAGAATCTGAGCGATGTC	CTTAGGCTCCACCCAG	NM_004829.1
S00857.C09	CTGGGTGGAGCCTAAG	CTACCGAGACAAGCAGTG	NM_004829.1
S01310.A04	CGACAGAGCAAGACTCC	AAGTGCTGGGATTACAGG	NM_004829.1
S00878.F09	TTTACCTGCTGGATGAAG	CCATTTAGATTCCCTTCC	NM_004829.1
S01317.A12	GGCGACAAGACTGAGG	AGGGATGGAGAGCTAGAG	NM_004829.1
S00700.B06	GAAACCCAAAGTAACGTG	GCTGGGTCTCAGATTAGG	NM_004843.2
S00757.G06	TCTGGTGAGGATATCTGG	CAGCAGTGTTGGGATTAC	NM_004843.2
S01166.H12	CCTTATCTCAGGGTGTCC	GGGAGGAAGGCAGTAG	NM_004843.2
S01342.A06	AGGGCAAGACTCTGTCTC	AGGGTTCATGAATGTGAC	NM_004843.2
S00747.E09	ATTCATGAACCCTGCAC	GATGAGCCTGTAATCCTG	NM_004843.2
S01135.C08	ACACACCTGTAGTCCGAG	CAGAATCACAGCGTCATC	NM_004843.2
S00730.E11	GAGGTGAGTCAAAGGGC	GAGGGCTAATCCAGGAC	NM_004843.2
S00938.B01	TTGTGTCTTATGCCTGTG	GACCAGACGTGAATGAAG	NM_004887.2
S01135.A05	GCTAGATGACCTGGTGG	CCCTGACTTAGCCCAG	NM_004887.2
S01097.G09	CAAAGTCGGAGAGAAATG	CACCAAGGTGGTCGAG	NM_004887.2
S01054.G08	CAGGATGCCTAGAAATTG	GCATATTAATGAGCTCGC	NM_004887.2
S00384.B10	ATTGCACCCAATACCAG	GAAGGAGAGAGAGGGATG	NM_004942.2
S00385.G02	ACTGACACAGGGTTTGTG	AGGTCAAGGAATCCAAAG	NM_004942.2
S00146.C04	CTTTAACCTCACCTTCCC	TCAGAGGTCAGATTGGAG	NM_005217.2
S00385.H08	TGGTACGTGTATCCCAAG	AGCTAGCATGTGACTTCC	NM_005217.2
S00385.C10	TAAGTGAAGCCACCTCAG	GGAAGGTTTCTTGTCTCC	NM_005217.2
S00388.H01	TCAGAGGTCAGATTGGAG	CTTTAACCTCACCTTCCC	NM_005217.2
S00390.C06	GACCTGTCTCACGTTCC	GCGAGATGTTCTCAAATC	NM_005218.2
S00383.E10	ATCCGAGACTCACATCAG	CTTGACTGTGGCACCTC	NM_005218.2
S00252.C05	TGTGTTCTGCAATGCTC	ACAAGTGCTTTTCTTCG	NM_005283.1
S00802.G09	CTCCACGTAGCAGAACAG	TATGACCTTCAGAGCCAG	NM_005283.1
S00275.D06	TTCATGATGACGGATAGG	TATGCATCATTTGGTTTG	NM_005409.3
S01190.G09	TTTGCCAGTATCCCATAG	TGTGAAGGATGAAAGGTG	NM_005409.3
S01191.B07	GATGGTAACCAGCCTTTC	GACAACGATGCCTAAATC	NM_005409.3
S01190.G08	TTCATGATGACGGATAGG	TATGCATCATTTGGTTTG	NM_005409.3
S00260.B07	GCTGTTACAACCAAGGAC	AAGATGACAATGGTGCAG	NM_005409.3
S01213.C01	GCTGTTACAACCAAGGAC	AAGATGACAATGGTGCAG	NM_005409.3
S00260.D07	ATTTGGGATTTAGGCATC	AATTCTGCTCACGTTTAC	NM_005409.3
S01214.B10	ATTTGGGATTTAGGCATC	AATTCTGCTCACGTTTAC	NM_005409.3
S01214.C01	ATGTCCACCATTCTGTG	GTGCATGACTCAAAGAGG	NM_005409.3
S00261.A12	ATGTCCACCATTCTGTG	GTGCATGACTCAAAGAGG	NM_005409.3
S00135.D01	GACTAACAGAAACGAAAGC	CCCTTGTGATTCTGGG	NM_005531.1
S00138.A06	GCCACTCACTCACATAGG	GTTGAGTCACAAACTGGG	NM_005531.1
S00098.B06	TCAAGCAGGAACTGAGAG	AGATTGAGTGGAAGAGCC	NM_005531.1
S00133.F12	TGCCCATCTCTTAAACTG	TAACCGGTGAAATCAGTC	NM_005531.1
S00124.F12	TGAGGTCACTGAATAGCAG	TAGGCAAAGCTTCATCTC	NM_005531.1
S00124.D01	TGCTGTTGTGCATCTTG	CTCCCGCTGAACTCTG	NM_005531.1

S00135.A11	GAGAGAGACCATGTTTGG	ACCAATCCATTACACAGAG	NM_005531.1
S00141.D12	ACTGGCAAAGTGAACATC	GTGAGGTGCTTTCAAGG	NM_005531.1
S00141.F01	CACTGAGGCTGAGATGAC	GACCAAACCTCCAGTTGAC	NM_005531.1
S00126.G12	AAGTTTCCAGAAACACCC	TTTCCACTTGCTAGACTCTC	NM_005531.1
S00121.F11	CAGTGTGATTGAAGGGAG	GATTTGCAGACCACAGAC	NM_005531.1
S00087.C09	CCATTTCTGCACTTTGAC	CAAGAACGATGTGTTTCC	NM_005534.1
S00090.G06	GTATCTCAATAAACCTGCG	AGAGGTGTGTGGAGTCG	NM_005534.1
S00091.A10	GCAAGAGAATTGCTTGAG	GCCCATGTAAAGGTTTC	NM_005534.1
S00082.E02	TCTTTGTTTGTCTGTTC	CAGCACTCTTCTCACTGG	NM_005534.1
S00086.G01	TAAGCATACCAGGTGAGG	TTGTACCATGACACTCCC	NM_005534.1
S00844.G07	AAGAGATCAAGCCATCG	AGAAAGCTGAAACTCTGC	NM_005534.1
S00093.G12	GGCAAGAGTAAGACTCCATC	CTCATGTCTGCAGGGAC	NM_005534.1
S01073.D03	ATGGCAGCATCTAGGG	CACTTATGGCATACCCAG	NM_005535.1
S01339.B03	TTTCGTTTCTCCCTCAG	TTAACCAGCAGTGACCTG	NM_005535.1
S01325.A02	TAATGCGTAACCCTTGTC	AGAGCAAGACTCCGTCTC	NM_005535.1
S01328.E08	ATTATTTCTGGGCAAAG	CAAGTTCATGGAGAAACC	NM_005535.1
S00817.E08	TGCTAAGATCATTGTGGG	ACAGGCTGTGGTAGCC	NM_005535.1
S01321.A08	GGGATTACATGCGTGAG	CAGTGCAAAGGTGCAG	NM_005535.1
S00901.E08	AGTAAGCAGCAACACCTC	TATAGACGAGAGGGTGGG	NM_005535.1
S01313.E05	ATCTCATCTCCCTCCATC	AAATGTGGAGAATCCATC	NM_005535.1
S00710.E06	GAAGGAGTGTTGACCCAG	AGATTTGTCTTAGGCACG	NM_005535.1
S00717.D07	GACTCCCAAGACCACAG	CTGATGATCACTTGGGTG	NM_005535.1
S00295.G08	TTTACATATGCCTCCTCG	AAGCATGTTTGTGTTTCC	NM_005546.3
S00296.F09	GATTTCTGGAGCAATCTG	AAGTGCTAGGATTACAGGC	NM_005546.3
S00282.F01	TATGACGATAAACACCCG	TCTATTGTGGAACCCAAC	NM_005546.3
S00304.E03	TCTGGGCAATACTCATTC	GCATTCTGTTCTTGACAC	NM_005546.3
S00298.A03	CCTGGCTGCTCACTTC	ATGCAAATAGGAACATGC	NM_005546.3
S00285.E04	AGTCTACCAGAGGAAGGC	CCTCAGTGCTGTGGTTAC	NM_005546.3
S00297.G12	GTAGAAACATACGTGTGCAG	GGATTCCAGACATGAGAC	NM_005546.3
S00291.A10	AAGAAAGTGGAGCTGGAG	CCTCTACCTCTTGCACTG	NM_005546.3
S00309.D06	ACAATATCTGCCACCTTG	ACGCTGATCTGACAGAAG	NM_005546.3
S00306.C07	ATTAGGCTTTGGGATTTG	CATGGCCAGTTTATTCAG	NM_005546.3
S00302.C08	AATTTATTTGCCATCTTTG	GGCATTTCAGAAGAACTG	NM_005546.3
S00291.E11	TCATCCAAACCATAAATTAG	CCCAGTCATTTCAGTGAG	NM_005546.3
S00283.D06	GATGCCCTTGATGACAG	AGGGAGAAGGTCAGAATG	NM_005546.3
S00282.D01	GTGAAGTCTCAGGAATGG	TAGGGTTGTCTGCATTTG	NM_005546.3
S00296.F02	GACTTGATGCACTTCTGG	TTTCTCTAGGGAAGGAGG	NM_005546.3
S01275.F08	TGAGCTAGGAGACTTCCC	CCTCCTCATGAAGTGTTT	NM_005546.3
S01263.B09	ACGAGCTTCAAAGCAAC	AGTTCTCTACAAACACAGGG	NM_005546.3
S01305.B04	ACAGCATTCTTGCACTTC	TTCTGTGCAGAAGAGGAG	NM_005546.3
S01372.A11	ACATTCTTCACCTCCTGG	TGTGTGCATGAACCATAG	NM_005546.3
S01151.G04	CCTACCATGGAGCTGG	ACAGGTGACTATCCTGCC	NM_005601.2
S00795.B08	TGCCCTCTGTCCTCAG	AAGGACTCTGGACTGGAC	NM_005601.2
S01104.D03	AAGGACAAGAGAGATGGC	CGATTTCTGGTTTGAGG	NM_005601.2
S01344.F03	AAGGACAAGAGAGATGGC	CGATTTCTGGTTTGAGG	NM_005601.2
S01034.G04	CTTACCACTTCCCTCCAC	CCGAGGAGATAAGAGAC	NM_005624.1
S00719.H06	GTGGTATGAGCAGACAGG	AGGTTAGGGTGTAGGCTG	NM_005624.1
S00706.A02	AGGTCCCAAGTCCTCAC	ATCTGTACAATGGGAGGG	NM_005755.2
S00732.E05	CCTGTTCTGCTCTC	GCTTAAGTGTGAAGGTGC	NM_005755.2
S01294.E10	TCAATTTCAATTGTGTGATG	GAGTCCTTTCTCTCCAG	NM_005874.1
S00734.A01	GGAAGGAGGACAGAGAAG	CTCCCTGCATCTCAGTAG	NM_005874.1
S00973.H10	CCATTGCTACGGAAAC	AGTGGAGGTAATTCTGCC	NM_005874.1
S01173.E08	GAGGAATGGGAGCTTTAG	TCCTTCCTTACCTTCGAG	NM_005874.1
S01105.H06	TGGTTTGGATTCTCTTG	CAGTCACCTGCACACAG	NM_005874.1

S01042.G11	ACCTAGGACAGAACCCAC	AGGCAGAGAGAAGTGTTG	NM_005874.1
S01062.A05	GCTCACTCCATCCCAG	AACAGAGACAGAGGCTCC	NM_005874.1
S01168.E09	CATCACTAATTGGATTCCC	ACACAGGAAGATCAGCAG	NM_005874.1
S01158.E02	GAAGTGCCTGAGACAC	TGTCTCCCTCTCACAGC	NM_005874.1
S00882.G06	TGTGAGAGGGAGACACC	TTCTGGACTGACTGATGG	NM_005874.1
S00823.H06	GGAAGGAAATCAAAGGTC	GCTCACAAGATCCCAG	NM_005874.1
S00688.D05	ACCAGAGTTTGGCTGTG	GAATGAGAGTCAGGCTCC	NM_005874.1
S00764.C05	TCCTTCTCACAGCTTCC	AAACCCACAATCCAGTG	NM_005874.1
S01031.F08	AACTAGAGGGCCTGAAAC	AAGATTACATGACCAGCG	NM_006058.2
S00885.D06	TCAGAAGGATGCAGTTTC	TAGAGGGTGATGAGATGG	NM_006058.2
S00704.D04	GTTAGCAGAGGATGTCCC	CTCGTGGCTGGTTAGG	NM_006058.2
S01161.B10	CATCCAGCCTCACCAG	AGGAGGCATGGGAGTC	NM_006058.2
S01305.B08	GTTCCATGTGATTCCAAG	TTCCCTGAGGATGACC	NM_006058.2
S00724.H04	TCCTAAGCTGAATGGTTG	CAGGCAGGACAGAGAATC	NM_006058.2
S00764.H11	TTGCTCCACAGAACTCTC	TAGCAGCTTTGAACCTTG	NM_006058.2
S00715.H12	TCAAAGCTGCTAAAGAGG	CACTATTCACACACACCG	NM_006058.2
S00740.D10	ACCATGCCAACTCCTC	TAGAGGAGCACCGAGAC	NM_006058.2
S01068.H12	CACTGGAGGTGGTAAGC	ACTCATGCGATAGTGAGC	NM_006058.2
S00877.F08	GTAACCTCCAAATAGGGC	CATCCTCTAGCTCAGCC	NM_006058.2
S01018.B10	CATGGTACCAGTGGATTC	TGAGAAATGAGGAAGCAG	NM_006058.2
S00845.D10	CAGGTTCTGTGCCTCTC	TATGTAACGGTCCCTGTG	NM_006058.2
S01315.G12	CCTCAACCCTCTTTCTTC	AATCCTGTCTGAGAACCC	NM_006058.2
S00914.G10	GGCATAAGAAGGGAGTTC	GGAGTTTGTCCCACTTG	NM_006058.2
S00754.A01	AGTAGAGGGACTGGCATC	AAGGAGGTGACTGTCCTG	NM_006058.2
S00787.H08	AAAGCATTGTAGGACCG	CGGCTTAAGCTCAGAAG	NM_006083.2
S01106.D12	TGACACTGTCGCTGTTT	TTCTTTACCATCACAC	NM_006083.2
S01093.G11	GATGTGGATTTCTGCTTG	TCTAGCTTCATAATTAGCCC	NM_006083.2
S01315.C07	AGATGTAGGGAAGCAAGC	AGGGCAGGAAAGTAAGAG	NM_006083.2
S01315.C08	CAAACCTCTGACCTTGTC	ATCTTGCCAGACCCATAC	NM_006083.2
S00785.C06	GTTCTCTGGTACAGTGTGG	GGATCCTCATCTTTCCTG	NM_006083.2
S01279.C10	GAGAATTTAGAAAGGTGGG	AGCATATCCTTCCCAGAG	NM_006083.2
S00716.F09	CCTCCCTTCACCTACTG	GAAAGCTCCAGGAGACC	NM_006083.2
S01315.C09	TAAGAGCTGGAGAGGATG	CCAGATTCTCATGTCAGC	NM_006083.2
S01169.C12	AGGTTGGGTAAAGGAATTG	TCTGAGCCCTACCAGG	NM_006083.2
S01063.E08	TCTGGATACCCTACCCTC	AGGGATGGTTTTCATTCTG	NM_006083.2
S01091.E07	ACCCATAACAGCTCACAG	TCAAATTTCCATTTACC	NM_006083.2
S00957.C05	GTGGTCATTCTATGCAG	TACTGCTGCAGCTAAAGG	NM_006083.2
S01056.A09	ATTATGGGAGAGTCTGGC	AGACCACACCCTCTAACC	NM_006083.2
S00691.D10	TAGAGGGTGTGGTCTGG	CCTGTTCTGAATCTGC	NM_006083.2
S00809.E11	CCATGGAAATGAGAGGTC	GAAGGAGAAATGGGTCAG	NM_006083.2
S00702.A05	ATTCTTCCTCTGTGGGAC	AACATCTTGCAACCTTTG	NM_006083.2
S00808.B05	AAGGTCTAAGCTCTTGAGG	AAGAATTTGGAATCCTGG	NM_006083.2
S00889.E07	AGCTTATCAGCACCCACAG	GGTTTCTTCTCTTCCAGC	NM_006083.2
S01315.D06	AGCTTATCAGCACCCACAG	GGTTTCTTCTCTTCCAGC	NM_006083.2
S00552.C02	AACCTTAACCTTAAGCCC	TTTCTCCAGGATGTTTCCAG	NM_006084.2
S00552.D09	TACTAGCCAGCTCTCTGC	CATTGAGCACAACCTCAG	NM_006084.2
S00548.E02	CTGAGGTTGTGCTGAATG	CTCCAGAAATGCTGAAC	NM_006084.2
S00545.E10	TGAATGTAAAGGACCAG	TCAAATTCTGAAAGCTGC	NM_006084.2
S00553.B05	TGGAAGACAAGGTTGAAG	CCAAGAAGACAGAGGAGC	NM_006084.2
S00555.E11	AAATTGTTTCCTTGGGTC	TTTAGCACAGAACTGGC	NM_006084.2
S00553.H08	CATGAGTTGTTACCCAGG	CTGGCTGAAGTTCACAAC	NM_006084.2
S00552.E11	CCCAACTCCCTGTATTTT	CAATGGTAACTGCCTCAG	NM_006084.2
S00551.B03	GAGCCACTGTCACCATC	AAAGCAAGCAAGGGAG	NM_006084.2
S00557.B10	ATATGGGATAGGGTTCAG	GCAATATGATTCAGGTGG	NM_006084.2

S00669.C05	ACCTAGAGGAGCAAGAGG	TGAAGAGCAGAAGACAGG	NM_006084.2
S00565.H12	TTCTTAGTGGACACCTGG	ATCTGGCTCTAGGCTCTC	NM_006084.2
S00549.C11	TTGACATCCAGGTACTGC	GTTATCAAAGGCCTGACC	NM_006084.2
S00547.E10	CCAAGTTCTTGTGGTGTG	TCCAGTACACAACTCCC	NM_006084.2
S00551.A07	AACCACTGGATGTGAGTG	GCCCTCAGGAAGAGAG	NM_006084.2
S00544.D09	CTCAGAAGCCTGTCATTG	CCACTCCTCAATAGCCTC	NM_006084.2
S00547.H11	CTCCAATGTCTCCATCTC	CAATTCTAGCACGGAG	NM_006084.2
S00548.A05	GCCAGGAGAGAAGAAGAC	CAATTAACCTTGCCAAAGG	NM_006084.2
S00544.C10	ATATCCCAGTTCTGGAGC	CCACTGCAAGACCTACTG	NM_006084.2
S00550.E11	TAATCTTGTTTCGTCCAGG	TCTTCTGTCAGCTTCTGC	NM_006084.2
S00546.C12	ACCCACCCTACAGAAGTC	CAAAGCTCTGTTACCC	NM_006084.2
S00143.G11	TCCTCTCCCTCTCACTTC	CCAGTAATTGTGAATGCC	NM_006147.1
S00141.E01	ATGGATGCTTGATGAGG	GGCTATTGTAATGGACAGC	NM_006147.1
S00123.H07	AGGAAGGTGAAAGACAGG	CTGAATGCTGGTTGAAAG	NM_006147.1
S00156.C10	TGCCTCTGAGACAGGTAG	GTCAGGGTTCAGTGTTTG	NM_006147.1
S00136.A05	ATTGACAGTCCCAAGGTC	CAGTCCCTAGCTTGAATG	NM_006147.1
S00116.E06	TTAAACTGTGTAAATCAGGC	TTGTGTCTATGAGAAAGGG	NM_006147.1
S00132.F10	CCCATCATAAGCATTCTC	AGTAGATGGGAAAGGTGG	NM_006147.1
S00110.A03	CAACTAAAGGTGAATGGG	GTGGAGACGTGTTCTCAG	NM_006147.1
S00412.G04	GACAGATCTATGGGTGCC	CATCCAGAGACTGCAGAG	NM_006274.2
S00405.E03	TAGAGGAGGAAGGAGAGG	AGGAAATCCCTGAAACAG	NM_006274.2
S00405.B12	GGAATAAGAAGGTGGGAG	ACACACACAGGTGTCCTC	NM_006274.2
S00407.C09	CTAAGCATTGCTGAAC	ACAGAATGGGACATGAAG	NM_006274.2
S00800.B09	ACTCAGAGGAAGGAGTGG	CCCTGTGAAGTCTGGG	NM_006332.1
S01006.B05	GATGAATTGCGTATCACAG	TGAGAGCCTGCTGGTAG	NM_006332.1
S00701.H03	GAGATCCTCAATGTCACG	CTCGTATTTGCCTCTG	NM_006332.1
S01332.A09	TATTCCTATCTCCTGGG	GACTTGAATTTGGGTCTG	NM_006332.1
S00860.B11	AAGCATGTATTGAGCACC	ATCTCTGGTCCCTCTGTC	NM_006332.1
S01103.F06	ACTTGGGAATATGTGCAG	CCATCACTTGAAGCAAAC	NM_006332.1
S01236.A11	GGGTATCAGTCACCCATC	AATACCAACAATACCTGGG	NM_006564.1
S00226.F07	GGGTATCAGTCACCCATC	AATACCAACAATACCTGGG	NM_006564.1
S01220.D09	TGTAGTGGTTAAGGCCAC	TTCCATTGATGTGAGACC	NM_006564.1
S01216.B07	AATGTCTGCCACACAAAC	GCCCAAGGTCTTACAAAC	NM_006564.1
S00879.G05	TCAGGTTCTCCTTGATTG	ATAGAATGTGCCGAAGTG	NM_006564.1
S01220.G03	CTAAATGTGGTCAATGGG	AGGGATATCACCCAGATG	NM_006564.1
S01031.E05	TAACCCTGTGCTCTATGC	TTGCCCAGTAGTCAGAAG	NM_006564.1
S01220.H09	TAACCCTGTGCTCTATGC	TTGCCCAGTAGTCAGAAG	NM_006564.1
S00253.E09	CTAAATGTGGTCAATGGG	AGGGATATCACCCAGATG	NM_006564.1
S00860.A11	TGTAGTGGTTAAGGCCAC	TTCCATTGATGTGAGACC	NM_006564.1
S01120.G06	AATGTCTGCCACACAAAC	GCCCAAGGTCTTACAAAC	NM_006564.1
S01216.G08	TCAGGTTCTCCTTGATTG	ATAGAATGTGCCGAAGTG	NM_006564.1
S01325.G06	ATGTATGTAGGTGCCTGG	TCATCTGGTCCTTGCTC	NM_006664.2
S01321.H02	TTAGGTTGGATTTCTG	AACAGGCCGAGAATTAG	NM_006664.2
S01095.G02	GAGGAGCTTGGCTCTG	CTATCTGTGGGCACTAGG	NM_006734.2
S00336.D10	CAGTGCATTATCAGGAGG	GTACGGACTCAGAACCAG	NM_006734.2
S00323.B06	ACTACCTCAGCCACAGAG	ACATTGAATTTGGAGCAG	NM_006734.2
S00322.E11	TTGATCACTTACTTGAGGG	TAAATTTACAGGCTTCG	NM_006734.2
S00335.H04	TTACCAGCCAGAGTTTACG	TGGAAGAGTGGGACATAG	NM_006734.2
S01329.E02	GGAAACTTTGGAAGAAGG	AGAGCGTGAAGCAAGAG	NM_006734.2
S01332.G09	TCTTGCTGAAGAGGAGG	CTTGACAGATATGGAGCAC	NM_006734.2
S01299.G04	GGTTGTCTGGACTCACTG	AAGAATCATTGGGAGGTC	NM_006734.2
S01311.B09	TTTGGTGTTTCAGAGTCC	CTGTTTCACAGCTGATCC	NM_006734.2
S01325.G12	GACAAGTTGCTTTCTTGG	GCCATTGATTCAGACAAG	NM_006734.2
S01325.G11	TTCCCTTCCTCTTCCAG	GCTTAGAATCCTCCATCC	NM_006734.2

S01314.E08	TTAGGCCTTATATCCTTCAC	GATATCGATGAGACGGC	NM_006734.2
S01307.E02	ACTAGGTTTGGCACACG	GGGACACAGCTCTAGGAC	NM_006734.2
S00679.A01	GGCTGCCAAGACACAC	ACTTCCCTCCTGTTTCAG	NM_006737.1
S00790.B07	CATGAACCAACCTCAAAG	CCTTTCAGTGTGGAGTG	NM_006737.1
S00739.G06	TCTGAGTCTGGATGTTGG	TGTTTCATCAGAGTCCTGG	NM_006737.1
S00863.C09	GAATAGGCAGGTAGGTCC	GATTGCAGCCTCAAGTAG	NM_006737.1
S01139.G05	TTTGTGCCTACACCTCAC	AACTACTAATCCCAGAGGC	NM_006764.2
S00989.G12	GGCCTCTGGGATTAGTAG	CCTCGAGAACAACCAAG	NM_006764.2
S00803.B10	ATCTCTGAGAGGGACACC	ACCGCTTCTTGTCTC	NM_006764.2
S00787.C04	GGGTGGAAGTTTGACAG	CTCTCAAGAGCACCCCTG	NM_006764.2
S00694.G09	AACTCCTACACCCAGCTC	GGATGCTTTCCAGTCAG	NM_006764.2
S00894.G12	AAAGTGCCTCAAGAAAGG	CCCTCAGAGTAAAGGAGG	NM_006764.2
S00760.F05	CCTCCTTTACTCTGAGGG	TAGGAGCACAGAGAGGC	NM_006764.2
S01143.G08	CTGACATCCAGGTGAGG	TTCAGTGGACAAGAGCTG	NM_006764.2
S00946.F10	CCTAGCACCCAAATCAG	CCCATCATGACATCTAGG	NM_006764.2
S01001.A11	CTCTCAGTGAAAGGAGGG	ACACAACCTGGGCTTGG	NM_006764.2
S00702.E11	GTGTCCTAGCAAGGGTG	CGGAGTAGCTCATTGTTC	NM_006764.2
S00687.H09	CTTCAAGGAAGTGCTGG	CTCTACAGAATTCCAGGC	NM_006764.2
S00743.G09	AGGCCTGGAATTCTGTAG	TAAGAGTGGGTCATCCTG	NM_006764.2
S00995.F05	AATATGTGCCTTCCTCAG	CTGATCTCTTCAAGCCAG	NM_006764.2
S01337.E06	AGGCCTGGAATTCTGTAG	TAAGAGTGGGTCATCCTG	NM_006764.2
S00810.B11	GGAAGGAGGACAGAGAAG	GTGGTCTGAACCCACAC	NM_006840.1
S00706.D02	GACTGTGATGTCCCTGAG	ATGAAGACCCAAGACTCC	NM_006840.1
S01061.D12	AATTTCTCCTGGATGTC	TCCAGGTTTCCTTCTTTC	NM_006840.1
S00836.H10	TCCTCTGTGTTTGTTTC	GCTCATGAAGGAAAGACC	NM_006840.1
S01012.B01	AGAGGAGCCTGAACCTAC	GAGAGATGTTGGGTGTTG	NM_006840.1
S01106.A03	CGCTTGAGTCTTTGAGG	CAAATGGTGAAAGGTGAG	NM_006840.1
S01105.A04	CTCACCTTTCACCATTTG	CTCCTAGAGAGGCCTGG	NM_006840.1
S01169.B08	CATCACTAATTGGATTCCC	AGACACAGAGCGTGAGAG	NM_006840.1
S00892.E01	TCCATCAACACATCCTTC	GGGACGTCTACCTCTCAC	NM_006840.1
S01060.D07	GGGCTGTGAGAGGTAGAC	TGGAGATAGCTGTTCTGG	NM_006840.1
S00725.H11	AGCCCAGAACAGCTATC	CTCCGAGGGAGGAGAG	NM_006840.1
S00960.E03	CTCTGATAGACCAGAGCC	GGGAAATGAGAGCCAG	NM_006840.1
S00898.F07	CAAATGAGGGCAGTTTC	TCTCCTAAAGAACCAGGG	NM_006847.2
S00743.B04	AAATCTCAGGGTAAAGAGAG	AGAAGTGTGTCTCCTCC	NM_006847.2
S00863.D04	AGTTCTGGGTGACTGATG	GCTGTGAGAGGGAGATG	NM_006847.2
S00846.F11	CATCTCCCTCTCACAGC	CCTCTGAGGGCTGAGTC	NM_006847.2
S00972.H04	GGCAGATATAGGGAGAGG	GAGAATTGGAACGAGGAC	NM_006847.2
S00768.G01	GGCTGAAGGAGATGTTG	ACCTAGGACAGAACCCAC	NM_006847.2
S00767.E04	ACCCAGCACACACAGTAG	TCTCCTATCTGGAGTCCC	NM_006847.2
S00719.B07	AGGTTTCCTTTCCTCTTG	TCTCTGCCTCTCACTCAC	NM_006847.2
S00683.F02	AAGACCTCAGACTCCAC	AATCCTAGCCTGTGCTC	NM_006847.2
S01011.B07	ACTCAGGGAGAAGTGGTC	GGAAGGAGGACAGAGAAG	NM_006847.2
S00917.C08	GATGTAATCGGATCACCC	TCTGAGGGTAAAGCTGTG	NM_006847.2
S01380.C01	TATACTGCTCTGGCCATC	GATGAAGGGAGGGAGAG	NM_006847.2
S01045.D05	TTTCTTCTGAGCTTCGTG	AACACCTCTGGCTTGTAG	NM_006858.1
S00756.H04	CAGTCAGGGCGGTAAC	CCTTGGTGGTCTGTATTG	NM_006858.1
S01145.G11	ATCTCTTTCTAGCTCCGC	CACATCAGGCATTCATTC	NM_006858.1
S00733.D07	AAACCCACAATCCAGTG	CTTCCCTTTCCTTCTCAC	NM_006863.1
S00832.G02	AGTTCTGCTTCCTGTGTG	TTAGGGACTAGAGGTCGG	NM_006863.1
S00858.H03	AAAGATCCCAGGGAGG	TCCAGAACTGCTATTCCC	NM_006863.1
S00909.E09	TTCTGGACTGACTGATGG	GCTGTGAGAGGGAGATG	NM_006863.1
S01057.C02	CATCTCCCTCTCACAGC	ATCATCCACCTGGAG	NM_006863.1
S00845.B05	GGGAGAGGGAGGATATG	CCCTGTCTCTGTCTGTCTC	NM_006863.1

S01345.A01	CCAGATAGAAGCCTGGG	TTACAGGTGTAAGCCACC	NM_006863.1
S01264.D05	ATGTCTACCCAGGACACC	AATGTCCACCCAGGAC	NM_006863.1
S00680.A06	GGGAAGATAAGAATGCAG	CACCTCCTTACCCTTGAC	NM_006863.1
S01317.B02	GTCAAGGGTAAGGAGGTG	GACCAGAGCACACAGATG	NM_006863.1
S00946.D04	TCAGTGTCTCTGTCCCTG	AGACTCAGAGCGTGAGAG	NM_006864.1
S00878.F06	ATCACTCTGGGTCCTTTC	TCTCCCTCTCACAGCC	NM_006864.1
S01355.A06	GGCTGTGAGAGGGAGAC	AGTTCTGGGTGACTGATG	NM_006864.1
S00762.F12	AGAACTACTGTCTCCTCCC	AAAGCTCAGGAGGCAC	NM_006864.1
S00938.H03	TTGAGGTCTCCTGATGG	TGAGGATGAGACAACCC	NM_006864.1
S00854.G06	TCATTATTGTCCCAGAGC	CAGAGAGACTGAGGGTCC	NM_006865.1
S00907.C03	TGTCTCTCCCTCCCTTAG	GGGAGAGGGAAAGTTTG	NM_006865.1
S00884.E06	ATCATCCACCTGGAG	CTTCTCCCTCTCACAGC	NM_006865.1
S00946.B10	GCTGTGAGAGGGAGAAG	ATAGCAGTTCTGGGCTG	NM_006865.1
S00771.D12	CCAGAACTGCTATTCCC	AAAGATCCCAGGGAGG	NM_006865.1
S00830.F04	GGTCTCCTTAGGGACAAG	TACAGGAAAGACAGCCAG	NM_006865.1
S00745.D03	AGCCCTAAAGGTATGACAG	TCTCCTTAGGGACCAGAG	NM_006866.1
S00731.C12	AAAGATCCCAGGGAGG	CCAGAACTGCTATTCCC	NM_006866.1
S01008.E02	ATAGCAGTTCTGGGCTG	GGGTTGAGCTGTGAGAG	NM_006866.1
S00941.A07	CTCTCACAGCTCAACCC	ATCATCCACCTGGAG	NM_006866.1
S01079.H11	ACAGGAAGATCAGCGG	CTCTCTGTCTCTCCCTCC	NM_006866.1
S01069.D02	AGAGACTAAGGGTCCCAG	TCATTATTGTCCCAGAGC	NM_006866.1
S01065.H08	TGCTCTCAGTTATGGGAC	AGGTGTGTGGAGGTGTG	NM_006866.1
S00823.F02	ATCTCCTCAAACCTGGAG	AACGCTTATGTCCTGTTG	NM_007051.2
S01080.C03	CAATGGAAGACTCAAAGC	CATAAATTGATTGGAACTG	NM_007051.2
S00914.G03	GCCATTGGAGAGTACTTG	TCTTTGAGAACATCAGCC	NM_007115.1
S00816.G05	TTCTGTGGGCTAGTCTTAC	ATCGCCAGAAGGTAATG	NM_012206.1
S01078.D01	TCAGTCGTATTCCAGAGC	AGGTGATGGTAATTCCTG	NM_012206.1
S00735.G05	ACATTAATCCACCACCAC	CTCTCATTTCCAGCAGAG	NM_012206.1
S00679.D08	GCTTCAGACTACACCTCC	GTGGGAGATAGAGGAAGC	NM_012206.1
S00763.F10	GAAACTGTCTCCAGAAGC	ATGTGAACAGCCTCCAC	NM_012275.1
S00938.D08	CTGAGGTATGCTCTGGG	GACAACGGGTCTATCCAG	NM_012275.1
S01116.A12	TTCTGGCACAGTAGGAAG	TTCTAAGCCCTCTTCAGG	NM_012275.1
S00707.H07	TAGAGCCCAGGACAGG	ATCCTGCTAGGGTGTCC	NM_012275.1
S01129.G02	AGCAGGATTCTGTTGATG	TGTTATTCCCAGTTTACCC	NM_012275.1
S01106.H08	AAATTCTGAGATTTGGAGC	TGCAATATATGCCACTTTG	NM_012275.1
S01239.G11	GAAACTGTCTCCAGAAGC	ATGTGAACAGCCTCCAC	NM_012275.2
S01224.G01	CTGAGGTATGCTCTGGG	GACAACGGGTCTATCCAG	NM_012275.2
S01238.B07	TTCTGGCACAGTAGGAAG	TTCTAAGCCCTCTTCAGG	NM_012275.2
S01243.E03	TAGAGCCCAGGACAGG	ATCCTGCTAGGGTGTCC	NM_012275.2
S01217.H04	AAATTCTGAGATTTGGAGC	TGCAATATATGCCACTTTG	NM_012275.2
S01203.E06	TGGAATCTCTGGGTAAGG	TAAACACGAGGAGACAGG	NM_012275.2
S01225.H09	AGCAGGATTCTGTTGATG	TGTTATTCCCAGTTTACCC	NM_012275.2
S01192.H12	GTAGGGTATGCTGATCCTC	CCAATGCCTTGGAATC	NM_012275.2
S01203.A10	AATCTCAGACTTCCAGCC	TTTGGGTAAATGAAGGATAG	NM_012275.2
S01310.A05	GAGCATGAGGTCACAGAG	GAGATTCTCCCAGTTATGG	NM_012276.1
S00691.F02	TGTAATCCTGGAGGTGTG	TATAAGAATGCATTGCC	NM_012276.1
S01347.G07	GCAGCAAGTGAGACAGAC	GAGACAGACTGAGGGTCC	NM_012276.1
S00965.A10	CTCTGTCTGTCTCTCCCTC	AAGGCTACAGAAGGAAGG	NM_012276.1
S01046.G06	GGGTAAGGCTCCCAAC	CCAGCCTTGTAAGGATAAG	NM_012276.1
S01111.E03	TATCCTACAAGGCTGGG	AAGACAGCAGTTCTGGG	NM_012276.1
S00818.F04	AAGATGTCCTCAACCCTC	CATAGCCATGCCTTAGTC	NM_012276.1
S00914.E11	AAGGTAGAAAGAGCCTGC	CTCTAGGCCATAACTCC	NM_012312.1
S00679.C05	CAAGACTCACAGCCAG	ACTTCCCTCCTGTTTCAG	NM_012312.1
S01319.B01	TCACTCATTCTAGGTGCC	CCTCAGCAAGTCAGTCTC	NM_012312.1

S01304.F02	CTCAGCTCAGGTGAAGG	CATCTGTCCATGCTTCTC	NM_012312.1
S00759.F08	CATGAACCATCTCAAAG	GCTGTGAGATGCTGAGTC	NM_012312.1
S01319.B02	TGTATGTGGTTACCTGCC	GAGGAACACACACCTGAG	NM_012312.1
S00857.C02	GTCTGAGTCTGCTGTTGG	AGAGAGGGAAATGCTGAG	NM_012312.1
S01386.A05	GTCTGAGTCTGCTGTTGG	AGAGAGGGAAATGCTGAG	NM_012312.1
S01165.D08	ACATGTAAACTGCATGGG	TAGGCTCATCACTCCATC	NM_012312.1
S00719.E10	TATCAAGACTCACAGCCC	CTGACAGGACTTCCCTC	NM_012312.1
S01069.C10	CACAGAGAGGAAGCAGAG	TTACAACCACCTGGGTC	NM_012312.1
S00727.A09	TCTCAGGTCAGGTGTGAG	AGCATCTGTAGGTCCCTC	NM_012312.1
S00816.C03	AAACCTTCTCTCTCAGCC	CATCTGTCCATGCTTCTC	NM_012312.1
S00784.C02	GAAGCCATGTTCTGCTC	CATATCTCCACCTCTGGG	NM_012314.1
S00850.H07	CTTCCTCAATTTCTGTGC	CTCTCATGTTGATCAGGG	NM_013416.1
S00968.H08	GAATGTTGGCTTCACAAC	ATTGGAGGTTTCAAGAGTC	NM_013416.1
S01092.E06	TCTCCTTCTCCAGAGACC	CACAGAACAGTGTGAGGG	NM_013416.1
S00777.C08	TAACAGGGAAGAATGCTG	CAGTTCCCAAAGCCATAC	NM_013416.1
S00819.C04	GGACATCTAGGCTGGG	TCCTTCTCTCCTTTTCAGG	NM_013416.1
S00920.B07	GACACAGGAGCAGGAAG	AGAGGCTGAGGCTGTAAC	NM_013416.1
S00774.C12	CCAAGCCTCAGTTTCTAC	TCCACCCTCACCTCTATC	NM_013416.1
S01087.G05	TCTTACTCCTGGCTTCAG	TTTCCTGGTCCCAATC	NM_013416.1
S01332.D01	TCTTACTCCTGGCTTCAG	TTTCCTGGTCCCAATC	NM_013416.1
S01051.G07	AAACATTTATGGCTCATTG	TCTGATTTTATGACTCAAAG	NM_013431.1
S01367.H08	TCCTGACTTTGACCTCTG	CTATACCAGGGATCCTGTC	NM_013431.1
S01049.F03	TGCAGCTGTGTGATGTC	AAACATTTGCCAAGACC	NM_013431.1
S01204.D07	GTAAGAGCTGCGTGATTC	CCTTGAGGGCATTGAC	NM_014442.1
S01195.F05	TAGTGGCGTAAGGATGAC	AGTAGGAAATACAGGGCAG	NM_014442.1
S01195.E01	AAAGTGGCAGCTCAGTC	TAGCTGGCATCTCTTCTC	NM_014442.1
S01241.B06	CTTCAGGGATTCTGTTCC	GTCTGGGAAGGAGAAGAG	NM_014442.1
S01205.F11	ACAGCTGAGCACAGACC	TGCTATTGTGAATAGTGCC	NM_014442.1
S01242.E12	ATTCCAGGATGAGGAGAG	CTCCTGGGAAGACAGG	NM_014442.1
S01244.E06	CAGAACCCAGTGTCCAG	TGGGATTGAAATAAGTCG	NM_014442.1
S01208.D05	CCGACTTATTTCAATCCC	GGGATGGTTACTTGCTG	NM_014442.1
S01208.D03	ACCAGTAGCCATGAAGT	ACCTCCACAAACAGTGAC	NM_014442.1
S00870.B02	ACCAGTAGCCATGAAGT	ACCTCCACAAACAGTGAC	NM_014442.1
S00302.D09	AATCTACCTCCCAGGAAC	TCTGATTAGGAAAGGCAG	NM_014443.1
S00293.H04	ACCATTACAATGACTGGG	GGTAGGCAGAGTCAGACC	NM_014443.1
S00283.H10	TAAACCAACAGAGGCAG	GCTCCCAGCTGATGAC	NM_014443.1
S01268.H01	AGAGATGTTAGGTGAAGGG	GACTCTCAGGTTAGCTGG	NM_015564.1
S01295.D03	TTGAGCACTGCCTAATTC	TGGAAATGAAATCAAAGC	NM_015564.1
S01371.B12	ATTCTACTTCCCACCCTG	GGTTATGGACAGTGCAAG	NM_015564.1
S01252.A08	GATAGTTGAGAGAGAGAGCG	CCACAACATCTTGCTGC	NM_015564.1
S01286.G01	AGGCGTACTGGGATAGTC	ATAGCCCATATGTTCTGC	NM_015564.1
S00300.A03	AATATGATGGTGATTTC	AAAGACACGTCATCCG	NM_015564.1
S00174.B10	GGCTACTCTTCCCAACTC	ACAACCTGGAAGCAAACCTG	NM_016232.2
S00191.E04	TCACAGTATATGACCGGC	CTCAGGCAATCAACCAC	NM_016232.2
S00200.A10	TGTTAGGGCTACTATGGG	GGATTACAGGCATGAGC	NM_016232.2
S00211.B07	GGCAACAAACATTCTGTC	AGCAGGAGGAAGTAAAGG	NM_016232.2
S00173.C01	GTGTGTTTGTGATTATGGG	AAGGGAATTCAGAACAGG	NM_016232.2
S00174.G03	TGAAGGTAATGGAAGCAG	TAATGCCTACTTTGCAGG	NM_016232.2
S00170.G04	AGAGAACCATCCTCTTCC	GAACCACACTCCATTCTG	NM_016232.2
S00189.G02	AATTCTTGTAATCCCAAGG	AATGGAATCTGGGCTTAG	NM_016232.2
S00193.D06	ATACATTCACCAACAGCC	TTCATTATCCAATGCAGG	NM_016232.2
S00198.C08	TCAGAGAATCTCACACCAG	CTGCTCCTCACACTTCAG	NM_016232.2
S00388.E02	GAGGAAAGGAGGGAGAG	CTTCCTCTGGTCTTCAGG	NM_016240.1
S00381.F01	GTAGAGGTGGGCATGG	GACAAATCTCTCACTGGC	NM_016240.1

S00389.F12	CAGGAACATGGAAGTAC	AGTGTCTTGTCTTTGCAGG	NM_016240.1
S00381.B11	TTCTCAAGGAATGACTGC	TAGAAGGCTGGTGAAGG	NM_016240.1
S01334.A02	AACCAATTTCTTATGCTCTG	CTCTCCAGTCTTGGTGG	NM_016240.1
S01143.C06	TCTGTCATCACTCCTTGG	CTGTTCTGCTCTCTCTG	NM_016240.1
S00982.H09	GCACACATACACATGCAC	AAACTCCTGCTTGGATTC	NM_016240.1
S00398.G01	GACTTGTTCAACCCTCG	ATTCTGTGTGACAGTGGC	NM_016240.1
S00858.F05	GACATTCTCTGGCCTTG	GAGTGTAGCCAACAGGAG	NM_016240.1
S01035.E05	TGATATAAGCTGGAAGGC	TATTGTCTCACTGCATGG	NM_016543.1
S00874.E02	TGTGCAACAAGACATCAG	AGGCCATGGAGTCAAC	NM_016543.1
S01205.G01	TGTGCAACAAGACATCAG	AGGCCATGGAGTCAAC	NM_016543.1
S01205.G05	CTTGTGACTCTCCCTGC	TACAGAGGAGAATGGTGG	NM_016543.1
S01282.E08	ACCTATTATTCGTTGGGC	GTTTGTGTGGATTAACATTG	NM_019846.2
S00696.G04	CTCAATCCTTCCAGCAC	GATACCCTGAACACCTCC	NM_019846.2
S01346.E08	AAGGTAGAAAGAGCCTGC	GGCCTATATCTCCACCTC	NM_020535.1
S01330.D02	AGGAGCCTTAGAAACGAG	CACCAAATACAGTCAGGG	NM_020535.1
S01337.C02	GTGGAGGGTGAGAGAGAG	TCTCTCCATCATCAGCAG	NM_020535.1
S01385.C05	CATGAACCAACCTCAAAG	GCTGTTGTAGTGTCTGGG	NM_020535.1
S01387.E09	GCAACCAAGAAATGAGAG	GTCAGGAACACACACCAG	NM_020535.1
S01323.A09	GTGTGTTGGTGTCTGCTC	TGATCATCAGAGTCCTGG	NM_020535.1
S00427.G08	AATGGCAGATCATGAAAG	AAGTCAAGCTGCTCTCTG	NM_021002.1
S00390.H11	AAGGAACCATACAAACCAC	CAGTTAGTCTGGCTGTGC	NM_021010.1
S00395.E05	TGACTCCAGATCCTTCTC	TTGAGAACAAAGGCAGTC	NM_021010.1
S00428.F06	AGGAGACATCAGAATGGTC	AATTCAGATTCCCAGAGG	NM_021057.1
S00617.A08	TGAGCTCACAGCTTGG	GGACCACTCCTCACTACC	NM_021137.2
S00644.D07	AGTACGGTCGTGTTTCTG	TTCTAGATCTGGTCATTTC	NM_021137.2
S00626.G03	GTGCTAGAACCTCCATCC	CTCCATCCCACAAGAAG	NM_021137.2
S00640.G07	TGACACTTCCTCACCAAG	AGGAGTTCAGAGTGAGGG	NM_021137.2
S00616.C08	AAGGTACCAGGACCTCTG	TCCCAATTTCCCTTCTAC	NM_021137.2
S00631.D12	ACTTGTCTAGCACCTCC	ACCATTACCGTGTTTGG	NM_021137.2
S00960.G03	CTCACTGACATGATCTTAGC	TAAATCACAGTTCCAGCC	NM_021137.2
S01055.H12	ACCTGAAGTGACATGACG	TGCTTTCTGAATAGGGC	NM_021137.2
S01018.H11	CCTGTGGGATCTGTTTC	CACCAACCAAGAGCATAG	NM_021137.2
S00655.E09	TTATGAGAGGTAGCGGAG	AAGGGTGATGGTGAGC	NM_021137.2
S00820.E01	CTCAGAGGTCAGAGGGTC	CCTCCCTCAGATTGATTC	NM_021137.2
S00838.H06	TGAGGACAGCAAACCTCC	ACCTGAGAGTCTTAGTGCTG	NM_021137.2
S01093.A10	AGAAAGCTCTCCCTCTTG	CAGTAGGGCAGTCTTGG	NM_021270.1
S00870.H04	ATCCCTGAATTGTGATCC	ACAGAGAGAGGACAGCAG	NM_021270.1
S01010.B10	ATCGTATTCGTGGTGATG	AGACCCAGCTACAGTTCC	NM_021706.1
S01000.D03	CATTGCATCTGGATTGG	GAATGACTCCTGGACCTC	NM_021706.1
S00796.A04	ACATCAACAGCCAGGTC	CGCCAGAATCAGATAAAG	NM_021706.1
S00824.G03	GGTGTGAATTAAGGAGACC	AAGTCTATGAAACGCACG	NM_021706.1
S00948.C12	AAGCCTGACCTCTTCTC	AGGACTCAGAGCCTTCTC	NM_021706.1
S00960.A06	AAGGTTGGCCACAGAG	AATCCCTGAATTGTGATG	NM_021706.1
S00995.A11	GGCCCTCTAAGAATCAAC	ATGGAGACAGTGATGTCG	NM_021706.1
S01044.E06	GAGGAGGAGGACACTTTC	TCTTCCTCTTGTGTGAGG	NM_021706.1
S01120.D01	TGAAGAGGAATCCAACAG	GCAATTTAGGAGAGGGTC	NM_021708.1
S00729.C03	GTTCCCAAAGATTCTTCC	CGCCAGAATCAGATAAAG	NM_021708.1
S00961.C01	TCCCTAGACCTTGACTCC	ACATTGTCTGGGATTGC	NM_021708.1
S01146.A12	TAAGGAAGACACCAGCAG	ATAGAGGATTGGGAAAGC	NM_021803.1
S00806.E06	TCATCAATTATTAGACCGC	TGTGAATGACTTGGTAAGAC	NM_021803.1
S00428.G11	CAGAAATGGAAAGTGGC	TTCTTCACAGCCAAGATG	NM_024013.1
S01126.B12	TTCTGCACCGAACTCTAC	ATCAGGTTGCACAGTCAG	NM_024013.1
S01356.H03	GCCAGTGACTCTTGTCTG	ACTACCTGAGCTTCCTGAC	NM_024298.1
S00824.E11	GTACCTCACCTGGGAC	AGCTAAATACCCTGCCTG	NM_024298.1

S00842.A04	CTGGGTGGTACAGTTCAC	TCCAGCTGCTAGAGAGAG	NM_024298.1
S00827.A10	CCTTTAGGAGTGAGGACC	ATAGCAATTTCCAATCCC	NM_024298.1
S00735.A03	GACTTAACCACATCCGTG	TCTCTGGTGAACAAGGC	NM_024317.1
S00770.H01	GCTACTGGTGCTCCAAC	TTCTCACCCTCAGTTCAG	NM_024317.1
S00799.F02	TTCTGAACTGAGGGTGAG	TATTAGAACGGAGATGCC	NM_024317.1
S00949.G06	ACTTACTCTCACGGAGCC	CTGTCTGTCTCTCCCTCC	NM_024317.1
S01166.G09	GACAGAGACTGAGGGTCC	TTCCTTAGCGTCCTGAG	NM_024317.1
S00788.F11	GTCAGGTCCTGTGAAGG	ATCAGACTCATTGCCAAG	NM_024317.1
S01144.E04	GCTGGGTTTATAGGTGTG	TTCAGCATATTGCTGTTG	NM_024873.2
S00917.A08	CACACACACACATATGCAC	CGCTTCTTGATTTCTCAG	NM_024873.2
S00784.A02	CCCAAGTACGAATGAATG	GAGTGAGGTTGGCAATAG	NM_024873.2
S00896.E07	GCTGAAATTCCAGAGATG	TGCCAGATTAAGTGGAAC	NM_024873.2
S01133.B01	CTGTCTATCCGTTGATGG	TAGGTCAAGAGTGGCTTG	NM_024873.2
S01134.B12	AACAGAAGTCCAAACGTC	TCAAAGCCCTTGTGTTAG	NM_024873.2
S01122.G05	AAATGCCCAAAGAAGC	AATGCATATTTGTGGGTG	NM_024873.2
S01269.C02	GCGACTGTCAGTAAGAATG	TTAAAGTCTTGACAGTCC	NM_024873.2
S00726.F09	CGGTCGTTGCTCAGTAG	TCTGCCAAAGTTCATAGC	NM_024873.2
S00798.H11	TAAGAAAGAAGGCGTTTG	TAAATCGCAACAGGAGAG	NM_024873.2
S00759.H07	AAAGCAAAGTAGCCATTTT	TGCCTATTTGAGACATCC	NM_024873.2
S01238.B03	GATTGCTGGAAGCTACAC	CATAGCAGCACACAAGT	NM_031200.1
S00225.G01	GATTGCTGGAAGCTACAC	CATAGCAGCACACAAGT	NM_031200.1
S00222.H09	GACTCTAACTCCTGCTTGG	ACACAGATAAATCCTTCCC	NM_031200.1
S01234.F04	GACTCTAACTCCTGCTTGG	ACACAGATAAATCCTTCCC	NM_031200.1
S01115.G08	TGGTGACAGTGTCTCTCC	ACTACCTTCAGACCAGCC	NM_031200.1
S01137.G02	TGTCACCTTTCTTTACCCTG	TGTCTGCTCACTTTATTCC	NM_031200.1
S01153.A02	CGTGGACAGGTACATTG	ATGCAACCCAAGTTCTTC	NM_031200.1
S00254.C12	GGAAGGGTCAAGAGGTC	CCAGATGGTAAAGCAAAC	NM_031200.1
S00977.H06	ACCAACATTGACATCTGC	CATGAGAACTGAAGCCAC	NM_031200.1
S01388.G12	CTGGAAGCATTGTAGTGG	AGACAGACCAGACCCTTC	NM_031908.2
S01314.H08	CATGGAGGTTTCAGAGTG	TACTGGACAGACAGCCTC	NM_031908.2
S01134.F10	CATGGAGGTTTCAGAGTG	TACTGGACAGACAGCCTC	NM_031908.2
S01160.H03	CTCATTCAATTGAGAAGCG	ACAGGAGACAGGGAAGAG	NM_031908.2
S01048.B08	GAGTCCTCCTCCTCCTC	GTCATCAGCACTGCAAG	NM_031908.2
S01194.G07	CTCAACCTCCCAAAGTG	GTGCTGTAAATCAGTGCC	NM_033130.1
S01188.F01	CACCTTGATGTCGCTAAG	TCAGGTAGTAAACGTGGC	NM_033130.1
S01221.D08	GTTGATCACGACCTTCAC	TTAATGCCGAGTGATGAG	NM_033130.1
S01229.H03	AACCACAGGACCCTACTC	GTCTCTCTCAGCCTCTCC	NM_033130.1
S01230.D04	GGAGGGAGGACAGGAC	CAGGACAGGTAGGAAAGG	NM_033130.1
S01244.B04	GACCCTCCAGACTCCTG	CAGGATGGTTCCCTTTAC	NM_033130.1
S01244.G01	GCATGAGGGTCTACACAG	TGCTCCTCCCTGTACC	NM_033130.1
S01209.H05	GAGAGAAAGGGAGGGAG	GTTGTCACTTGTCTTCCC	NM_033130.1
S01227.C05	TTCTCTCCCTGGATG	CTATGGGCTGAGCAGAG	NM_033130.1
S01226.E05	CTCTGCTCAGCCCATAG	GAGATGCTACTGCCACTG	NM_033130.1
S01243.G11	GAATCTCCCATCCATAGC	CTGAAGCTCATTTTCATGC	NM_033130.1
S01023.E12	TTATTTGGAACAACACGG	GAGGAAGGAGAGATCCAG	NM_053003.1
S00718.F03	GGAAGAAAGGAAGGACAG	AATAGGAAATACAGGGCAG	NM_053003.1
S00827.D01	CAAGCTCTTGACCCATC	GCAGTGGGAGGAGAAG	NM_053003.1
S00989.G06	AAGAGGACTGTGATGCTG	CTGTTCCATTCACTACTC	NM_053003.1
S00799.G01	TGAGTCCTGGCTCTCC	ATCTGGGTCCTGGAATC	NM_053003.1
S00906.E12	GATCCTTGAGTCTGGGTC	TTGGAGGTGAAGCATATC	NM_053003.1
S00922.G05	TCTGGTCTTACTCCTCCC	CCTCTGCCTCAGAGATG	NM_053003.1
S01347.C08	TCTGGTCTTACTCCTCCC	CCTCTGCCTCAGAGATG	NM_053003.1
S01112.C12	ACCAGTAGCCATGAAGT	TGTCACCTCTGACCTACAG	NM_053003.1
S01341.G05	GACATGTGTCCCGTCTC	GGAACAGAAGGATTACCTG	NM_053003.1

S00423.A07	AAGCCAACTAGCTTCCTC	AAATAAACAAACCAGGGC	NM_138554.1
S00420.G05	CTCTGGTCTAGGAGAGGG	AAACCAAGCTTTCCAGTC	NM_138554.1
S00950.H08	TCTACTCAAGCCAGGATG	CTGAACAAGTGTTGGACC	NM_138554.1
S00990.D07	TCCCTGAACCCTATGAAC	ACTTTAGGCTGGTTGTCC	NM_138554.1
S00678.B04	GAAGAGCTGGATGACTAGG	CAGCCAGACCTTGAATAC	NM_138554.1
S00872.F10	CACTCTCCAGTCTTCAGG	CTGTAGTGAAGGCAGAGC	NM_138554.1
S01139.B09	ACTGCAGTCGTCAAGG	AAACTTCTGCTGCAACTC	NM_138554.1
S01213.G02	TCCCTGAACCCTATGAAC	ACTTTAGGCTGGTTGTCC	NM_138554.1
S01219.F02	TCTACTCAAGCCAGGATG	CTGAACAAGTGTTGGACC	NM_138554.1
S00411.B10	CCATGCTCATCTTCTCTG	TTCATCCATCTGTCCATC	NM_138556.1
S00894.D05	AATGCTCTGCTCCAGG	TGTGGAAGAGACTCAAGG	NM_145021.1
S00455.A05	TAGCATCCACTAATTCCC	GAGCCAGCAGAGTTCC	NM_145021.1
S01171.D06	AGTTGGGCTCTGTTAGTG	TTCTGGAGCATGAGAATC	NM_145021.1
S00435.A04	CCTAACTGATGTCCCTCC	TGCATCTAGTTTGGGAAG	NM_145021.1
S00436.C08	TCTGAGACACCAGCTTTC	TGTGCCCATAGTCACTTC	NM_145021.1
S00436.G12	TAGACCAAAGGCAGATTG	CTAGGGTTTCTCCCTGTC	NM_145021.1
S00440.B11	CTTATGGTCCCAGAACAG	CAGGGAATGATTTGTCAG	NM_145021.1
S00440.B03	AAGCACTGTTCTAGGTCATC	CCAAACATTTATGTTGCC	NM_145021.1
S00438.H01	TTTCAAGCCTTTGATGAG	TCTGTGCCATAAATAGCC	NM_145021.1
S01071.E11	GGTGGAGGTTAGGACATC	GACTGAGCCACTCTGAAG	NM_145256.1
S00824.A06	AGAAGAAACCAGGGACAG	TCTCCATCTGAGACTCCC	NM_145256.1
S00964.G12	GAGCAGTTGTCTCGGC	GGTTATCTACCCATTCCC	NM_145256.1
S00689.B03	TGCTGAAAGGGTCCTC	CTCTGTCTTCATTCTTCCC	NM_145256.1
S00411.B02	GGGCAAGACTTGTAAGG	AAGAACCAGGCTTTG	NM_147162.1
S00404.E02	GAATCTCAGGTCCTCCTC	GCTGTGAGTATGGAATGG	NM_147164.1

Table 8: Sequence Primers

RefSeq	HUGO ID	Ens_start	Ens_end	Chr	Strand	selected TSS	Start_ex	End_ex
NM_001243	TNFRSF8	11832980	11913808	1	1	11832980	11829480	11833980
NM_001066	TNFRSF1B	11936606	11978822	1	1	11936606	11933106	11937606
NM_000760	CSF3R	36359306	36372782	1	-1	36372782	36371782	36376282
NM_007051	FAF1	50276853	50795854	1	-1	50795854	50794854	50799354
NM_005531	IFI16	156196500	156241730	1	1	156196489	156192989	156197489
NM_002995	XCL1	165733233	165738692	1	1	165733233	165729733	165734233
NM_000639	TNFSF6	169867561	169875384	1	1	169867561	169864061	169868561
NM_003326	TNFSF4	170392247	170415847	1	-1	170415847	170414847	170419347
NM_000572	IL10	204024647	204029538	1	-1	204029538	204028538	204033038
NM_006147	IRF6	207040651	207058868	1	-1	207058868	207057868	207062368
NM_006147	IRF6	207040651	207058868	1	-1	207058873	207057873	207062373
NM_004619	TRAF5	208579429	208627671	1	1	208579429	208575929	208580429
NM_001768	CD8A	86986274	86992607	2	-1	86992601	86991601	86996101
NM_000877	IL1R1	102391802	102417734	2	1	102342498	102338998	102343498
NM_003854	IL1RL2	102424833	102477211	2	1	102424833	102421333	102425833
NM_003856	NM_003856	102549362	102589781	2	1	102549362	102545862	102550362
NM_016232	IL1RL1	102549362	102589781	2	1	102575117	102571617	102576117
NM_003855	IL18R1	102600497	102636618	2	1	102600497	102596997	102601497

NM_003581	NCK2	106054430	106132124	2	1	106054326	106050826	106055326
NM_000575	IL1A	113626641	113638117	2	-1	113637216	113636216	113640716
NM_000576	IL1B	113682483	113689502	2	-1	113689502	113688502	113693002
NM_012275	IL1F5	113911361	113917464	2	1	113911361	113907861	113912361
NM_003467	CXCR4	137083208	137084257	2	-1	137086488	137085488	137089988
NM_007115	TNFAIP6	152416650	152439104	2	1	152416651	152413151	152417651
NM_000564	IL5RA	3086421	3127031	3	-1	3127031	3126031	3130531
NM_001337	CX3CR1	39265579	39282114	3	-1	39282119	39281119	39285619
NM_001296	CCBP2	42821712	42869366	3	1	42811529	42808029	42812529
NM_031200	CCR9	45888611	45905259	3	1	45888611	45885111	45889611
NM_006564	CXCR6	45945565	45950437	3	1	45945565	45942065	45946565
NM_005283	XCR1	46023030	46024031	3	-1	46024031	46023031	46027531
NM_001295	CCR1	46204320	46210412	3	-1	46210395	46209395	46213895
NM_001837	CCR3	46244280	46268754	3	1	46244280	46240780	46245280
NM_000647 _NM_000648	CCR2	46356232	46363011	3	1	46356232	46352732	46357232
NM_000579	CCR5	46372225	46378283	3	1	46372225	46368725	46373225
NM_003965	CCRL2	46409271	46411605	3	1	46409271	46405771	46410271
NM_002447	MST1R	49883452	49900082	3	-1	49900318	49899318	49903818
NM_006764	IFRD2	50284186	50295911	3	-1	50295911	50294911	50299411
NM_000882	IL12A	161027542	161034718	3	1	161027542	161024042	161028542
NM_000584	IL8	75072526	75075682	4	1	75072537	75069037	75073537
NM_001657	AREG	75777104	75786978	4	1	75777104	75773604	75778104
NM_001729	BTC	76128372	76178082	4	-1	76178082	76177082	76181582
NM_005409	CXCL11	77413346	77415747	4	-1	77415548	77414548	77419048
NM_024873	TNIP3	122511388	122544297	4	-1	122544297	122543297	122547797
NM_021803	IL21	123992686	124001033	4	-1	124001033	124000033	124004533
NM_002006	FGF2	124206684	124278211	4	1	124206684	124203184	124207684
NM_000585	IL15	143135381	143232238	4	1	143135363	143131863	143136363
NM_002185	IL7R	35902492	35922422	5	1	35902492	35898992	35903492
NM_019846	CCL28	43422251	43457973	5	-1	43457973	43456973	43461473
NM_002184	IL6ST	55252580	55287992	5	-1	55287992	55286992	55291492
NM_000588	IL3	131472563	131475112	5	1	131472563	131469063	131473563
NM_000758	CSF2	131485701	131488075	5	1	131485701	131482201	131486701
NM_002198	IRF1	131894996	131901386	5	-1	131901386	131900386	131904886
NM_000879	IL5	131953352	131955430	5	-1	131955430	131954430	131958930
NM_002188	IL13	132070081	132073017	5	1	132070081	132066581	132071081
NM_000589	IL4	132085589	132094584	5	1	132085589	132082089	132086589
NM_004887	CXCL14	134982585	134991185	5	-1	134991185	134990185	134994685
NM_000590	IL9	135304151	135307732	5	-1	135307732	135306732	135311232

NM_015564	NM_015564	138284915	138286462	5	-1	138287209	138286209	138290709
NM_006083	IK	140055885	140070565	5	1	140055915	140052415	140056915
NM_014443	IL17B	148782342	148787348	5	-1	148787348	148786348	148790848
NM_006058	TNIP1	150438027	150495229	5	-1	150489055	150488055	150492555
NM_012206	HAVCR1	156437332	156465867	5	-1	156465867	156464867	156469367
NM_005546	ITK	156588802	156663004	5	1	156588799	156585299	156589799
NM_002187	IL12B	158722686	158738376	5	-1	158738376	158737376	158741876
NM_031908	C1QTNF2	159755672	159778526	5	-1	159778526	159777526	159782026
NM_000416	IFNGR1	137499199	137521116	6	-1	137521111	137520111	137524611
NM_006734	HIVEP2	143053176	143076552	6	-1	143076552	143075552	143080052
NM_000600	IL6	22509154	22513888	7	1	22509091	22505591	22510091
NM_005218	DEFB1	6715511	6722856	8	-1	6722856	6721856	6726356
NM_004084	DEFA1	6822585	6825017	8	-1	6825017	6824017	6828517
NM_005217	DEFA3	6860805	6863226	8	-1	6863226	6862226	6866726
NM_021010	DEFA5	6900239	6901669	8	-1	6901669	6900669	6905169
-NM_004942	-DEFB4	7259788	7261795	8	-1	7261795	7260795	7265295
NM_004942	DEFB4	7789609	7791647	8	1	7789609	7786109	7790609
NM_003842	TNFRSF10B	22899591	22948630	8	-1	22948630	22947630	22952130
NM_003841	TNFRSF10C	22982372	22996884	8	1	22982372	22978872	22983372
NM_003840	TNFRSF10D	23016838	23043468	8	-1	23043468	23042468	23046968
NM_003844	TNFRSF10A	23070909	23104577	8	-1	23104550	23103550	23108050
NM_016240	SCARA3	27513489	27556198	8	1	27513489	27509989	27514489
NM_000880	IL7	79694971	79760406	8	-1	79767317	79766317	79770817
NM_002175	IFNA21	21156042	21156611	9	-1	21156611	21155611	21160111
NM_021057	IFNA7	21191595	21192164	9	-1	21192164	21191164	21195664
NM_002169	IFNA5	21294686	21295255	9	-1	21295255	21294255	21298755
NM_021002	IFNA6	21340317	21340886	9	-1	21340886	21339886	21344386
-NM_024013	-IFNA13	21357437	21358006	9	-1	21358006	21357006	21361506
NM_024013	IFNA1_IFNA13	21430440	21431315	9	1	21430440	21426940	21431440
NM_001842 _NM_14716 4	CNTFR	34541432	34579722	9	-1	34579722	34578722	34583222
NM_147162 _NM_00451 2	IL11RA	34640699	34650935	9	1	34640699	34637199	34641699
NM_006274	CCL19	34679567	34681274	9	-1	34681273	34680273	34684773
NM_002989	CCL21	34699002	34700147	9	-1	34700133	34699133	34703633
NM_001782	CD72	35599976	35608408	9	-1	35636834	35635834	35640334
NM_001244	TNFSF8	113041169	113068815	9	-1	113068815	113067815	113072315
NM_138554 _NM_13855 6	TLR4	115842629	115854098	9	1	115842629	115839129	115843629

NM_001735	C5	119091062	119188599	9	-1	119188599	119187599	119192099
NM_002189	IL15RA	5998340	6023887	10	-1	6023898	6022898	6027398
NM_000609	CXCL12	44156588	44164551	10	-1	44164551	44163551	44168051
NM_145021	NM_145021	45236966	45314827	10	-1	45374035	45373035	45377535
NM_001548	IFIT1	90826613	90828046	10	1	90816976	90813476	90817976
NM_001562	IL18	111551625	111563425	11	-1	111572466	111571466	111575966
NM_001558	IL10RA	117394835	117409846	11	1	117394835	117391335	117395835
NM_013431	KLRC4	10451250	10453623	12	-1	10453623	10452623	10457123
NM_000619	IFNG	66834816	66839770	12	-1	66839770	66838770	66843270
NM_003701	TNFSF11	40934872	40979054	13	1	40934872	40931372	40935872
NM_006084	ISGF3G	22620652	22625900	14	1	22620630	22617130	22621630
NM_006084	ISGF3G	22620652	22625900	14	1	22620652	22617152	22621652
NM_003300	TRAF3	101233857	101362669	14	1	101233857	101230357	101234857
NM_004513	IL16	79190912	79320920	15	1	79305148	79301648	79306148
NM_003789	TRADD	66964341	66970017	16	-1	66970017	66969017	66973517
NM_002163	ICSBP1	85718101	85736578	16	1	85718101	85714601	85719101
NM_003809	TNFSF12	7652940	7665483	17	1	7652940	7649440	7653940
NM_021137	TNFAIP1	26808348	26819597	17	1	26808353	26804853	26809353
NM_004295	TRAF4	27216603	27222660	17	1	27216593	27213093	27217593
NM_002982	CCL2	32727848	32729768	17	1	32727851	32724351	32728851
NM_002986	CCL11	32758237	32760749	17	1	32758237	32754737	32759237
NM_002981	CCL1	32832949	32835802	17	-1	32835802	32834802	32839302
NM_004590	CCL16	34449088	34454082	17	-1	34454082	34453082	34457582
NM_001838	CCR7	39083189	39094889	17	-1	39094889	39093889	39098389
NM_003839	TNFRSF11A	58141555	58201236	18	1	58141555	58138055	58142555
NM_005755	EBI3	4180495	4188506	19	1	4180520	4177020	4181520
NM_001252	TNFSF7	6536850	6542163	19	-1	6542163	6541163	6545663
NM_003807	TNFSF14	6615568	6621599	19	-1	6621599	6620599	6625099
NM_005624	CCL25	8023933	8033547	19	1	8023933	8020433	8024933
NM_004516	ILF3	10625988	10664095	19	1	10626046	10622546	10627046
NM_006858	NM_006858	10804115	10807983	19	-1	10807955	10806955	10811455
NM_004843	NM_004843	14003262	14025026	19	1	14003581	14000081	14004581
NM_004335	BST2	17374759	17377457	19	-1	17377404	17376404	17380904
NM_005535	IL12RB1	18031701	18058702	19	-1	18058745	18057745	18062245
NM_006332	IFI30	18145579	18149927	19	1	18145623	18142123	18146623
NM_145256	LRRC25	18362959	18369408	19	-1	18369038	18368038	18372538
NM_002975	SCGF	55918417	55920776	19	1	55918433	55914933	55919433
NM_016543	SIGLEC7	56337376	56348595	19	1	56337370	56333870	56338370
NM_005601	NKG7	56566688	56567701	19	-1	56567701	56566701	56571201
NM_033130	SIGLEC10	56606115	56612803	19	-1	56612862	56611862	56616362
NM_014442	SIGLEC8	56646064	56653509	19	-1	56653522	56652522	56657022

NM_053003	SIGLECL1	56686707	56696855	19	-1	56696838	56695838	56700338
NM_024298	NM_024298	59368921	59385478	19	-1	59385265	59384265	59388765
NM_006864	LILRB3	59412565	59418660	19	-1	59438492	59437492	59441992
NM_006840	LILRB5	59446143	59452937	19	-1	59452939	59451939	59456439
NM_005874	LILRB2	59470349	59476163	19	-1	59476163	59475163	59479663
NM_006865	LILRA3	59491669	59495985	19	-1	59495985	59494985	59499485
NM_012276	NM_012276	59536505	59541992	19	-1	59542245	59541245	59545745
NM_021706	NM_021706	59557945	59568287	19	-1	59568287	59567287	59571787
NM_021708	LAIR1	59557945	59568287	19	-1	59568350	59567350	59571850
NM_002288 _NM_01231 2_NM_0123 14_NM_021 270	NM_002288	59705825	59713707	19	1	59705825	59702325	59706825
NM_006866	LILRA2	59777158	59790625	19	1	59777079	59773579	59778079
NM_006863	LILRA1	59796937	59805499	19	1	59796904	59793404	59797904
NM_006847	LILRB4	59866264	59873619	19	1	59866264	59862764	59867264
NM_024317	NM_024317	59911413	59916501	19	1	59911413	59907913	59912413
NM_006737 _NM_00225 5_NM_0048 29	KIR3DL2_KI R2DL4_NCR 1	60006878	60116153	19	1	60006878	60003378	60007878
NM_000641	IL11	60567569	60573626	19	-1	60573626	60572626	60577126
NM_000629	IFNAR1	33617679	33649252	21	1	33617674	33614174	33618674
NM_005534	IFNGR2	33695598	33730216	21	1	33696125	33692625	33697125
NM_013416	NCF4	35500069	35517096	22	1	35500069	35496569	35501069
NM_000395	CSF2RB	35561289	35577583	22	1	35561289	35557789	35562289
NM_000878	IL2RB	35764924	35789001	22	-1	35789001	35788001	35792501
NM_000206	IL2RG	69194050	69198194	X	-1	69198216	69197216	69201716
NM_001504	CXCR3	69702558	69705151	X	-1	69705152	69704152	69708652
NM_000074	TNFSF5	134435976	134448156	X	1	134435976	134432476	134436976
NM_001569	IRAK1	151743864	151753246	X	-1	151753246	151752246	151756746
NM_002186	IL9R	153659077	153672313	X	1	153659077	153655577	153660077

Table 9: Out of the 166 redundant genes, 160 promoters were annotated by DBTSS and Ensembl.

Gene Symbol	Gene Length [bp]	Exon Length [bp]	CDS Length [bp]	Exon Coverage [bp]	Exon Coverage [%]	CDS Coverage [bp]	CDS Coverage [%]
CCR1	6074	2129	1067	2103	99%	1052	99%
CXCL11	2404	1488	281	1451	98%	244	87%
IL10	4903	1625	532	1566	96%	473	89%
IL6ST	15754	329	329	313	95%	313	95%
IL9	3592	586	430	548	94%	403	94%
CD72	8713	1522	1072	1377	90%	927	86%

TNFSF7	1111	344	193	311	90%	161	83%
IL18R1	22610	824	800	743	90%	743	93%
IL16	11132	1869	1572	1683	90%	1471	94%
IL1RL2	52389	1952	1717	1735	89%	1500	87%
IFNA6	570	569	569	503	88%	503	88%
IL10RA	15114	3664	1730	3235	88%	1375	79%
SIGLEC10	6564	2164	2083	1902	88%	1821	87%
CSF3R	13486	2833	2496	2453	87%	2139	86%
CSF2RB	4941	1809	1533	1559	86%	1283	84%
IRAK1	6127	2408	1072	2035	85%	1046	98%
CSF3R	13433	2359	2336	1979	84%	1979	85%
IFIT1	1434	1433	1433	1197	84%	1197	84%
CX3CR1	16620	3088	1076	2470	80%	704	65%
IL6ST	12050	1174	1174	910	78%	910	78%
ITK	74496	4348	1846	3365	77%	1313	71%
CX3CR1	18295	3108	1162	2404	77%	704	61%
IL6ST	1884	1033	818	793	77%	578	71%
IL9R	1713	451	451	346	77%	346	77%
IL7R	19920	1796	1372	1376	77%	1215	89%
TNFRSF8	28378	1144	1144	876	77%	876	77%
LILRA1	7430	1891	1452	1430	76%	1172	81%
IL12B	15678	2336	981	1759	75%	864	88%
IL9R	1684	422	420	317	75%	317	75%
TNFRSF10C	14506	1377	775	1033	75%	670	86%
CXCR3	2603	1621	1105	1207	74%	691	63%
IFRD2	5170	2256	1314	1679	74%	1232	94%
TNFSF14	6039	1475	719	1082	73%	697	97%
IRF6	18170	2160	1397	1581	73%	1008	72%
NCK2	30936	995	946	721	72%	721	76%
IRAK1	1324	600	600	429	72%	429	72%
TNFRSF10B	7692	3101	568	2208	71%	313	55%
MST1R	17032	4509	4181	3203	71%	2903	69%
IL15	94282	1035	192	735	71%	181	94%
CNTFR	32801	885	600	626	71%	516	86%
IFNA21	570	569	569	391	69%	391	69%
IFI30	4343	1025	773	704	69%	658	85%
CNTFR	32801	775	600	516	67%	516	86%
XCL1	5804	1221	341	772	63%	60	18%
SCARA3	38525	3637	1815	2280	63%	1341	74%
IL11RA	3399	903	686	531	59%	314	46%
TNFRSF11A	44602	1558	1558	915	59%	915	59%

CCL17	1919	282	282	165	59%	165	59%
IL1R1	26043	4893	1700	2761	56%	1380	81%
SIGLEC8	6745	2422	1040	1352	56%	786	76%
IL1RL1	94695	1503	1387	818	54%	702	51%
C1QTNF2	23733	2371	856	1288	54%	466	54%
IL1A	10956	2927	810	1569	54%	610	75%
IL3	2547	918	454	487	53%	434	96%
TRAF4	2869	1765	1264	933	53%	933	74%
IL2RB	11926	3515	1263	1818	52%	564	45%
IK	30728	1800	1650	922	51%	772	47%
TNIP1	35434	2702	1900	1324	49%	1288	68%
TRAF3	36072	1623	1623	793	49%	793	49%
IL5RA	20170	1684	1000	796	47%	554	55%
IL11RA	3205	506	442	239	47%	180	41%
IL6	4803	1120	634	529	47%	467	74%
SCARA3	42566	1903	1395	890	47%	890	64%
TRAF3	36072	1697	1697	793	47%	793	47%
DEFA5	1421	447	283	207	46%	167	59%
IL16	83179	3632	1572	1671	46%	1471	94%
IL16	83179	3632	3525	1671	46%	1671	47%
TNFSF8	27968	1975	701	908	46%	264	38%
CSF2	2374	777	431	356	46%	324	75%
IL11RA	3221	522	442	239	46%	180	41%
CCR3	24897	1858	1067	850	46%	411	39%
CCR3	56431	1725	1067	787	46%	411	39%
CNTFR	895	796	159	363	46%	159	100%
TNIP1	51482	2898	1900	1319	46%	1288	68%
IL9R	4340	181	143	81	45%	43	30%
IL11RA	4472	1183	780	520	44%	395	51%
CCR3	24897	1936	1067	850	44%	411	39%
IL11RA	4467	1178	780	515	44%	395	51%
BTC	50510	2061	532	881	43%	117	22%
CCBP2	45375	2906	1154	1193	41%	875	76%
NCR1	5653	1013	904	412	41%	405	45%
LAIR1	10414	1790	854	720	40%	656	77%
IFNAR1	42649	6013	1666	2399	40%	1380	83%
IL5RA	41033	2283	1253	880	39%	638	51%
CCR9	16854	2537	1107	961	38%	360	33%
CCR9	16854	2537	1072	961	38%	340	32%
IL5RA	41033	2351	1253	880	37%	638	51%
CCL11	2497	914	291	341	37%	0	0%

CCR9	16821	2456	1072	881	36%	340	32%
IL18	20871	1077	583	381	35%	230	39%
IL11	6082	2343	595	813	35%	236	40%
IL2RB	6464	349	201	120	34%	87	43%
IL12RB1	22032	2349	1736	793	34%	675	39%
ISGF3G	17253	4734	1132	1588	34%	0	0%
TRADD	4597	565	248	158	28%	0	0%
HIVP2	17210	3787	2149	1049	28%	1049	49%
TRADD	4613	581	427	158	27%	150	35%
TRAF4	2368	450	450	119	26%	119	26%
AREG	9814	1233	754	312	25%	294	39%
CCL28	222253	520	381	126	24%	126	33%
IL6ST	7998	515	488	120	23%	120	25%
TRAF5	28745	3965	1664	783	20%	782	47%
IFNGR2	35119	2572	1028	496	19%	496	48%
TRAF5	48884	4098	1664	783	19%	782	47%
IL21	8444	624	484	115	18%	115	24%
IL15	3615	860	247	137	16%	137	55%
EBI3	8033	1153	685	178	15%	178	26%
CXCL12	1661	1660	90	251	15%	90	100%
IL1RL1	86351	1203	503	172	14%	172	34%
IL7	73098	2069	528	264	13%	264	50%
BST2	2721	1028	554	126	12%	126	23%
TNFSF4	23708	3492	549	356	10%	200	36%
IL11RA	6438	1797	442	180	10%	180	41%
IL18R1	4306	2404	513	158	7%	158	31%
CCL28	36693	2539	381	126	5%	126	33%
FAF1	521025	2564	1934	126	5%	126	7%
IL15	7488	5252	112	181	3%	84	75%
TNFRSF10D	27704	3546	1152	111	3%	111	10%
CD8A	6382	2019	592	30	1%	30	5%
CD8A	6382	2129	702	30	1%	30	4%

Table 12: This table shows 22 redundant or 19 non-redundant genes, listing only genes categorized as B. The exon areas in this category are covered to at least 65%. The coding areas (CDS) could be fully determined (100%).

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9. Eidesstattliche Erklärung

Die selbständige Anfertigung versichere ich an Eides statt.

A handwritten signature in black ink, appearing to read 'Sven M. Dillenburger', written in a cursive style.

Sven M. Dillenburger