HUMAN GENES AND GENE EXPRESSION PRODUCTS

Cross-Reference to Related Application

[0001] Ths application claims the benefit of earlier-filed U.S. provisional application serial no. 60/226,326 filed August 16, 2000, which application is incorporated herein by reference in its entirety.

Field of the Invention

[0002] The present invention relates to polynucleotides of human origin, particularly in human colon, breast, prostate, and/or lung tissue, and the encoded gene products.

Background of the Invention

[0003] Identification of novel polynucleotides, particularly those that encode an expressed gene product, is important in the advancement of drug discovery, diagnostic technologies, and the understanding of the progression and nature of complex diseases such as cancer. Identification of genes expressed in different cell types isolated from sources that differ in disease state or stage, developmental stage, exposure to various environmental factors, the tissue of origin, the species from which the tissue was isolated, and the like is key to identifying the genetic factors that are responsible for the phenotypes associated with these various differences.

[0004] This invention provides novel human polynucleotides, the polypeptides encoded by these polynucleotides, and the genes and proteins corresponding to these novel polynucleotides.

Summary of the Invention

[0005] This invention relates to novel human polynucleotides and variants thereof, their encoded polypeptides and variants thereof, to genes corresponding to these polynucleotides and to proteins expressed by the genes. The invention also relates to diagnostics and therapeutics comprising such novel human polynucleotides, their corresponding genes or gene products, including probes, antisense nucleotides, and antibodies. The polynucleotides of the invention correspond to a polynucleotide comprising the sequence information of at least one of SEQ ID NOS:1-6010.

[0006] Various aspects and embodiments of the invention will be readily apparent to the ordinarily skilled artisan upon reading the description provided herein.

Detailed Description of the Invention

[0007] Before the present invention is described, it is to be understood that this invention is not limited to particular embodiments described, as such may, of course, vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to be limiting.

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although any methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, the preferred methods and materials are now described.

All publications and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference. The citation of any publication is for its disclosure prior to the filing date and should not be construed as an admission that the present invention is not entitled to antedate such publication by virtue of prior invention.

It must be noted that as used herein and in the appended claims, the singular forms "a," "and," and "the" include plural referents unless the context clearly dictates otherwise. Thus, for example, reference to "a polynucleotide" includes a plurality of such polynucleotides and reference to "the colon cancer cell" includes reference to one or more cells and equivalents thereof known to those skilled in the art, and so forth.

The publications and applications discussed herein are provided solely for their disclosure prior to the filing date of the present application. Nothing herein is to be construed as an admission that the present invention is not entitled to antedate such publication by virtue of prior invention. Further, the dates of publication provided may be different from the actual publication dates which may need to be independently confirmed.

Definitions

The terms "polynucleotide" and "nucleic acid," used interchangeably herein, refer to a polymeric forms of nucleotides of any length, either ribonucleotides or deoxynucleotides. Thus, these terms include, but are not limited to, single-, double-, or multi-stranded DNA or RNA, genomic DNA, cDNA, DNA-RNA hybrids, branched nucleic acid (see, *e.g.*, U.S. Pat. Nos. 5,124,246; 5,710,264; and 5,849,481) , or a polymer comprising purine and pyrimidine bases or other natural, chemically or biochemically modified, non-natural, or derivatized nucleotide bases. These terms furhter include, but are not limited to, mRNA or cDNA that comprise intronic sequences (see, *e.g.*, Niwa et al. (1999) Cell 99(7):691-702). The backbone of the polynucleotide can comprise sugars and phosphate groups (as may typically be found in RNA or DNA), or modified or substituted sugar or phosphate groups. Alternatively, the backbone of the polynucleotide can comprise a polymer of synthetic subunits such as phosphoramidites and thus can be an oligodeoxynucleoside phosphoramidate or a mixed phosphoramidate-phosphodiester oligomer. Peyrottes et al. (1996) Nucl. Acids Res. 24:1841-1848; Chaturvedi et al. (1996) Nucl. Acids Res. 24:2318-2323. A polynuclotide may comprise modified nucleotides, such as methylated nucleotides and nucleotide analogs, uracyl, other sugars, and linking

groups such as fluororibose and thioate, and nucleotide branches. The sequence of nucleotides may be interrupted by non-nucleotide components. A polynucleotide may be further modified after polymerization, such as by conjugation with a labeling component. Other types of modifications included in this definition are caps, substitution of one or more of the naturally occurring nucleotides with an analog, and introduction of means for attaching the polynucleotide to proteins, metal ions, labeling components, other polynucleotides, or a solid support.

The terms "polypeptide" and "protein," used interchangebly herein, refer to a polymeric form of amino acids of any length, which can include coded and non-coded amino acids, chemically or biochemically modified or derivatized amino acids, and polypeptides having modified peptide backbones. The term includes fusion proteins, including, but not limited to, fusion proteins with a heterologous amino acid sequence, fusions with heterologous and homologous leader sequences, with or without N-terminal methionine residues; immunologically tagged proteins; and the like.

"Diagnosis" as used herein generally includes determination of a subject's susceptibility to a disease or disorder, determination as to whether a subject is presently affected by a disease or disorder, prognosis of a subject affected by a disease or disorder (*e.g.*, identification of pre-metastatic or metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy), and therametrics (*e.g.*, monitoring a subject's condition to provide information as to the effect or efficacy of therapy).

"Sample" or "biological sample" as used herein encompasses a variety of sample types, and are generally meant to refer to samples of biological fluids or tissues, particularly samples obtained from tissues, especially from cells of the type associated with a disease or condition for which a diagnostic application is designed (e.g., ductal adenocarcinoma), and the like. "Sample" or "biological sample" are meant to encompass blood and other liquid samples of biological origin, solid tissue samples, such as a biopsy specimen or tissue cultures or cells derived therefrom and the progeny thereof. These terms encompass samples that have been manipulated in any way after their procurement as well as derivatives and fractions of samples, where the samples may be maniuplated by, for example, treatment with reagents, solubilization, or enrichment for certain components. The terms also encompass clinical samples, and also includes cells in cell culture, cell supernatants, cell lysates, serum, plasma, biological fluids, and tissue samples. Where the sample is solid tissue, the cells of the tissue can be dissociated or tissue sections can be analyzed.

The terms "treatment," "treating," "treat" and the like are used herein to generally refer to obtaining a desired pharmacologic and/or physiologic effect. The effect may be prophylactic in terms of completely or partially preventing a disease or symptom thereof and/or may be therapeutic in terms of a partial or complete stabilization or cure for a disease and/or adverse effect attributable to the disease. "Treatment" as used herein covers any treatment of a disease in a mammal, particularly a

human, and includes: (a) preventing the disease or symptom from occurring in a subject which may be predisposed to the disease or symptom but has not yet been diagnosed as having it; (b) inhibiting the disease symptom, i.e., arresting its development; or relieving the disease symptom, i.e., causing regression of the disease or symptom.

The terms "individual," "subject," "host," and "patient," used interchangeably herein and refer to any mammalian subject for whom diagnosis, treatment, or therapy is desired, particularly humans. Other subjects may include cattle, dogs, cats, guinea pigs, rabbits, rats, mice, horses, and so on.

As used herein the term "isolated" refers to a polynucleotide, a polypeptide, an antibody, or a host cell that is in an environment different from that in which the polynucleotide, the polypeptide, the antibody, or the host cell naturally occurs. A polynucleotide, a polypeptide, an antibody, or a host cell which is isolated is generally substantially purified. As used herein, the term "substantially purified" refers to a compound (e.g., either a polynucleotide or a polypeptide or an antibody) that is removed from its natural environment and is at least 60% free, preferably 75% free, and most preferably 90% free from other components with which it is naturally associated. Thus, for example, a composition containing A is "substantially free of" B when at least 85% by weight of the total A+B in the composition is A. Preferably, A comprises at least about 90% by weight of the total of A+B in the composition, more preferably at least about 95% or even 99% by weight.

A "host cell," as used herein, refers to a microorganism or a eukaryotic cell or cell line cultured as a unicellular entity which can be, or has been, used as a recipient for a recombinant vector or other transfer polynucleotides, and include the progeny of the original cell which has been transfected. It is understood that the progeny of a single cell may not necessarily be completely identical in morphology or in genomic or total DNA complement as the original parent, due to natural, accidental, or deliberate mutation.

The terms "cancer," "neoplasm," "tumor," and "carcinoma," are used interchangeably herein to refer to cells which exhibit relatively autonomous growth, so that they exhibit an aberrant growth phenotype characterized by a significant loss of control of cell proliferation. In general, cells of interest for detection or treatment in the present application include precancerous (*e.g.*, benign), malignant, metastatic, and non-metastatic cells. Detection of cancerous cell is of particular interest.

The use of "e", as in 10e-3, indicates that the number to the left of "e" is raised to the power of the number to the right of "e" (thus, 10e-3 is 10^{-3}).

The term "heterologous" as used herein in the context of, for example, heterologous nucleic acid or amino acid sequences, heterologous polypeptides, or heterologous nucleic acid, is meant to refer to material that originates from a source different from that with which it is joined or associated. For example, two DNA sequences are heterologous to one another if the sequences are from different genes

or from different species. A recombinant host cell containing a sequence that is heterologous to the host cell can be, for example, a bacterial cell containing a sequence encoding a human polypeptide.

The invention relates to polynucleotides comprising the disclosed nucleotide sequences, to full length cDNA, mRNA, genomic sequences, and genes corresponding to these sequences and degenerate variants thereof, and to polypeptides encoded by the polynucleotides of the invention and polypeptide variants. The following detailed description describes the polynucleotide compositions encompassed by the invention, methods for obtaining cDNA or genomic DNA encoding a full-length gene product, expression of these polynucleotides and genes, identification of structural motifs of the polynucleotides and genes, identification of the function of a gene product encoded by a gene corresponding to a polynucleotide of the invention, use of the provided polynucleotides as probes and in mapping and in tissue profiling, use of the corresponding polypeptides and other gene products to raise antibodies, and use of the polynucleotides and their encoded gene products for therapeutic and diagnostic purposes.

Polynucleotide Compositions

The scope of the invention with respect to polynucleotide compositions includes, but is not necessarily limited to, polynucleotides having a sequence set forth in any one of SEQ ID NOS:1-6010; polynucleotides obtained from the biological materials described herein or other biological sources (particularly human sources) by hybridization under stringent conditions (particularly conditions of high stringency); genes corresponding to the provided polynucleotides; variants of the provided polynucleotides and their corresponding genes, particularly those variants that retain a biological activity of the encoded gene product (*e.g.*, a biological activity ascribed to a gene product corresponding to the provided polynucleotides as a result of the assignment of the gene product to a protein family(ies) and/or identification of a functional domain present in the gene product). Other nucleic acid compositions contemplated by and within the scope of the present invention will be readily apparent to one of ordinary skill in the art when provided with the disclosure here. "Polynucleotide" and "nucleic acid" as used herein with reference to nucleic acids of the composition is not intended to be limiting as to the length or structure of the nucleic acid unless specifically indicated.

The invention features polynucleotides that are expressed in human tissue, especially human colon, prostate, breast, lung and/or endothelial tissue. Novel nucleic acid compositions of the invention of particular interest comprise a sequence set forth in any one of SEQ ID NOS:1-6010 or an identifying sequence thereof. An "identifying sequence" is a contiguous sequence of residues at least about 10 nt to about 20 nt in length, usually at least about 50 nt to about 100 nt in length, that uniquely identifies a polynucleotide sequence, *e.g.*, exhibits less than 90%, usually less than about 80% to about 85% sequence identity to any contiguous nucleotide sequence of more than about 20 nt. Thus, the

subject novel nucleic acid compositions include full length cDNAs or mRNAs that encompass an identifying sequence of contiguous nucleotides from any one of SEQ ID NOS: 1-6010.

The polynucleotides of the invention also include polynucleotides having sequence similarity or sequence identity. Nucleic acids having sequence similarity are detected by hybridization under low stringency conditions, for example, at 50°C and 10XSSC (0.9 M saline/0.09 M sodium citrate) and remain bound when subjected to washing at 55°C in 1XSSC. Sequence identity can be determined by hybridization under stringent conditions, for example, at 50°C or higher and 0.1XSSC (9 mM saline/0.9 mM sodium citrate). Hybridization methods and conditions are well known in the art, see, *e.g.*, USPN 5,707,829. Nucleic acids that are substantially identical to the provided polynucleotide sequences, *e.g.* allelic variants, genetically altered versions of the gene, *etc.*, bind to the provided polynucleotide sequences (SEQ ID NOS:1-6010) under stringent hybridization conditions. By using probes, particularly labeled probes of DNA sequences, one can isolate homologous or related genes. The source of homologous genes can be any species, *e.g.* primate species, particularly human; rodents, such as rats and mice; canines, felines, bovines, ovines, equines, yeast, nematodes, *etc.*

Preferably, hybridization is performed using at least 15 contiguous nucleotides (nt) of at least one of SEQ ID NOS:1-6010. That is, when at least 15 contiguous nt of one of the disclosed SEQ ID NOS. is used as a probe, the probe will preferentially hybridize with a nucleic acid comprising the complementary sequence, allowing the identification and retrieval of the nucleic acids that uniquely hybridize to the selected probe. Probes from more than one SEQ ID NO. can hybridize with the same nucleic acid if the cDNA from which they were derived corresponds to one mRNA. Probes of more than 15 nt can be used, *e.g.*, probes of from about 18 nt to about 100 nt, but 15 nt represents sufficient sequence for unique identification.

The polynucleotides of the invention also include naturally occurring variants of the nucleotide sequences (*e.g.*, degenerate variants, allelic variants, *etc.*). Variants of the polynucleotides of the invention are identified by hybridization of putative variants with nucleotide sequences disclosed herein, preferably by hybridization under stringent conditions. For example, by using appropriate wash conditions, variants of the polynucleotides of the invention can be identified where the allelic variant exhibits at most about 25-30% base pair (bp) mismatches relative to the selected polynucleotide probe. In general, allelic variants contain 15-25% bp mismatches, and can contain as little as even 5-15%, or 2-5%, or 1-2% bp mismatches, as well as a single bp mismatch.

The invention also encompasses homologs corresponding to the polynucleotides of SEQ ID NOS:1-6010, where the source of homologous genes can be any mammalian species, *e.g.*, primate species, particularly human; rodents, such as rats; canines, felines, bovines, ovines, equines, yeast, nematodes, *etc.* Between mammalian species, *e.g.*, human and mouse, homologs generally have

substantial sequence similarity, *e.g.*, at least 75% sequence identity, usually at least 90%, more usually at least 95% between nucleotide sequences. Sequence similarity is calculated based on a reference sequence, which may be a subset of a larger sequence, such as a conserved motif, coding region, flanking region, *etc.* A reference sequence will usually be at least about 18 contiguous nt long, more usually at least about 30 nt long, and may extend to the complete sequence that is being compared. Algorithms for sequence analysis are known in the art, such as gapped BLAST, described in Altschul, et al. *Nucleic Acids Res.* (1997) *25*:3389-3402.

In general, variants of the invention have a sequence identity greater than at least about 65%, preferably at least about 75%, more preferably at least about 85%, and can be greater than at least about 90% or more as determined by the Smith-Waterman homology search algorithm as implemented in MPSRCH program (Oxford Molecular). For the purposes of this invention, a preferred method of calculating percent identity is the Smith-Waterman algorithm, using the following. Global DNA sequence identity must be greater than 65% as determined by the Smith-Waterman homology search algorithm as implemented in MPSRCH program (Oxford Molecular) using an affine gap search with the following search parameters: gap open penalty, 12; and gap extension penalty, 1.

The subject nucleic acids can be cDNAs or genomic DNAs, as well as fragments thereof, particularly fragments that encode a biologically active gene product and/or are useful in the methods disclosed herein (*e.g.*, in diagnosis, as a unique identifier of a differentially expressed gene of interest, *etc.*). The term "cDNA" as used herein is intended to include all nucleic acids that share the arrangement of sequence elements found in native mature mRNA species, where sequence elements are exons and 3' and 5' non-coding regions. Normally mRNA species have contiguous exons, with the intervening introns, when present, being removed by nuclear RNA splicing, to create a continuous open reading frame encoding a polypeptide of the invention.

A genomic sequence of interest comprises the nucleic acid present between the initiation codon and the stop codon, as defined in the listed sequences, including all of the introns that are normally present in a native chromosome. It can further include the 3' and 5' untranslated regions found in the mature mRNA. It can further include specific transcriptional and translational regulatory sequences, such as promoters, enhancers, *etc.*, including about 1 kb, but possibly more, of flanking genomic DNA at either the 5' and 3' end of the transcribed region. The genomic DNA can be isolated as a fragment of 100 kbp or smaller; and substantially free of flanking chromosomal sequence. The genomic DNA flanking the coding region, either 3' and 5', or internal regulatory sequences as sometimes found in introns, contains sequences required for proper tissue, stage-specific, or disease-state specific expression.

The nucleic acid compositions of the subject invention can encode all or a part of the subject polypeptides. Double or single stranded fragments can be obtained from the DNA sequence by chemically synthesizing oligonucleotides in accordance with conventional methods, by restriction enzyme digestion, by PCR amplification, *etc.* Isolated polynucleotides and polynucleotide fragments of the invention comprise at least about 10, about 15, about 20, about 35, about 50, about 100, about 150 to about 200, about 250 to about 300, or about 350 contiguous nt selected from the polynucleotide sequences as shown in SEQ ID NOS:1-6010. For the most part, fragments will be of at least 15 nt, usually at least 18 nt or 25 nt, and up to at least about 50 contiguous nt in length or more. In a preferred embodiment, the polynucleotide molecules comprise a contiguous sequence of at least 12 nt selected from the group consisting of the polynucleotides shown in SEQ ID NOS:1-6010.

Probes specific to the polynucleotides of the invention can be generated using the polynucleotide sequences disclosed in SEQ ID NOS:1-6010. The probes are preferably at least about 12, 15, 16, 18, 20, 22, 24, or 25 nt fragment of a corresponding contiguous sequence of SEQ ID NOS:1-6010, and can be less than 2, 1, 0.5, 0.1, or 0.05 kb in length. The probes can be synthesized chemically or can be generated from longer polynucleotides using restriction enzymes. The probes can be labeled, for example, with a radioactive, biotinylated, or fluorescent tag. Preferably, probes are designed based upon an identifying sequence of a polynucleotide of one of SEQ ID NOS:1-6010. More preferably, probes are designed based on a contiguous sequence of one of the subject polynucleotides that remain unmasked following application of a masking program for masking low complexity (*e.g.*,XBLAST) to the sequence., *i.e.*, one would select an unmasked region, as indicated by the polynucleotides outside the poly-n stretches of the masked sequence produced by the masking program.

The polynucleotides of the subject invention are isolated and obtained in substantial purity, generally as other than an intact chromosome. Usually, the polynucleotides, either as DNA or RNA, will be obtained substantially free of other naturally-occurring nucleic acid sequences, generally being at least about 50%, usually at least about 90% pure and are typically "recombinant," e.g., flanked by one or more nucleotides with which it is not normally associated on a naturally occurring chromosome.

The polynucleotides of the invention can be provided as a linear molecule or within a circular molecule, and can be provided within autonomously replicating molecules (vectors) or within molecules without replication sequences. Expression of the polynucleotides can be regulated by their own or by other regulatory sequences known in the art. The polynucleotides of the invention can be introduced into suitable host cells using a variety of techniques available in the art, such as transferrin polycation-mediated DNA transfer, transfection with naked or encapsulated nucleic acids, liposome-

mediated DNA transfer, intracellular transportation of DNA-coated latex beads, protoplast fusion, viral infection, electroporation, gene gun, calcium phosphate-mediated transfection, and the like.

The subject nucleic acid compositions can be used to, for example, produce polypeptides, as probes for the detection of mRNA of the invention in biological samples (e.g., extracts of human cells) to generate additional copies of the polynucleotides, to generate ribozymes or antisense oligonucleotides, and as single stranded DNA probes or as triple-strand forming oligonucleotides. The probes described herein can be used to, for example, determine the presence or absence of the polynucleotide sequences as shown in SEQ ID NOS:1-6010 or variants thereof in a sample. These and other uses are described in more detail below.

Use of Polynucleotides to Obtain Full-Length cDNA, Gene, and Promoter Region

In one embodiment, the polynucleotides are useful as starting materials to construct larger molecules. In one example, the polynucleotides of the invention are used to construct polynucleotides that encode a larger polypeptide (*e.g.*, up to the full-length native polypeptide as well as fusion proteins comprising all or a portion of the native polypeptide) or may be used to produce haptens of the polypeptide (*e.g.*, polypeptides useful to generate antibodies).

In one particular example, the polynucleotides of the invention are used to make or isolate cDNA molecules encoding all or portion of a naturally-occuring polypeptide. Full-length cDNA molecules comprising the disclosed polynucleotides are obtained as follows. A polynucleotide having a sequence of one of SEQ ID NOS:1-6010, or a portion thereof comprising at least 12, 15, 18, or 20 nt, is used as a hybridization probe to detect hybridizing members of a cDNA library using probe design methods, cloning methods, and clone selection techniques such as those described in USPN 5,654,173. Libraries of cDNA are made from selected tissues, such as normal or tumor tissue, or from tissues of a mammal treated with, for example, a pharmaceutical agent. Preferably, the tissue is the same as the tissue from which the polynucleotides of the invention were isolated, as both the polynucleotides described herein and the cDNA represent expressed genes. Most preferably, the cDNA library is made from the biological material described herein in the Examples. The choice of cell type for library construction can be made after the identity of the protein encoded by the gene corresponding to the polynucleotide of the invention is known. This will indicate which tissue and cell types are likely to express the related gene, and thus represent a suitable source for the mRNA for generating the cDNA. Where the provided polynucleotides are isolated from cDNA libraries, the libraries are prepared from mRNA of human colon cells, more preferably, human colon cancer cells, even more preferably, from a highly metastatic colon cell, Km12L4-A.

Techniques for producing and probing nucleic acid sequence libraries are described, for example, in Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Ed., (1989) Cold Spring

Harbor Press, Cold Spring Harbor, NY. The cDNA can be prepared by using primers based on polynucleotides comprising a sequence of SEQ ID NOS:1-6010. In one embodiment, the cDNA library can be made from only poly-adenylated mRNA. Thus, poly-T primers can be used to prepare cDNA from the mRNA.

Members of the library that are larger than the provided polynucleotides, and preferably that encompass the complete coding sequence of the native message, are obtained. In order to confirm that the entire cDNA has been obtained, RNA protection experiments are performed as follows. Hybridization of a full-length cDNA to an mRNA will protect the RNA from RNase degradation. If the cDNA is not full length, then the portions of the mRNA that are not hybridized will be subject to RNase degradation. This is assayed, as is known in the art, by changes in electrophoretic mobility on polyacrylamide gels, or by detection of released monoribonucleotides. Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Ed., (1989) Cold Spring Harbor Press, Cold Spring Harbor, NY. In order to obtain additional sequences 5' to the end of a partial cDNA, 5' RACE (PCR Protocols: A Guide to Methods and Applications, (1990) Academic Press, Inc.) can be performed.

Genomic DNA is isolated using the provided polynucleotides in a manner similar to the isolation of full-length cDNAs. Briefly, the provided polynucleotides, or portions thereof, are used as probes to libraries of genomic DNA. Preferably, the library is obtained from the cell type that was used to generate the polynucleotides of the invention, but this is not essential. Most preferably, the genomic DNA is obtained from the biological material described herein in the Examples. Such libraries can be in vectors suitable for carrying large segments of a genome, such as P1 or YAC, as described in detail in Sambrook et al., supra, 9.4-9.30. In addition, genomic sequences can be isolated from human BAC libraries, which are commercially available from Research Genetics, Inc., Huntsville, Alabama, USA, for example. In order to obtain additional 5' or 3' sequences, chromosome walking is performed, as described in Sambrook et al., such that adjacent and overlapping fragments of genomic DNA are isolated. These are mapped and pieced together, as is known in the art, using restriction digestion enzymes and DNA ligase.

Using the polynucleotide sequences of the invention, corresponding full-length genes can be isolated using both classical and PCR methods to construct and probe cDNA libraries. Using either method, Northern blots, preferably, are performed on a number of cell types to determine which cell lines express the gene of interest at the highest level. Classical methods of constructing cDNA libraries are taught in Sambrook et al., supra. With these methods, cDNA can be produced from mRNA and inserted into viral or expression vectors. Typically, libraries of mRNA comprising poly(A) tails can be produced with poly(T) primers. Similarly, cDNA libraries can be produced using the instant sequences as primers.

PCR methods are used to amplify the members of a cDNA library that comprise the desired insert. In this case, the desired insert will contain sequence from the full length cDNA that corresponds to the instant polynucleotides. Such PCR methods include gene trapping and RACE methods. Gene trapping entails inserting a member of a cDNA library into a vector. The vector then is denatured to produce single stranded molecules. Next, a substrate-bound probe, such as a biotinylated oligo, is used to trap cDNA inserts of interest. Biotinylated probes can be linked to an avidin-bound solid substrate. PCR methods can be used to amplify the trapped cDNA. To trap sequences corresponding to the full length genes, the labeled probe sequence is based on the polynucleotide sequences of the invention. Random primers or primers specific to the library vector can be used to amplify the trapped cDNA. Such gene trapping techniques are described in Gruber et al., WO 95/04745 and Gruber et al., USPN 5,500,356. Kits are commercially available to perform gene trapping experiments from, for example, Life Technologies, Gaithersburg, Maryland, USA.

"Rapid amplification of cDNA ends," or RACE, is a PCR method of amplifying cDNAs from a number of different RNAs. The cDNAs are ligated to an oligonucleotide linker, and amplified by PCR using two primers. One primer is based on sequence from the instant polynucleotides, for which full length sequence is desired, and a second primer comprises sequence that hybridizes to the oligonucleotide linker to amplify the cDNA. A description of this method is reported in WO 97/19110. In preferred embodiments of RACE, a common primer is designed to anneal to an arbitrary adaptor sequence ligated to cDNA ends (Apte and Siebert, Biotechniques (1993) 15:890-893; Edwards et al., Nuc. Acids Res. (1991) 19:5227-5232). When a single gene-specific RACE primer is paired with the common primer, preferential amplification of sequences between the single gene specific primer and the common primer occurs. Commercial cDNA pools modified for use in RACE are available.

Another PCR-based method generates full-length cDNA library with anchored ends without needing specific knowledge of the cDNA sequence. The method uses lock-docking primers (I-VI), where one primer, poly TV (I-III) locks over the polyA tail of eukaryotic mRNA producing first strand synthesis and a second primer, polyGH (IV-VI) locks onto the polyC tail added by terminal deoxynucleotidyl transferase (TdT)(see, e.g., WO 96/40998).

The promoter region of a gene generally is located 5' to the initiation site for RNA polymerase II. Hundreds of promoter regions contain the "TATA" box, a sequence such as TATTA or TATAA, which is sensitive to mutations. The promoter region can be obtained by performing 5' RACE using a primer from the coding region of the gene. Alternatively, the cDNA can be used as a probe for the genomic sequence, and the region 5' to the coding region is identified by "walking up." If the gene is

highly expressed or differentially expressed, the promoter from the gene can be of use in a regulatory construct for a heterologous gene.

Once the full-length cDNA or gene is obtained, DNA encoding variants can be prepared by site-directed mutagenesis, described in detail in Sambrook et al., 15.3-15.63. The choice of codon or nucleotide to be replaced can be based on disclosure herein on optional changes in amino acids to achieve altered protein structure and/or function.

As an alternative method to obtaining DNA or RNA from a biological material, nucleic acid comprising nucleotides having the sequence of one or more polynucleotides of the invention can be synthesized. Thus, the invention encompasses nucleic acid molecules ranging in length from 15 nt (corresponding to at least 15 contiguous nt of one of SEQ ID NOS:1-6010) up to a maximum length suitable for one or more biological manipulations, including replication and expression, of the nucleic acid molecule. The invention includes but is not limited to (a) nucleic acid having the size of a full gene, and comprising at least one of SEQ ID NOS:1-6010; (b) the nucleic acid of (a) also comprising at least one additional gene, operably linked to permit expression of a fusion protein; (c) an expression vector comprising (a) or (b); (d) a plasmid comprising (a) or (b); and (e) a recombinant viral particle comprising (a) or (b). Once provided with the polynucleotides disclosed herein, construction or preparation of (a) - (e) are well within the skill in the art.

The sequence of a nucleic acid comprising at least 15 contiguous nt of at least any one of SEQ ID NOS:1-6010, preferably the entire sequence of at least any one of SEQ ID NOS:1-6010, is not limited and can be any sequence of A, T, G, and/or C (for DNA) and A, U, G, and/or C (for RNA) or modified bases thereof, including inosine and pseudouridine. The choice of sequence will depend on the desired function and can be dictated by coding regions desired, the intron-like regions desired, and the regulatory regions desired. Where the entire sequence of any one of SEQ ID NOS:1-6010 is within the nucleic acid, the nucleic acid obtained is referred to herein as a polynucleotide comprising the sequence of any one of SEQ ID NOS:1-6010.

Expression of Polypeptide Encoded by Full-Length cDNA or Full-Length Gene

The provided polynucleotides (*e.g.*, a polynucleotide having a sequence of one of SEQ ID NOS:1-6010), the corresponding cDNA, or the full-length gene is used to express a partial or complete gene product. Constructs of polynucleotides having sequences of SEQ ID NOS:1-6010 can also be generated synthetically. Alternatively, single-step assembly of a gene and entire plasmid from large numbers of oligodeoxyribonucleotides is described by, e.g., Stemmer et al., Gene (Amsterdam) (1995) 164(1):49-53. In this method, assembly PCR (the synthesis of long DNA sequences from large numbers of oligodeoxyribonucleotides (oligos)) is described. The method is derived from DNA

shuffling (Stemmer, Nature (1994) 370:389-391), and does not rely on DNA ligase, but instead relies on DNA polymerase to build increasingly longer DNA fragments during the assembly process.

Appropriate polynucleotide constructs are purified using standard recombinant DNA techniques as described in, for example, Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual, 2nd Ed.*, (1989) Cold Spring Harbor Press, Cold Spring Harbor, NY, and under current regulations described in United States Dept. of HHS, National Institute of Health (NIH) Guidelines for Recombinant DNA Research. The gene product encoded by a polynucleotide of the invention is expressed in any expression system, including, for example, bacterial, yeast, insect, amphibian and mammalian systems. Vectors, host cells and methods for obtaining expression in same are well known in the art. Suitable vectors and host cells are described in USPN 5,654,173.

Polynucleotide molecules comprising a polynucleotide sequence provided herein are generally propagated by placing the molecule in a vector. Viral and non-viral vectors are used, including plasmids. The choice of plasmid will depend on the type of cell in which propagation is desired and the purpose of propagation. Certain vectors are useful for amplifying and making large amounts of the desired DNA sequence. Other vectors are suitable for expression in cells in culture. Still other vectors are suitable for transfer and expression in cells in a whole animal or person. The choice of appropriate vector is well within the skill of the art. Many such vectors are available commercially. Methods for preparation of vectors comprising a desired sequence are well known in the art.

The polynucleotides set forth in SEQ ID NOS:1-6010 or their corresponding full-length polynucleotides are linked to regulatory sequences as appropriate to obtain the desired expression properties. These can include promoters (attached either at the 5' end of the sense strand or at the 3' end of the antisense strand), enhancers, terminators, operators, repressors, and inducers. The promoters can be regulated or constitutive. In some situations it may be desirable to use conditionally active promoters, such as tissue-specific or developmental stage-specific promoters. These are linked to the desired nucleotide sequence using the techniques described above for linkage to vectors. Any techniques known in the art can be used.

When any of the above host cells, or other appropriate host cells or organisms, are used to replicate and/or express the polynucleotides or nucleic acids of the invention, the resulting replicated nucleic acid, RNA, expressed protein or polypeptide, is within the scope of the invention as a product of the host cell or organism. The product is recovered by any appropriate means known in the art.

Once the gene corresponding to a selected polynucleotide is identified, its expression can be regulated in the cell to which the gene is native. For example, an endogenous gene of a cell can be regulated by an exogenous regulatory sequence as disclosed in USPN 5,641,670.

Identification of Functional and Structural Motifs

Translations of the nucleotide sequence of the provided polynucleotides, cDNAs or full genes can be aligned with individual known sequences. Similarity with individual sequences can be used to determine the activity of the polypeptides encoded by the polynucleotides of the invention. Also, sequences exhibiting similarity with more than one individual sequence can exhibit activities that are characteristic of either or both individual sequences.

The full length sequences and fragments of the polynucleotide sequences of the nearest neighbors can be used as probes and primers to identify and isolate the full length sequence corresponding to provided polynucleotides. The nearest neighbors can indicate a tissue or cell type to be used to construct a library for the full-length sequences corresponding to the provided polynucleotides.

Typically, a selected polynucleotide is translated in all six frames to determine the best alignment with the individual sequences. The sequences disclosed herein in the Sequence Listing are in a 5' to 3' orientation and translation in three frames can be sufficient (with a few specific exceptions as described in the Examples). These amino acid sequences are referred to, generally, as query sequences, which will be aligned with the individual sequences. Databases with individual sequences are described in "Computer Methods for Macromolecular Sequence Analysis" *Methods in Enzymology* (1996) *266*, Doolittle, Academic Press, Inc., a division of Harcourt Brace & Co., San Diego, California, USA. Databases include GenBank, EMBL, and DNA Database of Japan (DDBJ).

Query and individual sequences can be aligned using the methods and computer programs described above, and include BLAST 2.0, available over the world wide web at a site supported by the National Center for Biotechnology Information, which is supported by the National Library of Medicine and the National Institutes of Health. See also Altschul, et al. Nucleic Acids Res. (1997) 25:3389-3402. Another alignment algorithm is Fasta, available in the Genetics Computing Group (GCG) package, Madison, Wisconsin, USA, a wholly owned subsidiary of Oxford Molecular Group, Inc. Other techniques for alignment are described in Doolittle, supra. Preferably, an alignment program that permits gaps in the sequence is utilized to align the sequences. The Smith-Waterman is one type of algorithm that permits gaps in sequence alignments. See Meth. Mol. Biol. (1997) *70*: 173-187. Also, the GAP program using the Needleman and Wunsch alignment method can be utilized to align sequences. An alternative search strategy uses MPSRCH software, which runs on a MASPAR computer. MPSRCH uses a Smith-Waterman algorithm to score sequences on a massively parallel computer. This approach improves ability to identify sequences that are distantly related matches, and is especially tolerant of small gaps and nucleotide sequence errors. Amino acid sequences encoded by the provided polynucleotides can be used to search both protein and DNA databases. Incorporated

herein by reference are all sequences that have been made public as of the filing date of this application by any of the DNA or protein sequence databases, including the patent databases (*e.g.*, GeneSeq). Also incorporated by reference are those sequences that have been submitted to these databases as of the filing date of the present application but not made public until after the filing date of the present application.

Results of individual and query sequence alignments can be divided into three categories: high similarity, weak similarity, and no similarity. Individual alignment results ranging from high similarity to weak similarity provide a basis for determining polypeptide activity and/or structure. Parameters for categorizing individual results include: percentage of the alignment region length where the strongest alignment is found, percent sequence identity, and p value. The percentage of the alignment region length is calculated by counting the number of residues of the individual sequence found in the region of strongest alignment, *e.g.*, contiguous region of the individual sequence that contains the greatest number of residues that are identical to the residues of the corresponding region of the aligned query sequence. This number is divided by the total residue length of the query sequence to calculate a percentage. For example, a query sequence of 20 amino acid residues might be aligned with a 20 amino acid region of an individual sequence. The individual sequence might be identical to amino acid residues 5, 9-15, and 17-19 of the query sequence. The region of strongest alignment is thus the region stretching from residue 9-19, an 11 amino acid stretch. The percentage of the alignment region length is: 11 (length of the region of strongest alignment) divided by (query sequence length) 20 or 55%.

Percent sequence identity is calculated by counting the number of amino acid matches between the query and individual sequence and dividing total number of matches by the number of residues of the individual sequences found in the region of strongest alignment. Thus, the percent identity in the example above would be 10 matches divided by 11 amino acids, or approximately, 90.9%

P value is the probability that the alignment was produced by chance. For a single alignment, the p value can be calculated according to Karlin et al., Proc. Natl. Acad. Sci. (1990) 87:2264 and Karlin et al., Proc. Natl. Acad. Sci. (1993) 90. The p value of multiple alignments using the same query sequence can be calculated using an heuristic approach described in Altschul et al., Nat. Genet. (1994) 6:119. Alignment programs such as BLAST program can calculate the p value. See also Altschul et al., Nucleic Acids Res. (1997) 25:3389-3402.

Another factor to consider for determining identity or similarity is the location of the similarity or identity. Strong local alignment can indicate similarity even if the length of alignment is short. Sequence identity scattered throughout the length of the query sequence also can indicate a similarity between the query and profile sequences. The boundaries of the region where the sequences align can be determined according to Doolittle, supra; BLAST 2.0 (see, e.g., Altschul, et al. Nucleic Acids Res.

(1997) 25:3389-3402) or FAST programs; or by determining the area where sequence identity is highest.

High Similarity. In general, in alignment results considered to be of high similarity, the percent of the alignment region length is typically at least about 55% of total length query sequence; more typically, at least about 58%; even more typically; at least about 60% of the total residue length of the query sequence. Usually, percent length of the alignment region can be as much as about 62%; more usually, as much as about 64%; even more usually, as much as about 66%. Further, for high similarity, the region of alignment, typically, exhibits at least about 75% of sequence identity; more typically, at least about 78%; even more typically; at least about 80% sequence identity. Usually, percent sequence identity can be as much as about 82%; more usually, as much as about 84%; even more usually, as much as about 86%.

The p value is used in conjunction with these methods. If high similarity is found, the query sequence is considered to have high similarity with a profile sequence when the p value is less than or equal to about 10e-2; more usually; less than or equal to about 10e-3; even more usually; less than or equal to about 10e-4. More typically, the p value is no more than about 10e-5; more typically; no more than or equal to about 10e-10; even more typically, no more than or equal to about 10e-15 for the query sequence to be considered high similarity.

Weak Similarity. In general, where alignment results considered to be of weak similarity, there is no minimum percent length of the alignment region nor minimum length of alignment. A better showing of weak similarity is considered when the region of alignment is, typically, at least about 15 amino acid residues in length; more typically, at least about 20; even more typically, at least about 25 amino acid residues in length. Usually, length of the alignment region can be as much as about 30 amino acid residues; more usually, as much as about 40; even more usually, as much as about 60 amino acid residues. Further, for weak similarity, the region of alignment, typically, exhibits at least about 35% of sequence identity; more typically, at least about 40%; even more typically, at least about 45% sequence identity. Usually, percent sequence identity can be as much as about 50%; more usually, as much as about 55%; even more usually, as much as about 60%.

If low similarity is found, the query sequence is considered to have weak similarity with a profile sequence when the p value is usually less than or equal to about 10e-2; more usually, less than or equal to about 10e-3; even more usually; less than or equal to about 10e-4. More typically, the p value is no more than about 10e-5; more usually; no more than or equal to about 10e-10; even more usually, no more than or equal to about 10e-15 for the query sequence to be considered weak similarity.

Similarity Determined by Sequence Identity Alone. Sequence identity alone can be used to determine similarity of a query sequence to an individual sequence and can indicate the activity of the

sequence. Such an alignment, preferably, permits gaps to align sequences. Typically, the query sequence is related to the profile sequence if the sequence identity over the entire query sequence is at least about 15%; more typically, at least about 20%; even more typically, at least about 25%; even more typically, at least about 50%. Sequence identity alone as a measure of similarity is most useful when the query sequence is usually, at least 80 residues in length; more usually, at least 90 residues in length; even more usually, at least 95 amino acid residues in length. More typically, similarity can be concluded based on sequence identity alone when the query sequence is preferably 100 residues in length; more preferably, 120 residues in length; even more preferably, 150 amino acid residues in length.

Alignments with Profile and Multiple Aligned Sequences. Translations of the provided polynucleotides can be aligned with amino acid profiles that define either protein families or common motifs. Also, translations of the provided polynucleotides can be aligned to multiple sequence alignments (MSA) comprising the polypeptide sequences of members of protein families or motifs. Similarity or identity with profile sequences or MSAs can be used to determine the activity of the gene products (e.g., polypeptides) encoded by the provided polynucleotides or corresponding cDNA or genes. For example, sequences that show an identity or similarity with a chemokine profile or MSA can exhibit chemokine activities.

Profiles can be designed manually by (1) creating an MSA, which is an alignment of the amino acid sequence of members that belong to the family and (2) constructing a statistical representation of the alignment. Such methods are described, for example, in Birney et al., Nucl. Acid Res. (1996) 24(14): 2730-2739. MSAs of some protein families and motifs are publicly available. For example, the Genome Sequencing Center at thw Washington University School of Medicine provides a web set (Pfam) which provides MSAs of 547 different families and motifs. These MSAs are described also in Sonnhammer et al., Proteins (1997) 28: 405-420. Other sources over the world wide web include the site supported by the European Molecular Biology Laboratories in Heidelberg, Germany. A brief description of these MSAs is reported in Pascarella et al., Prot. Eng. (1996) 9(3):249-251. Techniques for building profiles from MSAs are described in Sonnhammer et al., supra; Birney et al., supra; and "Computer Methods for Macromolecular Sequence Analysis," Methods in Enzymology (1996) 266, Doolittle, Academic Press, Inc., San Diego, California, USA.

Similarity between a query sequence and a protein family or motif can be determined by (a) comparing the query sequence against the profile and/or (b) aligning the query sequence with the members of the family or motif. Typically, a program such as Searchwise is used to compare the query sequence to the statistical representation of the multiple alignment, also known as a profile (see Birney

et al., supra). Other techniques to compare the sequence and profile are described in Sonnhammer et al., supra and Doolittle, supra.

Next, methods described by Feng et al., J. Mol. Evol. (1987) 25:351 and Higgins et al., CABIOS (1989) 5:151 can be used align the query sequence with the members of a family or motif, also known as a MSA. Sequence alignments can be generated using any of a variety of software tools. Examples include PileUp, which creates a multiple sequence alignment, and is described in Feng et al., J. Mol. Evol. (1987) 25:351. Another method, GAP, uses the alignment method of Needleman et al., J. Mol. Biol. (1970) 48:443. GAP is best suited for global alignment of sequences. A third method, BestFit, functions by inserting gaps to maximize the number of matches using the local homology algorithm of Smith et al., Adv. Appl. Math. (1981) 2:482. In general, the following factors are used to determine if a similarity between a query sequence and a profile or MSA exists: (1) number of conserved residues found in the query sequence, (2) percentage of conserved residues found in the query sequence, (3) number of frameshifts, and (4) spacing between conserved residues.

Some alignment programs that both translate and align sequences can make any number of frameshifts when translating the nucleotide sequence to produce the best alignment. The fewer frameshifts needed to produce an alignment, the stronger the similarity or identity between the query and profile or MSAs. For example, a weak similarity resulting from no frameshifts can be a better indication of activity or structure of a query sequence, than a strong similarity resulting from two frameshifts. Preferably, three or fewer frameshifts are found in an alignment; more preferably two or fewer frameshifts; even more preferably, one or fewer frameshifts; even more preferably, no frameshifts are found in an alignment of query and profile or MSAs.

Conserved residues are those amino acids found at a particular position in all or some of the family or motif members. Alternatively, a position is considered conserved if only a certain class of amino acids is found in a particular position in all or some of the family members. For example, the N-terminal position can contain a positively charged amino acid, such as lysine, arginine, or histidine.

Typically, a residue of a polypeptide is conserved when a class of amino acids or a single amino acid is found at a particular position in at least about 40% of all class members; more typically, at least about 50%; even more typically, at least about 60% of the members. Usually, a residue is conserved when a class or single amino acid is found in at least about 70% of the members of a family or motif; more usually, at least about 80%; even more usually, at least about 90%; even more usually, at least about 95%.

A residue is considered conserved when three unrelated amino acids are found at a particular position in some or all of the members; more usually, two unrelated amino acids. These residues are conserved when the unrelated amino acids are found at particular positions in at least about 40% of all

class member; more typically, at least about 50%; even more typically, at least about 60% of the members. Usually, a residue is conserved when a class or single amino acid is found in at least about 70% of the members of a family or motif; more usually, at least about 80%; even more usually, at least about 90%; even more usually, at least about 95%.

A query sequence has similarity to a profile or MSA when the query sequence comprises at least about 25% of the conserved residues of the profile or MSA; more usually, at least about 30%; even more usually; at least about 40%. Typically, the query sequence has a stronger similarity to a profile sequence or MSA when the query sequence comprises at least about 45% of the conserved residues of the profile or MSA; more typically, at least about 50%; even more typically, at least about 55%.

Identification of Secreted & Membrane-Bound Polypeptides. Both secreted and membrane-bound polypeptides of the present invention are of particular interest. For example, levels of secreted polypeptides can be assayed in body fluids that are convenient, such as blood, plasma, serum, and other body fluids such as urine, prostatic fluid and semen. Membrane-bound polypeptides are useful for constructing vaccine antigens or inducing an immune response. Such antigens would comprise all or part of the extracellular region of the membrane-bound polypeptides. Because both secreted and membrane-bound polypeptides comprise a fragment of contiguous hydrophobic amino acids, hydrophobicity predicting algorithms can be used to identify such polypeptides.

A signal sequence is usually encoded by both secreted and membrane-bound polypeptide genes to direct a polypeptide to the surface of the cell. The signal sequence usually comprises a stretch of hydrophobic residues. Such signal sequences can fold into helical structures. Membrane-bound polypeptides typically comprise at least one transmembrane region that possesses a stretch of hydrophobic amino acids that can transverse the membrane. Some transmembrane regions also exhibit a helical structure. Hydrophobic fragments within a polypeptide can be identified by using computer algorithms. Such algorithms include Hopp & Woods, Proc. Natl. Acad. Sci. USA (1981) 78:3824-3828; Kyte & Doolittle, J. Mol. Biol. (1982) 157: 105-132; and RAOAR algorithm, Degli Esposti et al., Eur. J. Biochem. (1990) 190: 207-219.

Another method of identifying secreted and membrane-bound polypeptides is to translate the polynucleotides of the invention in all six frames and determine if at least 8 contiguous hydrophobic amino acids are present. Those translated polypeptides with at least 8; more typically, 10; even more typically, 12 contiguous hydrophobic amino acids are considered to be either a putative secreted or membrane bound polypeptide. Hydrophobic amino acids include alanine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, threonine, tryptophan, tyrosine, and valine

Identification of the Function of an Expression Product of a Full-Length Gene

Ribozymes, antisense constructs, and dominant negative mutants can be used to determine function of the expression product of a gene corresponding to a polynucleotide provided herein. These methods and compositions are particularly useful where the provided novel polynucleotide exhibits no significant or substantial homology to a sequence encoding a gene of known function. Antisense molecules and ribozymes can be constructed from synthetic polynucleotides. Typically, the phosphoramidite method of oligonucleotide synthesis is used. See Beaucage et al., Tet. Lett. (1981) 22:1859 and USPN 4,668,777. Automated devices for synthesis are available to create oligonucleotides using this chemistry. Examples of such devices include Biosearch 8600, Models 392 and 394 by Applied Biosystems, a division of Perkin-Elmer Corp., Foster City, California, USA; and Expedite by Perceptive Biosystems, Framingham, Massachusetts, USA. Synthetic RNA, phosphate analog oligonucleotides, and chemically derivatized oligonucleotides can also be produced, and can be covalently attached to other molecules. RNA oligonucleotides can be synthesized, for example, using RNA phosphoramidites. This method can be performed on an automated synthesizer, such as Applied Biosystems, Models 392 and 394, Foster City, California, USA.

Phosphorothioate oligonucleotides can also be synthesized for antisense construction. A sulfurizing reagent, such as tetraethylthiruam disulfide (TETD) in acetonitrile can be used to convert the internucleotide cyanoethyl phosphite to the phosphorothioate triester within 15 minutes at room temperature. TETD replaces the iodine reagent, while all other reagents used for standard phosphoramidite chemistry remain the same. Such a synthesis method can be automated using Models 392 and 394 by Applied Biosystems, for example.

Oligonucleotides of up to 200 nt can be synthesized, more typically, 100 nt; more typically 50 nt; even more typically, 30 to 40 nt. These synthetic fragments can be annealed and ligated together to construct larger fragments. See, for example, Sambrook et al., supra. Trans-cleaving catalytic RNAs (ribozymes) are RNA molecules possessing endoribonuclease activity. Ribozymes are specifically designed for a particular target, and the target message must contain a specific nucleotide sequence. They are engineered to cleave any RNA species site-specifically in the background of cellular RNA. The cleavage event renders the mRNA unstable and prevents protein expression. Importantly, ribozymes can be used to inhibit expression of a gene of unknown function for the purpose of determining its function in an in vitro or in vivo context, by detecting the phenotypic effect. One commonly used ribozyme motif is the hammerhead, for which the substrate sequence requirements are minimal. Design of the hammerhead ribozyme, as well as therapeutic uses of ribozymes, are disclosed in Usman et al., Current Opin. Struct. Biol. (1996) 6:527. Methods for production of ribozymes,

including hairpin structure ribozyme fragments, methods of increasing ribozyme specificity, and the like are known in the art.

The hybridizing region of the ribozyme can be modified or can be prepared as a branched structure as described in Horn and Urdea, Nucleic Acids Res. (1989) 17:6959. The basic structure of the ribozymes can also be chemically altered in ways familiar to those skilled in the art, and chemically synthesized ribozymes can be administered as synthetic oligonucleotide derivatives modified by monomeric units. In a therapeutic context, liposome mediated delivery of ribozymes improves cellular uptake, as described in Birikh et al., Eur. J. Biochem. (1997) 245:1.

Antisense nucleic acids are designed to specifically bind to RNA, resulting in the formation of RNA-DNA or RNA-RNA hybrids, with an arrest of DNA replication, reverse transcription or messenger RNA translation. Antisense polynucleotides based on a selected polynucleotide sequence can interfere with expression of the corresponding gene. Antisense polynucleotides are typically generated within the cell by expression from antisense constructs that contain the antisense strand as the transcribed strand. Antisense polynucleotides based on the disclosed polynucleotides will bind and/or interfere with the translation of mRNA comprising a sequence complementary to the antisense polynucleotide. The expression products of control cells and cells treated with the antisense construct are compared to detect the protein product of the gene corresponding to the polynucleotide upon which the antisense construct is based. The protein is isolated and identified using routine biochemical methods.

Given the extensive background literature and clinical experience in antisense therapy, one skilled in the art can use selected polynucleotides of the invention as additional potential therapeutics. The choice of polynucleotide can be narrowed by first testing them for binding to "hot spot" regions of the genome of cancerous cells. If a polynucleotide is identified as binding to a "hot spot," testing the polynucleotide as an antisense compound in the corresponding cancer cells is warranted.

As an alternative method for identifying function of the gene corresponding to a polynucleotide disclosed herein, dominant negative mutations are readily generated for corresponding proteins that are active as homomultimers. A mutant polypeptide will interact with wild-type polypeptides (made from the other allele) and form a non-functional multimer. Thus, a mutation is in a substrate-binding domain, a catalytic domain, or a cellular localization domain. Preferably, the mutant polypeptide will be overproduced. Point mutations are made that have such an effect. In addition, fusion of different polypeptides of various lengths to the terminus of a protein can yield dominant negative mutants. General strategies are available for making dominant negative mutants (see, e.g., Herskowitz, Nature (1987) 329:219). Such techniques can be used to create loss of function mutations, which are useful for determining protein function.

Polypeptides and Variants Thereof

The polypeptides of the invention include those encoded by the disclosed polynucleotides, as well as nucleic acids that, by virtue of the degeneracy of the genetic code, are not identical in sequence to the disclosed polynucleotides. Thus, the invention includes within its scope a polypeptide encoded by a polynucleotide having the sequence of any one of SEQ ID NOS:1-6010 or a variant thereof.

In general, the term "polypeptide" as used herein refers to both the full length polypeptide encoded by the recited polynucleotide, the polypeptide encoded by the gene represented by the recited polynucleotide, as well as portions or fragments thereof. "Polypeptides" also includes variants of the naturally occurring proteins, where such variants are homologous or substantially similar to the naturally occurring protein, and can be of an origin of the same or different species as the naturally occurring protein (e.g., human, murine, or some other species that naturally expresses the recited polypeptide, usually a mammalian species). In general, variant polypeptides have a sequence that has at least about 80%, usually at least about 90%, and more usually at least about 98% sequence identity with a differentially expressed polypeptide of the invention, as measured by BLAST 2.0 using the parameters described above. The variant polypeptides can be naturally or non-naturally glycosylated, i.e., the polypeptide has a glycosylation pattern that differs from the glycosylation pattern found in the corresponding naturally occurring protein.

The invention also encompasses homologs of the disclosed polypeptides (or fragments thereof) where the homologs are isolated from other species, i.e. other animal or plant species, where such homologs, usually mammalian species, e.g. rodents, such as mice, rats; domestic animals, e.g., horse, cow, dog, cat; and humans. By "homolog" is meant a polypeptide having at least about 35%, usually at least about 40% and more usually at least about 60% amino acid sequence identity to a particular differentially expressed protein as identified above, where sequence identity is determined using the BLAST 2.0 algorithm, with the parameters described supra.

In general, the polypeptides of the subject invention are provided in a non-naturally occurring environment, e.g. are separated from their naturally occurring environment. In certain embodiments, the subject protein is present in a composition that is enriched for the protein as compared to a control. As such, purified polypeptide is provided, where by purified is meant that the protein is present in a composition that is substantially free of non-differentially expressed polypeptides, where by substantially free is meant that less than 90%, usually less than 60% and more usually less than 50% of the composition is made up of non-differentially expressed polypeptides.

Also within the scope of the invention are variants; variants of polypeptides include mutants, fragments, and fusions. Mutants can include amino acid substitutions, additions or deletions. The amino acid substitutions can be conservative amino acid substitutions or substitutions to eliminate non-

essential amino acids, such as to alter a glycosylation site, a phosphorylation site or an acetylation site, or to minimize misfolding by substitution or deletion of one or more cysteine residues that are not necessary for function. Conservative amino acid substitutions are those that preserve the general charge, hydrophobicity/ hydrophilicity, and/or steric bulk of the amino acid substituted. Variants can be designed so as to retain or have enhanced biological activity of a particular region of the protein (e.g., a functional domain and/or, where the polypeptide is a member of a protein family, a region associated with a consensus sequence). Selection of amino acid alterations for production of variants can be based upon the accessibility (interior vs. exterior) of the amino acid (see, e.g., Go et al, Int. J. Peptide Protein Res. (1980) 15:211), the thermostability of the variant polypeptide (see, e.g., Querol et al., Prot. Eng. (1996) 9:265), desired glycosylation sites (see, e.g., Olsen and Thomsen, J. Gen. Microbiol. (1991) 137:579), desired disulfide bridges (see, e.g., Clarke et al., Biochemistry (1993) 32:4322; and Wakarchuk et al., Protein Eng. (1994) 7:1379), desired metal binding sites (see, e.g., Toma et al., Biochemistry (1991) 30:97, and Haezerbrouck et al., Protein Eng. (1993) 6:643), and desired substitutions within proline loops (see, e.g., Masul et al., Appl. Env. Microbiol. (1994) 60:3579). Cysteine-depleted muteins can be produced as disclosed in USPN 4,959,314.

Variants also include fragments of the polypeptides disclosed herein, particularly haptens, biologically active fragments, and/or fragments corresponding to functional domains. Fragments of interest will typically be at least about 10 aa to at least about 15 aa in length, usually at least about 50 aa in length, and can be as long as 300 aa in length or longer, but will usually not exceed about 1000 aa in length, where the fragment will have a stretch of amino acids that is identical to a polypeptide encoded by a polynucleotide having a sequence of any SEQ ID NOS:1-6010, or a homolog thereof. The protein variants described herein are encoded by polynucleotides that are within the scope of the invention. The genetic code can be used to select the appropriate codons to construct the corresponding variants.

Computer-Related Embodiments

In general, a library of polynucleotides is a collection of sequence information, which information is provided in either biochemical form (e.g., as a collection of polynucleotide molecules), or in electronic form (e.g., as a collection of polynucleotide sequences stored in a computer-readable form, as in a computer system and/or as part of a computer program). The sequence information of the polynucleotides can be used in a variety of ways, e.g., as a resource for gene discovery, as a representation of sequences expressed in a selected cell type (e.g., cell type markers), and/or as markers of a given disease or disease state. In general, a disease marker is a representation of a gene product that is present in all cells affected by disease either at an increased or decreased level relative to a normal cell (e.g., a cell of the same or similar type that is not substantially affected by disease). For

example, a polynucleotide sequence in a library can be a polynucleotide that represents an mRNA, polypeptide, or other gene product encoded by the polynucleotide, that is either overexpressed or underexpressed in a breast ductal cell affected by cancer relative to a normal (i.e., substantially disease-free) breast cell.

The nucleotide sequence information of the library can be embodied in any suitable form, e.g., electronic or biochemical forms. For example, a library of sequence information embodied in electronic form comprises an accessible computer data file (or, in biochemical form, a collection of nucleic acid molecules) that contains the representative nucleotide sequences of genes that are differentially expressed (e.g., overexpressed or underexpressed) as between, for example, i) a cancerous cell and a normal cell; ii) a cancerous cell and a dysplastic cell; iii) a cancerous cell and a cell affected by a disease or condition other than cancer; iv) a metastatic cancerous cell and a normal cell and/or non-metastatic cancerous cell; v) a malignant cancerous cell and a non-malignant cancerous cell (or a normal cell) and/or vi) a dysplastic cell relative to a normal cell. Other combinations and comparisons of cells affected by various diseases or stages of disease will be readily apparent to the ordinarily skilled artisan. Biochemical embodiments of the library include a collection of nucleic acids that have the sequences of the genes in the library, where the nucleic acids can correspond to the entire gene in the library or to a fragment thereof, as described in greater detail below.

The polynucleotide libraries of the subject invention generally comprise sequence information of a plurality of polynucleotide sequences, where at least one of the polynucleotides has a sequence of any of SEQ ID NOS:1-6010. By plurality is meant at least 2, usually at least 3 and can include up to all of SEQ ID NOS:1-6010. The length and number of polynucleotides in the library will vary with the nature of the library, e.g., if the library is an oligonucleotide array, a cDNA array, a computer database of the sequence information, etc.

Where the library is an electronic library, the nucleic acid sequence information can be present in a variety of media. "Media" refers to a manufacture, other than an isolated nucleic acid molecule, that contains the sequence information of the present invention. Such a manufacture provides the genome sequence or a subset thereof in a form that can be examined by means not directly applicable to the sequence as it exists in a nucleic acid. For example, the nucleotide sequence of the present invention, e.g. the nucleic acid sequences of any of the polynucleotides of SEQ ID NOS:1-6010, can be recorded on computer readable media, e.g. any medium that can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as a floppy disc, a hard disc storage medium, and a magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. One of skill in the art can readily appreciate how any of the presently known computer

readable mediums can be used to create a manufacture comprising a recording of the present sequence information. "Recorded" refers to a process for storing information on computer readable medium, using any such methods as known in the art. Any convenient data storage structure can be chosen, based on the means used to access the stored information. A variety of data processor programs and formats can be used for storage, e.g. word processing text file, database format, etc. In addition to the sequence information, electronic versions of the libraries of the invention can be provided in conjunction or connection with other computer-readable information and/or other types of computer-readable files (e.g., searchable files, executable files, etc, including, but not limited to, for example, search program software, etc.).

By providing the nucleotide sequence in computer readable form, the information can be accessed for a variety of purposes. Computer software to access sequence information is publicly available. For example, the gapped BLAST (Altschul et al. Nucleic Acids Res. (1997) 25:3389-3402) and BLAZE (Brutlag et al. Comp. Chem. (1993) 17:203) search algorithms on a Sybase system can be used to identify open reading frames (ORFs) within the genome that contain homology to ORFs from other organisms.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based system are suitable for use in the present invention. The data storage means can comprise any manufacture comprising a recording of the present sequence information as described above, or a memory access means that can access such a manufacture.

"Search means" refers to one or more programs implemented on the computer-based system, to compare a target sequence or target structural motif, or expression levels of a polynucleotide in a sample, with the stored sequence information. Search means can be used to identify fragments or regions of the genome that match a particular target sequence or target motif. A variety of known algorithms are publicly known and commercially available, e.g. MacPattern (EMBL), BLASTN and BLASTX (NCBI). A "target sequence" can be any polynucleotide or amino acid sequence of six or more contiguous nucleotides or two or more amino acids, preferably from about 10 to 100 amino acids or from about 30 to 300 nt A variety of comparing means can be used to accomplish comparison of sequence information from a sample (e.g., to analyze target sequences, target motifs, or relative expression levels) with the data storage means. A skilled artisan can readily recognize that any one of the publicly available homology search programs can be used as the search means for the computer

based systems of the present invention to accomplish comparison of target sequences and motifs. Computer programs to analyze expression levels in a sample and in controls are also known in the art.

A "target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration that is formed upon the folding of the target motif, or on consensus sequences of regulatory or active sites. There are a variety of target motifs known in the art. Protein target motifs include, but arc not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, hairpin structures, promoter sequences and other expression elements such as binding sites for transcription factors.

A variety of structural formats for the input and output means can be used to input and output the information in the computer-based systems of the present invention. One format for an output means ranks the relative expression levels of different polynucleotides. Such presentation provides a skilled artisan with a ranking of relative expression levels to determine a gene expression profile.

As discussed above, the "library" of the invention also encompasses biochemical libraries of the polynucleotides of SEQ ID NOS:1-6010 , e.g., collections of nucleic acids representing the provided polynucleotides. The biochemical libraries can take a variety of forms, e.g., a solution of cDNAs, a pattern of probe nucleic acids stably associated with a surface of a solid support (i.e., an array) and the like. Of particular interest are nucleic acid arrays in which one or more of SEQ ID NOS:1-6010 is represented on the array. By array is meant a an article of manufacture that has at least a substrate with at least two distinct nucleic acid targets on one of its surfaces, where the number of distinct nucleic acids can be considerably higher, typically being at least 10, usually at least 20, and often at least 25 distinct nucleic acid molecules. A variety of different array formats have been developed and are known to those of skill in the art. The arrays of the subject invention find use in a variety of applications, including gene expression analysis, drug screening, mutation analysis and the like, as disclosed in the above-listed exemplary patent documents.

In addition to the above nucleic acid libraries, analogous libraries of polypeptides are also provided, where the polypeptides of the library will represent at least a portion of the polypeptides encoded by a gene corresponding to one or more of SEQ ID NOS:1-6010.

Utilities

The polynucleotides of the invention are useful in a variety of applications. Exemplary utilies of the polynucleotides of the invention are described below.

Construction of Larger Molecules: Recombinant DNAs and Nucleic Acid Multimers. In one embodiment of particular interest, the polynucleotides described herein as useful as the building blocks for larger molecules. In one example, the polynucleotide is a component of a larger cDNA molecule

which in turn can be adapted for expression in a host cell (*e.g.*, a bacterial or eukaryotic (*e.g.*, yeast or mammalian) host cell). The cDNA can include, in addition to the polypeptide encoded by the starting material polynucleotide (*i.e.*, a polynucleotide described herein), an amino acid sequence that is heterologous to the polypeptide encoded by the polynucleotide described herein (*e.g.*, as in a sequence encoding a fusion protein). In some embodiments, the polynucleotides described herein is used as starting material polynucleotide for synthesizing all or a portion of the gene to which the described polynucleotide corresponds. For example, a DNA molecule encoding a full-length human polypeptide can be constructed using a polynucleotide described herein as starting material.

In another embodiment, the polynucleotides of the invention are used in nucleic acid multimers . Nucleic acid multimers can be linear or branched polymers of the same repeating single-stranded oligonucleotide unit or different single-stranded oligonucleotide units. Where the molecules are branched, the multimers are generally described as either "fork" or "comb" structures. The oligonucleotide units of the multimer may be composed of RNA, DNA, modified nucleotides or combinations thereof. At least one of the units has a sequence, length, and composition that permits it to bind specifically to a first single-stranded nucleotide sequence of interest, typically analyte or an oligonucleotide bound to the analyte. In order to achieve such specificity and stability, this unit will normally be 15 to 50 nt, preferably 15 to 30 nt, in length and have a GC content in the range of 40% to 60%. In addition to such unit(s), the multimer includes a multiplicity of units that are capable of hybridizing specifically and stably to a second single-stranded nucleotide of interest, typically a labeled oligonucleotide or another multimer. These units will also normally be 15 to 50 nt, preferably 15 to 30 nt, in length and have a GC content in the range of 40% to 60%. When a multimer is designed to be hybridized to another multimer, the first and second oligonucleotide units are heterogeneous (different). One or more of the polynucleotides described herein, or a portion of a polynucleotide described herein, can be used as a repeating unit of such nucleic acid multimers.

The total number of oligonucleotide units in the multimer will usually be in the range of 3 to 50, more usually 10 to 20. In multimers in which the unit that hybridizes to the nucleotide sequence of interest is different from the unit that hybridizes to the labeled oligonucleotide, the number ratio of the latter to the former will usually be 2:1 to 30:1, more usually 5:1 to 20:1, and preferably 10:1 to 15:1.

The oligonucleotide units of the multimer may be covalently linked directly to each other through phosphodiester bonds or through interposed linking agents such as nucleic acid, amino acid, carbohydrate or polyol bridges, or through other cross-linking agents that are capable of cross-linking nucleic acid or modified nucleic acid strands. The site(s) of linkage may be at the ends of the unit (in either normal 3,-5' orientation or randomly oriented) and/or at one or more internal nucleotides in the strand. In linear multimers the individual units are linked end-to-end to form a linear polymer. In one

type of branched multimer three or more oligonucleotide units emanate from a point of origin to form a branched structure. The point of origin may be another oligonucleotide unit or a multifunctional molecule to which at least three units can be covalently bound. In another type, there is an oligonucleotide unit backbone with one or more pendant oligonucleotide units. These latter-type multimers are "fork-like", "comb-like" or combination "fork-" and "comb-like" in structure. The pendant units will normally depend from a modified nucleotide or other organic moiety having appropriate functional groups to which oligonucleotides may be conjugated or otherwise attached. The multimer may be totally linear, totally branched, or a combination of linear and branched portions. Preferably there will be at least two branch points in the multimer, more preferably at least 3, preferably 5 to 10. The multimer may include one or more segments of double-stranded sequences.

Multimeric nucleic acid molecules are useful in amplifying the signal that results from hybridization of one the first sequence of the multimeric molecule to a target sequence. The amplification is theoretically proportional to the number of iterations of the second segment.

Without being held to theory, forked structures of greater than about eight branches exhibited steric hindrance which inhibited binding of labeled probes to the multimer. On the other hand, comb structures exhibit little or no steric problems and are thus a preferred type of branched multimer. For a description of branched nucleic acid multimers of both the fork and comb types, as well as methods of use and synthesis, see, *e.g.*, U.S. Pat. Nos. 5,124,246 (fork-type structures); 5,710,264 (synthesis of comb structures); and 5,849,481.

Use of Polynucleotide Probes in Mapping, and in Tissue Profiling. Polynucleotide probes, generally comprising at least 12 contiguous nt of a polynucleotide as shown in the Sequence Listing, are used for a variety of purposes, such as chromosome mapping of the polynucleotide and detection of transcription levels. Additional disclosure about preferred regions of the disclosed polynucleotide sequences is found in the Examples. A probe that hybridizes specifically to a polynucleotide disclosed herein should provide a detection signal at least 5-, 10-, or 20-fold higher than the background hybridization provided with other unrelated sequences.

Detection of Expression Levels. Nucleotide probes are used to detect expression of a gene corresponding to the provided polynucleotide. In Northern blots, mRNA is separated electrophoretically and contacted with a probe. A probe is detected as hybridizing to an mRNA species of a particular size. The amount of hybridization is quantitated to determine relative amounts of expression, for example under a particular condition. Probes are used for in situ hybridization to cells to detect expression. Probes can also be used in vivo for diagnostic detection of hybridizing sequences. Probes are typically labeled with a radioactive isotope. Other types of detectable labels can be used

such as chromophores, fluors, and enzymes. Other examples of nucleotide hybridization assays are described in WO92/02526 and USPN 5,124,246.

Alternatively, the Polymerase Chain Reaction (PCR) is another means for detecting small amounts of target nucleic acids (see, e.g., Mullis et al., Meth. Enzymol. (1987) 155:335; USPN 4,683,195; and USPN 4,683,202). Two primer polynucleotides nucleotides that hybridize with the target nucleic acids are used to prime the reaction. The primers can be composed of sequence within or 3' and 5' to the polynucleotides of the Sequence Listing. Alternatively, if the primers are 3' and 5' to these polynucleotides, they need not hybridize to them or the complements. After amplification of the target with a thermostable polymerase, the amplified target nucleic acids can be detected by methods known in the art, e.g., Southern blot. mRNA or cDNA can also be detected by traditional blotting techniques (e.g., Southern blot, Northern blot, etc.) described in Sambrook et al., "Molecular Cloning: A Laboratory Manual" (New York, Cold Spring Harbor Laboratory, 1989) (e.g., without PCR amplification). In general, mRNA or cDNA generated from mRNA using a polymerase enzyme can be purified and separated using gel electrophoresis, and transferred to a solid support, such as nitrocellulose. The solid support is exposed to a labeled probe, washed to remove any unhybridized probe, and duplexes containing the labeled probe are detected.

Mapping. Polynucleotides of the present invention can be used to identify a chromosome on which the corresponding gene resides. Such mapping can be useful in identifying the function of the polynucleotide-related gene by its proximity to other genes with known function. Function can also be assigned to the polynucleotide-related gene when particular syndromes or diseases map to the same chromosome. For example, use of polynucleotide probes in identification and quantification of nucleic acid sequence aberrations is described in USPN 5,783,387. An exemplary mapping method is fluorescence in situ hybridization (FISH), which facilitates comparative genomic hybridization to allow total genome assessment of changes in relative copy number of DNA sequences (see, e.g., Valdes et al., Methods in Molecular Biology (1997) 68:1). Polynucleotides can also be mapped to particular chromosomes using, for example, radiation hybrids or chromosome-specific hybrid panels. See Leach et al., Advances in Genetics, (1995) 33:63-99; Walter et al., Nature Genetics (1994) 7:22; Walter and Goodfellow, Trends in Genetics (1992) 9:352. Panels for radiation hybrid mapping are available from Research Genetics, Inc., Huntsville, Alabama, USA. Databases for markers using various panels are available via the world wide web at sites supported by the Stanford Human Genome Center (Stanford University) and the Whitehead Institute for Biomedical Research/MIT Center for Genome Research. The statistical program RHMAP can be used to construct a map based on the data from radiation hybridization with a measure of the relative likelihood of one order versus another. RHMAP is available via the world wide web at a site supported by the University of Michigan. In addition,

commercial programs are available for identifying regions of chromosomes commonly associated with disease, such as cancer.

Tissue Typing or Profiling. Expression of specific mRNA corresponding to the provided polynucleotides can vary in different cell types and can be tissue-specific. This variation of mRNA levels in different cell types can be exploited with nucleic acid probe assays to determine tissue types. For example, PCR, branched DNA probe assays, or blotting techniques utilizing nucleic acid probes substantially identical or complementary to polynucleotides listed in the Sequence Listing can determine the presence or absence of the corresponding cDNA or mRNA.

Tissue typing can be used to identify the developmental organ or tissue source of a metastatic lesion by identifying the expression of a particular marker of that organ or tissue. If a polynucleotide is expressed only in a specific tissue type, and a metastatic lesion is found to express that polynucleotide, then the developmental source of the lesion has been identified. Expression of a particular polynucleotide can be assayed by detection of either the corresponding mRNA or the protein product. As would be readily apparent to any forensic scientist, the sequences disclosed herein are useful in differentiating human tissue from non-human tissue. In particular, these sequences are useful to differentiate human tissue from bird, reptile, and amphibian tissue, for example.

Use of Polymorphisms. A polynucleotide of the invention can be used in forensics, genetic analysis, mapping, and diagnostic applications where the corresponding region of a gene is polymorphic in the human population. Any means for detecting a polymorphism in a gene can be used, including, but not limited to electrophoresis of protein polymorphic variants, differential sensitivity to restriction enzyme cleavage, and hybridization to allele-specific probes.

Antibody Production. Expression products of a polynucleotide of the invention, as well as the corresponding mRNA, cDNA, or complete gene, can be prepared and used for raising antibodies for experimental, diagnostic, and therapeutic purposes. For polynucleotides to which a corresponding gene has not been assigned, this provides an additional method of identifying the corresponding gene. The polynucleotide or related cDNA is expressed as described above, and antibodies are prepared. These antibodies are specific to an epitope on the polypeptide encoded by the polynucleotide, and can precipitate or bind to the corresponding native protein in a cell or tissue preparation or in a cell-free extract of an in vitro expression system.

Methods for production of antibodies that specifically bind a selected antigen are well known in the art. Immunogens for raising antibodies can be prepared by mixing a polypeptide encoded by a polynucleotide of the invention with an adjuvant, and/or by making fusion proteins with larger immunogenic proteins. Polypeptides can also be covalently linked to other larger immunogenic proteins, such as keyhole limpet hemocyanin. Immunogens are typically administered intradermally,

subcutaneously, or intramuscularly to experimental animals such as rabbits, sheep, and mice, to generate antibodies. Monoclonal antibodies can be generated by isolating spleen cells and fusing myeloma cells to form hybridomas. Alternatively, the selected polynucleotide is administered directly, such as by intramuscular injection, and expressed in vivo. The expressed protein generates a variety of protein-specific immune responses, including production of antibodies, comparable to administration of the protein.

Preparations of polyclonal and monoclonal antibodies specific for polypeptides encoded by a selected polynucleotide are made using standard methods known in the art. The antibodies specifically bind to epitopes present in the polypeptides encoded by polynucleotides disclosed in the Sequence Listing. Typically, at least 6, 8, 10, or 12 contiguous amino acids are required to form an epitope. Epitopes that involve non-contiguous amino acids may require a longer polypeptide, e.g., at least 15, 25, or 50 amino acids. Antibodies that specifically bind to human polypeptides encoded by the provided polypeptides should provide a detection signal at least 5-, 10-, or 20-fold higher than a detection signal provided with other proteins when used in Western blots or other immunochemical assays. Preferably, antibodies that specifically bind polypeptides contemplated by the invention do not bind to other proteins in immunochemical assays at detectable levels and can immunoprecipitate the specific polypeptide from solution.

The invention also contemplates naturally occurring antibodies specific for a polypeptide of the invention. For example, serum antibodies to a polypeptide of the invention in a human population can be purified by methods well known in the art, e.g., by passing antiserum over a column to which the corresponding selected polypeptide or fusion protein is bound. The bound antibodies can then be eluted from the column, for example, using a buffer with a high salt concentration.

In addition to the antibodies discussed above, the invention also contemplates genetically engineered antibodies antibodies (e.g., chimeric antibodies, humanized antibodies, human antibodies produced by a transgenic animal (e.g., a transgenic mouse such as the XenomousTM), antibody derivatives (e.g., single chain antibodies, antibody fragments (e.g., Fab, etc.)), according to methods well known in the art.

Polynucleotides or Arrays for Diagnostics.

Polynucleotide arrays provide a high throughput technique that can assay a large number of polynucleotides in a sample. This technology can be used as a diagnostic and as tool to test for differential expression expression, e.g., to determine function of an encoded protein. A variety of methods of producing arrays, as well as variations of these methods, are known in the art and contemplated for use in the invention. For example, arrays can be created by spotting polynucleotide probes onto a substrate (e.g., glass, nitrocellulose, etc.) in a two-dimensional matrix or array having

bound probes. The probes can be bound to the substrate by either covalent bonds or by non-specific interactions, such as hydrophobic interactions. Samples of polynucleotides can be detectably labeled (e.g., using radioactive or fluorescent labels) and then hybridized to the probes. Double stranded polynucleotides, comprising the labeled sample polynucleotides bound to probe polynucleotides, can be detected once the unbound portion of the sample is washed away. Alternatively, the polynucleotides of the test sample can be immobilized on the array, and the probes detectably labeled. Techniques for constructing arrays and methods of using these arrays are described in, for example, Schena et al. (1996) Proc Natl Acad Sci U S A. 93(20):10614-9; Schena et al. (1995) Science 270(5235):467-70; Shalon et al. (1996) Genome Res. 6(7):639-45, USPN 5,807,522, EP 799 897; WO 97/29212; WO 97/27317; EP 785 280; WO 97/02357; USPN 5,593,839; USPN 5,578,832; EP 728 520; USPN 5,599,695; EP 721 016; USPN 5,556,752; WO 95/22058; and USPN 5,631,734.

Arrays can be used to, for example, examine differential expression of genes and can be used to determine gene function. For example, arrays can be used to detect differential expression of a gene corresponding to a polynucleotide of the invention, where expression is compared between a test cell and control cell (e.g., cancer cells and normal cells). For example, high expression of a particular message in a cancer cell, which is not observed in a corresponding normal cell, can indicate a cancer specific gene product. Exemplary uses of arrays are further described in, for example, Pappalarado et al., Sem. Radiation Oncol. (1998) 8:217; and Ramsay Nature Biotechnol. (1998) 16:40. Furthermore, many variations on methods of detection using arrays are well within the skill in the art and within the scope of the present invention. For example, rather than immobilizing the probe to a solid support, the test sample can be immobilized on a solid support which is then contacted with the probe.

Differential Expression in Diagnosis

The polynucleotides of the invention can also be used to detect differences in expression levels between two cells, e.g., as a method to identify abnormal or diseased tissue in a human. For polynucleotides corresponding to profiles of protein families, the choice of tissue can be selected according to the putative biological function. In general, the expression of a gene corresponding to a specific polynucleotide is compared between a first tissue that is suspected of being diseased and a second, normal tissue of the human. The tissue suspected of being abnormal or diseased can be derived from a different tissue type of the human, but preferably it is derived from the same tissue type; for example, an intestinal polyp or other abnormal growth should be compared with normal intestinal tissue. The normal tissue can be the same tissue as that of the test sample, or any normal tissue of the patient, especially those that express the polynucleotide-related gene of interest (e.g., brain, thymus, testis, heart, prostate, placenta, spleen, small intestine, skeletal muscle, pancreas, and the mucosal lining of the colon). A difference between the polynucleotide-related gene, mRNA, or protein in the

two tissues which are compared, for example, in molecular weight, amino acid or nucleotide sequence, or relative abundance, indicates a change in the gene, or a gene which regulates it, in the tissue of the human that was suspected of being diseased. Examples of detection of differential expression and its use in diagnosis of cancer are described in USPNs 5,688,641 and 5,677,125.

A genetic predisposition to disease in a human can also be detected by comparing expression levels of an mRNA or protein corresponding to a polynucleotide of the invention in a fetal tissue with levels associated in normal fetal tissue. Fetal tissues that are used for this purpose include, but are not limited to, amniotic fluid, chorionic villi, blood, and the blastomere of an in vitro-fertilized embryo. The comparable normal polynucleotide-related gene is obtained from any tissue. The mRNA or protein is obtained from a normal tissue of a human in which the polynucleotide-related gene is expressed. Differences such as alterations in the nucleotide sequence or size of the same product of the fetal polynucleotide-related gene or mRNA, or alterations in the molecular weight, amino acid sequence, or relative abundance of fetal protein, can indicate a germline mutation in the polynucleotide-related gene of the fetus, which indicates a genetic predisposition to disease. In general, diagnostic, prognostic, and other methods of the invention based on differential expression involve detection of a level or amount of a gene product, particularly a differentially expressed gene product, in a test sample obtained from a patient suspected of having or being susceptible to a disease (e.g., breast cancer, lung cancer, colon cancer and/or metastatic forms thereof), and comparing the detected levels to those levels found in normal cells (e.g., cells substantially unaffected by cancer) and/or other control cells (e.g., to differentiate a cancerous cell from a cell affected by dysplasia). Furthermore, the severity of the disease can be assessed by comparing the detected levels of a differentially expressed gene product with those levels detected in samples representing the levels of differentially expressed gene product associated with varying degrees of severity of disease. It should be noted that use of the term "diagnostic" herein is not necessarily meant to exclude "prognostic" or "prognosis," but rather is used as a matter of convenience.

The term "differentially expressed gene" is generally intended to encompass a polynucleotide that can, for example, include an open reading frame encoding a gene product (e.g., a polypeptide), and/or introns of such genes and adjacent 5' and 3' non-coding nucleotide sequences involved in the regulation of expression, up to about 20 kb beyond the coding region, but possibly further in either direction. The gene can be introduced into an appropriate vector for extrachromosomal maintenance or for integration into a host genome. In general, a difference in expression level associated with a decrease in expression level of at least about 25%, usually at least about 50% to 75%, more usually at least about 90% or more is indicative of a differentially expressed gene of interest, i.e., a gene that is underexpressed or down-regulated in the test sample relative to a control sample. Furthermore, a

difference in expression level associated with an increase in expression of at least about 25%, usually at least about 50% to 75%, more usually at least about 90% and can be at least about 1½-fold, usually at least about 2-fold to about 10-fold, and can be about 100-fold to about 1,000-fold increase relative to a control sample is indicative of a differentially expressed gene of interest, i.e., an overexpressed or up-regulated gene.

"Differentially expressed polynucleotide" as used herein means a nucleic acid molecule (RNA or DNA) comprising a sequence that represents a differentially expressed gene, e.g., the differentially expressed polynucleotide comprises a sequence (e.g., an open reading frame encoding a gene product) that uniquely identifies a differentially expressed gene so that detection of the differentially expressed polynucleotide in a sample is correlated with the presence of a differentially expressed gene in a sample. "Differentially expressed polynucleotide" is also meant to encompass fragments of the disclosed polynucleotides, e.g., fragments retaining biological activity, as well as nucleic acids homologous, substantially similar, or substantially identical (e.g., having about 90% sequence identity) to the disclosed polynucleotides.

Methods of the subject invention useful in diagnosis or prognosis typically involve comparison of the abundance of a selected differentially expressed gene product in a sample of interest with that of a control to determine any relative differences in the expression of the gene product, where the difference can be measured qualitatively and/or quantitatively. Quantitation can be accomplished, for example, by comparing the level of expression product detected in the sample with the amounts of product present in a standard curve. A comparison can be made visually; by using a technique such as densitometry, with or without computerized assistance; by preparing a representative library of cDNA clones of mRNA isolated from a test sample, sequencing the clones in the library to determine that number of cDNA clones corresponding to the same gene product, and analyzing the number of clones corresponding to that same gene product relative to the number of clones of the same gene product in a control sample; or by using an array to detect relative levels of hybridization to a selected sequence or set of sequences, and comparing the hybridization pattern to that of a control. The differences in expression are then correlated with the presence or absence of an abnormal expression pattern. A variety of different methods for determining the nucleic acid abundance in a sample are known to those of skill in the art (see, e.g., WO 97/27317).

In general, diagnostic assays of the invention involve detection of a gene product of a polynucleotide sequence (e.g., mRNA or polypeptide) that corresponds to a sequence of SEQ ID NOS:1-6010. The patient from whom the sample is obtained can be apparently healthy, susceptible to disease (e.g., as determined by family history or exposure to certain environmental factors), or can

already be identified as having a condition in which altered expression of a gene product of the invention is implicated.

Diagnosis can be determined based on detected gene product expression levels of a gene product encoded by at least one, preferably at least two or more, at least 3 or more, or at least 4 or more of the polynucleotides having a sequence set forth in SEQ ID NOS:1-6010, and can involve detection of expression of genes corresponding to all of SEQ ID NOS:1-6010 and/or additional sequences that can serve as additional diagnostic markers and/or reference sequences. Where the diagnostic method is designed to detect the presence or susceptibility of a patient to cancer, the assay preferably involves detection of a gene product encoded by a gene corresponding to a polynucleotide that is differentially expressed in cancer. Examples of such differentially expressed polynucleotides are described in the Examples below. Given the provided polynucleotides and information regarding their relative expression levels provided herein, assays using such polynucleotides and detection of their expression levels in diagnosis and prognosis will be readily apparent to the ordinarily skilled artisan.

Any of a variety of detectable labels can be used in connection with the various embodiments of the diagnostic methods of the invention. Suitable detectable labels include fluorochromes,(e.g. fluorescein isothiocyanate (FITC), rhodamine, Texas Red, phycoerythrin, allophycocyanin, 6-carboxyfluorescein (6-FAM), 2',7'-dimethoxy-4',5'-dichloro-6-carboxyfluorescein, 6-carboxy-X-rhodamine (ROX), 6-carboxy-2',4',7',4,7-hexachlorofluorescein (HEX), 5-carboxyfluorescein (5-FAM) or N,N,N',N'-tetramethyl-6-carboxyrhodamine (TAMRA)), radioactive labels, (e.g. 32P, 35S, 3H, etc.), and the like. The detectable label can involve a two stage systems (e.g., biotin-avidin, hapten-anti-hapten antibody, etc.).

Reagents specific for the polynucleotides and polypeptides of the invention, such as antibodies and nucleotide probes, can be supplied in a kit for detecting the presence of an expression product in a biological sample. The kit can also contain buffers or labeling components, as well as instructions for using the reagents to detect and quantify expression products in the biological sample. Exemplary embodiments of the diagnostic methods of the invention are described below in more detail.

Polypeptide detection in diagnosis. In one embodiment, the test sample is assayed for the level of a differentially expressed polypeptide. Diagnosis can be accomplished using any of a number of methods to determine the absence or presence or altered amounts of the differentially expressed polypeptide in the test sample. For example, detection can utilize staining of cells or histological sections with labeled antibodies, performed in accordance with conventional methods. Cells can be permeabilized to stain cytoplasmic molecules. In general, antibodies that specifically bind a differentially expressed polypeptide of the invention are added to a sample, and incubated for a period of time sufficient to allow binding to the epitope, usually at least about 10 minutes. The antibody can

be detectably labeled for direct detection (e.g., using radioisotopes, enzymes, fluorescers, chemiluminescers, and the like), or can be used in conjunction with a second stage antibody or reagent to detect binding (e.g., biotin with horseradish peroxidase-conjugated avidin, a secondary antibody conjugated to a fluorescent compound, e.g. fluorescein, rhodamine, Texas red, etc.). The absence or presence of antibody binding can be determined by various methods, including flow cytometry of dissociated cells, microscopy, radiography, scintillation counting, etc. Any suitable alternative methods of qualitative or quantitative detection of levels or amounts of differentially expressed polypeptide can be used, for example, ELISA, western blot, immunoprecipitation, radioimmunoassay, etc.

mRNA detection. The diagnostic methods of the invention can also or alternatively involve detection of mRNA encoded by a gene corresponding to a differentially expressed polynucleotide of the invention. Any suitable qualitative or quantitative methods known in the art for detecting specific mRNAs can be used. mRNA can be detected by, for example, in situ hybridization in tissue sections, by reverse transcriptase-PCR, or in Northern blots containing poly A+ mRNA. One of skill in the art can readily use these methods to determine differences in the size or amount of mRNA transcripts between two samples. mRNA expression levels in a sample can also be determined by generation of a library of expressed sequence tags (ESTs) from the sample, where the EST library is representative of sequences present in the sample (Adams, et al., (1991) Science 252:1651). Enumeration of the relative representation of ESTs within the library can be used to approximate the relative representation of the gene transcript within the starting sample. The results of EST analysis of a test sample can then be compared to EST analysis of a reference sample to determine the relative expression levels of a selected polynucleotide, particularly a polynucleotide corresponding to one or more of the differentially expressed genes described herein. Alternatively, gene expression in a test sample can be performed using serial analysis of gene expression (SAGE) methodology (e.g., Velculescu et al., Science (1995) 270:484) or differential display (DD) methodology (see, e.g., USPN 5,776,683 and USPN 5,807,680).

Alternatively, gene expression can be analyzed using hybridization analysis. Oligonucleotides or cDNA can be used to selectively identify or capture DNA or RNA of specific sequence composition, and the amount of RNA or cDNA hybridized to a known capture sequence determined qualitatively or quantitatively, to provide information about the relative representation of a particular message within the pool of cellular messages in a sample. Hybridization analysis can be designed to allow for concurrent screening of the relative expression of hundreds to thousands of genes by using, for example, array-based technologies having high density formats, including filters, microscope slides, or microchips, or solution-based technologies that use spectroscopic analysis (e.g., mass spectrometry).

One exemplary use of arrays in the diagnostic methods of the invention is described below in more detail.

Use of a single gene in diagnostic applications. The diagnostic methods of the invention can focus on the expression of a single differentially expressed gene. For example, the diagnostic method can involve detecting a differentially expressed gene, or a polymorphism of such a gene (e.g., a polymorphism in a coding region or control region), that is associated with disease. Disease-associated polymorphisms can include deletion or truncation of the gene, mutations that alter expression level and/or affect activity of the encoded protein, etc.

A number of methods are available for analyzing nucleic acids for the presence of a specific sequence, e.g. a disease associated polymorphism. Where large amounts of DNA are available, genomic DNA is used directly. Alternatively, the region of interest is cloned into a suitable vector and grown in sufficient quantity for analysis. Cells that express a differentially expressed gene can be used as a source of mRNA, which can be assayed directly or reverse transcribed into cDNA for analysis. The nucleic acid can be amplified by conventional techniques, such as the polymerase chain reaction (PCR), to provide sufficient amounts for analysis, and a detectable label can be included in the amplification reaction (e.g., using a detectably labeled primer or detectably labeled oligonucleotides) to facilitate detection. Alternatively, various methods are also known in the art that utilize oligonucleotide ligation as a means of detecting polymorphisms, see, e.g., Riley et al., Nucl. Acids Res. (1990) 18:2887; and Delahunty et al., Am. J. Hum. Genet. (1996) 58:1239.

The amplified or cloned sample nucleic acid can be analyzed by one of a number of methods known in the art. The nucleic acid can be sequenced by dideoxy or other methods, and the sequence of bases compared to a selected sequence, e.g., to a wild-type sequence. Hybridization with the polymorphic or variant sequence can also be used to determine its presence in a sample (e.g., by Southern blot, dot blot, etc.). The hybridization pattern of a polymorphic or variant sequence and a control sequence to an array of oligonucleotide probes immobilized on a solid support, as described in US 5,445,934, or in WO 95/35505, can also be used as a means of identifying polymorphic or variant sequences associated with disease. Single strand conformational polymorphism (SSCP) analysis, denaturing gradient gel electrophoresis (DGGE), and heteroduplex analysis in gel matrices are used to detect conformational changes created by DNA sequence variation as alterations in electrophoretic mobility. Alternatively, where a polymorphism creates or destroys a recognition site for a restriction endonuclease, the sample is digested with that endonuclease, and the products size fractionated to determine whether the fragment was digested. Fractionation is performed by gel or capillary electrophoresis, particularly acrylamide or agarose gels.

Screening for mutations in a gene can be based on the functional or antigenic characteristics of the protein. Protein truncation assays are useful in detecting deletions that can affect the biological activity of the protein. Various immunoassays designed to detect polymorphisms in proteins can be used in screening. Where many diverse genetic mutations lead to a particular disease phenotype, functional protein assays have proven to be effective screening tools. The activity of the encoded protein can be determined by comparison with the wild-type protein.

Diagnosis, Prognosis, Assessment of Therapy (Therametrics), and Management of Cancer

The polynucleotides of the invention, as well as their gene products, are of particular interest as genetic or biochemical markers (e.g., in blood or tissues) that will detect the earliest changes along the carcinogenesis pathway and/or to monitor the efficacy of various therapies and preventive interventions. For example, the level of expression of certain polynucleotides can be indicative of a poorer prognosis, and therefore warrant more aggressive chemo- or radio-therapy for a patient or vice versa. The correlation of novel surrogate tumor specific features with response to treatment and outcome in patients can define prognostic indicators that allow the design of tailored therapy based on the molecular profile of the tumor. These therapies include antibody targeting, antagonists (e.g., small molecules), and gene therapy. Determining expression of certain polynucleotides and comparison of a patient's profile with known expression in normal tissue and variants of the disease allows a determination of the best possible treatment for a patient, both in terms of specificity of treatment and in terms of comfort level of the patient. Surrogate tumor markers, such as polynucleotide expression, can also be used to better classify, and thus diagnose and treat, different forms and disease states of cancer. Two classifications widely used in oncology that can benefit from identification of the expression levels of the genes corresponding to the polynucleotides of the invention are staging of the cancerous disorder, and grading the nature of the cancerous tissue.

The polynucleotides that correspond to differentially expressed genes, as well as their encoded gene products, can be useful to monitor patients having or susceptible to cancer to detect potentially malignant events at a molecular level before they are detectable at a gross morphological level. In addition, the polynucleotides of the invention, as well as the genes corresponding to such polynucleotides, can be useful as therametrics, e.g., to assess the effectiveness of therapy by using the polynucleotides or their encoded gene products, to assess, for example, tumor burden in the patient before, during, and after therapy.

Furthermore, a polynucleotide identified as corresponding to a gene that is differentially expressed in, and thus is important for, one type of cancer can also have implications for development or risk of development of other types of cancer, e.g., where a polynucleotide represents a gene differentially expressed across various cancer types. Thus, for example, expression of a polynucleotide

corresponding to a gene that has clinical implications for metastatic colon cancer can also have clinical implications for stomach cancer or endometrial cancer.

Staging. Staging is a process used by physicians to describe how advanced the cancerous state is in a patient. Staging assists the physician in determining a prognosis, planning treatment and evaluating the results of such treatment. Staging systems vary with the types of cancer, but generally involve the following "TNM" system: the type of tumor, indicated by T; whether the cancer has metastasized to nearby lymph nodes, indicated by N; and whether the cancer has metastasized to more distant parts of the body, indicated by M. Generally, if a cancer is only detectable in the area of the primary lesion without having spread to any lymph nodes it is called Stage I. If it has spread only to the closest lymph nodes, it is called Stage II. In Stage III, the cancer has generally spread to the lymph nodes in near proximity to the site of the primary lesion. Cancers that have spread to a distant part of the body, such as the liver, bone, brain or other site, are Stage IV, the most advanced stage.

The polynucleotides of the invention can facilitate fine-tuning of the staging process by identifying markers for the aggresivity of a cancer, e.g., the metastatic potential, as well as the presence in different areas of the body. Thus, a Stage II cancer with a polynucleotide signifying a high metastatic potential cancer can be used to change a borderline Stage II tumor to a Stage III tumor, justifying more aggressive therapy. Conversely, the presence of a polynucleotide signifying a lower metastatic potential allows more conservative staging of a tumor.

Grading of cancers. Grade is a term used to describe how closely a tumor resembles normal tissue of its same type. The microscopic appearance of a tumor is used to identify tumor grade based on parameters such as cell morphology, cellular organization, and other markers of differentiation. As a general rule, the grade of a tumor corresponds to its rate of growth or aggressiveness, with undifferentiated or high-grade tumors being more aggressive than well-differentiated or low-grade tumors. The following guidelines are generally used for grading tumors: 1) GX Grade cannot be assessed; 2) G1 Well differentiated; 3) G2 Moderately well differentiated; 4) G3 Poorly differentiated; 5) G4 Undifferentiated. The polynucleotides of the invention can be especially valuable in determining the grade of the tumor, as they not only can aid in determining the differentiation status of the cells of a tumor, they can also identify factors other than differentiation that are valuable in determining the aggressiveness of a tumor, such as metastatic potential.

Detection of colon cancer. The polynucleotides corresponding to genes that exhibit the appropriate expression pattern can be used to detect colon cancer in a subject. Colorectal cancer is one of the most common neoplasms in humans and perhaps the most frequent form of hereditary neoplasia. Prevention and early detection are key factors in controlling and curing colorectal cancer. Colorectal cancer begins as polyps, which are small, benign growths of cells that form on the inner lining of the

colon. Over a period of several years, some of these polyps accumulate additional mutations and become cancerous. Multiple familial colorectal cancer disorders have been identified, which are summarized as follows: 1) Familial adenomatous polyposis (FAP); 2) Gardner's syndrome; 3) Hereditary nonpolyposis colon cancer (HNPCC); and 4) Familial colorectal cancer in Ashkenazi Jews. The expression of appropriate polynucleotides of the invention can be used in the diagnosis, prognosis and management of colorectal cancer. Detection of colon cancer can be determined using expression levels of any of these sequences alone or in combination with the levels of expression. Determination of the aggressive nature and/or the metastatic potential of a colon cancer can be determined by comparing levels of one or more polynucleotides of the invention and comparing total levels of another sequence known to vary in cancerous tissue, e.g., expression of p53, DCC ras, lor FAP (see, e.g., Fearon ER, et al., Cell (1990) 61(5):759; Hamilton SR et al., Cancer (1993) 72:957; Bodmer W, et al., Nat Genet. (1994) 4(3):217; Fearon ER, Ann N Y Acad Sci. (1995) 768:101). For example, development of colon cancer can be detected by examining the ratio of any of the polynucleotides of the invention to the levels of oncogenes (e.g., ras) or tumor suppressor genes (e.g., FAP or p53). Thus, expression of specific marker polynucleotides can be used to discriminate between normal and cancerous colon tissue, to discriminate between colon cancers with different cells of origin, to discriminate between colon cancers with different potential metastatic rates, etc. For a review of markers of cancer, see, e.g., Hanahan et al. (2000) Cell 100:57-70.

Detection of prostate cancer. The polynucleotides and their corresponding genes and gene products exhibiting the appropriate differential expression pattern can be used to detect prostate cancer in a subject. Over 95% of primary prostate cancers are adenocarcinomas. Signs and symptoms may include: frequent urination, especially at night; inability to urinate; trouble starting or holding back urination; a weak or interrupted urine flow; and frequent pain or stiffness in the lower back, hips or upper thighs.

Many of the signs and symptoms of prostate cancer can be caused by a variety of other non-cancerous conditions. For example, one common cause of many of these signs and symptoms is a condition called benign prostatic hypertrophy, or BPH. In BPH, the prostate gets bigger and may block the flow of urine or interfere with sexual function. The methods and compositions of the invention can be used to distinguish between prostate cancer and such non-cancerous conditions. The methods of the invention can be used in conjunction with conventional methods of diagnosis, e.g., digital rectal exam and/or detection of the level of prostate specific antigen (PSA), a substance produced and secreted by the prostate.

Detection of breast cancer. The majority of breast cancers are adenocarcinoma subtypes, which can be summarized as follows: 1) ductal carcinoma in situ (DCIS), including comedocarcinoma;

2) infiltrating (or invasive) ductal carcinoma (IDC); 3) lobular carcinoma in situ (LCIS); 4) infiltrating (or invasive) lobular carcinoma (ILC); 5) inflammatory breast cancer; 6) medullary carcinoma; 7) mucinous carcinoma; 8) Paget's disease of the nipple; 9) Phyllodes tumor; and 10) tubular carcinoma;

The expression of polynucleotides of the invention can be used in the diagnosis and management of breast cancer, as well as to distinguish between types of breast cancer. Detection of breast cancer can be determined using expression levels of any of the appropriate polynucleotides of the invention, either alone or in combination. Determination of the aggressive nature and/or the metastatic potential of a breast cancer can also be determined by comparing levels of one or more polynucleotides of the invention and comparing levels of another sequence known to vary in cancerous tissue, e.g., ER expression. In addition, development of breast cancer can be detected by examining the ratio of expression of a differentially expressed polynucleotide to the levels of steroid hormones (e.g., testosterone or estrogen) or to other hormones (e.g., growth hormone, insulin). Thus, expression of specific marker polynucleotides can be used to discriminate between normal and cancerous breast tissue, to discriminate between breast cancers with different cells of origin, to discriminate between breast cancers with different potential metastatic rates, etc.

Detection of lung cancer. The polynucleotides of the invention can be used to detect lung cancer in a subject. Although there are more than a dozen different kinds of lung cancer, the two main types of lung cancer are small cell and nonsmall cell, which encompass about 90% of all lung cancer cases. Small cell carcinoma (also called oat cell carcinoma) usually starts in one of the larger bronchial tubes, grows fairly rapidly, and is likely to be large by the time of diagnosis. Nonsmall cell lung cancer (NSCLC) is made up of three general subtypes of lung cancer. Epidermoid carcinoma (also called squamous cell carcinoma) usually starts in one of the larger bronchial tubes and grows relatively slowly. The size of these tumors can range from very small to quite large. Adenocarcinoma starts growing near the outside surface of the lung and can vary in both size and growth rate. Some slowly growing adenocarcinomas are described as alveolar cell cancer. Large cell carcinoma starts near the surface of the lung, grows rapidly, and the growth is usually fairly large when diagnosed. Other less common forms of lung cancer are carcinoid, cylindroma, mucoepidermoid, and malignant mesothelioma.

The polynucleotides of the invention, e.g., polynucleotides differentially expressed in normal cells versus cancerous lung cells (e.g., tumor cells of high or low metastatic potential) or between types of cancerous lung cells (e.g., high metastatic versus low metastatic), can be used to distinguish types of lung cancer as well as identifying traits specific to a certain patient's cancer and selecting an appropriate therapy. For example, if the patient's biopsy expresses a polynucleotide that is associated with a low metastatic potential, it may justify leaving a larger portion of the patient's lung in surgery to

remove the lesion. Alternatively, a smaller lesion with expression of a polynucleotide that is associated with high metastatic potential may justify a more radical removal of lung tissue and/or the surrounding lymph nodes, even if no metastasis can be identified through pathological examination.

Use of Polynucleotides to Screen for Peptide Analogs and Antagonists

Polypeptides encoded by the instant polynucleotides and corresponding full-length genes can be used to screen peptide libraries to identify binding partners, such as receptors, from among the encoded polypeptides. Peptide libraries can be synthesized according to methods known in the art (see, e.g., USPN 5,010,175 , and WO 91/17823). Agonists or antagonists of the polypeptides of the invention can be screened using any available method known in the art, such as signal transduction, antibody binding, receptor binding, mitogenic assays, chemotaxis assays, etc. The assay conditions ideally should resemble the conditions under which the native activity is exhibited in vivo, that is, under physiologic pH, temperature, and ionic strength. Suitable agonists or antagonists will exhibit strong inhibition or enhancement of the native activity at concentrations that do not cause toxic side effects in the subject. Agonists or antagonists that compete for binding to the native polypeptide can require concentrations equal to or greater than the native concentration, while inhibitors capable of binding irreversibly to the polypeptide can be added in concentrations on the order of the native concentration.

Such screening and experimentation can lead to identification of a novel polypeptide binding partner, such as a receptor, encoded by a gene or a cDNA corresponding to a polynucleotide of the invention, and at least one peptide agonist or antagonist of the novel binding partner. Such agonists and antagonists can be used to modulate, enhance, or inhibit receptor function in cells to which the receptor is native, or in cells that possess the receptor as a result of genetic engineering. Further, if the novel receptor shares biologically important characteristics with a known receptor, information about agonist/antagonist binding can facilitate development of improved agonists/antagonists of the known receptor.

Pharmaceutical Compositions and Uses

Pharmaceutical compositions can comprise polypeptides, receptors that specifically bind a polypeptide produced by a differentially expressed gene (e.g., antibodies, or polynucleotides (including antisense nucleotides and ribozymes) of the claimed invention in a therapeutically effective amount. The compositions can be used to treat primary tumors as well as metastases of primary tumors. In addition, the pharmaceutical compositions can be used in conjunction with conventional methods of cancer treatment, e.g., to sensitize tumors to radiation or conventional chemotherapy.

Where the pharmaceutical composition comprises a receptor (such as an antibody) that specifically binds to a gene product encoded by a differentially expressed gene, the receptor can be coupled to a drug for delivery to a treatment site or coupled to a detectable label to facilitate imaging of

a site comprising colon cancer cells. Methods for coupling antibodies to drugs and detectable labels are well known in the art, as are methods for imaging using detectable labels.

The term "therapeutically effective amount" as used herein refers to an amount of a therapeutic agent to treat, ameliorate, or prevent a desired disease or condition, or to exhibit a detectable therapeutic or preventative effect. The effect can be detected by, for example, chemical markers or antigen levels. Therapeutic effects also include reduction in physical symptoms, such as decreased body temperature. The precise effective amount for a subject will depend upon the subject's size and health, the nature and extent of the condition, and the therapeutics or combination of therapeutics selected for administration. Thus, it is not useful to specify an exact effective amount in advance. However, the effective amount for a given situation is determined by routine experimentation and is within the judgment of the clinician. For purposes of the present invention, an effective dose will generally be from about 0.01 mg/kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

A pharmaceutical composition can also contain a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable carrier" refers to a carrier for administration of a therapeutic agent, such as antibodies or a polypeptide, genes, and other therapeutic agents. The term refers to any pharmaceutical carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition, and which can be administered without undue toxicity. Suitable carriers can be large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, and inactive virus particles. Such carriers are well known to those of ordinary skill in the art. Pharmaceutically acceptable carriers in therapeutic compositions can include liquids such as water, saline, glycerol and ethanol. Auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, can also be present in such vehicles. Typically, the therapeutic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection can also be prepared. Liposomes are included within the definition of a pharmaceutically acceptable carrier. Pharmaceutically acceptable salts can also be present in the pharmaceutical composition, e.g., mineral acid salts such as hydrochlorides, hydrobromides, phosphates, sulfates, and the like; and the salts of organic acids such as acetates, propionates, malonates, benzoates, and the like. A thorough discussion of pharmaceutically acceptable excipients is available in Remington's Pharmaceutical Sciences (Mack Pub. Co., N.J. 1991).

Delivery Methods

Once formulated, the compositions of the invention can be (1) administered directly to the subject (e.g., as polynucleotide or polypeptides); or (2) delivered ex vivo, to cells derived from the

subject (e.g., as in ex vivo gene therapy). Direct delivery of the compositions will generally be accomplished by parenteral injection, e.g., subcutaneously, intraperitoneally, intravenously or intramuscularly, intratumorally or to the interstitial space of a tissue. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal applications, needles, and gene guns or hyposprays. Dosage treatment can be a single dose schedule or a multiple dose schedule.

Methods for the ex vivo delivery and reimplantation of transformed cells into a subject are known in the art and described in, e.g., WO 93/14778. Examples of cells useful in ex vivo applications include, for example, stem cells, particularly hematopoetic, lymph cells, macrophages, dendritic cells, or tumor cells. Generally, delivery of nucleic acids for both ex vivo and in vitro applications can be accomplished by, for example, dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei, all well known in the art.

Once differential expression of a gene corresponding to a polynucleotide of the invention has been found to correlate with a proliferative disorder, such as neoplasia, dysplasia, and hyperplasia, the disorder can be amenable to treatment by administration of a therapeutic agent based on the provided polynucleotide, corresponding polypeptide or other corresponding molecule (e.g., antisense, ribozyme, etc.). In other embodiments, the disorder can be amenable to treatment by administration of a small molecule drug that, for example, serves as an inhibitor (antagonist) of the function of the encoded gene product of a gene having increased expression in cancerous cells relative to normal cells or as an agonist for gene products that are decreased in expression in cancerous cells (e.g., to promote the activity of gene products that act as tumor suppressors).

The dose and the means of administration of the inventive pharmaceutical compositions are determined based on the specific qualities of the therapeutic composition, the condition, age, and weight of the patient, the progression of the disease, and other relevant factors. For example, administration of polynucleotide therapeutic composition agents of the invention includes local or systemic administration, including injection, oral administration, particle gun or catheterized administration, and topical administration. Preferably, the therapeutic polynucleotide composition contains an expression construct comprising a promoter operably linked to a polynucleotide of at least 12, 22, 25, 30, or 35 contiguous nt of the polynucleotide of the invention. Various methods can be used to administer the therapeutic composition directly to a specific site in the body. For example, a small metastatic lesion is located and the therapeutic composition injected several times in several different locations within the body of tumor. Alternatively, arteries that serve a tumor are identified, and the therapeutic composition injected into such an artery, in order to deliver the composition directly into

the tumor. A tumor that has a necrotic center is aspirated and the composition injected directly into the now empty center of the tumor. The antisense composition is directly administered to the surface of the tumor, for example, by topical application of the composition. X-ray imaging is used to assist in certain of the above delivery methods.

Targeted delivery of therapeutic compositions containing an antisense polynucleotide, subgenomic polynucleotides, or antibodies to specific tissues can also be used. Receptor-mediated DNA delivery techniques are described in, for example, Findeis et al., Trends Biotechnol. (1993) 11:202; Chiou et al., Gene Therapeutics: Methods And Applications Of Direct Gene Transfer (J.A. Wolff, ed.) (1994); Wu et al., J. Biol. Chem. (1988) 263:621; Wu et al., J. Biol. Chem. (1994) 269:542; Zenke et al., Proc. Natl. Acad. Sci. (USA) (1990) 87:3655; Wu et al., J. Biol. Chem. (1991) 266:338. Therapeutic compositions containing a polynucleotide are administered in a range of about 100 ng to about 200 mg of DNA for local administration in a gene therapy protocol. Concentration ranges of about 500 ng to about 50 mg, about 1 micrograms to about 2 mg, about 5 micrograms to about 500 micrograms, and about 20 micrograms to about 100 micrograms of DNA can also be used during a gene therapy protocol. Factors such as method of action (e.g., for enhancing or inhibiting levels of the encoded gene product) and efficacy of transformation and expression are considerations which will affect the dosage required for ultimate efficacy of the antisense subgenomic polynucleotides. Where greater expression is desired over a larger area of tissue, larger amounts of antisense subgenomic polynucleotides or the same amounts readministered in a successive protocol of administrations, or several administrations to different adjacent or close tissue portions of, for example, a tumor site, may be required to effect a positive therapeutic outcome. In all cases, routine experimentation in clinical trials will determine specific ranges for optimal therapeutic effect. For polynucleotide related genes encoding polypeptides or proteins with anti-inflammatory activity, suitable use, doses, and administration are described in USPN 5,654,173.

The therapeutic polynucleotides and polypeptides of the present invention can be delivered using gene delivery vehicles. The gene delivery vehicle can be of viral or non-viral origin (see generally, Jolly, Cancer Gene Therapy (1994) 1:51; Kimura, Human Gene Therapy (1994) 5:845; Connelly, Human Gene Therapy (1995) 1:185; and Kaplitt, Nature Genetics (1994) 6:148). Expression of such coding sequences can be induced using endogenous mammalian or heterologous promoters. Expression of the coding sequence can be either constitutive or regulated.

Viral-based vectors for delivery of a desired polynucleotide and expression in a desired cell are well known in the art. Exemplary viral-based vehicles include, but are not limited to, recombinant retroviruses (see, e.g., WO 90/07936; WO 94/03622; WO 93/25698; WO 93/25234; USPN 5, 219,740; WO 93/11230; WO 93/10218; USPN 4,777,127; GB Patent No. 2,200,651; EP 0 345 242;

and WO 91/02805), alphavirus-based vectors (e.g., Sindbis virus vectors, Semliki forest virus (ATCC VR-67; ATCC VR-1247), Ross River virus (ATCC VR-373; ATCC VR-1246) and Venezuelan equine encephalitis virus (ATCC VR-923; ATCC VR-1250; ATCC VR 1249; ATCC VR-532), and adeno-associated virus (AAV) vectors (see, e.g., WO 94/12649, WO 93/03769; WO 93/19191; WO 94/28938; WO 95/11984 and WO 95/00655). Administration of DNA linked to killed adenovirus, as described in Curiel, Hum. Gene Ther. (1992) 3:147, can also be employed.

Non-viral delivery vehicles and methods can also be employed, including, but not limited to, polycationic condensed DNA linked or unlinked to killed adenovirus alone (see, e.g., Curiel, Hum. Gene Ther. (1992) 3:147); ligand-linked DNA (see, e.g., Wu, J. Biol. Chem. (1989) 264:16985); eukaryotic cell delivery vehicles cells (see, e.g., USPN 5,814,482; WO 95/07994; WO 96/17072; WO 95/30763; and WO 97/42338) and nucleic charge neutralization or fusion with cell membranes. Naked DNA can also be employed. Exemplary naked DNA introduction methods are described in WO 90/11092 and USPN 5,580,859. Liposomes that can act as gene delivery vehicles are described in USPN 5,422,120; WO 95/13796; WO 94/23697; WO 91/14445; and EP 0524968. Additional approaches are described in Philip, Mol. Cell Biol. (1994) 14:2411, and in Woffendin, Proc. Natl. Acad. Sci. (1994) 91:1581

Further non-viral delivery suitable for use includes mechanical delivery systems such as the approach described in Woffendin et al., Proc. Natl. Acad. Sci. USA (1994) 91(24):11581. Moreover, the coding sequence and the product of expression of such can be delivered through deposition of photopolymerized hydrogel materials or use of ionizing radiation (see, e.g., USPN 5,206,152 and WO 92/11033). Other conventional methods for gene delivery that can be used for delivery of the coding sequence include, for example, use of hand-held gene transfer particle gun (see, e.g., USPN 5,149,655); use of ionizing radiation for activating transferred gene (see, e.g., USPN 5,206,152 and WO 92/11033).

The present invention will now be illustrated by reference to the following examples which set forth particularly advantageous embodiments. However, it should be noted that these embodiments are illustrative and are not to be construed as restricting the invention in any way.

EXAMPLES

The following examples are put forth so as to provide those of ordinary skill in the art with a complete disclosure and description of how to make and use the present invention, and are not intended to limit the scope of what the inventors regard as their invention nor are they intended to represent that the experiments below are all or the only experiments performed. It will be readily apparent to those skilled in the art that the formulations, dosages, methods of administration, and other parameters of

this invention may be further modified or substituted in various ways without departing from the spirit and scope of the invention. Efforts have been made to ensure accuracy with respect to numbers used (e.g. amounts, temperature, etc.) but some experimental errors and deviations should be accounted for. Unless indicated otherwise, parts are parts by weight, molecular weight is weight average molecular weight, temperature is in degrees Centigrade, and pressure is at or near atmospheric.

Example 1:Source of Biological Materials and Overview of Novel Polynucleotides Expressed by the Biological Materials

Candidate polynucleotides that may represent novel polynucleotides were obtained from cDNA libraries generated from selected cell lines and patient tissues. In order to obtain the candidate polynucleotides, mRNA was isolated from several selected cell lines and patient tissues, and used to construct cDNA libraries. The cells and tissues that served as sources for these cDNA libraries are summarized in Table 1 below.

Human colon cancer cell line Km12L4-A (Morikawa, et al., Cancer Research (1988) 48:6863) is derived from the KM12C cell line. The KM12C cell line (Morikawa et al. Cancer Res. (1988) 48:1943-1948), which is poorly metastatic (low metastatic) was established in culture from a Dukes' stage B2 surgical specimen (Morikawa et al. Cancer Res. (1988) 48:6863). The KM12L4-A is a highly metastatic subline derived from KM12C (Yeatman et al. Nucl. Acids. Res. (1995) 23:4007; Bao-Ling et al. Proc. Annu. Meet. Am. Assoc. Cancer. Res. (1995) 21:3269). The KM12C and KM12C-derived cell lines (e.g., KM12L4, KM12L4-A, etc.) are well-recognized in the art as a model cell line for the study of colon cancer (see, e.g., Moriakawa et al., supra; Radinsky et al. Clin. Cancer Res. (1995) 1:19; Yeatman et al., (1995) supra; Yeatman et al. Clin. Exp. Metastasis (1996) 14:246).

The MDA-MB-231 cell line (Brinkley et al. Cancer Res. (1980) 40:3118-3129) was originally isolated from pleural effusions (Cailleau, J. Natl. Cancer. Inst. (1974) 53:661), is of high metastatic potential, and forms poorly differentiated adenocarcinoma grade II in nude mice consistent with breast carcinoma. The MCF7 cell line was derived from a pleural effusion of a breast adenocarcinoma and is non-metastatic. The MV-522 cell line is derived from a human lung carcinoma and is of high metastatic potential. The UCP-3 cell line is a low metastatic human lung carcinoma cell line; the MV-522 is a high metastatic variant of UCP-3. These cell lines are well-recognized in the art as models for the study of human breast and lung cancer (see, e.g., Chandrasekaran et al., Cancer Res. (1979) 39:870 (MDA-MB-231 and MCF-7); Gastpar et al., J Med Chem (1998) 41:4965 (MDA-MB-231 and MCF-7); Ranson et al., Br J Cancer (1998) 77:1586 (MDA-MB-231 and MCF-7); Kuang et al., Nucleic Acids Res (1998) 26:1116 (MDA-MB-231 and MCF-7); Varki et al., Int J Cancer (1987) 40:46 (UCP-3); Varki et al., Tumour Biol. (1990) 11:327; (MV-522 and UCP-3); Varki et al., Anticancer

Res. (1990) 10:637; (MV-522); Kelner et al., Anticancer Res (1995) 15:867 (MV-522); and Zhang et al., Anticancer Drugs (1997) 8:696 (MV522)).

The samples of libraries 15-20 are derived from two different patients (UC#2, and UC#3). The bFGF-treated HMVEC were prepared by incubation with bFGF at 10ng/ml for 2 hrs; the VEGF-treated HMVEC were prepared by incubation with 20ng/ml VEGF for 2 hrs. Following incubation with the respective growth factor, the cells were washed and lysis buffer added for RNA preparation. The GRRpz and WOca cell lines were provided by Dr. Donna M. Peehl, Department of Medicine, Stanford University School of Medicine. GRRpz was derived from normal prostate epithelium. The WOca cell line is a Gleason Grade 4 cell line.

Table 1. Description of cDNA Libraries

Library (lib #)	Description	Number of Clones in Library
0	Artificial library composed of deselected clones (clones with no associated variant or cluster)	673
1	Human Colon Cell Line Km12 L4: High Metastatic Potential (derived from Km12C)	308731
2	Human Colon Cell Line Km12C: Low Metastatic Potential	284771
3	Human Breast Cancer Cell Line MDA-MB-231: High Metastatic Potential; micro-mets in lung	326937
4	Human Breast Cancer Cell Line MCF7: Non Metastatic	318979
8	Human Lung Cancer Cell Line MV-522: High Metastatic Potential	223620
9	Human Lung Cancer Cell Line UCP-3: Low Metastatic Potential	312503
12	Human microvascular endothelial cells (HMEC) - UNTREATED (PCR (OligodT) cDNA library)	41938
13	Human microvascular endothelial cells (HMEC) - bFGF TREATED (PCR (OligodT) cDNA library)	42100
14	Human microvascular endothelial cells (HMEC) - VEGF TREATED (PCR (OligodT) cDNA library)	42825
15	Normal Colon - UC#2 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	282722
16	Colon Tumor - UC#2 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	298831
17	Liver Metastasis from Colon Tumor of UC#2 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	303467
18	Normal Colon - UC#3 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	36216
19	Colon Tumor - UC#3 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	41388
20	Liver Metastasis from Colon Tumor of UC#3 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	30956
21	GRRpz Cells derived from normal prostate epithelium	164801
22	WOca Cells derived from Gleason Grade 4 prostate cancer epithelium	162088
23	Normal Lung Epithelium of Patient #1006 (MICRODISSECTED PCR (OligodT) cDNA library)	306198

Library (lib #)	Description	Number of Clones in Library
24	Primary tumor, Large Cell Carcinoma of Patient #1006 (MICRODISSECTED PCR (OligodT) cDNA library)	309349
25	Normal Prostate Epithelium from Patient IF97-26811	279444
26	Prostate Cancer Epithelium Gleason 3+3 Patient IF97-26811	269406
27	Normal Breast Epithelium from Patient 515	239494
28	Primary Breast tumor from Patient 515	259960
29	Lymph node metastasis from Patient 515	326786
30	Normal Prostate Epithelium from Chiron Patient ID 884	298431
31	Prostate Cancer Epithelium (Gleason 4+4) from Chiron Patient ID 884	331941

Characterization of sequences in the libraries

After using the software program Phred (ver 0.000925.c, Green and Weing,, ©1993-2000) to select those polynucleotides having the best quality sequence, the polyncueltoides were compared against the public databases to identify any homolgous sequences. The sequences of the isolated polynucleotides were first masked to eliminate low complexity sequences using the BLASTX masking program (Claverie "Effective Large-Scale Sequence Similarity Searches," In: Computer Methods for Macromolecular Sequence Analysis, Doolittle, ed., Meth. Enzymol. 266:212-227 Academic Press, NY, NY (1996); see particularly Claverie, in "Automated DNA Sequencing and Analysis Techniques" Adams et al., eds., Chap. 36, p. 267 Academic Press, San Diego, 1994 and Claverie et al. Comput. Chem. (1993) 17:191). Generally, masking does not influence the final search results, except to eliminate sequences of relatively little interest due to their low complexity, and to eliminate multiple "hits" based on similarity to repetitive regions common to multiple sequences, e.g., Alu repeats. The remaining sequences were then used in a BLASTN vs. GenBank search; sequences that exhibited greater than 70% overlap, 99% identity, and a p value of less than 1 x 10e-40 were discarded. Sequences from this search also were discarded if the inclusive parameters were met, but the sequence was ribosomal or vector-derived.

The resulting sequences from the previous search were classified into three groups (1, 2 and 3 below) and searched in a BLASTX vs. NRP (non-redundant proteins) database search: (1) unknown (no hits in the GenBank search), (2) weak similarity (greater than 45% identity and p value of less than 1 x 10e-5), and (3) high similarity (greater than 60% overlap, greater than 80% identity, and p value less than 1 x 10e-5). Sequences having greater than 70% overlap, greater than 99% identity, and p value of less than 1 x 10e-40 were discarded.

The remaining sequences were classified as unknown (no hits), weak similarity, and high similarity (parameters as above). Two searches were performed on these sequences. First, a BLAST vs. EST database search was performed and sequences with greater than 99% overlap, greater than

99% similarity and a p value of less than 1 x 10e-40 were discarded. Sequences with a p value of less than 1 x 10e-65 when compared to a database sequence of human origin were also excluded. Second, a BLASTN vs. Patent GeneSeq database was performed and sequences having greater than 99% identity, p value less than 1 x 10e-40, and greater than 99% overlap were discarded.

The remaining sequences were subjected to screening using other rules and redundancies in the dataset. Sequences with a p value of less than 1 x 10e-111 in relation to a database sequence of human origin were specifically excluded. The final result provided the 8064 sequences listed as SEQ ID NOS:1-6010 in the accompanying Sequence Listing and summarized in Table 2 (inserted prior to claims). Each identified polynucleotide represents sequence from at least a partial mRNA transcript.

Summary of polynucleotides of the invention

Table 2 (inserted prior to claims) provides a summary of polynucleotides isolated as described. Specifically, Table 2 provides: 1) the SEQ ID NO ("SEQ ID") assigned to each sequence for use in the present specification; 2) theCluster Identification No. ("CLUSTER"); 3) the Sequence Name assigned to each sequence; 3) the sequence name ("SEQ NAME") used as an internal identifier of the sequence; 4) the orientation of the sequence ("ORIENT") (either forward (F) or reverse (R)); 5) the name assigned to the clone from which the sequence was isolated ("CLONE ID"); and the name of the library from which the sequence was isolated ("LIBRARY"), where the notatiion indicates that name of the cell line or patient sample (*e.g.*, UC2-NormColon indicates the sequence was isolated from normla colon tissue of the patient assigned the idnetification UC#2). Because at least some of the provided polynucleotides represent partial mRNA transcripts, two or more polynucleotides may represent different regions of the same mRNA transcript and the same gene and/or may be contained within the same clone. Thus, for example, if two or more SEQ ID NOS: are identified as belonging to the same clone, then either sequence can be used to obtain the full-length mRNA or gene

Example 2:Results of Public Database Search to Identify Function of Gene Products

SEQ ID NOS:1-6010 were translated in all three reading frames, and the nucleotide sequences and translated amino acid sequences used as query sequences to search for homologous sequences in either the GenBank (nucleotide sequences) or Non-Redundant Protein (amino acid sequences) databases. Query and individual sequences were aligned using the BLAST 2.0 programs, available over the world wide at a site sponsored by the National Center for Biotechnology Information, which is supported by the National Library of Medicine and the National Institutes of Health (see also Altschul, et al. Nucleic Acids Res. (1997) 25:3389-3402). The sequences were masked to various extents to prevent searching of repetitive sequences or poly-A sequences, using the BLASTX program for masking low complexity as described above in Example 1.

Tables 3A and 3B (inserted prior to claims) provides the alignment summaries having a p value of 1 x 10e-2 or less indicating substantial homology between the sequences of the present invention and those of the indicated public databases. Specifically, Table 3A provides the SEQ ID NO of the query sequence, the accession number of the GenBank database entry of the homologous sequence, and the individual p value of each alignment. Table 3A provides the SEQ ID NO of the query sequence, the accession number of the Non-Redundant Protein database entry of the homologous sequence, and the individual p value of each alignment. The alignments provided in Tables 3A and 3B are the best available alignment to a DNA or amino acid sequence at a time just prior to filing of the present specification. The activity of the polypeptide encoded by the SEQ ID NOS listed in these tables can be extrapolated to be substantially the same or substantially similar to the activity of the reported nearest neighbor or closely related sequence. The accession number of the nearest neighbor is reported, providing a publicly available reference to the activities and functions exhibited by the nearest neighbor. The public information regarding the activities and functions of each of the nearest neighbor sequences is incorporated by reference in this application. Also incorporated by reference is all publicly available information regarding the sequence, as well as the putative and actual activities and functions of the nearest neighbor sequences listed in Tables 3A and 3B and their related sequences. The search program and database used for the alignment, as well as the calculation of the p value are also indicated.

Full length sequences or fragments of the polynucleotide sequences of the nearest neighbors can be used as probes and primers to identify and isolate the full length sequence of the corresponding polynucleotide. The nearest neighbors can indicate a tissue or cell type to be used to construct a library for the full-length sequences of the corresponding polynucleotides.

Example 3:Members of Protein Families

SEQ ID NOS:1-6010 were used to conduct a profile search as described in the specification above. Several of the polynucleotides of the invention were found to encode polypeptides having characteristics of a polypeptide belonging to a known protein family (and thus represent members of these protein families) and/or comprising a known functional domain. Table 4 (inserted before claims) provides the SEQ ID NO: of the query sequence, the Sequence Name, the Cluster to which the sequence is assigned, a brief description of the profile hit, the orientation (Direction, "Dir") of the query sequence with respect to the individual sequence)where forward (for) indicates that the alignment is in the same direction (left to right) as the sequence provided in the Sequence Listing and reverse (rev) indicates that the alignment is with a sequence complementary to the sequence provided in the Sequence Listing), and the score of the profile hit.

Some polynucleotides exhibited multiple profile hits where the query sequence contains overlapping profile regions, and/or where the sequence contains two different functional domains. Each of the profile hits of Table 4 is described in more detail below. The acronyms for the profiles (provided in parentheses) are those used to identify the profile in the Pfam, Prosite, and InterPro databases. The Pfam database can be accessed through web sites supported by Genome Sequencing Center at the Washington University School of Medicine or by the European Molecular Biology Laboratories in Heidelberg, Germany. The Prosite database can be accessed at the ExPASy Molecular Biology Server on the internet. The InterPro database can be accessed at a web site supported by the EMBL European Bioinformatics Institute. The public information available on the Pfam, Prosite, and InterPro databases regarding the various profiles, including but not limited to the activities, function, and consensus sequences of various proteins families and protein domains, is incorporated herein by reference.

Seven Transmembrane Integral Membrane Proteins -- Rhodopsin Family (7tm_1; Pfam Accession No. PF00001). SEQ ID NOS:2973, 5467, and 5508 correspond to sequences encoding a polypeptides that are members of the seven transmembrane (7tm) receptor rhodopsin family. G-protein coupled receptors of the (7tm) rhodopsin family (also called R7G) are an extensive group of hormones, neurotransmitters, and light receptors which transduce extracellular signals by interaction with guanine nucleotide-binding (G) proteins (Strosberg, Eur. J. Biochem. (1991) 196:1; Kerlavage, Curr. Opin. Struct. Biol. (1991) 1:394; Probst et al., DNA Cell Biol. (1992) 11:1; Savarese et al., Biochem. J. (1992) 283:1. The consensus pattern that contains the conserved triplet and that also spans the major part of the third transmembrane helix is used to detect this widespread family of proteins: [GSTALIVMFYWC]-[GSTANCPDE]-{EDPKRH}-x(2)-[LIVMNQGA]-x(2)- [LIVMFT]-[GSTANC]-[LIVMFYWSTAC]-[DENH]-R-[FYWCSH]-x(2)- [LIVM].

Ank Repeats (ANK; Pfam Accession No. PF0023). SEQ ID NOS:445, 487 and 3013 represent polynucleotides encoding Ank repeat-containing proteins. The ankyrin motif is a 33 amino acid sequence named after the protein ankyrin which has 24 tandem 33-amino-acid motifs. Ank repeats were originally identified in the cell-cycle-control protein cdc10 (Breeden et al., Nature (1987) 329:651). Proteins containing ankyrin repeats include ankyrin, myotropin, I-kappaB proteins, cell cycle protein cdc10, the Notch receptor (Matsuno et al., Development (1997) 124(21):4265); G9a (or BAT8) of the class III region of the major histocompatibility complex (Biochem J. (1993) 290:811-818); FABP, GABP, 53BP2, Lin12, glp-1, SW14, and SW16. The functions of the ankyrin repeats are compatible with a role in protein-protein interactions (Bork, Proteins (1993) 17(4):363; Lambert and Bennet, Eur. J. Biochem. (1993) 211:1; Kerr et al., Current Op. Cell Biol. (1992) *4*:496; Bennet *et al., J. Biol. Chem.* (1980) *255*:6424).

Basic Region Plus Leucine Zipper Transcription Factors (BZIP; Pfam Accession No. PF00170). SEQ ID NOS:108, 1714, 3931, and 4356 represent polynucleotides encoding novel members of the family of basic region plus leucine zipper transcription factors. The bZIP superfamily (Hurst, *Protein Prof.* (1995) *2*:105; and Ellenberger, *Curr. Opin. Struct. Biol.* (1994) *4*:12) of eukaryotic DNA-binding transcription factors encompasses proteins that contain a basic region mediating sequence-specific DNA-binding followed by a leucine zipper required for dimerization. The consensus pattern for this protein family is: [KR]-x(1,3)-[RKSAQ]-N-x(2)-[SAQ](2)-x-[RKTAENQ]-x-R-x-[RK].

DEAD and DEAH box families ATP-dependent helicases (Dead_box_helic; Pfam Accession No. PF00270. SEQ ID NOS:38, 415, and 5756 correspond to sequences encoding a polypeptides that are members of the DEAD box family. A number of eukaryotic and prokaryotic proteins have been characterized (Schmid *et al., Mol. Microbiol.* (1992) *6*:283; Linder *et al., Nature* (1989) *337*:121; Wassarman *et al., Nature* (1991) *349*:463) on the basis of their structural similarity. All are involved in ATP-dependent, nucleic-acid unwinding. All DEAD box family members of the above proteins share a number of conserved sequence motifs, some of which are specific to the DEAD family while others are shared by other ATP-binding proteins or by proteins belonging to the helicases 'superfamily' (Hodgman, Nature (1988) 333:22 and Nature (1988) 333:578 (Errata)). One of these motifs, called the 'D-E-A-D-box', represents a special version of the B motif of ATP-binding proteins. Some other proteins belong to a subfamily which have His instead of the second Asp and are thus said to be 'D-E-A-H-box' proteins (Wassarman et al., Nature (1991) 349:463; Harosh et al., Nucleic Acids Res. (1991) 19:6331; Koonin et al., J. Gen. Virol. (1992) 73:989). The following signature patterns are used to identify member for both subfamilies: 1) [LIVMF](2)-D-E-A-D-[RKEN]-x-[LIVMFYGSTN]; and 2) [GSAH]-x-[LIVMF](3)-D-E-[ALIV]-H-[NECR].

Defensins (defensins; Pfam Accession No. PF00323. SEQ ID NO:486 corresponds to a sequence encoding a polypeptide that is a member of the mammalian defensin family. Defensins are a family of structurally related cysteine-rich peptides which are active against many Gram-positive bacteria, fungi, and enveloped viruses (Lehrer *et al., ASM News* (1990) *56*:315-318; Lehrer *et al., Cell* (1991) *64*:229-230; Kagan *et al., Toxicology* (1994) *87*:131-149; Lehrer *et al., Annu. Rev. Immunol.* (1993) *11*:105-128; White *et al., Curr. Opin. Struc/ Biol.* (1995) *5*:521-527). Some defensins inhibit corticotropoid-stimulated corticosteroid production and also play a significant role in innate immunity to infection and neoplasia. The peptides known to belong to this family range in length from 29 to 35 amino acids and have seven invariant residues, including six cysteines that are all involved in intrachain disulfide bonds. The following consensus pattern is used to identify members of this protein family: C-x-C-x(3,5)-C-x(7)-G-x-C-x(9)-C-C.

EF Hand (Efhand; Pfam Accession No. PF00036). SEQ ID NO:4373 corresponds to a polynucleotide encoding a member of the EF-hand protein family, a calcium binding domain shared by many calcium-binding proteins belonging to the same evolutionary family (Kawasaki *et al.*, *Protein. Prof.* (1995) *2*:305-490). The domain is a twelve residue loop flanked on both sides by a twelve residue alpha-helical domain, with a calcium ion coordinated in a pentagonal bipyramidal configuration. The six residues involved in the binding are in positions 1, 3, 5, 7, 9 and 12; these residues are denoted by X, Y, Z, -Y, -X and -Z. The invariant Glu or Asp at position 12 provides two oxygens for liganding Ca (bidentate ligand). The consensus pattern includes the complete EF-hand loop as well as the first residue which follows the loop and which seem to always be hydrophobic: D-x-[DNS]-{ILVFYW}-[DENSTG]-[DNQGHRK]-{GP}-[LIVMC]-[DENQSTAGC]-x(2)-[DE]-[LIVMFYW].

Epidermal Growth Factor (EGF; Pfam Accession No. PF00008). SEQ ID NO:3689 represents a polynucleotide encoding a member of the EGF family of proteins. The distinguishing characteristic of this family is the presence of a sequence of about thirty to forty amino acid residues found in epidermal growth factor (EGF) which has been shown to be present, in a more or less conserved form, in a large number of other proteins (Davis, *New Biol.* (1990) *2*:410-419; Blomquist *et al.*, *Proc. Natl. Acad. Sci. U.S.A.* (1984) *81*:7363-7367; Barkert *et al.*, *Protein Nucl. Acid Enz.* (1986) *29*:54-86; Doolittle *et al.*, *Nature.* (1984) *307*:558-560; Appella *et al.*, *FEBS Lett.* (1988) *231*:1-4; Campbell and Bork, *Curr. Opin. Struct. Biol.* (1993) *3*:385-392). A common feature of the domain is that the conserved pattern is generally found in the extracellular domain of membrane-bound proteins or in proteins known to be secreted. The EGF domain includes six cysteine residues which have been shown to be involved in disulfide bonds. The main structure is a two-stranded beta-sheet followed by a loop to a C-terminal short two-stranded sheet. Subdomains between the conserved cysteines strongly vary in length. The following consensus patterns are used to identify members of this family: C-x-C-x(5)-G-x(2)-C and C-x-C-x(s)-[GP]-[FYW]-x(4,8)-C.

Ets Domain (Ets_Cterm; Pfam Accession No. PF00178). SEQ ID NO:6 represents a polynucleotide encoding a polypeptide with C-terminal homology in the ETS domain. Proteins of this family contain a conserved domain, the "ETS-domain," that is involved in DNA binding. The domain appears to recognize purine-rich sequences; it is about 85 to 90 amino acids in length, and is rich in aromatic and positively charged residues (Wasylyk *et al.*, *Eur. J. Biochem.* (1993) *211*:718). The *ets* gene family encodes a novel class of DNA-binding proteins, each of which binds a specific DNA sequence and comprises an *ets* domain that specifically interacts with sequences containing the common core tri-nucleotide sequence GGA. In addition to an *ets* domain, native *ets* proteins comprise other sequences which can modulate the biological specificity of the protein. *Ets* genes and proteins

are involved in a variety of essential biological processes including cell growth, differentiation and development, and three members are implicated in oncogenic process.

Pleckstrin Homology (PH; Pfam Accession No. PF00169). SEQ ID NOS:228 and 6001 correspond to polynucleotides encoding members of the PH family. The pleckstrin homology domain is a domain of about 100 residues that occurs in a wide range of proteins involved in intracellular signaling or as constituents of the cytoskeleton (Mayer *et al., Cell* (1993) *73*:629-630; Haslam *et al., Nature* (1993) *363*:309-310; Musacchio *et al., Trends Biochem.* Sci. (1993) *18*:343-348; Gibson *et al., Trends Biochem. Sci.* (1994) *19*:349-353; Pawson, *Nature* (1995) *373*:573-580; Ingley and Hemmings, *J. Cell. Biochem.* (1994) *56*:436-443; Saraste and Hyvonen, *Curr. Opin. Struct. Biol.* (1995) *5*:403-408). All known structures of PH domains have two perpendicular anti-parallel beta sheets, followed by a C-terminal amphipathic helix. The loops connecting the beta-strands differ greatly in length, making the PH domain relatively difficult to detect (Riddihough, *Nat. Struct. Biol.* (1994) *1*:755-757). There are no totally invariant residues within this domain.

Protein Kinase (protkinase; Pfam Accession No. PF00069). SEQ ID NOS:9, 39, 69, 118, 229 and 4151 represent polynucleotides encoding protein kinases, which catalyze phosphorylation of proteins in a variety of pathways, and are implicated in cancer. Eukaryotic protein kinases (Hanks *et al., FASEB J.* (1995) *9*:576; Hunter, *Meth. Enzymol.* (1991) *200*:3; Hanks *et al., Meth. Enzymol.* (1991) *200*:38; Hanks, *Curr. Opin. Struct. Biol.* (1991) *1*:369; Hanks *et al., Science* (1988) *241*:42) belong to a very extensive family of proteins that share a conserved catalytic core common to both serine/threonine and tyrosine protein kinases. There are a number of conserved regions in the catalytic domain of protein kinases. The first region, located in the N-terminal extremity of the catalytic domain, is a glycine-rich stretch of residues in the vicinity of a lysine residue, which has been shown to be involved in ATP binding. The second region, located in the central part of the catalytic domain, contains a conserved aspartic acid residue that is important for the catalytic activity of the enzyme (Knighton *et al., Science* (1991) *253*:407).

The protein kinase profile includes two signature patterns for this second region: one specific for serine/threonine kinases and the other for tyrosine kinases. A third profile is based on the alignment in Hanks *et al.* (*FASEB J.* (1995) *9*:576) and covers the entire catalytic domain. The consensus patterns are as follows: 1) [LIV]-G-{P}-G-{P}-[FYWMGSTNH]-[SGA]-{PW}-[LIVCAT]-{PD}-x-[GSTACLIVMFY]-x(5,18)-[LIVMFYWCSTAR]-[AIVP]-[LIVMFAGCKR]-K, where K binds ATP; 2) [LIVMFYC]-x-[HY]-x-D-[LIVMFY]-K-x(2)-N-[LIVMFYCT](3), where D is an active site residue; and 3) [LIVMFYC]-x-[HY]-x-D-[LIVMFY]-[RSTAC]-x(2)-N-[LIVMFYC], where D is an active site residue.

Retroviral_aspartyl_protease (RVP; Pfam Accession No. PF00077). SEQ ID NO:2038 corresponds to a polynucleotide encoding a member of the Aspartyl Protease family. Aspartyl proteases, also know as acid proteases, are a widely distributed family of proteolytic enzymes known to exist in vertebrates, fungi, plants, retroviruses and some plant viruses (Foltmann, *Essays Biochem.* (1981) *17*:52-84; Davies, *Annu. Rev.* Biophys. *Chem.* (1990) *19*:189-215; Rao *et al., Biochemistry* (1991) *30*:4663-4671). Most retroviral aspartyl proteases (RVP) are homodimers of a chain of about 95 to 125 amino acids. In most retroviruses, the protease is encoded as a segment of a polyprotein which is cleaved during the maturation process of the virus. RVP is generally part of the pol polyprotein and, more rarely, of the gag polyprotein. The consensus pattern is as follows: [LIVMFGAC]-[LIVMTADN]-[LIVFSA]-D-[ST]-G-[STAV]-[STAPDENQ]-x-[LIVMFSTNC]-x-[LIVMFGTA] [D is the active site residue].

Reverse Transcriptase (rvt; Pfam Accession No. PF00078). SEQ ID NOS:1511 and 2514 represent polynucleotides encoding reverse transcriptases, which occur in a variety of mobile elements, including retrotransposons, retroviruses, group II introns, bacterial msDNAs, hepadnaviruses, and caulimoviruses (Xiong and Eickbush, *EMBO J* (1990) *9*:3353-3362). Reverse transcriptases catalyze RNA-template-directed extension of the 3'-end of a DNA strand by one deoxynucleotide at a time and require an RNA or DNA primer.

Transforming growth factor beta like domain (TGF_beta; Pfam Accession No. PF00019). SEQ ID NO:5522 represents a polynucleotide encoding a polypeptide of the TGF-beta family. Proteins from the transforming growth factor-beta family are active as homo- or hetero-dimers with the two chains being linked by a single disulfide bond (Roberts and Sporn, *In* Peptide growth factors and their receptors, Handbook of Experimental Pharmacology, Vol. 95, pp419-475, Springer Verlag, Heidelberg, (1990); Burt, *Biochem. Biophys. Res. Commun.* (1992) *184*:590-595; Burt and Law, *Prog. Growth Factor Res.* (1994) *5*:99-118). It is known from X-ray studies that all the other cysteines of the sequence are involved in interchain disulfide bonds (Daopin *et al., Science* (1992) *257*:369-373). Members of this family can be recognized by the following consensus pattern: [LIVM]-x(2)-P-x(2)-[FY]-x(4)-C-x-G-x-C (The two C's are involved in disulfide bonds).

WD Domain (WD40), G-Beta Repeats (WD_domain; Pfam Accession No. PF00400). SEQ ID NO:117 represents a member of the WD domain/G-beta repeat family. Beta-transducin (G-beta) is one of the three subunits (alpha, beta, and gamma) of the guanine nucleotide-binding proteins (G proteins) which act as intermediaries in the transduction of signals generated by transmembrane receptors (Gilman, *Annu. Rev. Biochem.* (1987) *56*:615). The alpha subunit binds to and hydrolyzes GTP; the beta and gamma subunits are required for the replacement of GDP by GTP as well as for membrane anchoring and receptor recognition. In higher eukaryotes, G-beta exists as a small

multigene family of highly conserved proteins of about 340 amino acid residues. Structurally, G-beta has eight tandem repeats of about 40 residues, each containing a central Trp-Asp motif (this type of repeat is sometimes called a WD-40 repeat). The consensus pattern for the WD domain/G-Beta repeat family is: [LIVMSTAC]-[LIVMFYWSTAGC]-[LIMSTAG]-[LIVMSTAGC]-x(2)-[DN]-x(2)-[LIVMWSTAC]-x-[LIVMFSTAG]-W-[DEN]-[LIVMFSTAGCN].

Zinc Finger, C2H2 Type (Zincfing_C2H2; Pfam Accession No. PF00096). SEQ ID NOS: 61, 502, 700, 847, 2034, 2054, 3403, 3524, 3653, 3723, 4688, and 4979 correspond to polynucleotides encoding members of the C2H2 type zinc finger protein family, which contain zinc finger domains that facilitate nucleic acid binding (Klug *et al.*, *Trends Biochem. Sci.* (1987) *12*:464; Evans *et al.*, *Cell* (1988) *52*:1; Payre *et al.*, *FEBS Lett.* (1988) *234*:245; Miller *et al.*, *EMBO J.* (1985) *4*:1609; and Berg, *Proc. Natl. Acad. Sci. USA* (1988) *85*:99). In addition to the conserved zinc ligand residues, a number of other positions are also important for the structural integrity of the C2H2 zinc fingers (Rosenfeld *et al.*, *J. Biomol. Struct. Dyn.* (1993) *11*:557). The best conserved position, which is generally an aromatic or aliphatic residue, is located four residues after the second cysteine. The consensus pattern for C2H2 zinc fingers is: C-x(2,4)-C-x(3)-[LIVMFYWC]-x(8)-H-x(3,5)-H. The two C's and two H's are zinc ligands.

Zinc Finger, C2HC Type (Zincfing_C2HC; Pfam Accession No. PF01530). SEQ ID NO:3814 represents a member of the C2HC zinc finger family. The 18 residue C2HC domain is mainly found in the retroviral nucleocapsid protein, and is required for viral genome packaging and for the early infection process (Katz and Jentoft, *Bioessays* (1989) *11*:176-181; Urbaneja *et al.*, *J Mol Biol.* (1999) *287*:59-75). In addition, the CCHC domain is found in eukaryotic proteins involved in RNA binding or single-strand DNA binding.

Zinc finger, C3HC4 type (RING finger), signature (Zincfing_C3HC4; Pfam Accession No. PF00097). SEQ ID NO:3140 represents a polynucleotide encoding a polypeptide having a C3HC4 type zinc finger signature. A number of eukaryotic and viral proteins contain this signature, which is primarily a conserved cysteine-rich domain of 40 to 60 residues (Borden *et al.*, *Curr. Opin. Struct. Biol.* (1996) *6*:395) that binds two atoms of zinc, and is probably involved in mediating protein-protein interactions. The 3D structure of the zinc ligation system is unique to the RING domain and is referred to as the "cross-brace" motif. The spacing of the cysteines in such a domain is C-x(2)-C-x(9 to 39)-C-x(1 to 3)-H-x(2 to 3)-C-x(2)-C-x(4 to 48)-C-x(2)-C. The signature pattern for the C3HC4 finger is based on the domain's central region: C-x-H-x-[LIVMFY]-C-x(2)-C-[LIVMYA].

Zinc finger, CCCH type, (Zincfing_CCCH; Pfam Accession No. PF00642). SEQ ID NO:877 corresponds to a polyncleotide encoding a member of the CCCH zinc finger protein family. This domain is present in many eukaryotic proteins, including zinc finger proteins involved in cell cycle or

growth phase–related regulation and regulatory proteins involved in regulating the response to growth factors. It has been shown that proteins containing the CCCH zinc finger interact with the 3' untranslated region of various mRNA (Carballo *et al.*, *Science* (1998) *281*:1001-1005; Lai *et al.*, *Mol. Cell. Biol.* (1999) *19*:4311-4323) and that this domain is often present in two copies. The consensus pattern for the CCCH zinc fingers is: C-x8-C-x5-C-x3-H.

Example 4: Description of Libraries and Detection of Differential Expression

The relative expression levels of the polynucleotides of the invention were assessed in several libraries prepared from various sources, including cell lines and patient tissue samples. Table 1 above provides a summary of these libraries, including the shortened library name, the mRNA source used to prepared the cDNA library, the "nickname" of the library that is used in the tables below (in quotes), and the approximate number of clones in the library.

Each of the libraries is composed of a collection of cDNA clones that in turn are representative of the mRNAs expressed in the indicated mRNA source. In order to facilitate the analysis of the millions of sequences in each library, the sequences were assigned to clusters. The concept of "cluster of clones" is derived from a sorting/grouping of cDNA clones based on their hybridization pattern to a panel of roughly 300 7bp oligonucleotide probes (see Drmanac *et al.*, *Genomics* (1996) *37*(1):29). Random cDNA clones from a tissue library are hybridized at moderate stringency to 300 7bp oligonucleotides. Each oligonucleotide has some measure of specific hybridization to that specific clone. The combination of 300 of these measures of hybridization for 300 probes equals the "hybridization signature" for a specific clone. Clones with similar sequence will have similar hybridization signatures. By developing a sorting/grouping algorithm to analyze these signatures, groups of clones in a library can be identified and brought together computationally. These groups of clones are termed "clusters". Depending on the stringency of the selection in the algorithm (similar to the stringency of hybridization in a classic library cDNA screening protocol), the "purity" of each cluster can be controlled. For example, artifacts of clustering may occur in computational clustering just as artifacts can occur in "wet-lab" screening of a cDNA library with 400 bp cDNA fragments, at even the highest stringency. The stringency used in the implementation of cluster herein provides groups of clones that are in general from the same cDNA or closely related cDNAs. Closely related clones can be a result of different length clones of the same cDNA, closely related clones from highly related gene families, or splice variants of the same cDNA.

Differential expression for a selected cluster was assessed by first determining the number of cDNA clones corresponding to the selected cluster in the first library (Clones in 1st), and the determining the number of cDNA clones corresponding to the selected cluster in the second library

(Clones in 2nd). Differential expression of the selected cluster in the first library relative to the second library is expressed as a "ratio" of percent expression between the two libraries. In general, the "ratio" is calculated by: 1) calculating the percent expression of the selected cluster in the first library by dividing the number of clones corresponding to a selected cluster in the first library by the total number of clones analyzed from the first library; 2) calculating the percent expression of the selected cluster in the second library by dividing the number of clones corresponding to a selected cluster in a second library by the total number of clones analyzed from the second library; 3) dividing the calculated percent expression from the first library by the calculated percent expression from the second library. If the "number of clones" corresponding to a selected cluster in a library is zero, the value is set at 1 to aid in calculation. The formula used in calculating the ratio takes into account the "depth" of each of the libraries being compared, *i.e.*, the total number of clones analyzed in each library.

In general, a polynucleotide is significantly differentially expressed between two samples when the ratio value is greater than at least about 2, preferably greater than at least about 3, more preferably greater than at least about 5 , where the ratio value is calculated using the method described above. The significance of differential expression is determined using a z score test (Zar, Biostatistical Analysis, Prentice Hall, Inc., USA, "Differences Between Proportions," pp 296-298 (1974).

Using this approach, a number of polynucleotide sequences were identified as being differentially expressed between, for example, cells derived from high metastatic potential cancer tissue and low metastatic cancer cells, and between cells derived from metastatic cancer tissue and normal tissue. Evaluation of the levels of expression of the genes corresponding to these sequences can be valuable in diagnosis, prognosis, and/or treatment (*e.g.*, to facilitate rationale design of therapy, monitoring during and after therapy, *etc.*). Moreover, the genes corresponding to differentially expressed sequences described herein can be therapeutic targets due to their involvement in regulation (*e.g.*, inhibition or promotion) of development of, for example, the metastatic phenotype. For example, sequences that correspond to genes that are increased in expression in high metastatic potential cells relative to normal or non-metastatic tumor cells may encode genes or regulatory sequences involved in processes such as angiogenesis, differentiation, cell replication, and metastasis.

Detection of the relative expression levels of differentially expressed polynucleotides described herein can provide valuable information to guide the clinician in the choice of therapy. For example, a patient sample exhibiting an expression level of one or more of these polynucleotides that corresponds to a gene that is increased in expression in metastatic or high metastatic potential cells may warrant more aggressive treatment for the patient. In contrast, detection of expression levels of a polynucleotide sequence that corresponds to expression levels associated with that of low metastatic potential cells may warrant a more positive prognosis than the gross pathology would suggest.

A number of polynucleotide sequences of the present invention are differentially expressed between human microvascular endothelial cells (HMVEC) that have been treated with growth factors relative to untreated HMVEC. Sequences that are differentially expressed between growth factor-treated HMVEC and untreated HMVEC can represent sequences encoding gene products involved in angiogenesis, metastasis (cell migration), and other development and oncogenic processes. For example, sequences that are more highly expressed in HMVEC treated with growth factors (such as bFGF or VEGF) relative to untreated HMVEC can serve as drug targets for chemotherapeutics, *e.g.*, decreasing expression of such up-regulated genes or inhibiting the activity of the encoded gene product would serve to inhibit tumor cell angiogenesis. Detection of expression of these sequences in colon cancer tissue can be valuable in determining diagnostic, prognostic and/or treatment information associated with the prevention of achieving the malignant state in these tissues, and can be important in risk assessment for a patient. A patient sample displaying an increased level of one or more of these polynucleotides may thus warrant closer attention or more frequent screening procedures to catch the malignant state as early as possible.

The differential expression of the polynucleotides can thus be used as, for example, diagnostic and/or prognostic markers, for risk assessment, patient treatment and the like. These polynucleotides can also be used in combination with other molecular and/or biochemical markers.

The differential expression data for polynucleotides of the invention that have been identified as being differentially expressed across various combinations of the libraries described above is summarized in Table 5 (inserted prior to the claims). Table 5 provides: 1) the Sequence Identification Number ("SEQ ID NO") assigned to the polynucleotide; 2) the cluster ("CLUSTER") to which the polynucleotide has been assigned as described above; 3) the library comparisons that resulted in identifcation of the polynucleotide as being differentially expressed ("PAIR AB"), where the cDNA libraries used are referenced by their library numbers; 4) the number of clones corresponding to the polynucleotide in the first library listed ("CLONES A"); 5) the number of clones corresponding to the polynucleotide in the second library listed ("CLONES B"); 6) the "RATIO PLUS" where the comparison resulted in a finding that the number of clones in library A is greater than the number of clones in library B; and 7) the "RATIO MINUS" where the comparison resulted in a finding that the number of clones in library B is greater than the number of clones in library A.

Detection of expression of genes that correspond to the above polynucleotides may be of particular interest in diagnosis, prognosis, risk assessment, and monitoring of treatment. Furthermore, differential expression of a specific gene across multiple libraries can also be indicative of a gene whose expression is associated with, for example, suppression of the metastatic phenotype or with development of the cell toward a metastatic phenotype. For example, SEQ ID NO:3744 corresponds

to a gene that is expressed at relatively higher levels in metastatized colon tumor than in normal colon tissue. Thus a relatively increased level of expression of the gene corresponding to SEQ ID NO:3744 may be used as marker of a metastatic or pre-metastatic colon cels either alone or in combination with other markers.

Some polynucleotides exhibited similar differential expression trends in libraries of different tissue origin (see, *e.g.*., SEQ ID NO:337). These data suggest that the differential expression patterns of some genes associated with development of tumors indicate a role for those genes that is non-specific to the tissue of origin.

Example 5: Detection of Differential Expression Using Arrays

mRNA isolated from samples of cancerous and normal colon tissue obtained from patients were analyzed to identify genes differentially expressed in cancerous and normal cells. Normal and cancerous cells collected from cryopreserved patient tissues were isolated using laser capture microdissection (LCM) techniques, which techniques are well known in the art (see, *e.g.*, Ohyama *et al.* (2000) *Biotechniques* 29:530-6; Curran *et al.* (2000) *Mol. Pathol.* 53:64-8; Suarez-Quian *et al.* (1999) *Biotechniques* 26:328-35; Simone *et al.* (1998) *Trends Genet* 14:272-6; Conia *et al.* (1997) *J. Clin. Lab. Anal.* 11:28-38; Emmert-Buck *et al.* (1996) *Science* 274:998-1001).

Table 6 (inserted before the claims) provides information about each patient from which colon tissue samples were isolated, including: the Patient ID ("PT ID")and Path ReportID (}Path ID"), which are numbers assigned to the patient and the pathology reports for identification purposes; the group ("Grp")to which the patients have been assigned; the anatomical location of the tumor ("Anatom Loc"); the primary tumor size ("Size"); the primary tumor grade ("Grade"); the identification of the histopathological grade ("Histo Grade"); a description of local sites to which the tumor had invaded ("Local Invasion"); the presence of lymph node metastases ("LN Met"); the incidence of lymph node metastases (provided as a number of lymph nodes positive for metastasis over the number of lymph nodes examined) ("Incidence Lymphnode Met"); the "Regional Lymphnode Grade"; the identification or detection of metastases to sites distant to the tumor and their location ("Dist Met & Loc"); the grade of distant metastasis ("Dist Met Grade"); and general comments about the patient or the tumor ("Comments"). Histophatology of all primary tumors incidated the tumor was adenocarcinmoa except for Patient ID Nos. 130 (for which no information was provided), 392 (in which greater than 50% of the cells were mucinous carcinoma), and 784 (adenosquamous carcinoma). Extranodal extensions were described in three patients, Patient ID Nos. 784, 789, and 791. Lymphovascular invasion was described in Patient ID Nos. 128, 278, 517, 534, 784, 786, 789, 791, 890, and 892. Crohn's-like

infiltrates were described in seven patients, Patient ID Nos. 52, 264, 268, 392, 393, 784, and 791. Table 7 (below) provides information about the patients from whom the prostate tissue was isolated.

Table 7. Prostate paitent data.

Prostate Patient ID	Tumor Gleason Grade	Normal Prostate Description
96	3+3 Adenocarcinoma	Normal prostate; Benign hyperplasia
282	4+3 Adenocarcinoma	Normal prostate; Benign hyperplasia
286	3+3 Adenocarcinoma	Normal prostate; Benign hyperplasia
294	3+4 Adenocarcinoma	Normal prostate; Benign hyperplasia
362	3+3 Adenocarcinoma	Normal prostate; Benign hyperplasia
428	4+3 Adenocarcinoma	Normal prostate; Benign hyperplasia
492	3+3 Adenocarcinoma	Normal prostate; Benign hyperplasia
492	3+3 Adenocarcinoma	Normal prostate; Benign hyperplasia
493	3+4 Adenocarcinoma	Normal prostate; Benign hyperplasia
510	3+3 Adenocarcinoma	Normal Prostate; Benign hyperplasia

Identification of differentially expressed genes

cDNA probes were prepared from total RNA isolated from the patient cells described above. Since LCM provides for the isolation of specific cell types to provide a substantially homogenous cell sample, this provided for a similarly pure RNA sample.

Total RNA was first reverse transcribed into cDNA using a primer containing a T7 RNA polymerase promoter, followed by second strand DNA synthesis. cDNA was then transcribed *in vitro* to produce antisense RNA using the T7 promoter-mediated expression (see, *e.g.*, Luo *et al.* (1999) *Nature Med* 5:117-122), and the antisense RNA was then converted into cDNA. The second set of cDNAs were again transcribed *in vitro*, using the T7 promoter, to provide antisense RNA. Optionally, the RNA was again converted into cDNA, allowing for up to a third round of T7-mediated amplification to produce more antisense RNA. Thus the procedure provided for two or three rounds of *in vitro* transcription to produce the final RNA used for fluorescent labeling.

Fluorescent probes were generated by first adding control RNA to the antisense RNA mix, and producing fluorescently labeled cDNA from the RNA starting material. Fluorescently labeled cDNAs prepared from the tumor RNA sample were compared to fluorescently labeled cDNAs prepared from normal cell RNA sample. For example, the cDNA probes from the normal cells were labeled with Cy3 fluorescent dye (green) and the cDNA probes prepared from the tumor cells were labeled with Cy5 fluorescent dye (red), and vice versa.

Each array used had an identical spatial layout and control spot set. Each microarray was divided into two areas, each area having an array with, on each half, twelve groupings of 32 x 12 spots, for a total of about 9,216 spots on each array. The two areas are spotted identically which provide for at least two duplicates of each clone per array.

Polynucleotides for use on the arrays were obtained from both publicly available sources and from cDNA libraries generated from selected cell lines and patient tissues. PCR products of from about 0.5kb to 2.0 kb amplified from these sources were spotted onto the array using a Molecular Dynamics Gen III spotter according to the manufacturer's recommendations. For polynucleotides described herein, the microarray spot contained a clone having a cDNA from which the sequence was derived. The first row of each of the 24 regions on the array had about 32 control spots, including 4 negative control spots and 8 test polynucleotides. The test polynucleotides were spiked into each sample before the labeling reaction with a range of concentrations from 2-600 pg/slide and ratios of 1:1. For each array design, two slides were hybridized with the test samples reverse-labeled in the labeling reaction. This provided for about four duplicate measurements for each clone, two of one color and two of the other, for each sample.

Table 8 (inserted before the claims) describes sequences present on the arrays. Table 8 includes: 1) athe SEQ ID NO of the sequence of the polynucleotide; and 2)the Spot ID, which is a unique identifier for each spot ontaining target sequence of interest on all arrays used.

The differential expression assay was performed by mixing equal amounts of probes from tumor cells and normal cells of the same patient. The arrays were prehybridized by incubation for about 2 hrs at 60°C in 5X SSC/0.2% SDS/1 mM EDTA, and then washed three times in water and twice in isopropanol. Following prehybridization of the array, the probe mixture was then hybridized to the array under conditions of high stringency (overnight at 42°C in 50% formamide, 5X SSC, and 0.2% SDS. After hybridization, the array was washed at 55°C three times as follows: 1) first wash in 1X SSC/0.2% SDS; 2) second wash in 0.1X SSC/0.2% SDS; and 3) third wash in 0.1X SSC.

The arrays were then scanned for green and red fluorescence using a Molecular Dynamics Generation III dual color laser-scanner/detector. The images were processed using BioDiscovery Autogene software, and the data from each scan set normalized to provide for a ratio of expression relative to normal. Data from the microarray experiments was analyzed according to the algorithms described in U.S. application serial no. 60/252,358, filed November 20, 2000, by E.J. Moler, M.A. Boyle, and F.M. Randazzo, and entitled "Precision and accuracy in cDNA microarray data," which application is specifically incorporated herein by reference.

The experiment was repeated, this time labeling the two probes with the opposite color in order to perform the assay in both "color directions." Each experiment was sometimes repeated with two more slides (one in each color direction). The level fluorescence for each sequence on the array expressed as a ratio of the geometric mean of 8 replicate spots/genes from the four arrays or 4 replicate spots/gene from 2 arrays or some other permutation. The data were normalized using the spiked positive controls present in each duplicated area, and the precision of this normalization was included

in the final determination of the significance of each differential. The fluorescent intensity of each spot was also compared to the negative controls in each duplicated area to determine which spots have detected significant expression levels in each sample.

A statistical analysis of the fluorescent intensities was applied to each set of duplicate spots to assess the precision and significance of each differential measurement, resulting in a p-value testing the null hypothesis that there is no differential in the expression level between the tumor and normal samples of each patient. During initial analysis of the microarrays, the hypothesis was accepted if $p > 10^{-3}$, and the differential ratio was set to 1.000 for those spots. All other spots have a significant difference in expression between the tumor and normal sample. If the tumor sample has detectable expression and the normal does not, the ratio is truncated at 1000 since the value for expression in the normal sample would be zero, and the ratio would not be a mathematically useful value (e.g., infinity). If the normal sample has detectable expression and the tumor does not, the ratio is truncated to 0.001, since the value for expression in the tumor sample would be zero and the ratio would not be a mathematically useful value. These latter two situations are referred to herein as "on/off." Database tables were populated using a 95% confidence level ($p>0.05$).

Table 8 (inserted before the claims) provides the results for gene products differentially expressed in the colon tumor samples relative to normal tissue samples. Table 8 includes: 1) the SEQ ID NO; 2) the spot identification number ("SpotID"); 3) the percentage of patients tested in which expression levels of the gene (as detected using the correponding clone) was at least 2-fold greater in cancerous colon tissue (primary colon tumor) than in matched normal tissue ("Colon>2x T/N "); 4) the percentage of patients tested in which expression levels of the gene was less than or equal to one-half of the expression level in matched normal cells ("Colon <=halfx T/N"); and 5) the colon number ratios, indicating the number of patients upon which the provided ratios was based.

Table 9 below provides the data for differential expression analysis on the arrays using samples from metastazed colon tissue. In this example, the samples used for hybridization to sequences on the microarray were derived from the matched metastasized (MT) colon tissue and normal (N) colon tissues of the patients. Table 9 includes: 1) the SEQ ID NO; 2) the percentage of patients tested in which expression levels of the gene (as detected using the correponding clone) was at least 2-fold greater in metastisized cancerous colon tissue (MT) than in matched normal tissue ("Colon>2x MT/N "); 5) the percentage of patients tested in which expression levels of the gene was less than or equal to one-half of the expression level in matched normal cells ("Colon <=halfx T/N"); and 8) the colon number ratios, indicating the number of patients upon which the provided ratios was based. The corresponding data with the same sequence of the colon tumor tissue versus matched normal colon tissue (T/N) are provided for convenience in comparison.

Table 9. Polynucleotides Corresponding to Differnetially Expressed Genes in Metastasized Colon Cancer Tissue

SEQ ID NO	Colon MT/N >2x	Colon MT/N <halfx	Colon MT/N Num Ratios by Clone	Colon T/N >2x	Colon T/N <halfx	Colon T/N Num Ratios
217	40.0	0.0	5.0	0.0	50.0	8.0
324	0.0	40.0	5.0	0.0	37.5	8.0
1653	0.0	40.0	5.0	0.0	37.5	8.0
1972	40.0	0.0	5.0	0.0	42.9	7.0
2346	20.0	40.0	5.0	0.0	85.7	7.0
2352	20.0	80.0	5.0	0.0	71.4	7.0
2353	20.0	40.0	5.0	0.0	85.7	7.0
2647	0.0	40.0	5.0	0.0	62.5	8.0
5341	0.0	40.0	5.0	0.0	37.5	8.0

Table 10 below provides the data for differential expression analysis on the arrays using samples from matched cancerous and normal prostate tissue (PT/N). Table 10 includes: 1) the SEQ ID NO; 2) the percentage of patients tested in which expression levels of the gene (as detected using the correponding clone) was at least 2-fold greater in metastisized cancerous prostate tissue (PT) than in matched normal tissue ("Colon>2x PT/N "); 3) the percentage of patients tested in which expression levels of the gene was less than or equal to one-half of the expression level in matched normal cells ("Colon <=halfx PT/N"); and 4) the prostate PT/N number ratios, indicating the number of patients upon which the provided ratios was based. The corresponding data with the same sequences for the colon tumor versus normal (T/N) and metastasized colon tissue versus normal (MT/N) are provided for convenience in comparison.

Table 10. Polynucleotides Corresponding to Differnetially Expressed Genes in Prostate Cancer Tissue

SEQ ID NO	Prostate (PT/N) >2x	Prostate (PT/N) <halfx	Prostate (PT/N) Num Ratios	Colon T/N >2x	Colon T/N <halfx	Colon T/N Num Ratios	Colon MT/N >2x	Colon MT/N <halfx	Colon MT/N Num Ratios
139	11.1	33.3	9.0	0.0	50.0	8.0			
490	37.5	12.5	8.0	0.0	71.4	7.0			
629	33.3	11.1	9.0						
644	12.5	37.5	8.0	0.0	42.9	7.0			
1674	33.3	0.0	9.0						
2346	37.5	25.0	8.0	0.0	85.7	7.0	20.0	40.0	5.0
2352	37.5	12.5	8.0	0.0	71.4	7.0	20.0	80.0	5.0
2420	22.2	33.3	9.0						

SEQ ID NO	Prostate (PT/N) >2x	Prostate (PT/N) <halfx	Prostate (PT/N) Num Ratios	Colon T/N >2x	Colon T/N <halfx	Colon T/N Num Ratios	Colon MT/N >2x	Colon MT/N <halfx	Colon MT/N Num Ratios
3296	33.3	0.0	9.0	0.0	37.5	8.0			

Example 6: Antisense Regulation of Gene Expression

The expression of the differentially expressed genes represented by the polynucleotides in the cancerous cells can be further analyzed using antisense knockout technology to confirm the role and function of the gene product in tumorigenesis, *e.g.*, in promoting a metastatic phenotype.

Methods for analysis using antisense technology are well known in the art. For example, a number of different oligonucleotides complementary to the mRNA generated by the differentially expressed genes identified herein can be designed as antisense oligonucleotides, and tested for their ability to suppress expression of the genes. Sets of antisense oligomers specific to each candidate target are designed using the sequences of the polynucleotides corresponding to a differentially expressed gene and the software program HYBsimulator Version 4 (available for Windows 95/Windows NT or for Power Macintosh, RNAture, Inc. 1003 Health Sciences Road, West, Irvine, CA 92612 USA). Factors considered when designing antisense oligonucleotides include: 1) the secondary structure of oligonucleotides; 2) the secondary structure of the target gene; 3) the specificity with no or minimum cross-hybridization to other expressed genes; 4) stability; 5) length and 6) terminal GC content. The antisense oligonucleotide is designed to so that it will hybridize to its target sequence under conditions of high stringency at physiological temperatures (*e.g.*, an optimal temperature for the cells in culture to provide for hybridization in the cell, e.g., about 37°C), but with minimal formation of homodimers.

Once synthesized and quantitated, the oligomers are screened for efficiency of a transcript knock-out in a panel of cancer cell lines. The efficiency of the knock-out is determined by analyzing mRNA levels using lightcycler quantification. The oligomers that resulted in the highest level of transcript knock-out, wherein the level was at least about 50%, preferably about 80-90%, up to 95% or more up to undetectable message, are selected for use in a cell-based proliferation assay, an anchorage independent growth assay, and an apoptosis assay.

For example, where the polynucleotide is identified as having a role in colon cancer, the ability of the corresponding designed antisense oligonucleotide to inhibit gene expression is tested through transfection into SW620 colon colorectal carcinoma cells. For each transfection mixture, a carrier molecule, preferably a lipitoid or cholesteroid, is prepared to a working concentration of 0.5 mM in water, sonicated to yield a uniform solution, and filtered through a 0.45 μm PVDF membrane. The

antisense or control oligonucleotide is then prepared to a working concentration of 100 μM in sterile Millipore water. The oligonucleotide is further diluted in OptiMEM™ (Gibco/BRL), in a microfuge tube, to 2 μM, or approximately 20 μg oligo/ml of OptiMEM™. In a separate microfuge tube, lipitoid or cholesteroid, typically in the amount of about 1.5-2 nmol lipitoid/μg antisense oligonucleotide, is diluted into the same volume of OptiMEM™ used to dilute the oligonucleotide. The diluted antisense oligonucleotide is immediately added to the diluted lipitoid and mixed by pipetting up and down. Oligonucleotide is added to the cells to a final concentration of 30 nM.

The level of target mRNA that corresponds to a target gene of interest in the transfected cells is quantitated in the cancer cell lines using the Roche LightCycler™ real-time PCR machine. Values for the target mRNA are normalized versus an internal control (*e.g.*, beta-actin). For each 20 μl reaction, extracted RNA (generally 0.2-1 μg total) is placed into a sterile 0.5 or 1.5 ml microcentrifuge tube, and water added to a total volume of 12.5 μl. To each tube 7.5 μl of a buffer/enzyme mixture is added, which is prepared by mixing (in the order listed) 2.5 μl H_2O, 2.0 μl 10X reaction buffer, 10 μl oligo dT (20 pmol), 1.0 μl dNTP mix (10 mM each), 0.5 μl RNAsin® (20u) (Ambion, Inc., Hialeah, FL), and 0.5 μl MMLV reverse transcriptase (50u) (Ambion, Inc.). The contents are mixed by pipetting up and down, and the reaction mixture incubated at 42°C for 1 hour. The contents of each tube are centrifuged prior to amplification.

An amplification mixture is prepared by mixing in the following order: 1X PCR buffer II, 3 mM $MgCl_2$, 140 μM each dNTP, 0.175 pmol each oligo, 1:50,000 dil of SYBR® Green, 0.25 mg/ml BSA, 1 unit *Taq* polymerase, and H_2O to 20 μl. (PCR buffer II is available in 10X concentration from Perkin-Elmer, Norwalk, CT). In 1X concentration it contains 10 mM Tris pH 8.3 and 50 mM KCl. SYBR® Green (Molecular Probes, Eugene, OR) is a dye which fluoresces when bound to double stranded DNA. As double stranded PCR product is produced during amplification, the fluorescence from SYBR® Green increases. To each 20 μl aliquot of amplification mixture, 2 μl of template RT are added, and amplification carried out according to standard protocols.

The results can be expressed as the percent decrease in expression of the corresponding gene product relative to non-transfected cells, vehicle-only transfected (mock-transfected) cells, or cells transfected with reverse control oligonucleotides.

Example 7: Effect of Expression on Proliferation

The effect of gene expression on the inhibition of cell proliferation can be assessed in, for example, metastatic breast cancer cell lines (MDA-MB-231 ("231")), SW620 colon colorectal carcinoma cells, or SKOV3 cells (a human ovarian carcinoma cell line).

Cells are plated to approximately 60-80% confluency in 96-well dishes. Antisense or reverse control oligonucleotide iss diluted to 2 μM in OptiMEM™ and added to OptiMEM™ into which the delivery vehicle, lipitoid 116-6 in the case of SW620 cells or 1:1 lipitoid 1:cholesteroid 1 in the case of MDA-MB-231 cells, had been diluted. The oligo/delivery vehicle mixture is then further diluted into medium with serum on the cells. The final concentration of oligonucleotide for all experiments was 300 nM, and the final ratio of oligo to delivery vehicle for all experiments iss 1.5 nmol lipitoid/μg oligonucleotide.

Antisense oligonucleotides are prepared as described above (see Example 6). Cells are transfected overnight at 37°C and the transfection mixture replaced with fresh medium the next morning. Transfection is carried out as described above in Example 3.

Those antisense oligonucleotides that inhibit proliferation represent genes that play a role in production or maintenance of the cancerous phenotype.

Example 8: Effect of Gene Expression on Colony Formation

The effect of gene expression upon colony formation of, for example, SW620 cells, SKOV3 cells, and MD-MBA-231 cells can be tested in a soft agar assay. Soft agar assays are conducted by first establishing a bottom layer of 2 ml of 0.6% agar in media plated fresh within a few hours of layering on the cells. The cell layer is formed on the bottom layer by removing cells transfected as described above from plates using 0.05% trypsin and washing twice in media. The cells are counted in a Coulter counter, and resuspended to 10^6 per ml in media. 10 μl aliquots are placed with media in 96-well plates (to check counting with WST1), or diluted further for the soft agar assay. 2000 cells are plated in 800 μl 0.4% agar in duplicate wells above 0.6% agar bottom layer. After the cell layer agar solidifies, 2 ml of media is dribbled on top and antisense or reverse control oligo (produced as described in Example 6) added without delivery vehicles. Fresh media and oligos are added every 3-4 days. Colonies usually are expected to form in 10 days to 3 weeks. Fields of colonies are counted by eye. Wst-1 metabolism values can be used to compensate for small differences in starting cell number. Larger fields can be scanned for visual record of differences.

Those antisense oligonucleotides that inhibited colony formation represent genes that play a role in production or maintenance of the cancerous phenotype.

Example 9: Induction of Cell Death upon Depletion of Polypeptides by Depletion of mRNA ("Antisense Knockout")

In order to assess the effect of depletion of a target message upon cell death, SW620 cells, or other cells derived from a cancer of interest, are transfected for proliferation assays. For cytotoxic

effect in the presence of cisplatin (cis), the same protocol is followed but cells are left in the presence of 2 μM drug. Each day, cytotoxicity was monitored by measuring the amount of LDH enzyme released in the medium due to membrane damage. The activity of LDH is measured using the Cytotoxicity Detection Kit from Roche Molecular Biochemicals. The data is provided as a ratio of LDH released in the medium vs. the total LDH present in the well at the same time point and treatment (rLDH/tLDH). A positive control using antisense and reverse control oligonucleotides for BCL2 (a known anti-apoptotic gene) is included; loss of message for BCL2 leads to an increase in cell death compared with treatment with the control oligonucleotide (background cytotoxicity due to transfection).

Example 10: Functional Analysis of Gene Products Differentially Expressed in Cancer

The gene products of sequences of a gene differentially expressed in cancerous cells can be further analyzed to confirm the role and function of the gene product in tumorigenesis, *e.g.*, in promoting or inhibiting development of a metastatic phenotype. For example, the function of gene products corresponding to genes identified herein can be assessed by blocking function of the gene products in the cell. For example, where the gene product is secreted or associated with a cell surface membrane, blocking antibodies can be generated and added to cells to examine the effect upon the cell phenotype in the context of, for example, the transformation of the cell to a cancerous, particularly a metastatic, phenotype.

Where the gene product of the differentially expressed genes identified herein exhibits sequence homology to a protein of known function (*e.g.*, to a specific kinase or protease) and/or to a protein family of known function (*e.g.*, contains a domain or other consensus sequence present in a protease family or in a kinase family), then the role of the gene product in tumorigenesis, as well as the activity of the gene product, can be examined using small molecules that inhibit or enhance function of the corresponding protein or protein family.

Additional functional assays include, but are not necessarily limited to, those that analyze the effect of expression of the corresponding gene upon cell cycle and cell migration. Methods for performing such assays are well known in the art.

Example 11: Contig Assembly and Additional Gene Characterization

The sequences of the polynucleotides provided in the present invention can be used to extend the sequence information of the gene to which the polynucleotides correspond (*e.g.*, a gene, or mRNA encoded by the gene, having a sequence of the polynucleotide described herein). This expanded sequence information can in turn be used to further characterize the corresponding gene, which in turn

provides additional information about the nature of the gene product (*e.g.*, the normal function of the gene product). The additional information can serve to provide additional evidence of the gene product's use as a therapeutic target, and provide further guidance as to the types of agents that can modulate its activity.

For example, a contig can be assembled using the sequence of a polynucleotide described herein. A "contig" is a contiguous sequence of nucleotides that is assembled from nucleic acid sequences having overlapping (*e.g.*, shared or substantially similar) sequence information. The sequences of publicly-available ESTs (Expressed Sequence Tags) and the sequences of various clones from several cDNA libraries synthesized at Chiron were used in the contig assembly. The contig is assembled using the software program Sequencher, version 4.05, according to the manufacturer's instructions. The resulting contig can then be used to search both the public databases as well as databases internal to the applicatns to matchthe polynucleotide contiged with homology data and/or differential gene expressed data.

The sequence information obtained in the contig assembly described above can be used to obtain a consensus sequence derived from the contig using the Sequencher program. The consensus sequence can then be used as a query sequence in a BLASTN search of the DGTI DoubleTwist Gene Index (DoubleTwist, Inc., Oakland, CA), which contains all the EST and non-redundant sequence in public databases. Alternatively, a sequence of a polynucleotide described herein can be used directly as a query sequence in a BLASTN search of the DGTI DoubleTwist Gene Index.

Through contig assembly and the use of homology searching software programs, the sequence information provided herein can be readily extended to confirm, or confirm a predicted, gene having the sequence of the polynucleotides described in the present invention. Further the information obtained can be used to identify the function of the gene product of the gene corresponding to the polynucleotides described herein. While not necessary to the practice of the invention, identification of the function of the corresponding gene, can provide guidance in the design of therapeutics that target the gene to modulate its activity and modulate the cancerous phenotype (*e.g.*, inhibit metastasis, proliferation, and the like).

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it is readily apparent to those of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims. Those skilled in the art will recognize, or be able to ascertain, using not more than routine experimentation, many equivalents to the

specific embodiments of the invention described herein. Such specific embodiments and equivalents are intended to be encompassed by the following claims.

Deposit Information.

A deposit of the biological materials in the tables referenced below was made with the American Type Culture Collection, 10801 University Blvd., Manasas, VA 20110-2209, under the provisions of the Budapest Treaty, on or before the filing date of the present application. The accession number indicated is assigned after successful viability testing, and the requisite fees were paid. Access to said cultures will be available during pendency of the patent application to one determined by the Commissioner to be entitled to such under 37 C.F.R. §1.14 and 35 U.S.C. §122. All restriction on availability of said cultures to the public will be irrevocably removed upon the granting of a patent based upon the application. Moreover, the designated deposits will be maintained for a period of thirty (30) years from the date of deposit, or for five (5) years after the last request for the deposit; or for the enforceable life of the U.S. patent, whichever is longer. Should a culture become nonviable or be inadvertently destroyed, or, in the case of plasmid-containing strains, lose its plasmid, it will be replaced with a viable culture(s) of the same taxonomic description.

These deposits are provided merely as a convenience to those of skill in the art, and are not an admission that a deposit is required. A license may be required to make, use, or sell the deposited materials, and no such license is hereby granted. The deposit below was received by the ATCC on or before the filing date of the present application.

Table 11. Cell Lines Deposited with ATCC

Cell Line	Deposit Date	ATCC Accession No.	CMCC Accession No.
KM12L4-A	March 19, 1998	CRL-12496	11606
Km12C	May 15, 1998	CRL-12533	11611
MDA-MB-231	May 15, 1998	CRL-12532	10583
MCF-7	October 9, 1998	CRL-12584	10377

In addition, pools of selected clones, as well as libraries containing specific clones, were assigned an "ES" number (internal reference) and deposited with the ATCC. Table 13 below provides the ATCC Accession Nos. of the ES deposits, all of which were deposited on or before June 13, 2000. The names of the clones contained within each of these deposits are provided in the tables numbered 22 and greater (inserted before the claims).

Table 12: Pools of Clones and Libraries Deposited with ATCC on or before June 13, 2000.

Library No.	CMCC No.	ATCC Accession No.	Library No.	CMCC No.	ATCC Accession No.
ES168	5276	PTA-2027	ES 189	5304	PTA-2052
ES169	5277	PTA-2028	ES 190	5305	PTA-2053
ES170	5284	PTA-2029	ES 191	5306	PTA-2054
ES171	5285	PTA-2030	ES 192	5307	PTA-2055

Library No.	CMCC No.	ATCC Accession No.	Library No.	CMCC No.	ATCC Accession No.
ES172	5286	PTA-2031	ES 193	5308	PTA-2056
ES173	5287	PTA-2032	ES 194	5309	PTA-2057
ES174	5288	PTA-2033	ES 195	5310	PTA-2058
ES175	5289	PTA-2034	ES 196	5311	PTA-2059
ES176	5290	PTA-2035	ES 197	5312	PTA-2060
ES177	5291	PTA-2036	ES 198	5313	PTA-2061
ES178	5292	PTA-2037	ES 199	5314	PTA-2062
ES179	5293	PTA-2038	ES 200	5315	PTA-2048
ES180	5294	PTA-2039	ES 201	5316	PTA-2049
ES181	5295	PTA-2040	ES 202	5317	PTA-2063
ES182	5296	PTA-2041	ES 203	5318	PTA-2064
ES183	5297	PTA-2042	ES 204	5319	PTA-2065
ES184	5298	PTA-2043	ES 205	5320	PTA-2066
ES185	5299	PTA-2044	ES 206	5321	PTA-2067
ES 186	5301	PTA-2045	ES 207	5322	PTA-2068
ES 187	5302	PTA-2046	ES 208	5253	PTA-2050
ES 188	5303	PTA-2047	ES 209	5324	PTA-2051

Table 13 (inserted before the claims) provides the names of the clones in each of the above libraries.

Retrieval of Individual Clones from Deposit of Pooled Clones. Where the ATCC deposit is composed of a pool of cDNA clones or a library of cDNA clones, the deposit was prepared by first transfecting each of the clones into separate bacterial cells. The clones in the pool or library were then deposited as a pool of equal mixtures in the composite deposit. Particular clones can be obtained from the composite deposit using methods well known in the art. For example, a bacterial cell containing a particular clone can be identified by isolating single colonies, and identifying colonies containing the specific clone through standard colony hybridization techniques, using an oligonucleotide probe or probes designed to specifically hybridize to a sequence of the clone insert (*e.g.*, a probe based upon unmasked sequence of the encoded polynucleotide having the indicated SEQ ID NO). The probe should be designed to have a T_m of approximately 80°C (assuming 2°C for each A or T and 4°C for each G or C). Positive colonies can then be picked, grown in culture, and the recombinant clone isolated. Alternatively, probes designed in this manner can be used to PCR to isolate a nucleic acid molecule from the pooled clones according to methods well known in the art, *e.g.*, by purifying the cDNA from the deposited culture pool, and using the probes in PCR reactions to produce an amplified product having the corresponding desired polynucleotide sequence.

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
1	498509	2102.H02.gz43_275066	F	M00063514B:E04	GRRpz
2	644927	2102.F08.gz43_275160	F	M00063493D:G07	GRRpz
3	621081	2102.G10.gz43_275193	F	M00063507B:B08	GRRpz
4	558900	2102.F14.gz43_275256	F	M00063496B:F07	GRRpz
5	464791	2102.A16.gz43_275283	F	M00063157B:B09	GRRpz
6	558147	2102.B18.gz43_275316	F	M00063457A:B12	GRRpz
7	379154	2102.I24.gz43_275419	F	M00063601D:C05	GRRpz
8	643609	2103.F01.gz43_275432	F	M00063866B:H02	GRRpz
9	377696	2103.M06.gz43_275519	F	M00063943B:G12	GRRpz
10	554395	2103.K10.gz43_275581	F	M00063927A:B08	GRRpz
11	402353	2103.B13.gz43_275620	F	M00063803B:F11	GRRpz
12	380514	2103.E17.gz43_275687	F	M00063864A:H10	GRRpz
13	147279	2103.J21.gz43_275756	F	M00063923B:A04	GRRpz
14	884	2128.K06.gz43_277507	F	M00028627B:F12	MV-522
15	188377	2128.H15.gz43_277648	F	M00028359D:F09	MV-522
16	155615	2128.P17.gz43_277688	F	M00032476D:F07	MV-522
17	125604	2128.P18.gz43_277704	F	M00032477A:B02	MV-522
18	432159	2128.A24.gz43_277785	F	M00028061D:D10	MV-522
19	429735	2130.N02.gz43_277847	F	M00032736A:B06	MV-522
20	72838	2130.O05.gz43_277896	F	M00032745C:F03	MV-522
21	436888	2130.N09.gz43_277959	F	M00032738D:G11	MV-522
22	427571	2130.H13.gz43_278017	F	M00032685B:C10	MV-522
23	38494	2130.H16.gz43_278065	F	M00032686C:D10	MV-522
24	78607	2130.H18.gz43_278097	F	M00032686D:G09	MV-522
25	90192	2130.J18.gz43_278099	F	M00032703D:E10	MV-522
26	44615	2130.I20.gz43_278130	F	M00032695B:A01	MV-522
27	376753	2130.M21.gz43_278150	F	M00032732A:A03	MV-522
28	6342	2152.H10.gz43_278370	F	M00039109A:H09	UCP-3
29	387530	2152.D12.gz43_278398	F	M00039069D:E12	UCP-3
30	36453	2152.B14.gz43_278428	F	M00039052B:H03	UCP-3
31	376044	2152.A18.gz43_278491	F	M00039047C:A05	UCP-3
32	375415	2152.J18.gz43_278500	F	M00039121C:C06	UCP-3
33	375706	2153.F03.gz43_278756	F	M00039222C:G06	UCP-3
34	379046	2153.J06.gz43_278808	F	M00039244C:F10	UCP-3
35	390017	2153.I08.gz43_278839	F	M00039240A:H08	UCP-3
36	377596	2153.O08.gz43_278845	F	M00039274C:D12	UCP-3
37	376384	2153.I11.gz43_278887	F	M00039241A:H11	UCP-3
38	372952	2153.K14.gz43_278937	F	M00039251A:G12	UCP-3
39	377696	2154.M04.gz43_279163	F	M00039404B:G11	UCP-3
40	60037	2154.G05.gz43_279173	F	M00039330B:H09	UCP-3
41	390968	2154.I18.gz43_279383	F	M00039346C:G08	UCP-3
42	376044	2154.G21.gz43_279429	F	M00039336A:C07	UCP-3

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
43	60037	2155.J03.gz43_279528	F	M00039632A:C01	UCP-3
44	376839	2155.N05.gz43_279564	F	M00039664B:H10	UCP-3
45	373680	2155.P11.gz43_279662	F	M00039674B:G11	UCP-3
46	373973	2155.C12.gz43_279665	F	M00039457A:D07	UCP-3
47	379805	2155.N15.gz43_279724	F	M00039665C:B01	UCP-3
48	376439	2155.F16.gz43_279732	F	M00039479A:A10	UCP-3
49	376994	2155.I16.gz43_279735	F	M00039619C:B01	UCP-3
50	378420	2155.B21.gz43_279808	F	M00039451B:F01	UCP-3
51	375510	2155.F21.gz43_279812	F	M00039479D:C06	UCP-3
52	24210	2155.P22.gz43_279838	F	M00039675C:C05	UCP-3
53	397167	2164.J03.gz43_279912	F	M00039778D:D05	UCP-3
54	380025	2164.I10.gz43_280023	F	M00039774A:E11	UCP-3
55	216179	2164.P10.gz43_280030	F	M00039823D:D09	UCP-3
56	379046	2164.B15.gz43_280096	F	M00039681B:F05	UCP-3
57	379279	2164.A24.gz43_280239	F	M00039679C:A02	UCP-3
58	376074	2164.O24.gz43_280253	F	M00039820D:F08	UCP-3
59	373905	2165.H01.gz43_280262	F	M00039883D:G06	UCP-3
60	1300	2165.K01.gz43_280265	F	M00039905B:F09	UCP-3
61	393635	2165.H06.gz43_280342	F	M00039885B:A10	UCP-3
62	396969	2165.P07.gz43_280366	F	M00039978D:C04	UCP-3
63	398061	2165.F09.gz43_280388	F	M00039871C:C01	UCP-3
64	376808	2165.I10.gz43_280407	F	M00039893A:G12	UCP-3
65	6342	2166.A06.gz43_281279	F	M00039986B:A11	UCP-3
66	233814	2166.K07.gz43_281305	F	M00040076B:D01	UCP-3
67	24210	2166.N07.gz43_281308	F	M00040096D:C03	UCP-3
68	24210	2166.A11.gz43_281359	F	M00039988B:C08	UCP-3
69	377696	2166.J11.gz43_281368	F	M00040070C:D11	UCP-3
70	398831	2166.A23.gz43_281551	F	M00040001A:H02	UCP-3
71	185432	2166.P24.gz43_281582	F	M00040113C:H09	UCP-3
72	505275	2104.D01.gz43_297323	F	M00064082C:D11	GRRpz
73	11379	2104.N01.gz43_297333	F	M00064194B:A02	GRRpz
74	446397	2104.N03.gz43_297365	F	M00064195C:B02	GRRpz
75	418763	2104.P04.gz43_297383	F	M00064220B:E01	GRRpz
76	469367	2104.N05.gz43_297397	F	M00064196D:C10	GRRpz
77	639578	2104.C08.gz43_297434	F	M00064077B:H02	GRRpz
78	376559	2104.E08.gz43_297436	F	M00064101B:E12	GRRpz
79	649035	2104.D11.gz43_297483	F	M00064085B:A12	GRRpz
80	647586	2104.H11.gz43_297487	F	M00064131B:A09	GRRpz
81	646187	2104.F12.gz43_297501	F	M00064112A:G03	GRRpz
82	727888	2104.N13.gz43_297525	F	M00064201A:C08	GRRpz
83	558382	2104.E17.gz43_297580	F	M00064104B:A01	GRRpz
84	52644	2104.C19.gz43_297610	F	M00064081A:D04	GRRpz

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
85	454622	2104.I20.gz43_297632	F	M00064147B:G08	GRRpz
86	554032	2104.A21.gz43_297640	F	M00064064D:D11	GRRpz
87	463217	2104.E23.gz43_297676	F	M00064107C:E03	GRRpz
88	189073	1521.H06.gz43_303496	F	M00027103D:B05	MCF-7
89	188309	1521.J06.gz43_303498	F	M00027219B:G12	MCF-7
90	187525	1521.N10.gz43_303566	F	M00027514C:F01	MCF-7
91	215366	1521.N12.gz43_303598	F	M00027517C:F08	MCF-7
92	186594	1521.H13.gz43_303608	F	M00027123D:F02	MCF-7
93	218904	1521.O13.gz43_303615	F	M00027586B:B03	MCF-7
94	189993	1521.C14.gz43_303619	F	M00023406A:G03	MCF-7
95	222818	1521.H14.gz43_303624	F	M00027126C:H05	MCF-7
96	185056	1521.O16.gz43_303663	F	M00027587C:F02	MCF-7
97	186404	1521.P20.gz43_303728	F	M00027694C:C11	MCF-7
98	649744	2116.I06.gz43_306217	F	M00063580A:A07	WOca
99	535955	2116.P08.gz43_306256	F	M00063994B:D10	WOca
100	375328	2116.J09.gz43_306266	F	M00063592B:E09	WOca
101	449206	2116.A13.gz43_306321	F	M00063165C:F10	WOca
102	89082	2116.E15.gz43_306357	F	M00063552B:B06	WOca
103	730600	2116.D21.gz43_306452	F	M00063546B:F01	WOca
104	372621	2116.O22.gz43_306479	F	M00063988A:C02	WOca
105	416886	2117.M03.gz43_306557	F	M00064394A:C02	WOca
106	372621	2117.D05.gz43_306580	F	M00064307C:E12	WOca
107	644919	2118.N03.gz43_306942	F	M00064601C:H06	WOca
108	446397	2118.A09.gz43_307025	F	M00064446D:C08	WOca
109	177443	2118.M09.gz43_307037	F	M00064592D:F05	WOca
110	730238	2118.H24.gz43_307272	F	M00064534D:H04	WOca
111	427907	2131.A01.gz43_307885	F	M00032766A:A10	MV-522
112	48238	2131.M02.gz43_307913	F	M00032886A:D04	MV-522
113	226324	2131.B04.gz43_307934	F	M00032783A:H08	MV-522
114	441801	2131.E06.gz43_307969	F	M00032809B:E10	MV-522
115	62016	2131.K11.gz43_308055	F	M00032872B:A02	MV-522
116	48238	2131.E12.gz43_308065	F	M00032811A:G10	MV-522
117	34071	2131.I13.gz43_308085	F	M00032857A:B02	MV-522
118	221686	2131.B14.gz43_308094	F	M00032786A:H04	MV-522
119	440284	2131.J16.gz43_308134	F	M00032865A:D11	MV-522
120	12481	2131.P18.gz43_308172	F	M00032914B:D09	MV-522
121	20453	2131.A19.gz43_308173	F	M00032779A:A04	MV-522
122	26926	2131.I19.gz43_308181	F	M00032858D:H11	MV-522
123	37805	2131.P19.gz43_308188	F	M00032915B:D01	MV-522
124	441874	2131.I21.gz43_308213	F	M00032859C:E04	MV-522
125	48238	2131.A23.gz43_308237	F	M00032780A:B09	MV-522
126	169458	1513.O03.gz43_300292	F	M00022648C:D08	MDA-MB-231

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
127	145815	1513.F09.gz43_300379	F	M00022135D:D06	MDA-MB-231
128	158321	1513.H09.gz43_300381	F	M00022255B:F12	MDA-MB-231
129	168195	1513.L10.gz43_300401	F	M00022537D:C05	MDA-MB-231
130	101499	1513.J13.gz43_300447	F	M00022445D:E12	MDA-MB-231
131	142842	1513.A14.gz43_300454	F	M00007960D:E09	MDA-MB-231
132	153316	1513.E14.gz43_300458	F	M00022072A:E12	MDA-MB-231
133	142614	1513.A15.gz43_300470	F	M00007963D:D03	MDA-MB-231
134	99011	1513.N16.gz43_300499	F	M00022622A:G01	MDA-MB-231
135	171073	1513.P18.gz43_300533	F	M00022710C:H03	MDA-MB-231
136	120049	1513.D19.gz43_300537	F	M00021925A:H07	MDA-MB-231
137	446572	1562.B01.gz43_207804	F	M00042546A:D03	UC2-NormColon
138	464091	1562.F01.gz43_207808	F	M00042552D:A11	UC2-NormColon
139	408386	1562.J01.gz43_207812	F	M00042560B:A01	UC2-NormColon
140	446829	1562.L02.gz43_207830	F	M00042563A:F10	UC2-NormColon
141	43338	1562.P03.gz43_207850	F	M00042569B:G07	UC2-NormColon
142	451780	1562.F04.gz43_207856	F	M00042554A:C02	UC2-NormColon
143	456462	1562.J04.gz43_207860	F	M00042560B:G10	UC2-NormColon
144	469511	1562.G05.gz43_207873	F	M00042555D:G10	UC2-NormColon
145	455075	1562.H05.gz43_207874	F	M00042557A:D09	UC2-NormColon
146	447346	1562.P05.gz43_207882	F	M00042569C:B05	UC2-NormColon
147	147196	1562.M06.gz43_207895	F	M00042564D:F10	UC2-NormColon
148	467262	1562.F08.gz43_207920	F	M00042554C:E02	UC2-NormColon
149	459536	1562.L09.gz43_207942	F	M00042563C:D08	UC2-NormColon
150	460190	1562.P09.gz43_207946	F	M00042569D:D02	UC2-NormColon
151	447597	1562.F10.gz43_207952	F	M00042554C:F09	UC2-NormColon
152	451737	1562.G10.gz43_207953	F	M00042556A:G12	UC2-NormColon
153	446614	1562.L10.gz43_207958	F	M00042563C:E02	UC2-NormColon
154	432159	1562.M10.gz43_207959	F	M00042565A:G05	UC2-NormColon
155	459523	1562.L11.gz43_207974	F	M00042563D:D02	UC2-NormColon
156	460516	1562.P11.gz43_207978	F	M00042570A:E08	UC2-NormColon
157	446674	1562.D12.gz43_207982	F	M00042550A:D12	UC2-NormColon
158	465594	1562.F12.gz43_207984	F	M00042554D:C08	UC2-NormColon
159	466719	1562.G12.gz43_207985	F	M00042556B:D12	UC2-NormColon
160	463487	1562.M12.gz43_207991	F	M00042565A:H03	UC2-NormColon
161	446389	1562.B13.gz43_207996	F	M00042546D:E06	UC2-NormColon
162	462149	1562.C14.gz43_208013	F	M00042548B:G01	UC2-NormColon
163	447174	1562.G14.gz43_208017	F	M00042556B:E10	UC2-NormColon
164	457405	1562.K14.gz43_208021	F	M00042562C:A07	UC2-NormColon
165	460766	1562.O15.gz43_208041	F	M00042568C:E08	UC2-NormColon
166	446703	1562.N16.gz43_208056	F	M00042567C:E02	UC2-NormColon
167	446981	1562.D18.gz43_208078	F	M00042550C:H10	UC2-NormColon
168	387077	1562.H18.gz43_208082	F	M00042558A:D03	UC2-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
169	460972	1562.N18.gz43_208088	F	M00042567C:E07	UC2-NormColon
170	417078	1562.P18.gz43_208090	F	M00042570B:F11	UC2-NormColon
171	461559	1562.L19.gz43_208102	F	M00042564A:F01	UC2-NormColon
172	464905	1562.F20.gz43_208112	F	M00042555B:B07	UC2-NormColon
173	468330	1562.H20.gz43_208114	F	M00042558A:F11	UC2-NormColon
174	446620	1562.J21.gz43_208132	F	M00042561B:E12	UC2-NormColon
175	457842	1562.P21.gz43_208138	F	M00042570C:B12	UC2-NormColon
176	446531	1562.B22.gz43_208140	F	M00042547B:D11	UC2-NormColon
177	446621	1562.J24.gz43_208180	F	M00042561C:E12	UC2-NormColon
178	380127	1562.N24.gz43_208184	F	M00042567D:E12	UC2-NormColon
179	464275	1563.D01.gz43_208190	F	M00042575D:A11	UC2-NormColon
180	456920	1563.C04.gz43_208237	F	M00042574C:A04	UC2-NormColon
181	466971	1563.B05.gz43_208252	F	M00042573A:D05	UC2-NormColon
182	142559	1563.J05.gz43_208260	F	M00042698A:A01	UC2-NormColon
183	457890	1563.G08.gz43_208305	F	M00042691D:B03	UC2-NormColon
184	453605	1563.K08.gz43_208309	F	M00042699C:H06	UC2-NormColon
185	465339	1563.N08.gz43_208312	F	M00042705A:B07	UC2-NormColon
186	461734	1563.I09.gz43_208323	F	M00042695C:F05	UC2-NormColon
187	459961	1563.D12.gz43_208366	F	M00042576B:D11	UC2-NormColon
188	463951	1563.F13.gz43_208384	F	M00042580C:A03	UC2-NormColon
189	468783	1563.A14.gz43_208395	F	M00042571C:F03	UC2-NormColon
190	447597	1563.E14.gz43_208399	F	M00042578A:E08	UC2-NormColon
191	463368	1563.I14.gz43_208403	F	M00042695D:H01	UC2-NormColon
192	451383	1563.C15.gz43_208413	F	M00042575A:E02	UC2-NormColon
193	467293	1563.G16.gz43_208433	F	M00042692A:E11	UC2-NormColon
194	446922	1563.O16.gz43_208441	F	M00042707C:A09	UC2-NormColon
195	446213	1563.D17.gz43_208446	F	M00042576D:A08	UC2-NormColon
196	460244	1563.F19.gz43_208480	F	M00042691A:D08	UC2-NormColon
197	460789	1563.A20.gz43_208491	F	M00042572B:E05	UC2-NormColon
198	451382	1563.C20.gz43_208493	F	M00042575B:F02	UC2-NormColon
199	468109	1563.K20.gz43_208501	F	M00042700C:F11	UC2-NormColon
200	447326	1563.L20.gz43_208502	F	M00042702B:B07	UC2-NormColon
201	463896	1563.B21.gz43_208508	F	M00042573D:A10	UC2-NormColon
202	446839	1563.D21.gz43_208510	F	M00042576D:F01	UC2-NormColon
203	446933	1563.E22.gz43_208527	F	M00042579A:B05	UC2-NormColon
204	447826	1563.L22.gz43_208534	F	M00042702B:G07	UC2-NormColon
205	446409	1563.B23.gz43_208540	F	M00042574A:F05	UC2-NormColon
206	453908	1573.N01.gz43_208584	F	M00042895C:C10	UC2-NormColon
207	447421	1573.D02.gz43_208590	F	M00042747D:C08	UC2-NormColon
208	447141	1573.P02.gz43_208602	F	M00042898A:H05	UC2-NormColon
209	447645	1573.E04.gz43_208623	F	M00042750D:E07	UC2-NormColon
210	401426	1573.K06.gz43_208661	F	M00042890D:G05	UC2-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
211	466894	1573.B07.gz43_208668	F	M00042744A:D11	UC2-NormColon
212	447161	1573.J08.gz43_208692	F	M00042889D:A01	UC2-NormColon
213	633946	1573.M08.gz43_208695	F	M00042894B:E05	UC2-NormColon
214	557974	1573.L09.gz43_208710	F	M00042892C:E03	UC2-NormColon
215	466920	1573.D10.gz43_208718	F	M00042748D:D08	UC2-NormColon
216	642146	1573.F10.gz43_208720	F	M00042882C:F06	UC2-NormColon
217	464205	1573.J10.gz43_208724	F	M00042889D:A12	UC2-NormColon
218	641890	1573.L10.gz43_208726	F	M00042892D:C04	UC2-NormColon
219	650195	1573.H11.gz43_208738	F	M00042886C:F01	UC2-NormColon
220	467293	1573.F12.gz43_208752	F	M00042882C:G07	UC2-NormColon
221	650756	1573.N12.gz43_208760	F	M00042896A:D04	UC2-NormColon
222	452611	1573.N13.gz43_208776	F	M00042896A:E03	UC2-NormColon
223	650944	1573.N14.gz43_208792	F	M00042896A:F09	UC2-NormColon
224	639372	1573.E15.gz43_208799	F	M00042881C:C11	UC2-NormColon
225	645690	1573.F15.gz43_208800	F	M00042882D:C04	UC2-NormColon
226	645470	1573.H16.gz43_208818	F	M00042886D:E10	UC2-NormColon
227	651029	1573.M17.gz43_208839	F	M00042894D:G05	UC2-NormColon
228	639849	1573.F18.gz43_208848	F	M00042883A:F06	UC2-NormColon
229	486238	1573.K19.gz43_208869	F	M00042891C:H01	UC2-NormColon
230	463060	1573.G21.gz43_208897	F	M00042885A:G09	UC2-NormColon
231	469150	1573.C22.gz43_208909	F	M00042747A:G12	UC2-NormColon
232	472101	1574.O01.gz43_208969	F	M00054797D:F01	UC2-NormColon
233	641875	1574.P02.gz43_208986	F	M00054799C:G11	UC2-NormColon
234	465104	1574.A03.gz43_208987	F	M00042900B:B10	UC2-NormColon
235	470641	1574.C03.gz43_208989	F	M00042904A:H10	UC2-NormColon
236	451624	1574.D04.gz43_209006	F	M00042906C:A10	UC2-NormColon
237	639391	1574.N04.gz43_209016	F	M00054796B:A01	UC2-NormColon
238	470462	1574.B05.gz43_209020	F	M00042902B:H01	UC2-NormColon
239	482043	1574.J05.gz43_209028	F	M00042915A:E06	UC2-NormColon
240	641525	1574.N05.gz43_209032	F	M00054796B:C08	UC2-NormColon
241	642691	1574.E06.gz43_209039	F	M00042908A:B01	UC2-NormColon
242	466697	1574.G06.gz43_209041	F	M00042910D:A02	UC2-NormColon
243	649965	1574.H06.gz43_209042	F	M00042912A:C01	UC2-NormColon
244	651051	1574.J06.gz43_209044	F	M00042915A:G10	UC2-NormColon
245	450506	1574.M06.gz43_209047	F	M00054794C:G11	UC2-NormColon
246	453572	1574.O06.gz43_209049	F	M00054798B:A01	UC2-NormColon
247	447660	1574.B07.gz43_209052	F	M00042902C:E11	UC2-NormColon
248	447147	1574.C07.gz43_209053	F	M00042905A:A07	UC2-NormColon
249	647639	1574.F07.gz43_209056	F	M00042909B:C04	UC2-NormColon
250	649965	1574.G08.gz43_209073	F	M00042910D:E11	UC2-NormColon
251	639371	1574.I09.gz43_209091	F	M00042914A:B05	UC2-NormColon
252	474298	1574.M09.gz43_209095	F	M00054794D:D02	UC2-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
253	646568	1574.M10.gz43_209111	F	M00054794D:D08	UC2-NormColon
254	639787	1574.P10.gz43_209114	F	M00054800B:C06	UC2-NormColon
255	447750	1574.A11.gz43_209115	F	M00042901A:F12	UC2-NormColon
256	649810	1574.G11.gz43_209121	F	M00042911A:A02	UC2-NormColon
257	645924	1574.H11.gz43_209122	F	M00042912B:F11	UC2-NormColon
258	413767	1574.L11.gz43_209126	F	M00054793C:D11	UC2-NormColon
259	641069	1574.E12.gz43_209135	F	M00042908B:A11	UC2-NormColon
260	649900	1574.G12.gz43_209137	F	M00042911A:B02	UC2-NormColon
261	560868	1574.J12.gz43_209140	F	M00042915C:E05	UC2-NormColon
262	513262	1574.P12.gz43_209146	F	M00054800B:C11	UC2-NormColon
263	640306	1574.L13.gz43_209158	F	M00054793D:H11	UC2-NormColon
264	389591	1574.A14.gz43_209163	F	M00042901A:H11	UC2-NormColon
265	447815	1574.C14.gz43_209165	F	M00042905C:G08	UC2-NormColon
266	95617	1574.D14.gz43_209166	F	M00042907A:B11	UC2-NormColon
267	465984	1574.B15.gz43_209180	F	M00042903B:C09	UC2-NormColon
268	447692	1574.D15.gz43_209182	F	M00042907A:F03	UC2-NormColon
269	641029	1574.G15.gz43_209185	F	M00042911A:D04	UC2-NormColon
270	650527	1574.J15.gz43_209188	F	M00042915D:A11	UC2-NormColon
271	641315	1574.O15.gz43_209193	F	M00054798D:A12	UC2-NormColon
272	474298	1574.P15.gz43_209194	F	M00054800B:E08	UC2-NormColon
273	645954	1574.H16.gz43_209202	F	M00042912D:H08	UC2-NormColon
274	640181	1574.M16.gz43_209207	F	M00054795A:A08	UC2-NormColon
275	650235	1574.F17.gz43_209216	F	M00042909C:F10	UC2-NormColon
276	640356	1574.H17.gz43_209218	F	M00042912D:H10	UC2-NormColon
277	649744	1574.E18.gz43_209231	F	M00042908C:A03	UC2-NormColon
278	650564	1574.F18.gz43_209232	F	M00042909D:B11	UC2-NormColon
279	527355	1574.G18.gz43_209233	F	M00042911A:H12	UC2-NormColon
280	452989	1574.H18.gz43_209234	F	M00042913A:D09	UC2-NormColon
281	648159	1574.K18.gz43_209237	F	M00054792B:A03	UC2-NormColon
282	714629	1574.E20.gz43_209263	F	M00042908C:D12	UC2-NormColon
283	467364	1574.I20.gz43_209267	F	M00042914B:H03	UC2-NormColon
284	644789	1574.N20.gz43_209272	F	M00054797C:F03	UC2-NormColon
285	646404	1574.J21.gz43_209284	F	M00054791A:G04	UC2-NormColon
286	639740	1574.H22.gz43_209298	F	M00042913B:E10	UC2-NormColon
287	649852	1574.I22.gz43_209299	F	M00042914D:B10	UC2-NormColon
288	644376	1574.G23.gz43_209313	F	M00042911B:H08	UC2-NormColon
289	639901	1574.P23.gz43_209322	F	M00054800D:D08	UC2-NormColon
290	647086	1574.E24.gz43_209327	F	M00042908D:G12	UC2-NormColon
291	562247	1574.G24.gz43_209329	F	M00042911C:D01	UC2-NormColon
292	446974	1574.J24.gz43_209332	F	M00054791B:C09	UC2-NormColon
293	513248	1575.A01.gz43_209339	F	M00054800D:F08	UC2-NormColon
294	467989	1575.M01.gz43_209351	F	M00055429B:B12	UC2-NormColon

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SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
295	650184	1575.N01.gz43_209352	F	M00055430D:F04	UC2-NormColon
296	649872	1575.E02.gz43_209359	F	M00054916A:A05	UC2-NormColon
297	649506	1575.G02.gz43_209361	F	M00054918A:D02	UC2-NormColon
298	446254	1575.M02.gz43_209367	F	M00055429B:E12	UC2-NormColon
299	641542	1575.O02.gz43_209369	F	M00055432B:H02	UC2-NormColon
300	649933	1575.I03.gz43_209379	F	M00054920B:C04	UC2-NormColon
301	639444	1575.M03.gz43_209383	F	M00055429B:G04	UC2-NormColon
302	553100	1575.G04.gz43_209393	F	M00054918A:F09	UC2-NormColon
303	549699	1575.A05.gz43_209403	F	M00054911A:C08	UC2-NormColon
304	639256	1575.E05.gz43_209407	F	M00054916A:E05	UC2-NormColon
305	644556	1575.H05.gz43_209410	F	M00054919C:F06	UC2-NormColon
306	500337	1575.I05.gz43_209411	F	M00054920B:C12	UC2-NormColon
307	643924	1575.K05.gz43_209413	F	M00055427A:F01	UC2-NormColon
308	639394	1575.E06.gz43_209423	F	M00054916A:F10	UC2-NormColon
309	452986	1575.J06.gz43_209428	F	M00055426B:B02	UC2-NormColon
310	654723	1575.K06.gz43_209429	F	M00055427A:F02	UC2-NormColon
311	645344	1575.N07.gz43_209448	F	M00055431A:H05	UC2-NormColon
312	645162	1575.O07.gz43_209449	F	M00055432C:F01	UC2-NormColon
313	589098	1575.B08.gz43_209452	F	M00054912B:C05	UC2-NormColon
314	643843	1575.F08.gz43_209456	F	M00054917C:D03	UC2-NormColon
315	647109	1575.P08.gz43_209466	F	M00055434A:A03	UC2-NormColon
316	467381	1575.D09.gz43_209470	F	M00054914D:G07	UC2-NormColon
317	570812	1575.N09.gz43_209480	F	M00055431B:A01	UC2-NormColon
318	559776	1575.A10.gz43_209483	F	M00054911A:G01	UC2-NormColon
319	648532	1575.F10.gz43_209488	F	M00054917C:F03	UC2-NormColon
320	449861	1575.G10.gz43_209489	F	M00054918B:H01	UC2-NormColon
321	643843	1575.I10.gz43_209491	F	M00054920C:A06	UC2-NormColon
322	41141	1575.K10.gz43_209493	F	M00055427B:E01	UC2-NormColon
323	648664	1575.E11.gz43_209503	F	M00054916B:E02	UC2-NormColon
324	640814	1575.K11.gz43_209509	F	M00055427B:F06	UC2-NormColon
325	584071	1575.M11.gz43_209511	F	M00055429D:G07	UC2-NormColon
326	450225	1575.C12.gz43_209517	F	M00054913C:G03	UC2-NormColon
327	452707	1575.I12.gz43_209523	F	M00054920C:D05	UC2-NormColon
328	243722	1575.L12.gz43_209526	F	M00055428C:G06	UC2-NormColon
329	641057	1575.B13.gz43_209532	F	M00054912C:C01	UC2-NormColon
330	413767	1575.D13.gz43_209534	F	M00054915A:G03	UC2-NormColon
331	504568	1575.K13.gz43_209541	F	M00055427C:A06	UC2-NormColon
332	639992	1575.A15.gz43_209563	F	M00054911B:E10	UC2-NormColon
333	456923	1575.G15.gz43_209569	F	M00054918D:C03	UC2-NormColon
334	649555	1575.I15.gz43_209571	F	M00054920C:F02	UC2-NormColon
335	649746	1575.J15.gz43_209572	F	M00055426C:C10	UC2-NormColon
336	644692	1575.F16.gz43_209584	F	M00054917D:A12	UC2-NormColon

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SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
337	452204	1575.G16.gz43_209585	F	M00054918D:C11	UC2-NormColon
338	61616	1575.H16.gz43_209586	F	M00054920A:A05	UC2-NormColon
339	495143	1575.M16.gz43_209591	F	M00055430B:E08	UC2-NormColon
340	644371	1575.O16.gz43_209593	F	M00055433A:B07	UC2-NormColon
341	630269	1575.K17.gz43_209605	F	M00055427C:E12	UC2-NormColon
342	446932	1575.O17.gz43_209609	F	M00055433A:B08	UC2-NormColon
343	639662	1575.F18.gz43_209616	F	M00054917D:D12	UC2-NormColon
344	611927	1575.L18.gz43_209622	F	M00055428D:G12	UC2-NormColon
345	641925	1575.O18.gz43_209625	F	M00055433A:C02	UC2-NormColon
346	651020	1575.P18.gz43_209626	F	M00055434C:B11	UC2-NormColon
347	639255	1575.F19.gz43_209632	F	M00054917D:E05	UC2-NormColon
348	468222	1575.G19.gz43_209633	F	M00054918D:H09	UC2-NormColon
349	468783	1575.K19.gz43_209637	F	M00055427C:H11	UC2-NormColon
350	417130	1575.B20.gz43_209644	F	M00054912D:G01	UC2-NormColon
351	448606	1575.B21.gz43_209660	F	M00054912D:G04	UC2-NormColon
352	456420	1575.K21.gz43_209669	F	M00055427D:E05	UC2-NormColon
353	640369	1575.P21.gz43_209674	F	M00055434D:B06	UC2-NormColon
354	473854	1575.E22.gz43_209679	F	M00054917A:F07	UC2-NormColon
355	564440	1575.H22.gz43_209682	F	M00054920A:C11	UC2-NormColon
356	639520	1575.L22.gz43_209686	F	M00055429A:H04	UC2-NormColon
357	649195	1575.O22.gz43_209689	F	M00055433A:E04	UC2-NormColon
358	57183	1575.P22.gz43_209690	F	M00055434D:E09	UC2-NormColon
359	648609	1575.E23.gz43_209695	F	M00054917B:A05	UC2-NormColon
360	648532	1575.F23.gz43_209696	F	M00054917D:H02	UC2-NormColon
361	642073	1575.N23.gz43_209704	F	M00055432B:B04	UC2-NormColon
362	377855	1575.B24.gz43_209708	F	M00054913A:B12	UC2-NormColon
363	452845	1575.G24.gz43_209713	F	M00054919A:H04	UC2-NormColon
364	638758	1575.O24.gz43_209721	F	M00055433C:A11	UC2-NormColon
365	639829	1576.A04.gz43_209771	F	M00055435B:C09	UC2-NormColon
366	484145	1576.I05.gz43_209795	F	M00055446B:A12	UC2-NormColon
367	640055	1576.A08.gz43_209835	F	M00055435C:E12	UC2-NormColon
368	639928	1576.I08.gz43_209843	F	M00055446B:D08	UC2-NormColon
369	526606	1576.L08.gz43_209846	F	M00055450B:G07	UC2-NormColon
370	653616	1576.E09.gz43_209855	F	M00055440D:D02	UC2-NormColon
371	624440	1576.M12.gz43_209911	F	M00055451C:B08	UC2-NormColon
372	560791	1576.O12.gz43_209913	F	M00055453D:E12	UC2-NormColon
373	639287	1576.A13.gz43_209915	F	M00055435D:G11	UC2-NormColon
374	475184	1576.M14.gz43_209943	F	M00055451C:E10	UC2-NormColon
375	626061	1576.A15.gz43_209947	F	M00055436A:E04	UC2-NormColon
376	640734	1576.E16.gz43_209967	F	M00055441A:G07	UC2-NormColon
377	466092	1576.B17.gz43_209980	F	M00055437D:B06	UC2-NormColon
378	639711	1576.A19.gz43_210011	F	M00055436B:B06	UC2-NormColon

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SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
379	640522	1576.C21.gz43_210045	F	M00055439B:B07	UC2-NormColon
380	651038	1585.I01.gz43_210211	F	M00055465A:C05	UC2-NormColon
381	466440	1585.B02.gz43_210220	F	M00055456C:A10	UC2-NormColon
382	648123	1585.C02.gz43_210221	F	M00055458B:B04	UC2-NormColon
383	646318	1585.K02.gz43_210229	F	M00055468A:A05	UC2-NormColon
384	598589	1585.E03.gz43_210239	F	M00055460B:G06	UC2-NormColon
385	447863	1585.F03.gz43_210240	F	M00055461A:H03	UC2-NormColon
386	562236	1585.P05.gz43_210282	F	M00055494C:G10	UC2-NormColon
387	559369	1585.A06.gz43_210283	F	M00055456A:B03	UC2-NormColon
388	484126	1585.B06.gz43_210284	F	M00055456C:G04	UC2-NormColon
389	558839	1585.P06.gz43_210298	F	M00055494C:G11	UC2-NormColon
390	555820	1585.J07.gz43_210308	F	M00055467A:A07	UC2-NormColon
391	544461	1585.H09.gz43_210338	F	M00055463D:G01	UC2-NormColon
392	642478	1585.A10.gz43_210347	F	M00055456A:F01	UC2-NormColon
393	643843	1585.C11.gz43_210365	F	M00055458C:G02	UC2-NormColon
394	640400	1585.G12.gz43_210385	F	M00055462C:A11	UC2-NormColon
395	645201	1585.L12.gz43_210390	F	M00055469C:F09	UC2-NormColon
396	640792	1585.F13.gz43_210400	F	M00055461C:E05	UC2-NormColon
397	640913	1585.H13.gz43_210402	F	M00055464B:E06	UC2-NormColon
398	639607	1585.I13.gz43_210403	F	M00055465D:F12	UC2-NormColon
399	639932	1585.B14.gz43_210412	F	M00055456D:G04	UC2-NormColon
400	640662	1585.D14.gz43_210414	F	M00055460A:D01	UC2-NormColon
401	598589	1585.G14.gz43_210417	F	M00055462C:C03	UC2-NormColon
402	556654	1585.H14.gz43_210418	F	M00055464B:E11	UC2-NormColon
403	555193	1585.O14.gz43_210425	F	M00055493D:B07	UC2-NormColon
404	641066	1585.E15.gz43_210431	F	M00055460D:B06	UC2-NormColon
405	664711	1585.H15.gz43_210434	F	M00055464B:G03	UC2-NormColon
406	549611	1585.I15.gz43_210435	F	M00055466A:C05	UC2-NormColon
407	639726	1585.K16.gz43_210453	F	M00055468C:B07	UC2-NormColon
408	607422	1585.F17.gz43_210464	F	M00055461D:C09	UC2-NormColon
409	584745	1585.M17.gz43_210471	F	M00055491A:H01	UC2-NormColon
410	661194	1585.H19.gz43_210498	F	M00055464D:A04	UC2-NormColon
411	559549	1585.J20.gz43_210516	F	M00055467D:A01	UC2-NormColon
412	641645	1585.A22.gz43_210539	F	M00055456B:G08	UC2-NormColon
413	641467	1585.C22.gz43_210541	F	M00055459B:A02	UC2-NormColon
414	640368	1585.F22.gz43_210544	F	M00055462A:A09	UC2-NormColon
415	412416	1585.G22.gz43_210545	F	M00055462D:H12	UC2-NormColon
416	650914	1585.H22.gz43_210546	F	M00055464D:F08	UC2-NormColon
417	3	1585.J22.gz43_210548	F	M00055467D:C10	UC2-NormColon
418	646318	1585.N22.gz43_210552	F	M00055492C:H07	UC2-NormColon
419	237288	1585.P22.gz43_210554	F	M00055495C:F03	UC2-NormColon
420	650605	1585.B23.gz43_210556	F	M00055457D:F09	UC2-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
421	643991	1585.E23.gz43_210559	F	M00055461A:A06	UC2-NormColon
422	398061	1585.G23.gz43_210561	F	M00055463A:A11	UC2-NormColon
423	505933	1585.J24.gz43_210580	F	M00055467D:G08	UC2-NormColon
424	640068	1585.K24.gz43_210581	F	M00055469A:D08	UC2-NormColon
425	474821	1585.N24.gz43_210584	F	M00055492D:B08	UC2-NormColon
426	234606	1587.C01.gz43_211361	F	M00055519A:F08	UC2-NormColon
427	597780	1587.E01.gz43_211363	F	M00055521C:B08	UC2-NormColon
428	492483	1587.B02.gz43_211376	F	M00055517C:H07	UC2-NormColon
429	644051	1587.C03.gz43_211393	F	M00055519A:H01	UC2-NormColon
430	639056	1587.E03.gz43_211395	F	M00055521C:C08	UC2-NormColon
431	643723	1587.L03.gz43_211402	F	M00055529D:D05	UC2-NormColon
432	639459	1587.N03.gz43_211404	F	M00055532C:G08	UC2-NormColon
433	639826	1587.P03.gz43_211406	F	M00055535B:A11	UC2-NormColon
434	552783	1587.A04.gz43_211407	F	M00055516B:E11	UC2-NormColon
435	590218	1587.D04.gz43_211410	F	M00055520B:D11	UC2-NormColon
436	559324	1587.E04.gz43_211411	F	M00055521C:D02	UC2-NormColon
437	646711	1587.L04.gz43_211418	F	M00055529D:D11	UC2-NormColon
438	639132	1587.M04.gz43_211419	F	M00055531B:D10	UC2-NormColon
439	207552	1587.N04.gz43_211420	F	M00055532D:A12	UC2-NormColon
440	116869	1587.O04.gz43_211421	F	M00055533D:G02	UC2-NormColon
441	481220	1587.D05.gz43_211426	F	M00055520B:E04	UC2-NormColon
442	645544	1587.K05.gz43_211433	F	M00055528D:B02	UC2-NormColon
443	650617	1587.M05.gz43_211435	F	M00055531B:E05	UC2-NormColon
444	194095	1587.O05.gz43_211437	F	M00055534A:E06	UC2-NormColon
445	446984	1587.B06.gz43_211440	F	M00055517D:D09	UC2-NormColon
446	290226	1587.B07.gz43_211456	F	M00055517D:D11	UC2-NormColon
447	634409	1587.P07.gz43_211470	F	M00055535C:A03	UC2-NormColon
448	640419	1587.G08.gz43_211477	F	M00055524B:B08	UC2-NormColon
449	649149	1587.L09.gz43_211498	F	M00055530A:C07	UC2-NormColon
450	640072	1587.P10.gz43_211518	F	M00055535C:E08	UC2-NormColon
451	641615	1587.J11.gz43_211528	F	M00055528A:E08	UC2-NormColon
452	639213	1587.M13.gz43_211563	F	M00055531D:E06	UC2-NormColon
453	641216	1587.N15.gz43_211596	F	M00055533B:B11	UC2-NormColon
454	650161	1587.A16.gz43_211599	F	M00055517A:D09	UC2-NormColon
455	558785	1587.B23.gz43_211712	F	M00055519A:C01	UC2-NormColon
456	642631	1588.B02.gz43_211780	F	M00055538C:E04	UC2-NormColon
457	639543	1588.F02.gz43_211784	F	M00055543D:H03	UC2-NormColon
458	473701	1588.F03.gz43_211800	F	M00055544A:A07	UC2-NormColon
459	562274	1588.G03.gz43_211801	F	M00055545B:A04	UC2-NormColon
460	643277	1588.D05.gz43_211830	F	M00055541C:D02	UC2-NormColon
461	556867	1588.G05.gz43_211833	F	M00055545B:C01	UC2-NormColon
462	646350	1588.P05.gz43_211842	F	M00055556A:A04	UC2-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
463	649335	1588.B06.gz43_211844	F	M00055538D:D12	UC2-NormColon
464	646159	1588.J06.gz43_211852	F	M00055548B:C03	UC2-NormColon
465	649099	1588.P06.gz43_211858	F	M00055556A:E07	UC2-NormColon
466	32812	1588.H09.gz43_211898	F	M00055546C:F11	UC2-NormColon
467	639480	1588.J09.gz43_211900	F	M00055548B:G06	UC2-NormColon
468	644242	1588.N09.gz43_211904	F	M00055553B:H04	UC2-NormColon
469	644723	1588.N11.gz43_211936	F	M00055553C:D06	UC2-NormColon
470	648748	1588.F13.gz43_211960	F	M00055544C:A01	UC2-NormColon
471	639099	1588.G13.gz43_211961	F	M00055545C:D09	UC2-NormColon
472	562414	1588.F15.gz43_211992	F	M00055544C:B07	UC2-NormColon
473	641078	1588.N15.gz43_212000	F	M00055553C:H12	UC2-NormColon
474	505042	1588.G16.gz43_212009	F	M00055545D:B06	UC2-NormColon
475	640747	1588.N16.gz43_212016	F	M00055553D:C07	UC2-NormColon
476	453606	1588.D17.gz43_212022	F	M00055542B:B11	UC2-NormColon
477	419706	1588.A18.gz43_212035	F	M00055538A:C05	UC2-NormColon
478	557983	1588.H21.gz43_212090	F	M00055547B:C05	UC2-NormColon
479	639114	1588.D22.gz43_212102	F	M00055542C:D07	UC2-NormColon
480	442531	1588.J22.gz43_212108	F	M00055549A:B04	UC2-NormColon
481	649668	1597.N02.gz43_212176	F	M00055574D:E02	UC2-NormColon
482	639781	1597.D05.gz43_212214	F	M00055561C:C07	UC2-NormColon
483	639056	1597.E05.gz43_212215	F	M00055562D:B06	UC2-NormColon
484	639698	1597.P05.gz43_212226	F	M00055577C:G02	UC2-NormColon
485	469731	1597.B06.gz43_212228	F	M00055559A:D06	UC2-NormColon
486	639593	1597.G06.gz43_212233	F	M00055566A:E02	UC2-NormColon
487	557975	1597.J06.gz43_212236	F	M00055569D:C02	UC2-NormColon
488	640356	1597.E08.gz43_212263	F	M00055563A:A02	UC2-NormColon
489	647431	1597.E09.gz43_212279	F	M00055563A:C03	UC2-NormColon
490	31112	1597.C10.gz43_212293	F	M00055560D:C03	UC2-NormColon
491	454825	1597.F10.gz43_212296	F	M00055565A:C08	UC2-NormColon
492	555021	1597.B12.gz43_212324	F	M00055559C:D07	UC2-NormColon
493	650740	1597.I12.gz43_212331	F	M00055569A:D01	UC2-NormColon
494	659031	1597.J12.gz43_212332	F	M00055570B:F07	UC2-NormColon
495	592122	1597.D14.gz43_212358	F	M00055562B:D03	UC2-NormColon
496	45921	1597.N14.gz43_212368	F	M00055575C:B04	UC2-NormColon
497	556511	1597.H15.gz43_212378	F	M00055568A:B04	UC2-NormColon
498	637966	1597.A16.gz43_212387	F	M00055558B:G11	UC2-NormColon
499	553318	1597.F16.gz43_212392	F	M00055565A:F11	UC2-NormColon
500	23961	1597.C17.gz43_212405	F	M00055561A:F07	UC2-NormColon
501	650235	1597.M17.gz43_212415	F	M00055574B:F06	UC2-NormColon
502	596882	1597.F18.gz43_212424	F	M00055565B:F04	UC2-NormColon
503	644928	1597.I18.gz43_212427	F	M00055569A:F06	UC2-NormColon
504	589483	1597.L18.gz43_212430	F	M00055573B:D11	UC2-NormColon

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SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
505	640956	1597.N18.gz43_212432	F	M00055575D:G04	UC2-NormColon
506	553602	1597.L19.gz43_212446	F	M00055573B:E01	UC2-NormColon
507	640851	1597.O20.gz43_212465	F	M00055577A:G09	UC2-NormColon
508	460666	1597.A21.gz43_212467	F	M00055558D:C08	UC2-NormColon
509	640195	1597.D22.gz43_212486	F	M00055562C:F02	UC2-NormColon
510	668852	1597.P22.gz43_212498	F	M00055578C:F11	UC2-NormColon
511	645913	1597.A23.gz43_212499	F	M00055558D:D07	UC2-NormColon
512	446230	1597.G23.gz43_212505	F	M00055567A:A06	UC2-NormColon
513	649349	1597.N23.gz43_212512	F	M00055576A:F07	UC2-NormColon
514	645538	1597.C24.gz43_212517	F	M00055561B:G12	UC2-NormColon
515	647069	1597.G24.gz43_212521	F	M00055567A:A11	UC2-NormColon
516	638869	1597.H24.gz43_212522	F	M00055568C:F07	UC2-NormColon
517	556	1597.I24.gz43_212523	F	M00055569B:G10	UC2-NormColon
518	648483	1597.O24.gz43_212529	F	M00055577B:F05	UC2-NormColon
519	447272	1598.M01.gz43_212543	F	M00055595C:F12	UC2-NormColon
520	640025	1598.B02.gz43_212548	F	M00055581A:C02	UC2-NormColon
521	415538	1598.E02.gz43_212551	F	M00055585B:F01	UC2-NormColon
522	478229	1598.M02.gz43_212559	F	M00055595C:G03	UC2-NormColon
523	644572	1598.H03.gz43_212570	F	M00055589B:E08	UC2-NormColon
524	648580	1598.B04.gz43_212580	F	M00055581C:A01	UC2-NormColon
525	470769	1598.L04.gz43_212590	F	M00055594C:B03	UC2-NormColon
526	554273	1598.M04.gz43_212591	F	M00055595D:C04	UC2-NormColon
527	641262	1598.C05.gz43_212597	F	M00055583A:A05	UC2-NormColon
528	645707	1598.F05.gz43_212600	F	M00055586D:G07	UC2-NormColon
529	463028	1598.N05.gz43_212608	F	M00055597B:B04	UC2-NormColon
530	640695	1598.P05.gz43_212610	F	M00055601B:D12	UC2-NormColon
531	641925	1598.D06.gz43_212614	F	M00055584A:G11	UC2-NormColon
532	449247	1598.E06.gz43_212615	F	M00055585C:F05	UC2-NormColon
533	646590	1598.L06.gz43_212622	F	M00055594C:F11	UC2-NormColon
534	641191	1598.A07.gz43_212627	F	M00055579C:D04	UC2-NormColon
535	641191	1598.P07.gz43_212642	F	M00055601B:H02	UC2-NormColon
536	641838	1598.K09.gz43_212669	F	M00055593A:F08	UC2-NormColon
537	641440	1598.N09.gz43_212672	F	M00055597D:B05	UC2-NormColon
538	640826	1598.M10.gz43_212687	F	M00055596A:E07	UC2-NormColon
539	459521	1598.A11.gz43_212691	F	M00055579D:C11	UC2-NormColon
540	140909	1598.G11.gz43_212697	F	M00055588B:H11	UC2-NormColon
541	641467	1598.J12.gz43_212716	F	M00055592B:C10	UC2-NormColon
542	455864	1598.L12.gz43_212718	F	M00055594D:F07	UC2-NormColon
543	641957	1598.A13.gz43_212723	F	M00055579D:G09	UC2-NormColon
544	638941	1598.K14.gz43_212749	F	M00055593C:D08	UC2-NormColon
545	648159	1598.B15.gz43_212756	F	M00055582B:A06	UC2-NormColon
546	509973	1598.G15.gz43_212761	F	M00055588C:G09	UC2-NormColon

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SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
547	641425	1598.A17.gz43_212787	F	M00055580B:B08	UC2-NormColon
548	647312	1598.O17.gz43_212801	F	M00055600C:C02	UC2-NormColon
549	86311	1598.C18.gz43_212805	F	M00055583C:A01	UC2-NormColon
550	515931	1598.O19.gz43_212833	F	M00055600D:B02	UC2-NormColon
551	651000	1598.D21.gz43_212854	F	M00055585A:E12	UC2-NormColon
552	553087	1598.E21.gz43_212855	F	M00055586C:A06	UC2-NormColon
553	646914	1598.G21.gz43_212857	F	M00055589A:B06	UC2-NormColon
554	446371	1598.K21.gz43_212861	F	M00055594B:A01	UC2-NormColon
555	640298	1598.N23.gz43_212896	F	M00055599D:C08	UC2-NormColon
556	201904	1599.A01.gz43_212923	F	M00055602B:B10	UC2-NormColon
557	641338	1599.B01.gz43_212924	F	M00055603D:A09	UC2-NormColon
558	640221	1599.L01.gz43_212934	F	M00055619C:F07	UC2-NormColon
559	454527	1599.F02.gz43_212944	F	M00055610B:E04	UC2-NormColon
560	640868	1599.I08.gz43_213043	F	M00055615C:E01	UC2-NormColon
561	641069	1599.N09.gz43_213064	F	M00055623D:G05	UC2-NormColon
562	559380	1599.B10.gz43_213068	F	M00055604D:F05	UC2-NormColon
563	641680	1599.D10.gz43_213070	F	M00055608C:E03	UC2-NormColon
564	639703	1599.I11.gz43_213091	F	M00055615D:C07	UC2-NormColon
565	641542	1599.C12.gz43_213101	F	M00055606D:C05	UC2-NormColon
566	5201	1599.A15.gz43_213147	F	M00055602D:G08	UC2-NormColon
567	607715	1599.D15.gz43_213150	F	M00055608C:G11	UC2-NormColon
568	640416	1599.L17.gz43_213190	F	M00055620D:D05	UC2-NormColon
569	554833	1599.B19.gz43_213212	F	M00055606A:B11	UC2-NormColon
570	639480	1599.K19.gz43_213221	F	M00055619B:H04	UC2-NormColon
571	607138	1599.P21.gz43_213258	F	M00055628B:B07	UC2-NormColon
572	561626	1599.L23.gz43_213286	F	M00055621B:G03	UC2-NormColon
573	548959	1600.I01.gz43_213315	F	M00055639D:D03	UC2-NormColon
574	639934	1600.H02.gz43_213330	F	M00055638D:D07	UC2-NormColon
575	640956	1600.I03.gz43_213347	F	M00055639D:F08	UC2-NormColon
576	554722	1600.L03.gz43_213350	F	M00055644A:D12	UC2-NormColon
577	649717	1600.D04.gz43_213358	F	M00055633D:A02	UC2-NormColon
578	646695	1600.H04.gz43_213362	F	M00055638D:E09	UC2-NormColon
579	639886	1600.N04.gz43_213368	F	M00055647C:D02	UC2-NormColon
580	451615	1600.K05.gz43_213381	F	M00055643A:C01	UC2-NormColon
581	635965	1600.I07.gz43_213411	F	M00055640A:G03	UC2-NormColon
582	379040	1600.L07.gz43_213414	F	M00055644B:H12	UC2-NormColon
583	640799	1600.C10.gz43_213453	F	M00055632D:A06	UC2-NormColon
584	642246	1600.K11.gz43_213477	F	M00055643B:E05	UC2-NormColon
585	467563	1600.N11.gz43_213480	F	M00055647D:B11	UC2-NormColon
586	640320	1600.O11.gz43_213481	F	M00055649A:H07	UC2-NormColon
587	557401	1600.I12.gz43_213491	F	M00055640C:E06	UC2-NormColon
588	646352	1600.M13.gz43_213511	F	M00055646C:B04	UC2-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
589	645004	1600.B15.gz43_213532	F	M00055630B:G04	UC2-NormColon
590	641702	1600.P17.gz43_213578	F	M00055651A:E06	UC2-NormColon
591	562000	1600.I19.gz43_213603	F	M00055641A:C12	UC2-NormColon
592	453441	1600.N19.gz43_213608	F	M00055648B:C01	UC2-NormColon
593	641210	1600.M20.gz43_213623	F	M00055647B:A05	UC2-NormColon
594	458736	1600.P20.gz43_213626	F	M00055651B:F08	UC2-NormColon
595	553285	1600.O21.gz43_213641	F	M00055650A:B05	UC2-NormColon
596	455075	1600.A22.gz43_213643	F	M00055629B:G09	UC2-NormColon
597	166041	1600.D23.gz43_213662	F	M00055634C:F09	UC2-NormColon
598	553516	1600.J23.gz43_213668	F	M00055642D:A05	UC2-NormColon
599	559423	1600.B24.gz43_213676	F	M00055632A:B11	UC2-NormColon
600	131348	1600.C24.gz43_213677	F	M00055633B:G02	UC2-NormColon
601	650180	1600.E24.gz43_213679	F	M00055636A:H12	UC2-NormColon
602	642361	1600.F24.gz43_213680	F	M00055637B:A01	UC2-NormColon
603	561069	1600.K24.gz43_213685	F	M00055643D:G11	UC2-NormColon
604	550515	1600.P24.gz43_213690	F	M00055651C:E01	UC2-NormColon
605	559854	1693.D01.gz43_213694	F	M00055819A:B10	UC2-NormColon
606	650579	1693.J01.gz43_213700	F	M00055827A:A12	UC2-NormColon
607	648567	1693.L02.gz43_213718	F	M00055829C:A07	UC2-NormColon
608	645155	1693.H03.gz43_213730	F	M00055825B:C11	UC2-NormColon
609	650204	1693.H04.gz43_213746	F	M00055825B:E03	UC2-NormColon
610	643054	1693.H06.gz43_213778	F	M00055825B:F09	UC2-NormColon
611	640464	1693.I06.gz43_213779	F	M00055826A:G04	UC2-NormColon
612	363172	1693.A07.gz43_213787	F	M00055816D:A10	UC2-NormColon
613	674526	1693.G08.gz43_213809	F	M00055823B:F02	UC2-NormColon
614	481864	1693.N08.gz43_213816	F	M00055832A:A08	UC2-NormColon
615	492242	1693.A09.gz43_213819	F	M00055816D:B11	UC2-NormColon
616	638837	1693.C10.gz43_213837	F	M00055818B:H03	UC2-NormColon
617	517280	1693.K10.gz43_213845	F	M00055828B:E10	UC2-NormColon
618	452863	1693.A13.gz43_213883	F	M00055816D:E10	UC2-NormColon
619	642962	1693.H13.gz43_213890	F	M00055825D:A03	UC2-NormColon
620	645746	1693.I13.gz43_213891	F	M00055826B:G07	UC2-NormColon
621	645146	1693.L15.gz43_213926	F	M00055829D:H10	UC2-NormColon
622	644781	1693.M15.gz43_213927	F	M00055831A:C06	UC2-NormColon
623	643397	1693.A17.gz43_213947	F	M00055817A:E05	UC2-NormColon
624	645073	1693.L17.gz43_213958	F	M00055830A:G10	UC2-NormColon
625	648580	1693.A19.gz43_213979	F	M00055817A:H07	UC2-NormColon
626	650487	1693.I19.gz43_213987	F	M00055826C:G06	UC2-NormColon
627	455716	1693.J19.gz43_213988	F	M00055827D:A01	UC2-NormColon
628	551681	1693.H20.gz43_214002	F	M00055825D:D11	UC2-NormColon
629	642054	1693.P21.gz43_214026	F	M00055835C:F08	UC2-NormColon
630	556286	1693.J22.gz43_214036	F	M00055827D:C02	UC2-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
631	449542	1693.A23.gz43_214043	F	M00055817B:C04	UC2-NormColon
632	517237	1693.M23.gz43_214055	F	M00055831B:C04	UC2-NormColon
633	647191	1694.J01.gz43_214084	F	M00055846B:F11	UC2-NormColon
634	644212	1694.G04.gz43_214129	F	M00055843B:D10	UC2-NormColon
635	549624	1694.P04.gz43_214138	F	M00055854C:C07	UC2-NormColon
636	645149	1694.A05.gz43_214139	F	M00055836A:B12	UC2-NormColon
637	981	1694.F05.gz43_214144	F	M00055842B:A04	UC2-NormColon
638	647448	1694.I05.gz43_214147	F	M00055845C:A11	UC2-NormColon
639	570939	1694.P05.gz43_214154	F	M00055854C:E03	UC2-NormColon
640	547841	1694.L06.gz43_214166	F	M00055849C:G07	UC2-NormColon
641	466265	1694.M06.gz43_214167	F	M00055851A:C03	UC2-NormColon
642	649842	1694.M07.gz43_214183	F	M00055851A:C09	UC2-NormColon
643	468222	1694.I08.gz43_214195	F	M00055845C:C12	UC2-NormColon
644	450949	1694.L08.gz43_214198	F	M00055849D:B04	UC2-NormColon
645	603388	1694.O08.gz43_214201	F	M00055853C:C12	UC2-NormColon
646	485237	1694.E09.gz43_214207	F	M00055841B:F09	UC2-NormColon
647	644063	1694.F09.gz43_214208	F	M00055842B:D04	UC2-NormColon
648	639341	1694.N09.gz43_214216	F	M00055852A:C12	UC2-NormColon
649	471364	1694.P09.gz43_214218	F	M00055854C:H11	UC2-NormColon
650	452735	1694.A10.gz43_214219	F	M00055836C:D01	UC2-NormColon
651	503546	1694.E10.gz43_214223	F	M00055841B:H03	UC2-NormColon
652	646420	1694.I10.gz43_214227	F	M00055845C:E02	UC2-NormColon
653	647577	1694.O10.gz43_214233	F	M00055853C:H03	UC2-NormColon
654	504944	1694.B11.gz43_214236	F	M00055837D:G10	UC2-NormColon
655	522869	1694.D11.gz43_214238	F	M00055840B:B02	UC2-NormColon
656	644548	1694.F11.gz43_214240	F	M00055842C:A11	UC2-NormColon
657	644314	1694.H11.gz43_214242	F	M00055844D:E12	UC2-NormColon
658	650492	1694.O11.gz43_214249	F	M00055853D:A07	UC2-NormColon
659	643800	1694.B12.gz43_214252	F	M00055838A:A03	UC2-NormColon
660	643843	1694.E12.gz43_214255	F	M00055841C:A03	UC2-NormColon
661	448450	1694.B13.gz43_214268	F	M00055838A:B02	UC2-NormColon
662	643804	1694.C13.gz43_214269	F	M00055839B:A10	UC2-NormColon
663	469511	1694.L13.gz43_214278	F	M00055849D:H09	UC2-NormColon
664	643130	1694.O13.gz43_214281	F	M00055853D:B04	UC2-NormColon
665	640171	1694.J14.gz43_214292	F	M00055846D:G11	UC2-NormColon
666	647522	1694.M14.gz43_214295	F	M00055851A:H10	UC2-NormColon
667	642293	1694.N14.gz43_214296	F	M00055852B:G09	UC2-NormColon
668	404816	1694.P14.gz43_214298	F	M00055855A:B11	UC2-NormColon
669	447597	1694.A15.gz43_214299	F	M00055837A:B08	UC2-NormColon
670	467901	1694.B15.gz43_214300	F	M00055838B:D06	UC2-NormColon
671	648039	1694.C15.gz43_214301	F	M00055839B:C07	UC2-NormColon
672	607430	1694.E15.gz43_214303	F	M00055841C:D05	UC2-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
673	645505	1694.F15.gz43_214304	F	M00055842D:C02	UC2-NormColon
674	472119	1694.G15.gz43_214305	F	M00055843D:H01	UC2-NormColon
675	645197	1694.K15.gz43_214309	F	M00055848C:A02	UC2-NormColon
676	650217	1694.O15.gz43_214313	F	M00055853D:C07	UC2-NormColon
677	644210	1694.A16.gz43_214315	F	M00055837A:D09	UC2-NormColon
678	466697	1694.H16.gz43_214322	F	M00055844D:H09	UC2-NormColon
679	650276	1694.I16.gz43_214323	F	M00055845D:G11	UC2-NormColon
680	562229	1694.M16.gz43_214327	F	M00055851B:B09	UC2-NormColon
681	462659	1694.P16.gz43_214330	F	M00055855A:G05	UC2-NormColon
682	644494	1694.B17.gz43_214332	F	M00055838B:H04	UC2-NormColon
683	24730	1694.D17.gz43_214334	F	M00055840C:D06	UC2-NormColon
684	599759	1694.E17.gz43_214335	F	M00055841C:D11	UC2-NormColon
685	15001	1694.F17.gz43_214336	F	M00055842D:D07	UC2-NormColon
686	558981	1694.K17.gz43_214341	F	M00055848C:G07	UC2-NormColon
687	592122	1694.O17.gz43_214345	F	M00055854A:B07	UC2-NormColon
688	489249	1694.A18.gz43_214347	F	M00055837A:F02	UC2-NormColon
689	447002	1694.B18.gz43_214348	F	M00055838C:A08	UC2-NormColon
690	558890	1694.C18.gz43_214349	F	M00055839B:E07	UC2-NormColon
691	644548	1694.D18.gz43_214350	F	M00055840C:H06	UC2-NormColon
692	643825	1694.G18.gz43_214353	F	M00055844A:D03	UC2-NormColon
693	645289	1694.A19.gz43_214363	F	M00055837A:H08	UC2-NormColon
694	643948	1694.B19.gz43_214364	F	M00055838C:B08	UC2-NormColon
695	537586	1694.C19.gz43_214365	F	M00055839B:H09	UC2-NormColon
696	462557	1694.F19.gz43_214368	F	M00055842D:F07	UC2-NormColon
697	647577	1694.G19.gz43_214369	F	M00055844A:D07	UC2-NormColon
698	643999	1694.H19.gz43_214370	F	M00055845A:C03	UC2-NormColon
699	651131	1694.J19.gz43_214372	F	M00055847B:G12	UC2-NormColon
700	425923	1694.M19.gz43_214375	F	M00055851B:G10	UC2-NormColon
701	639510	1694.O19.gz43_214377	F	M00055854A:D01	UC2-NormColon
702	643977	1694.D20.gz43_214382	F	M00055840D:B03	UC2-NormColon
703	140648	1694.E20.gz43_214383	F	M00055841C:H04	UC2-NormColon
704	649068	1694.G20.gz43_214385	F	M00055844A:F11	UC2-NormColon
705	644708	1694.N20.gz43_214392	F	M00055852D:B11	UC2-NormColon
706	643909	1694.P20.gz43_214394	F	M00055855B:B11	UC2-NormColon
707	650528	1694.E21.gz43_214399	F	M00055841D:C11	UC2-NormColon
708	644569	1694.H21.gz43_214402	F	M00055845A:H10	UC2-NormColon
709	646459	1694.J21.gz43_214404	F	M00055847C:A11	UC2-NormColon
710	608873	1694.L21.gz43_214406	F	M00055850C:D01	UC2-NormColon
711	649611	1694.N21.gz43_214408	F	M00055852D:G12	UC2-NormColon
712	465576	1694.P21.gz43_214410	F	M00055855B:D12	UC2-NormColon
713	467521	1694.C22.gz43_214413	F	M00055839C:B11	UC2-NormColon
714	646810	1694.J22.gz43_214420	F	M00055847C:C01	UC2-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
715	647318	1694.L22.gz43_214422	F	M00055850C:G05	UC2-NormColon
716	638854	1694.O22.gz43_214425	F	M00055854A:E04	UC2-NormColon
717	644987	1694.A23.gz43_214427	F	M00055837B:E07	UC2-NormColon
718	645948	1694.C23.gz43_214429	F	M00055839C:D06	UC2-NormColon
719	419751	1694.I23.gz43_214435	F	M00055846B:B12	UC2-NormColon
720	643594	1694.M23.gz43_214439	F	M00055851C:F12	UC2-NormColon
721	603388	1694.P23.gz43_214442	F	M00055855C:F11	UC2-NormColon
722	644075	1694.G24.gz43_214449	F	M00055844B:C12	UC2-NormColon
723	542282	1694.I24.gz43_214451	F	M00055846B:C12	UC2-NormColon
724	452976	1694.J24.gz43_214452	F	M00055847C:H09	UC2-NormColon
725	472801	1694.M24.gz43_214455	F	M00055851C:H05	UC2-NormColon
726	646633	1695.P03.gz43_214910	F	M00055875B:E09	UC2-NormColon
727	509027	1695.A04.gz43_214911	F	M00055855D:D12	UC2-NormColon
728	596882	1695.D05.gz43_214930	F	M00055860D:E04	UC2-NormColon
729	644442	1695.A07.gz43_214959	F	M00055855D:G08	UC2-NormColon
730	644047	1695.F07.gz43_214964	F	M00055863D:D09	UC2-NormColon
731	397399	1695.H07.gz43_214966	F	M00055866A:G10	UC2-NormColon
732	564854	1695.A08.gz43_214975	F	M00055856A:C06	UC2-NormColon
733	646372	1695.B08.gz43_214976	F	M00055857C:D09	UC2-NormColon
734	645848	1695.D08.gz43_214978	F	M00055861B:F04	UC2-NormColon
735	447035	1695.M08.gz43_214987	F	M00055872D:D12	UC2-NormColon
736	644149	1695.A09.gz43_214991	F	M00055856A:D12	UC2-NormColon
737	640147	1695.E09.gz43_214995	F	M00055862D:B02	UC2-NormColon
738	524261	1695.K09.gz43_215001	F	M00055871A:H06	UC2-NormColon
739	449500	1695.E11.gz43_215027	F	M00055862D:D06	UC2-NormColon
740	648819	1695.K11.gz43_215033	F	M00055871B:B03	UC2-NormColon
741	644755	1695.L11.gz43_215034	F	M00055872A:C08	UC2-NormColon
742	516512	1695.P11.gz43_215038	F	M00055875C:C07	UC2-NormColon
743	380550	1695.L12.gz43_215050	F	M00055872A:D08	UC2-NormColon
744	645538	1695.D13.gz43_215058	F	M00055861C:G03	UC2-NormColon
745	644047	1695.F13.gz43_215060	F	M00055864A:C09	UC2-NormColon
746	650773	1695.F14.gz43_215076	F	M00055864A:E11	UC2-NormColon
747	449936	1695.J14.gz43_215080	F	M00055869C:G06	UC2-NormColon
748	554646	1695.O14.gz43_215085	F	M00055875A:G05	UC2-NormColon
749	640534	1695.L15.gz43_215098	F	M00055872A:E11	UC2-NormColon
750	642411	1695.J16.gz43_215112	F	M00055869D:A07	UC2-NormColon
751	643451	1695.M16.gz43_215115	F	M00055873A:E03	UC2-NormColon
752	644435	1695.H17.gz43_215126	F	M00055866C:G09	UC2-NormColon
753	561877	1695.F18.gz43_215140	F	M00055864B:C09	UC2-NormColon
754	645497	1695.N18.gz43_215148	F	M00055874A:F06	UC2-NormColon
755	644030	1695.E20.gz43_215171	F	M00055863B:C07	UC2-NormColon
756	140224	1695.D21.gz43_215186	F	M00055862A:C01	UC2-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
757	643099	1695.K21.gz43_215193	F	M00055871C:C07	UC2-NormColon
758	643333	1695.P22.gz43_215214	F	M00055875D:D01	UC2-NormColon
759	649660	1695.G23.gz43_215221	F	M00055865C:G11	UC2-NormColon
760	645288	1695.H23.gz43_215222	F	M00055867A:B02	UC2-NormColon
761	650517	1695.G24.gz43_215237	F	M00055865C:H06	UC2-NormColon
762	552201	1696.J01.gz43_215256	F	M00055885C:B07	UC2-NormColon
763	643513	1696.P02.gz43_215278	F	M00055891B:F09	UC2-NormColon
764	447807	1696.D04.gz43_215298	F	M00055880B:A06	UC2-NormColon
765	639256	1696.M04.gz43_215307	F	M00055888C:F07	UC2-NormColon
766	179760	1696.G05.gz43_215317	F	M00055883A:C02	UC2-NormColon
767	459274	1696.G06.gz43_215333	F	M00055883A:C10	UC2-NormColon
768	345761	1696.I06.gz43_215335	F	M00055884D:F07	UC2-NormColon
769	640356	1696.M06.gz43_215339	F	M00055888C:G09	UC2-NormColon
770	645638	1696.A07.gz43_215343	F	M00055877A:H04	UC2-NormColon
771	464171	1696.N11.gz43_215420	F	M00055890A:A06	UC2-NormColon
772	446225	1696.E13.gz43_215443	F	M00055881A:G07	UC2-NormColon
773	450559	1696.F14.gz43_215460	F	M00055882C:A06	UC2-NormColon
774	643248	1696.L14.gz43_215466	F	M00055887D:C11	UC2-NormColon
775	549114	1696.N14.gz43_215468	F	M00055890A:D01	UC2-NormColon
776	645215	1696.D15.gz43_215474	F	M00055880C:F07	UC2-NormColon
777	555172	1696.I15.gz43_215479	F	M00055885B:A11	UC2-NormColon
778	593715	1696.B16.gz43_215488	F	M00055878C:C02	UC2-NormColon
779	586992	1696.I16.gz43_215495	F	M00055885B:B04	UC2-NormColon
780	451670	1696.H17.gz43_215510	F	M00055884B:F10	UC2-NormColon
781	552628	1696.H18.gz43_215526	F	M00055884B:H07	UC2-NormColon
782	643233	1696.A21.gz43_215567	F	M00055877D:C05	UC2-NormColon
783	640400	1696.F21.gz43_215572	F	M00055882D:B02	UC2-NormColon
784	644468	1696.G21.gz43_215573	F	M00055883D:B06	UC2-NormColon
785	643046	1696.H21.gz43_215574	F	M00055884C:B07	UC2-NormColon
786	649068	1696.N21.gz43_215580	F	M00055890A:G12	UC2-NormColon
787	648063	1696.E22.gz43_215587	F	M00055881D:A02	UC2-NormColon
788	570248	1696.M23.gz43_215611	F	M00055889B:E12	UC2-NormColon
789	643724	1696.N23.gz43_215612	F	M00055890A:H11	UC2-NormColon
790	649027	1696.P23.gz43_215614	F	M00055892A:F04	UC2-NormColon
791	643366	1696.P24.gz43_215630	F	M00055892B:D02	UC2-NormColon
792	526575	1705.E01.gz43_215635	F	M00055900D:D03	UC2-NormColon
793	449737	1705.O02.gz43_215661	F	M00055914A:A03	UC2-NormColon
794	394373	1705.B03.gz43_215664	F	M00055894B:E09	UC2-NormColon
795	557361	1705.C03.gz43_215665	F	M00055896D:G10	UC2-NormColon
796	644364	1705.K04.gz43_215689	F	M00055908D:F09	UC2-NormColon
797	644242	1705.M05.gz43_215707	F	M00055911B:E06	UC2-NormColon
798	644407	1705.N05.gz43_215708	F	M00055912D:F04	UC2-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
799	643513	1705.F06.gz43_215716	F	M00055902A:H11	UC2-NormColon
800	639194	1705.H06.gz43_215718	F	M00055905B:H01	UC2-NormColon
801	454720	1705.I06.gz43_215719	F	M00055906D:G03	UC2-NormColon
802	643300	1705.O09.gz43_215773	F	M00055914C:D12	UC2-NormColon
803	647522	1705.E10.gz43_215779	F	M00055901B:A02	UC2-NormColon
804	648576	1705.B11.gz43_215792	F	M00055896A:G01	UC2-NormColon
805	485237	1705.C11.gz43_215793	F	M00055898B:E07	UC2-NormColon
806	644108	1705.O11.gz43_215805	F	M00055914C:G01	UC2-NormColon
807	643914	1705.G12.gz43_215813	F	M00055904B:B01	UC2-NormColon
808	641645	1705.O12.gz43_215821	F	M00055914C:G11	UC2-NormColon
809	605596	1705.H13.gz43_215830	F	M00055905D:B06	UC2-NormColon
810	564134	1705.O13.gz43_215837	F	M00055914D:A08	UC2-NormColon
811	643948	1705.B14.gz43_215840	F	M00055896B:C06	UC2-NormColon
812	557947	1705.F14.gz43_215844	F	M00055902D:A07	UC2-NormColon
813	15001	1705.G15.gz43_215861	F	M00055904C:A07	UC2-NormColon
814	649170	1705.P15.gz43_215870	F	M00055916B:C02	UC2-NormColon
815	644390	1705.D16.gz43_215874	F	M00055900A:F08	UC2-NormColon
816	643089	1705.K16.gz43_215881	F	M00055909B:G10	UC2-NormColon
817	553587	1705.O16.gz43_215885	F	M00055914D:G06	UC2-NormColon
818	550242	1705.H17.gz43_215894	F	M00055905D:H02	UC2-NormColon
819	639413	1705.O17.gz43_215901	F	M00055915A:A06	UC2-NormColon
820	645844	1705.C18.gz43_215905	F	M00055899A:B03	UC2-NormColon
821	641087	1705.E18.gz43_215907	F	M00055901C:C10	UC2-NormColon
822	482163	1705.F18.gz43_215908	F	M00055902D:H10	UC2-NormColon
823	643808	1705.G18.gz43_215909	F	M00055904D:A06	UC2-NormColon
824	468147	1705.L19.gz43_215930	F	M00055910C:G01	UC2-NormColon
825	446728	1705.D20.gz43_215938	F	M00055900B:E12	UC2-NormColon
826	447326	1705.K20.gz43_215945	F	M00055909C:E08	UC2-NormColon
827	685001	1705.L20.gz43_215946	F	M00055910C:G04	UC2-NormColon
828	645781	1705.K21.gz43_215961	F	M00055909C:G09	UC2-NormColon
829	643825	1705.L21.gz43_215962	F	M00055910D:A03	UC2-NormColon
830	374340	1705.A22.gz43_215967	F	M00055894A:H08	UC2-NormColon
831	640756	1705.M22.gz43_215979	F	M00055912C:C08	UC2-NormColon
832	400741	1705.B23.gz43_215984	F	M00055896C:H10	UC2-NormColon
833	644063	1705.F24.gz43_216004	F	M00055903B:C10	UC2-NormColon
834	644354	1705.G24.gz43_216005	F	M00055905A:F11	UC2-NormColon
835	89082	1705.K24.gz43_216009	F	M00055909D:E01	UC2-NormColon
836	643991	1705.O24.gz43_216013	F	M00055915C:B09	UC2-NormColon
837	459881	1706.B01.gz43_216028	F	M00055918B:B10	UC2-NormColon
838	644554	1706.C01.gz43_216029	F	M00055919D:H07	UC2-NormColon
839	557175	1706.B03.gz43_216060	F	M00055918B:F10	UC2-NormColon
840	641484	1706.F03.gz43_216064	F	M00055924C:A09	UC2-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
841	651131	1706.B05.gz43_216092	F	M00055918C:C04	UC2-NormColon
842	644629	1706.J05.gz43_216100	F	M00055930A:G04	UC2-NormColon
843	419009	1706.E06.gz43_216111	F	M00055922D:G10	UC2-NormColon
844	446795	1706.M06.gz43_216119	F	M00055934C:E06	UC2-NormColon
845	638808	1706.L07.gz43_216134	F	M00055933A:E05	UC2-NormColon
846	646596	1706.N07.gz43_216136	F	M00055936C:B05	UC2-NormColon
847	639901	1706.P07.gz43_216138	F	M00055939B:A11	UC2-NormColon
848	648379	1706.N08.gz43_216152	F	M00055936C:D03	UC2-NormColon
849	650938	1706.J09.gz43_216164	F	M00055930C:D03	UC2-NormColon
850	643170	1706.E10.gz43_216175	F	M00055923B:C07	UC2-NormColon
851	643239	1706.H10.gz43_216178	F	M00055927D:E11	UC2-NormColon
852	639596	1706.J10.gz43_216180	F	M00055930C:F06	UC2-NormColon
853	605114	1706.L10.gz43_216182	F	M00055933B:B11	UC2-NormColon
854	456920	1706.N11.gz43_216200	F	M00055936D:F03	UC2-NormColon
855	647952	1706.B12.gz43_216204	F	M00055919A:A06	UC2-NormColon
856	650470	1706.M12.gz43_216215	F	M00055934D:H09	UC2-NormColon
857	465576	1706.D13.gz43_216222	F	M00055922A:F05	UC2-NormColon
858	455413	1706.P13.gz43_216234	F	M00055939D:D07	UC2-NormColon
859	639038	1706.H15.gz43_216258	F	M00055928A:C06	UC2-NormColon
860	556925	1706.J15.gz43_216260	F	M00055930C:H05	UC2-NormColon
861	644301	1706.A16.gz43_216267	F	M00055917D:E07	UC2-NormColon
862	447520	1706.J16.gz43_216276	F	M00055930D:B05	UC2-NormColon
863	447426	1706.D17.gz43_216286	F	M00055922B:A06	UC2-NormColon
864	610893	1706.H17.gz43_216290	F	M00055928A:E11	UC2-NormColon
865	613626	1706.J17.gz43_216292	F	M00055930D:B09	UC2-NormColon
866	645092	1706.N17.gz43_216296	F	M00055937A:F07	UC2-NormColon
867	649873	1706.P19.gz43_216330	F	M00055940B:A08	UC2-NormColon
868	645028	1706.A20.gz43_216331	F	M00055918A:F10	UC2-NormColon
869	639154	1706.F20.gz43_216336	F	M00055925B:D09	UC2-NormColon
870	649085	1706.D21.gz43_216350	F	M00055922B:G09	UC2-NormColon
871	643332	1706.F21.gz43_216352	F	M00055925B:D10	UC2-NormColon
872	643383	1706.H21.gz43_216354	F	M00055928B:E11	UC2-NormColon
873	204	1706.J21.gz43_216356	F	M00055930D:F05	UC2-NormColon
874	641716	1706.N21.gz43_216360	F	M00055937C:C08	UC2-NormColon
875	643627	1706.E22.gz43_216367	F	M00055924B:D02	UC2-NormColon
876	640672	1706.M23.gz43_216391	F	M00055935C:E03	UC2-NormColon
877	550237	1707.J02.gz43_216453	F	M00055956D:B01	UC2-NormColon
878	646317	1707.B04.gz43_216477	F	M00055942B:H10	UC2-NormColon
879	643968	1707.K05.gz43_216502	F	M00055958C:E03	UC2-NormColon
880	649549	1707.F06.gz43_216513	F	M00055949D:B07	UC2-NormColon
881	513619	1707.O07.gz43_216538	F	M00055967A:F11	UC2-NormColon
882	460245	1707.I08.gz43_216548	F	M00055955B:C06	UC2-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
883	646061	1707.O08.gz43_216554	F	M00055967A:G01	UC2-NormColon
884	645273	1707.O09.gz43_216570	F	M00055967B:B12	UC2-NormColon
885	524546	1707.A12.gz43_216604	F	M00055941B:A04	UC2-NormColon
886	648782	1707.B12.gz43_216605	F	M00055942D:A01	UC2-NormColon
887	645900	1707.O13.gz43_216634	F	M00055967B:F07	UC2-NormColon
888	648555	1707.D14.gz43_216639	F	M00055945C:D09	UC2-NormColon
889	452316	1707.J14.gz43_216645	F	M00055957B:F11	UC2-NormColon
890	461363	1707.D17.gz43_216687	F	M00055945D:D01	UC2-NormColon
891	644720	1707.D18.gz43_216703	F	M00055945D:E08	UC2-NormColon
892	647312	1707.L18.gz43_216711	F	M00055961D:F06	UC2-NormColon
893	646190	1707.N18.gz43_216713	F	M00055966B:H09	UC2-NormColon
894	531529	1707.H19.gz43_216723	F	M00055954C:G07	UC2-NormColon
895	393599	1707.E20.gz43_216736	F	M00055947C:E09	UC2-NormColon
896	645508	1707.N20.gz43_216745	F	M00055966C:D03	UC2-NormColon
897	383609	1707.O23.gz43_216794	F	M00055967D:C05	UC2-NormColon
898	447805	1707.B24.gz43_216797	F	M00055943B:E01	UC2-NormColon
899	694643	1707.P24.gz43_216811	F	M00055969A:F02	UC2-NormColon
900	647924	1708.I01.gz43_216820	F	M00055980B:B07	UC2-NormColon
901	645920	1708.P01.gz43_216827	F	M00055990A:F07	UC2-NormColon
902	641484	1708.M02.gz43_216840	F	M00055985D:E09	UC2-NormColon
903	640672	1708.A04.gz43_216860	F	M00055969B:B05	UC2-NormColon
904	644226	1708.K04.gz43_216870	F	M00055982C:H01	UC2-NormColon
905	557852	1708.C06.gz43_216894	F	M00055972C:C09	UC2-NormColon
906	558052	1708.C07.gz43_216910	F	M00055972C:F02	UC2-NormColon
907	644354	1708.I08.gz43_216932	F	M00055980C:G12	UC2-NormColon
908	645746	1708.L08.gz43_216935	F	M00055984D:E04	UC2-NormColon
909	647539	1708.M09.gz43_216952	F	M00055986A:F05	UC2-NormColon
910	645288	1708.L10.gz43_216967	F	M00055985A:B06	UC2-NormColon
911	645289	1708.A11.gz43_216972	F	M00055969D:B08	UC2-NormColon
912	642058	1708.G11.gz43_216978	F	M00055978A:H03	UC2-NormColon
913	642955	1708.A12.gz43_216988	F	M00055969D:F08	UC2-NormColon
914	640092	1708.H12.gz43_216995	F	M00055979B:G07	UC2-NormColon
915	558452	1708.P12.gz43_217003	F	M00055990D:B02	UC2-NormColon
916	645427	1708.L13.gz43_217015	F	M00055985B:C02	UC2-NormColon
917	649082	1708.B14.gz43_217021	F	M00055971B:A11	UC2-NormColon
918	451709	1708.K14.gz43_217030	F	M00055983C:C09	UC2-NormColon
919	640204	1708.H15.gz43_217043	F	M00055979C:B07	UC2-NormColon
920	640179	1708.N15.gz43_217049	F	M00055988A:A12	UC2-NormColon
921	582549	1708.P15.gz43_217051	F	M00055990D:G09	UC2-NormColon
922	484355	1708.G16.gz43_217058	F	M00055978B:F01	UC2-NormColon
923	646013	1708.J17.gz43_217077	F	M00055982A:G06	UC2-NormColon
924	649309	1708.P18.gz43_217099	F	M00055991A:D10	UC2-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
925	647333	1708.F19.gz43_217105	F	M00055977A:G09	UC2-NormColon
926	647058	1708.A21.gz43_217132	F	M00055970C:A05	UC2-NormColon
927	643723	1708.F21.gz43_217137	F	M00055977B:F06	UC2-NormColon
928	639359	1708.N21.gz43_217145	F	M00055988A:E05	UC2-NormColon
929	647539	1708.H23.gz43_217171	F	M00055980A:H06	UC2-NormColon
930	647211	1708.C24.gz43_217182	F	M00055973C:F10	UC2-NormColon
931	650018	1708.J24.gz43_217189	F	M00055982C:A12	UC2-NormColon
932	645848	1708.K24.gz43_217190	F	M00055984A:F05	UC2-NormColon
933	646212	1708.P24.gz43_217195	F	M00055991C:H11	UC2-NormColon
934	406436	1588.N01.gz43_217262	F	M00055553A:D08	UC2-NormColon
935	553651	1588.E02.gz43_217269	F	M00055542C:H05	UC2-NormColon
936	466092	1588.H02.gz43_217272	F	M00055546B:H03	UC2-NormColon
937	645891	1588.N02.gz43_217278	F	M00055553A:F11	UC2-NormColon
938	649390	1588.A03.gz43_217281	F	M00055536B:H11	UC2-NormColon
939	448358	1588.H04.gz43_217304	F	M00055546C:B01	UC2-NormColon
940	650982	1588.I04.gz43_217305	F	M00055547C:B07	UC2-NormColon
941	644012	1588.O05.gz43_217327	F	M00055554C:B04	UC2-NormColon
942	649099	1588.P06.gz43_217344	F	M00055556A:E07	UC2-NormColon
943	551662	1588.M07.gz43_217357	F	M00055551C:C08	UC2-NormColon
944	639316	1588.K08.gz43_217371	F	M00055549C:E10	UC2-NormColon
945	639480	1588.J09.gz43_217386	F	M00055548B:G06	UC2-NormColon
946	1318	1588.A11.gz43_217409	F	M00055537C:A01	UC2-NormColon
947	457146	1588.L11.gz43_217420	F	M00055550D:D02	UC2-NormColon
948	451671	1588.A15.gz43_217473	F	M00055537C:E04	UC2-NormColon
949	641401	1588.I15.gz43_217481	F	M00055547D:G06	UC2-NormColon
950	453606	1588.D17.gz43_217508	F	M00055542B:B11	UC2-NormColon
951	642414	1588.G17.gz43_217511	F	M00055545D:C03	UC2-NormColon
952	649564	1588.H18.gz43_217528	F	M00055547A:H11	UC2-NormColon
953	529799	1588.I18.gz43_217529	F	M00055548A:D07	UC2-NormColon
954	645781	1588.N18.gz43_217534	F	M00055553D:E06	UC2-NormColon
955	447379	1588.M20.gz43_217565	F	M00055552C:G03	UC2-NormColon
956	639461	1588.A21.gz43_217569	F	M00055538B:G09	UC2-NormColon
957	451361	1588.D21.gz43_217572	F	M00055542C:B02	UC2-NormColon
958	449891	1588.I22.gz43_217593	F	M00055548A:F04	UC2-NormColon
959	639395	1588.O22.gz43_217599	F	M00055555D:B05	UC2-NormColon
960	644173	1588.F23.gz43_217606	F	M00055545A:C01	UC2-NormColon
961	648494	1588.H24.gz43_217624	F	M00055547B:G09	UC2-NormColon
962	477064	1588.P24.gz43_217632	F	M00055557B:B10	UC2-NormColon
963	535436	1729.L02.gz43_217660	F	M00056092B:D10	UC2-NormColon
964	650900	1729.B04.gz43_217682	F	M00056078B:G02	UC2-NormColon
965	649149	1729.D04.gz43_217684	F	M00056081A:C05	UC2-NormColon
966	644054	1729.K04.gz43_217691	F	M00056091A:E04	UC2-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
967	649082	1729.P04.gz43_217696	F	M00056097B:C04	UC2-NormColon
968	454176	1729.J05.gz43_217706	F	M00056089D:A09	UC2-NormColon
969	448485	1729.A06.gz43_217713	F	M00056077B:E03	UC2-NormColon
970	643440	1729.N06.gz43_217726	F	M00056095B:A07	UC2-NormColon
971	649356	1729.J08.gz43_217754	F	M00056089D:E07	UC2-NormColon
972	710155	1729.L08.gz43_217756	F	M00056092C:E12	UC2-NormColon
973	560054	1729.E11.gz43_217797	F	M00056082A:E12	UC2-NormColon
974	644712	1729.K11.gz43_217803	F	M00056091C:C06	UC2-NormColon
975	646696	1729.A12.gz43_217809	F	M00056077C:H02	UC2-NormColon
976	644715	1729.H12.gz43_217816	F	M00056087B:G12	UC2-NormColon
977	644965	1729.N12.gz43_217822	F	M00056095C:E02	UC2-NormColon
978	645050	1729.K13.gz43_217835	F	M00056091C:D09	UC2-NormColon
979	649514	1729.N14.gz43_217854	F	M00056095C:G07	UC2-NormColon
980	570939	1729.E15.gz43_217861	F	M00056082B:G07	UC2-NormColon
981	647437	1729.F16.gz43_217878	F	M00056083D:D11	UC2-NormColon
982	650547	1729.L16.gz43_217884	F	M00056093A:B12	UC2-NormColon
983	649054	1729.P16.gz43_217888	F	M00056098B:C04	UC2-NormColon
984	645409	1729.K17.gz43_217899	F	M00056091D:C12	UC2-NormColon
985	613722	1729.B18.gz43_217906	F	M00056079A:B01	UC2-NormColon
986	418763	1729.L18.gz43_217916	F	M00056093A:F08	UC2-NormColon
987	619635	1729.K20.gz43_217947	F	M00056091D:E10	UC2-NormColon
988	645131	1729.L20.gz43_217948	F	M00056093B:D03	UC2-NormColon
989	451899	1729.M22.gz43_217981	F	M00056095A:C02	UC2-NormColon
990	597647	1729.P22.gz43_217984	F	M00056098D:A08	UC2-NormColon
991	560860	1717.F01.gz43_218406	F	M00055998B:D06	UC2-NormColon
992	640709	1717.P01.gz43_218416	F	M00056009D:C12	UC2-NormColon
993	447802	1717.O02.gz43_218431	F	M00056008B:G05	UC2-NormColon
994	641736	1717.I03.gz43_218441	F	M00056001D:B06	UC2-NormColon
995	464498	1717.J03.gz43_218442	F	M00056003B:G11	UC2-NormColon
996	452775	1717.K03.gz43_218443	F	M00056004D:F03	UC2-NormColon
997	561836	1717.L03.gz43_218444	F	M00056005C:F11	UC2-NormColon
998	444454	1717.K04.gz43_218459	F	M00056004D:F12	UC2-NormColon
999	639178	1717.O04.gz43_218463	F	M00056008C:D04	UC2-NormColon
1000	513888	1717.F05.gz43_218470	F	M00055998C:D04	UC2-NormColon
1001	643971	1717.I05.gz43_218473	F	M00056001D:G12	UC2-NormColon
1002	644824	1717.J05.gz43_218474	F	M00056003C:C09	UC2-NormColon
1003	448418	1717.N05.gz43_218478	F	M00056007C:A03	UC2-NormColon
1004	644030	1717.O05.gz43_218479	F	M00056008C:D08	UC2-NormColon
1005	644972	1717.P05.gz43_218480	F	M00056010A:E05	UC2-NormColon
1006	649556	1717.B06.gz43_218482	F	M00055993D:F12	UC2-NormColon
1007	644611	1717.I06.gz43_218489	F	M00056002A:A03	UC2-NormColon
1008	645162	1717.J07.gz43_218506	F	M00056003C:H10	UC2-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
1009	470462	1717.L07.gz43_218508	F	M00056005D:C04	UC2-NormColon
1010	645662	1717.A08.gz43_218513	F	M00055992A:D08	UC2-NormColon
1011	649259	1717.H08.gz43_218520	F	M00056000C:D09	UC2-NormColon
1012	650018	1717.D09.gz43_218532	F	M00055996C:A02	UC2-NormColon
1013	640645	1717.D10.gz43_218548	F	M00055996C:A08	UC2-NormColon
1014	643477	1717.M10.gz43_218557	F	M00056006D:E03	UC2-NormColon
1015	541214	1717.E11.gz43_218565	F	M00055997D:A11	UC2-NormColon
1016	651083	1717.M11.gz43_218573	F	M00056006D:F05	UC2-NormColon
1017	549889	1717.G12.gz43_218583	F	M00055999D:C05	UC2-NormColon
1018	558856	1717.D13.gz43_218596	F	M00055996D:D07	UC2-NormColon
1019	644022	1717.N13.gz43_218606	F	M00056007D:F07	UC2-NormColon
1020	644612	1717.O13.gz43_218607	F	M00056008D:D02	UC2-NormColon
1021	644949	1717.P13.gz43_218608	F	M00056011A:C11	UC2-NormColon
1022	643808	1717.C14.gz43_218611	F	M00055995A:G09	UC2-NormColon
1023	642260	1717.O14.gz43_218623	F	M00056008D:D03	UC2-NormColon
1024	651119	1717.B15.gz43_218626	F	M00055994B:B12	UC2-NormColon
1025	477521	1717.C15.gz43_218627	F	M00055995B:A02	UC2-NormColon
1026	587106	1717.D15.gz43_218628	F	M00055996D:G02	UC2-NormColon
1027	419443	1717.I15.gz43_218633	F	M00056002D:E09	UC2-NormColon
1028	643440	1717.L15.gz43_218636	F	M00056006A:E04	UC2-NormColon
1029	555736	1717.M16.gz43_218653	F	M00056007A:B02	UC2-NormColon
1030	644210	1717.G17.gz43_218663	F	M00055999D:H04	UC2-NormColon
1031	449261	1717.I17.gz43_218665	F	M00056003A:A08	UC2-NormColon
1032	643498	1717.J17.gz43_218666	F	M00056004B:F04	UC2-NormColon
1033	517274	1717.P17.gz43_218672	F	M00056011B:A06	UC2-NormColon
1034	532307	1717.L18.gz43_218684	F	M00056006A:G09	UC2-NormColon
1035	643288	1717.A19.gz43_218689	F	M00055993A:E02	UC2-NormColon
1036	478025	1717.F19.gz43_218694	F	M00055999A:A04	UC2-NormColon
1037	447822	1717.G19.gz43_218695	F	M00056000A:B02	UC2-NormColon
1038	641580	1717.I19.gz43_218697	F	M00056003A:B07	UC2-NormColon
1039	489426	1717.P19.gz43_218704	F	M00056011B:E10	UC2-NormColon
1040	650534	1717.C20.gz43_218707	F	M00055995C:F05	UC2-NormColon
1041	644990	1717.E20.gz43_218709	F	M00055998A:F06	UC2-NormColon
1042	207530	1717.F20.gz43_218710	F	M00055999A:B07	UC2-NormColon
1043	645197	1717.I20.gz43_218713	F	M00056003A:C01	UC2-NormColon
1044	414739	1717.K20.gz43_218715	F	M00056005B:H08	UC2-NormColon
1045	592941	1717.L20.gz43_218716	F	M00056006B:B05	UC2-NormColon
1046	447556	1717.H21.gz43_218728	F	M00056001C:F07	UC2-NormColon
1047	238586	1717.N21.gz43_218734	F	M00056008B:E04	UC2-NormColon
1048	644612	1717.E22.gz43_218741	F	M00055998B:A04	UC2-NormColon
1049	646387	1717.F22.gz43_218742	F	M00055999A:H10	UC2-NormColon
1050	647443	1717.G22.gz43_218743	F	M00056000A:E11	UC2-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
1051	555172	1717.P22.gz43_218752	F	M00056011C:D04	UC2-NormColon
1052	552846	1717.D23.gz43_218756	F	M00055997A:F04	UC2-NormColon
1053	639377	1717.B24.gz43_218770	F	M00055994C:F05	UC2-NormColon
1054	449713	1717.M24.gz43_218781	F	M00056007B:C10	UC2-NormColon
1055	456627	1717.N24.gz43_218782	F	M00056008B:G01	UC2-NormColon
1056	646143	1717.O24.gz43_218783	F	M00056009D:A02	UC2-NormColon
1057	639629	1718.H03.gz43_218827	F	M00056021C:H08	UC2-NormColon
1058	643744	1718.D04.gz43_218839	F	M00056016C:F11	UC2-NormColon
1059	397399	1718.P04.gz43_218851	F	M00056032B:H08	UC2-NormColon
1060	650391	1718.G06.gz43_218874	F	M00056020C:H03	UC2-NormColon
1061	447659	1718.N06.gz43_218881	F	M00056029D:D08	UC2-NormColon
1062	644967	1718.D07.gz43_218887	F	M00056016D:E02	UC2-NormColon
1063	545509	1718.G08.gz43_218906	F	M00056020D:D03	UC2-NormColon
1064	643975	1718.D09.gz43_218919	F	M00056017A:B08	UC2-NormColon
1065	645883	1718.M11.gz43_218960	F	M00056028D:F06	UC2-NormColon
1066	538808	1718.B12.gz43_218965	F	M00056013A:C09	UC2-NormColon
1067	425455	1718.P13.gz43_218995	F	M00056033A:C11	UC2-NormColon
1068	467057	1718.M20.gz43_219104	F	M00056029B:H03	UC2-NormColon
1069	640181	1718.B21.gz43_219109	F	M00056013D:D07	UC2-NormColon
1070	650348	1718.F23.gz43_219145	F	M00056020B:C09	UC2-NormColon
1071	451993	1718.P24.gz43_219171	F	M00056033C:H09	UC2-NormColon
1072	647976	1719.E01.gz43_219176	F	M00056039A:F04	UC2-NormColon
1073	557676	1719.I01.gz43_219180	F	M00056045A:D03	UC2-NormColon
1074	644639	1719.N01.gz43_219185	F	M00056050C:A09	UC2-NormColon
1075	644738	1719.J02.gz43_219197	F	M00056046A:B04	UC2-NormColon
1076	645973	1719.A03.gz43_219204	F	M00056033D:F06	UC2-NormColon
1077	550376	1719.B03.gz43_219205	F	M00056035B:A04	UC2-NormColon
1078	646088	1719.D03.gz43_219207	F	M00056037B:G02	UC2-NormColon
1079	506920	1719.P03.gz43_219219	F	M00056053A:F01	UC2-NormColon
1080	642198	1719.A04.gz43_219220	F	M00056033D:G07	UC2-NormColon
1081	649293	1719.E04.gz43_219224	F	M00056039B:C03	UC2-NormColon
1082	641193	1719.H04.gz43_219227	F	M00056043D:E03	UC2-NormColon
1083	461517	1719.J04.gz43_219229	F	M00056046A:B12	UC2-NormColon
1084	645070	1719.K04.gz43_219230	F	M00056046D:C11	UC2-NormColon
1085	645942	1719.M04.gz43_219232	F	M00056049B:E11	UC2-NormColon
1086	645151	1719.O05.gz43_219250	F	M00056051D:H02	UC2-NormColon
1087	566745	1719.B06.gz43_219253	F	M00056035B:D11	UC2-NormColon
1088	642184	1719.M06.gz43_219264	F	M00056049C:A08	UC2-NormColon
1089	649429	1719.O06.gz43_219266	F	M00056052A:A11	UC2-NormColon
1090	549786	1719.B07.gz43_219269	F	M00056035B:E10	UC2-NormColon
1091	452102	1719.J07.gz43_219277	F	M00056046A:G08	UC2-NormColon
1092	644819	1719.O07.gz43_219282	F	M00056052A:C07	UC2-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
1093	453804	1719.E08.gz43_219288	F	M00056039C:D05	UC2-NormColon
1094	650348	1719.K09.gz43_219310	F	M00056047A:E09	UC2-NormColon
1095	644894	1719.L09.gz43_219311	F	M00056048A:D12	UC2-NormColon
1096	646048	1719.A10.gz43_219316	F	M00056034A:G10	UC2-NormColon
1097	638912	1719.D10.gz43_219319	F	M00056037C:G11	UC2-NormColon
1098	644817	1719.F10.gz43_219321	F	M00056041B:F03	UC2-NormColon
1099	645973	1719.E11.gz43_219336	F	M00056039C:G05	UC2-NormColon
1100	643748	1719.M11.gz43_219344	F	M00056049C:H04	UC2-NormColon
1101	649259	1719.N11.gz43_219345	F	M00056051A:C03	UC2-NormColon
1102	642852	1719.E12.gz43_219352	F	M00056039C:H01	UC2-NormColon
1103	451544	1719.L12.gz43_219359	F	M00056048B:E01	UC2-NormColon
1104	528616	1719.N12.gz43_219361	F	M00056051A:H11	UC2-NormColon
1105	460727	1719.G13.gz43_219370	F	M00056043A:A09	UC2-NormColon
1106	468689	1719.C14.gz43_219382	F	M00056036D:B06	UC2-NormColon
1107	452729	1719.C15.gz43_219398	F	M00056036D:D01	UC2-NormColon
1108	481614	1719.D15.gz43_219399	F	M00056038B:G08	UC2-NormColon
1109	649900	1719.H15.gz43_219403	F	M00056044C:C01	UC2-NormColon
1110	645375	1719.N15.gz43_219409	F	M00056051B:B03	UC2-NormColon
1111	497101	1719.P15.gz43_219411	F	M00056053D:D07	UC2-NormColon
1112	556325	1719.G16.gz43_219418	F	M00056043A:H12	UC2-NormColon
1113	645431	1719.M16.gz43_219424	F	M00056049D:D03	UC2-NormColon
1114	452325	1719.A17.gz43_219428	F	M00056034C:D07	UC2-NormColon
1115	447645	1719.B17.gz43_219429	F	M00056035D:C08	UC2-NormColon
1116	644054	1719.C17.gz43_219430	F	M00056036D:F05	UC2-NormColon
1117	641715	1719.M17.gz43_219440	F	M00056049D:E01	UC2-NormColon
1118	644692	1719.P17.gz43_219443	F	M00056054A:B06	UC2-NormColon
1119	465589	1719.P18.gz43_219459	F	M00056054A:D09	UC2-NormColon
1120	643897	1719.G19.gz43_219466	F	M00056043B:E03	UC2-NormColon
1121	456840	1719.L19.gz43_219471	F	M00056048D:B09	UC2-NormColon
1122	467255	1719.P19.gz43_219475	F	M00056054A:E03	UC2-NormColon
1123	645530	1719.C20.gz43_219478	F	M00056037A:D11	UC2-NormColon
1124	648390	1719.A21.gz43_219492	F	M00056034C:H09	UC2-NormColon
1125	467597	1719.B21.gz43_219493	F	M00056035D:G10	UC2-NormColon
1126	468330	1719.D21.gz43_219495	F	M00056038D:F03	UC2-NormColon
1127	454438	1719.E21.gz43_219496	F	M00056040C:B03	UC2-NormColon
1128	402476	1719.I21.gz43_219500	F	M00056045D:C09	UC2-NormColon
1129	558439	1719.M21.gz43_219504	F	M00056050A:D02	UC2-NormColon
1130	595066	1719.N21.gz43_219505	F	M00056051C:C09	UC2-NormColon
1131	646687	1719.E22.gz43_219512	F	M00056040C:C12	UC2-NormColon
1132	452026	1719.H22.gz43_219515	F	M00056044D:F01	UC2-NormColon
1133	639255	1719.K22.gz43_219518	F	M00056047C:E03	UC2-NormColon
1134	612572	1719.L22.gz43_219519	F	M00056049A:C11	UC2-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
1135	641786	1719.O22.gz43_219522	F	M00056052D:G01	UC2-NormColon
1136	647306	1719.P22.gz43_219523	F	M00056054A:G07	UC2-NormColon
1137	640559	1719.A23.gz43_219524	F	M00056034D:E09	UC2-NormColon
1138	550365	1719.D23.gz43_219527	F	M00056039A:A02	UC2-NormColon
1139	462293	1719.I23.gz43_219532	F	M00056045D:E06	UC2-NormColon
1140	587106	1719.N23.gz43_219537	F	M00056051C:H09	UC2-NormColon
1141	483266	1719.F24.gz43_219545	F	M00056042B:B05	UC2-NormColon
1142	490898	1719.G24.gz43_219546	F	M00056043C:G03	UC2-NormColon
1143	640603	1719.N24.gz43_219553	F	M00056051D:A07	UC2-NormColon
1144	643510	1720.G01.gz43_219562	F	M00056062D:F12	UC2-NormColon
1145	645049	1720.A02.gz43_219572	F	M00056054B:G05	UC2-NormColon
1146	466795	1720.C02.gz43_219574	F	M00056057B:D01	UC2-NormColon
1147	14157	1720.I02.gz43_219580	F	M00056066B:H04	UC2-NormColon
1148	558494	1720.A04.gz43_219604	F	M00056054C:C09	UC2-NormColon
1149	644927	1720.C04.gz43_219606	F	M00056057B:E12	UC2-NormColon
1150	648688	1720.C05.gz43_219622	F	M00056057C:B02	UC2-NormColon
1151	454906	1720.A06.gz43_219636	F	M00056054C:E12	UC2-NormColon
1152	644597	1720.D06.gz43_219639	F	M00056059A:A02	UC2-NormColon
1153	460047	1720.K06.gz43_219646	F	M00056069A:F01	UC2-NormColon
1154	62053	1720.C08.gz43_219670	F	M00056057C:D06	UC2-NormColon
1155	649054	1720.D08.gz43_219671	F	M00056059A:B01	UC2-NormColon
1156	644225	1720.K08.gz43_219678	F	M00056069A:F06	UC2-NormColon
1157	447635	1720.C09.gz43_219686	F	M00056057C:E01	UC2-NormColon
1158	642166	1720.E10.gz43_219704	F	M00056060D:H11	UC2-NormColon
1159	473007	1720.D11.gz43_219719	F	M00056059B:D10	UC2-NormColon
1160	551181	1720.M11.gz43_219728	F	M00056072B:C06	UC2-NormColon
1161	644928	1720.C12.gz43_219734	F	M00056057C:E12	UC2-NormColon
1162	644916	1720.E12.gz43_219736	F	M00056061A:E05	UC2-NormColon
1163	644701	1720.L12.gz43_219743	F	M00056070C:B09	UC2-NormColon
1164	487567	1720.O12.gz43_219746	F	M00056074C:H08	UC2-NormColon
1165	641801	1720.E13.gz43_219752	F	M00056061B:A03	UC2-NormColon
1166	651108	1720.O13.gz43_219762	F	M00056074C:H09	UC2-NormColon
1167	447676	1720.A14.gz43_219764	F	M00056055A:E04	UC2-NormColon
1168	645076	1720.K14.gz43_219774	F	M00056069B:E04	UC2-NormColon
1169	641469	1720.C15.gz43_219782	F	M00056057D:E11	UC2-NormColon
1170	375577	1720.G15.gz43_219786	F	M00056063C:F10	UC2-NormColon
1171	558154	1720.C16.gz43_219798	F	M00056058A:B07	UC2-NormColon
1172	650549	1720.G16.gz43_219802	F	M00056063C:G11	UC2-NormColon
1173	461351	1720.I16.gz43_219804	F	M00056066D:G04	UC2-NormColon
1174	640818	1720.A18.gz43_219828	F	M00056055B:B06	UC2-NormColon
1175	455716	1720.I18.gz43_219836	F	M00056067A:A12	UC2-NormColon
1176	644822	1720.J18.gz43_219837	F	M00056068D:A06	UC2-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
1177	467780	1720.C19.gz43_219846	F	M00056058A:F08	UC2-NormColon
1178	446415	1720.F20.gz43_219865	F	M00056062D:D08	UC2-NormColon
1179	553923	1720.H20.gz43_219867	F	M00056066A:D03	UC2-NormColon
1180	645900	1720.I21.gz43_219884	F	M00056067B:D08	UC2-NormColon
1181	649364	1720.M21.gz43_219888	F	M00056072D:E08	UC2-NormColon
1182	643348	1720.N23.gz43_219921	F	M00056074B:D12	UC2-NormColon
1183	648654	1731.A01.gz43_219940	F	M00056120C:H04	UC2-NormColon
1184	648547	1731.C01.gz43_219942	F	M00056123B:G05	UC2-NormColon
1185	463824	1731.I01.gz43_219948	F	M00056133D:D09	UC2-NormColon
1186	648721	1731.N01.gz43_219953	F	M00056140C:E04	UC2-NormColon
1187	648481	1731.O01.gz43_219954	F	M00056142A:F03	UC2-NormColon
1188	644037	1731.A02.gz43_219956	F	M00056120D:F01	UC2-NormColon
1189	635354	1731.H02.gz43_219963	F	M00056132B:C12	UC2-NormColon
1190	711493	1731.J02.gz43_219965	F	M00056134D:G07	UC2-NormColon
1191	648742	1731.L02.gz43_219967	F	M00056137D:H05	UC2-NormColon
1192	476380	1731.F03.gz43_219977	F	M00056129C:F09	UC2-NormColon
1193	649617	1731.J03.gz43_219981	F	M00056134D:G11	UC2-NormColon
1194	639555	1731.B04.gz43_219989	F	M00056122B:A07	UC2-NormColon
1195	465127	1731.D04.gz43_219991	F	M00056125B:F01	UC2-NormColon
1196	458938	1731.L04.gz43_219999	F	M00056138A:B11	UC2-NormColon
1197	453726	1731.G05.gz43_220010	F	M00056131A:E09	UC2-NormColon
1198	557026	1731.H06.gz43_220027	F	M00056132C:F04	UC2-NormColon
1199	422242	1731.D07.gz43_220039	F	M00056127A:A10	UC2-NormColon
1200	456985	1731.E07.gz43_220040	F	M00056128B:A07	UC2-NormColon
1201	640695	1731.I07.gz43_220044	F	M00056134A:D04	UC2-NormColon
1202	627515	1731.B08.gz43_220053	F	M00056122B:G09	UC2-NormColon
1203	648341	1731.M08.gz43_220064	F	M00056139D:E05	UC2-NormColon
1204	464990	1731.A09.gz43_220068	F	M00056121A:E05	UC2-NormColon
1205	459521	1731.J10.gz43_220093	F	M00056135B:E03	UC2-NormColon
1206	549691	1731.L10.gz43_220095	F	M00056138B:F05	UC2-NormColon
1207	514838	1731.M10.gz43_220096	F	M00056139D:H04	UC2-NormColon
1208	452738	1731.O10.gz43_220098	F	M00056142C:A09	UC2-NormColon
1209	644928	1731.D11.gz43_220103	F	M00056127A:H03	UC2-NormColon
1210	460190	1731.B12.gz43_220117	F	M00056122C:H12	UC2-NormColon
1211	562378	1731.G12.gz43_220122	F	M00056131B:E01	UC2-NormColon
1212	647949	1731.P12.gz43_220131	F	M00056144D:C05	UC2-NormColon
1213	557419	1731.B13.gz43_220133	F	M00056122D:B07	UC2-NormColon
1214	638934	1731.D13.gz43_220135	F	M00056127B:E11	UC2-NormColon
1215	646785	1731.F13.gz43_220137	F	M00056130B:E11	UC2-NormColon
1216	647248	1731.E14.gz43_220152	F	M00056128C:F02	UC2-NormColon
1217	470006	1731.I14.gz43_220156	F	M00056134C:C06	UC2-NormColon
1218	648311	1731.K14.gz43_220158	F	M00056137B:F07	UC2-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
1219	649299	1731.F15.gz43_220169	F	M00056130C:C12	UC2-NormColon
1220	478393	1731.K15.gz43_220174	F	M00056137B:F11	UC2-NormColon
1221	647290	1731.F16.gz43_220185	F	M00056130C:F08	UC2-NormColon
1222	649735	1731.G16.gz43_220186	F	M00056131C:H03	UC2-NormColon
1223	646039	1731.J16.gz43_220189	F	M00056135C:C05	UC2-NormColon
1224	646581	1731.M16.gz43_220192	F	M00056140A:F12	UC2-NormColon
1225	470667	1731.N16.gz43_220193	F	M00056141C:H01	UC2-NormColon
1226	642650	1731.J17.gz43_220205	F	M00056135C:C08	UC2-NormColon
1227	642275	1731.K17.gz43_220206	F	M00056137C:A01	UC2-NormColon
1228	651015	1731.L17.gz43_220207	F	M00056138D:G08	UC2-NormColon
1229	642936	1731.H18.gz43_220219	F	M00056133B:F01	UC2-NormColon
1230	642204	1731.A19.gz43_220228	F	M00056121D:A12	UC2-NormColon
1231	557867	1731.J19.gz43_220237	F	M00056135C:H06	UC2-NormColon
1232	639395	1731.K19.gz43_220238	F	M00056137C:E01	UC2-NormColon
1233	645367	1731.K20.gz43_220254	F	M00056137C:G02	UC2-NormColon
1234	647232	1731.L20.gz43_220255	F	M00056139A:D12	UC2-NormColon
1235	647431	1731.E21.gz43_220264	F	M00056129A:G01	UC2-NormColon
1236	708175	1731.I21.gz43_220268	F	M00056134D:B07	UC2-NormColon
1237	503122	1731.A22.gz43_220276	F	M00056122A:A05	UC2-NormColon
1238	515350	1731.C22.gz43_220278	F	M00056124D:F06	UC2-NormColon
1239	556336	1731.F22.gz43_220281	F	M00056130D:E06	UC2-NormColon
1240	589098	1731.A23.gz43_220292	F	M00056122A:B05	UC2-NormColon
1241	531461	1731.B23.gz43_220293	F	M00056123B:F02	UC2-NormColon
1242	455808	1731.C23.gz43_220294	F	M00056124D:G03	UC2-NormColon
1243	643510	1731.D23.gz43_220295	F	M00056127D:G10	UC2-NormColon
1244	648996	1731.J23.gz43_220301	F	M00056136A:B11	UC2-NormColon
1245	446164	1731.N23.gz43_220305	F	M00056141D:E08	UC2-NormColon
1246	419114	1731.O23.gz43_220306	F	M00056143A:H08	UC2-NormColon
1247	648076	1731.A24.gz43_220308	F	M00056122A:D02	UC2-NormColon
1248	649482	1731.I24.gz43_220316	F	M00056134D:F02	UC2-NormColon
1249	646323	1732.H01.gz43_220331	F	M00056155B:A02	UC2-NormColon
1250	550714	1732.A05.gz43_220388	F	M00056146A:A09	UC2-NormColon
1251	649482	1732.J05.gz43_220397	F	M00056158C:D11	UC2-NormColon
1252	650987	1732.J06.gz43_220413	F	M00056158C:F09	UC2-NormColon
1253	644221	1732.F07.gz43_220425	F	M00056153A:G04	UC2-NormColon
1254	647412	1732.M07.gz43_220432	F	M00056162C:F02	UC2-NormColon
1255	416624	1732.I08.gz43_220444	F	M00056157A:B11	UC2-NormColon
1256	644801	1732.F09.gz43_220457	F	M00056153A:H07	UC2-NormColon
1257	650249	1732.G10.gz43_220474	F	M00056154B:F11	UC2-NormColon
1258	465734	1732.C11.gz43_220486	F	M00056149C:A02	UC2-NormColon
1259	605761	1732.E11.gz43_220488	F	M00056152A:B11	UC2-NormColon
1260	649782	1732.M11.gz43_220496	F	M00056162D:A01	UC2-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
1261	449956	1732.A12.gz43_220500	F	M00056146A:H09	UC2-NormColon
1262	642244	1732.I12.gz43_220508	F	M00056157B:A08	UC2-NormColon
1263	650348	1732.L12.gz43_220511	F	M00056161C:G06	UC2-NormColon
1264	461135	1732.E13.gz43_220520	F	M00056152A:D07	UC2-NormColon
1265	16092	1732.L13.gz43_220527	F	M00056161C:H10	UC2-NormColon
1266	650116	1732.M13.gz43_220528	F	M00056162D:D03	UC2-NormColon
1267	650534	1732.O13.gz43_220530	F	M00056165C:B11	UC2-NormColon
1268	640634	1732.A14.gz43_220532	F	M00056146B:E05	UC2-NormColon
1269	446184	1732.I14.gz43_220540	F	M00056157B:H06	UC2-NormColon
1270	380477	1732.M14.gz43_220544	F	M00056162D:D06	UC2-NormColon
1271	463966	1732.K15.gz43_220558	F	M00056160C:F12	UC2-NormColon
1272	649578	1732.O15.gz43_220562	F	M00056165D:D09	UC2-NormColon
1273	650877	1732.C16.gz43_220566	F	M00056149C:E10	UC2-NormColon
1274	449882	1732.F16.gz43_220569	F	M00056153B:F11	UC2-NormColon
1275	650909	1732.J16.gz43_220573	F	M00056159A:E03	UC2-NormColon
1276	645100	1732.K16.gz43_220574	F	M00056160C:G01	UC2-NormColon
1277	649883	1732.M17.gz43_220592	F	M00056163A:B10	UC2-NormColon
1278	554581	1732.I19.gz43_220620	F	M00056157C:E10	UC2-NormColon
1279	467972	1732.L19.gz43_220623	F	M00056162A:B06	UC2-NormColon
1280	488592	1732.A20.gz43_220628	F	M00056146D:D04	UC2-NormColon
1281	651075	1732.E20.gz43_220632	F	M00056152C:G08	UC2-NormColon
1282	649991	1732.K20.gz43_220638	F	M00056160D:C06	UC2-NormColon
1283	649947	1732.L20.gz43_220639	F	M00056162A:C09	UC2-NormColon
1284	224092	1732.N20.gz43_220641	F	M00056164A:H03	UC2-NormColon
1285	555634	1732.L21.gz43_220655	F	M00056162A:E09	UC2-NormColon
1286	639485	1732.C22.gz43_220662	F	M00056149D:F06	UC2-NormColon
1287	646596	1732.I23.gz43_220684	F	M00056157D:H08	UC2-NormColon
1288	459260	1732.J23.gz43_220685	F	M00056159C:C11	UC2-NormColon
1289	634409	1732.L23.gz43_220687	F	M00056162A:F01	UC2-NormColon
1290	650820	1732.C24.gz43_220694	F	M00056150A:E04	UC2-NormColon
1291	559349	1741.M01.gz43_220720	F	M00056184C:C07	UC2-NormColon
1292	650063	1741.D02.gz43_220727	F	M00056171C:A08	UC2-NormColon
1293	492982	1741.J02.gz43_220733	F	M00056180B:D05	UC2-NormColon
1294	557353	1741.K02.gz43_220734	F	M00056182A:B04	UC2-NormColon
1295	649299	1741.G03.gz43_220746	F	M00056175D:E05	UC2-NormColon
1296	648063	1741.F04.gz43_220761	F	M00056174C:H09	UC2-NormColon
1297	641193	1741.J04.gz43_220765	F	M00056180B:F11	UC2-NormColon
1298	561856	1741.L04.gz43_220767	F	M00056183B:G11	UC2-NormColon
1299	642631	1741.M04.gz43_220768	F	M00056184C:E08	UC2-NormColon
1300	648344	1741.P04.gz43_220771	F	M00056188B:E07	UC2-NormColon
1301	458085	1741.B05.gz43_220773	F	M00056169C:F07	UC2-NormColon
1302	394772	1741.C06.gz43_220790	F	M00056170C:C09	UC2-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
1303	646699	1741.E07.gz43_220808	F	M00056173D:C05	UC2-NormColon
1304	593173	1741.G07.gz43_220810	F	M00056176A:D06	UC2-NormColon
1305	643206	1741.K07.gz43_220814	F	M00056182A:G11	UC2-NormColon
1306	646309	1741.M07.gz43_220816	F	M00056184C:H03	UC2-NormColon
1307	553023	1741.N07.gz43_220817	F	M00056185D:C01	UC2-NormColon
1308	649705	1741.O07.gz43_220818	F	M00056186D:G05	UC2-NormColon
1309	555771	1741.B08.gz43_220821	F	M00056169D:A03	UC2-NormColon
1310	379805	1741.I08.gz43_220828	F	M00056179A:D12	UC2-NormColon
1311	710362	1741.L08.gz43_220831	F	M00056183C:F01	UC2-NormColon
1312	650188	1741.P08.gz43_220835	F	M00056188C:D02	UC2-NormColon
1313	649795	1741.A09.gz43_220836	F	M00056168C:A05	UC2-NormColon
1314	460506	1741.K09.gz43_220846	F	M00056182B:G12	UC2-NormColon
1315	502683	1741.N09.gz43_220849	F	M00056185D:D06	UC2-NormColon
1316	453768	1741.F10.gz43_220857	F	M00056175A:A06	UC2-NormColon
1317	457272	1741.G10.gz43_220858	F	M00056176B:B05	UC2-NormColon
1318	378694	1741.J10.gz43_220861	F	M00056180D:E06	UC2-NormColon
1319	649136	1741.F11.gz43_220873	F	M00056175A:C04	UC2-NormColon
1320	555655	1741.M11.gz43_220880	F	M00056184D:D06	UC2-NormColon
1321	648777	1741.B12.gz43_220885	F	M00056169D:D05	UC2-NormColon
1322	446289	1741.G12.gz43_220890	F	M00056176B:E10	UC2-NormColon
1323	449452	1741.J12.gz43_220893	F	M00056180D:F05	UC2-NormColon
1324	648665	1741.P12.gz43_220899	F	M00056188C:H04	UC2-NormColon
1325	561747	1741.D14.gz43_220919	F	M00056172A:H06	UC2-NormColon
1326	646915	1741.E14.gz43_220920	F	M00056174B:D02	UC2-NormColon
1327	648865	1741.G14.gz43_220922	F	M00056176C:B11	UC2-NormColon
1328	639886	1741.I14.gz43_220924	F	M00056179B:H12	UC2-NormColon
1329	183842	1741.J14.gz43_220925	F	M00056180D:G07	UC2-NormColon
1330	469409	1741.K14.gz43_220926	F	M00056182C:F08	UC2-NormColon
1331	649702	1741.L14.gz43_220927	F	M00056184A:B11	UC2-NormColon
1332	646581	1741.N14.gz43_220929	F	M00056186A:B09	UC2-NormColon
1333	638730	1741.H15.gz43_220939	F	M00056178B:A11	UC2-NormColon
1334	641525	1741.K15.gz43_220942	F	M00056182D:A07	UC2-NormColon
1335	650800	1741.B16.gz43_220949	F	M00056169D:H05	UC2-NormColon
1336	647086	1741.E16.gz43_220952	F	M00056174B:E02	UC2-NormColon
1337	471836	1741.J16.gz43_220957	F	M00056181A:B05	UC2-NormColon
1338	640285	1741.E17.gz43_220968	F	M00056174B:E04	UC2-NormColon
1339	459923	1741.H17.gz43_220971	F	M00056178B:H08	UC2-NormColon
1340	452729	1741.J17.gz43_220973	F	M00056181A:E07	UC2-NormColon
1341	209414	1741.H18.gz43_220987	F	M00056178C:C02	UC2-NormColon
1342	463487	1741.L18.gz43_220991	F	M00056184B:D08	UC2-NormColon
1343	645288	1741.F19.gz43_221001	F	M00056175C:A10	UC2-NormColon
1344	640514	1741.J19.gz43_221005	F	M00056181B:B02	UC2-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
1345	459974	1741.K19.gz43_221006	F	M00056183A:B09	UC2-NormColon
1346	465594	1741.P19.gz43_221011	F	M00056189B:A01	UC2-NormColon
1347	646173	1741.C20.gz43_221014	F	M00056171A:H01	UC2-NormColon
1348	557010	1741.E20.gz43_221016	F	M00056174B:H11	UC2-NormColon
1349	650146	1741.F20.gz43_221017	F	M00056175C:B11	UC2-NormColon
1350	499690	1741.G20.gz43_221018	F	M00056177A:D12	UC2-NormColon
1351	584745	1741.H20.gz43_221019	F	M00056178C:E12	UC2-NormColon
1352	446987	1741.L20.gz43_221023	F	M00056184B:H08	UC2-NormColon
1353	458683	1741.A21.gz43_221028	F	M00056169B:C02	UC2-NormColon
1354	640922	1741.H21.gz43_221035	F	M00056178C:F02	UC2-NormColon
1355	561793	1741.J21.gz43_221037	F	M00056181B:E11	UC2-NormColon
1356	641945	1741.O21.gz43_221042	F	M00056188A:E05	UC2-NormColon
1357	645578	1741.J22.gz43_221053	F	M00056181C:D02	UC2-NormColon
1358	647688	1741.L22.gz43_221055	F	M00056184C:A09	UC2-NormColon
1359	610986	1741.G23.gz43_221066	F	M00056177A:H01	UC2-NormColon
1360	644053	1741.I23.gz43_221068	F	M00056180B:A06	UC2-NormColon
1361	639132	1741.M23.gz43_221072	F	M00056185B:B06	UC2-NormColon
1362	642256	1741.B24.gz43_221077	F	M00056170B:B09	UC2-NormColon
1363	648820	1741.F24.gz43_221081	F	M00056175D:A06	UC2-NormColon
1364	650975	1741.L24.gz43_221087	F	M00056184C:C03	UC2-NormColon
1365	644801	1741.N24.gz43_221089	F	M00056186B:H09	UC2-NormColon
1366	637387	1742.G01.gz43_221098	F	M00056198A:B05	UC2-NormColon
1367	642118	1742.P01.gz43_221107	F	M00056212C:C09	UC2-NormColon
1368	397363	1742.F03.gz43_221129	F	M00056196C:B03	UC2-NormColon
1369	463168	1742.J03.gz43_221133	F	M00056203D:F05	UC2-NormColon
1370	172843	1742.M03.gz43_221136	F	M00056208B:C10	UC2-NormColon
1371	570939	1742.J04.gz43_221149	F	M00056203D:H03	UC2-NormColon
1372	463545	1742.L04.gz43_221151	F	M00056206D:F07	UC2-NormColon
1373	456920	1742.J05.gz43_221165	F	M00056204A:B08	UC2-NormColon
1374	644916	1742.E06.gz43_221176	F	M00056195C:F12	UC2-NormColon
1375	559955	1742.M06.gz43_221184	F	M00056208C:A10	UC2-NormColon
1376	453762	1742.B08.gz43_221205	F	M00056191B:E08	UC2-NormColon
1377	640913	1742.I08.gz43_221212	F	M00056201C:C03	UC2-NormColon
1378	648590	1742.F09.gz43_221225	F	M00056196C:G12	UC2-NormColon
1379	470801	1742.N09.gz43_221233	F	M00056210B:C11	UC2-NormColon
1380	645223	1742.M11.gz43_221264	F	M00056208D:A12	UC2-NormColon
1381	649402	1742.E12.gz43_221272	F	M00056195D:D07	UC2-NormColon
1382	649354	1742.N12.gz43_221281	F	M00056210B:E03	UC2-NormColon
1383	650756	1742.K15.gz43_221326	F	M00056205D:G04	UC2-NormColon
1384	648754	1742.J18.gz43_221373	F	M00056204C:H12	UC2-NormColon
1385	645177	1742.K19.gz43_221390	F	M00056206B:A10	UC2-NormColon
1386	507050	1742.M19.gz43_221392	F	M00056209B:D02	UC2-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
1387	646275	1742.P19.gz43_221395	F	M00056213C:C01	UC2-NormColon
1388	574166	1743.H01.gz43_221483	F	M00056223A:D10	UC2-NormColon
1389	649709	1743.H03.gz43_221515	F	M00056223A:H07	UC2-NormColon
1390	648155	1743.C04.gz43_221526	F	M00056217A:H11	UC2-NormColon
1391	578718	1743.K04.gz43_221534	F	M00056227D:A02	UC2-NormColon
1392	649272	1743.N04.gz43_221537	F	M00056232C:E06	UC2-NormColon
1393	648351	1743.D05.gz43_221543	F	M00056218C:C02	UC2-NormColon
1394	618670	1743.I06.gz43_221564	F	M00056225B:A11	UC2-NormColon
1395	706245	1743.P07.gz43_221587	F	M00056236A:G12	UC2-NormColon
1396	638807	1743.A08.gz43_221588	F	M00056214B:H03	UC2-NormColon
1397	562359	1743.C09.gz43_221606	F	M00056217B:G03	UC2-NormColon
1398	447892	1743.K09.gz43_221614	F	M00056228A:A02	UC2-NormColon
1399	502413	1743.N09.gz43_221617	F	M00056232D:C08	UC2-NormColon
1400	499517	1743.A10.gz43_221620	F	M00056214C:A04	UC2-NormColon
1401	570052	1743.G11.gz43_221642	F	M00056222A:E05	UC2-NormColon
1402	649351	1743.M11.gz43_221648	F	M00056231B:E01	UC2-NormColon
1403	650975	1743.A16.gz43_221716	F	M00056214D:F05	UC2-NormColon
1404	562625	1743.C16.gz43_221718	F	M00056217D:B07	UC2-NormColon
1405	644916	1743.E16.gz43_221720	F	M00056220A:H04	UC2-NormColon
1406	33738	1743.L16.gz43_221727	F	M00056229C:F05	UC2-NormColon
1407	645549	1743.H17.gz43_221739	F	M00056224B:F01	UC2-NormColon
1408	451487	1743.M21.gz43_221808	F	M00056232B:A11	UC2-NormColon
1409	448780	1743.C22.gz43_221814	F	M00056218A:G11	UC2-NormColon
1410	648816	1743.O22.gz43_221826	F	M00056235A:C12	UC2-NormColon
1411	648989	1743.G23.gz43_221834	F	M00056223A:B11	UC2-NormColon
1412	453470	1743.H23.gz43_221835	F	M00056224D:E08	UC2-NormColon
1413	649030	1743.M23.gz43_221840	F	M00056232B:C04	UC2-NormColon
1414	442347	1743.G24.gz43_221850	F	M00056223A:C03	UC2-NormColon
1415	645271	1744.O01.gz43_221874	F	M00056256A:C02	UC2-NormColon
1416	645872	1744.J02.gz43_221885	F	M00056249A:H07	UC2-NormColon
1417	651051	1744.N02.gz43_221889	F	M00056254A:F04	UC2-NormColon
1418	650463	1744.F03.gz43_221897	F	M00056244A:A01	UC2-NormColon
1419	506719	1744.J03.gz43_221901	F	M00056249B:C02	UC2-NormColon
1420	648989	1744.E04.gz43_221912	F	M00056242D:A02	UC2-NormColon
1421	703978	1744.A06.gz43_221940	F	M00056237B:D04	UC2-NormColon
1422	650661	1744.K07.gz43_221966	F	M00056250C:D05	UC2-NormColon
1423	419255	1744.H08.gz43_221979	F	M00056246C:G07	UC2-NormColon
1424	648996	1744.M08.gz43_221984	F	M00056253A:F12	UC2-NormColon
1425	451361	1744.N09.gz43_222001	F	M00056254D:C04	UC2-NormColon
1426	15296	1744.A10.gz43_222004	F	M00056237C:C05	UC2-NormColon
1427	649396	1744.C10.gz43_222006	F	M00056240B:F08	UC2-NormColon
1428	650860	1744.J10.gz43_222013	F	M00056249C:E06	UC2-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
1429	643327	1744.K14.gz43_222078	F	M00056251B:A12	UC2-NormColon
1430	639119	1744.M14.gz43_222080	F	M00056253B:H04	UC2-NormColon
1431	447272	1744.C15.gz43_222086	F	M00056240D:H07	UC2-NormColon
1432	452646	1744.K15.gz43_222094	F	M00056251B:B07	UC2-NormColon
1433	637387	1744.G17.gz43_222122	F	M00056246A:E01	UC2-NormColon
1434	162981	1744.H17.gz43_222123	F	M00056247A:D02	UC2-NormColon
1435	457221	1744.H18.gz43_222139	F	M00056247A:F07	UC2-NormColon
1436	703217	1744.M18.gz43_222144	F	M00056253C:C04	UC2-NormColon
1437	559324	1744.N18.gz43_222145	F	M00056255B:F09	UC2-NormColon
1438	707483	1744.A19.gz43_222148	F	M00056238A:A03	UC2-NormColon
1439	464091	1744.P19.gz43_222163	F	M00056258A:A11	UC2-NormColon
1440	645472	1744.N20.gz43_222177	F	M00056255C:C04	UC2-NormColon
1441	650018	1744.H21.gz43_222187	F	M00056247B:C11	UC2-NormColon
1442	651073	1744.E22.gz43_222200	F	M00056243C:G10	UC2-NormColon
1443	641874	1744.M23.gz43_222224	F	M00056253D:G04	UC2-NormColon
1444	610269	1744.P23.gz43_222227	F	M00056258A:E10	UC2-NormColon
1445	650463	1744.F24.gz43_222233	F	M00056245A:D11	UC2-NormColon
1446	650919	1744.I24.gz43_222236	F	M00056249A:F11	UC2-NormColon
1447	586794	1744.K24.gz43_222238	F	M00056251C:H04	UC2-NormColon
1448	642200	1753.K02.gz43_222270	F	M00056273A:A07	UC2-NormColon
1449	645271	1753.C03.gz43_222278	F	M00056261A:F12	UC2-NormColon
1450	528162	1753.J04.gz43_222301	F	M00056271C:C06	UC2-NormColon
1451	648609	1753.N05.gz43_222321	F	M00056277B:G05	UC2-NormColon
1452	213	1753.D06.gz43_222327	F	M00056262D:G08	UC2-NormColon
1453	648063	1753.E06.gz43_222328	F	M00056264B:C03	UC2-NormColon
1454	647828	1753.I06.gz43_222332	F	M00056270A:B09	UC2-NormColon
1455	476380	1753.L06.gz43_222335	F	M00056274D:E08	UC2-NormColon
1456	649262	1753.D10.gz43_222391	F	M00056263A:D08	UC2-NormColon
1457	648590	1753.A12.gz43_222420	F	M00056258D:H06	UC2-NormColon
1458	557857	1753.I12.gz43_222428	F	M00056270B:F02	UC2-NormColon
1459	649349	1753.P13.gz43_222451	F	M00056280B:E09	UC2-NormColon
1460	460245	1753.B14.gz43_222453	F	M00056260C:E11	UC2-NormColon
1461	648442	1753.M14.gz43_222464	F	M00056276A:F05	UC2-NormColon
1462	646609	1753.E15.gz43_222472	F	M00056265A:E01	UC2-NormColon
1463	562173	1753.G15.gz43_222474	F	M00056267D:B09	UC2-NormColon
1464	555021	1753.A17.gz43_222500	F	M00056259A:E08	UC2-NormColon
1465	486452	1753.D17.gz43_222503	F	M00056263B:E10	UC2-NormColon
1466	507066	1753.M17.gz43_222512	F	M00056276D:B12	UC2-NormColon
1467	649592	1753.O18.gz43_222530	F	M00056279B:G06	UC2-NormColon
1468	268336	1753.C23.gz43_222598	F	M00056262B:B08	UC2-NormColon
1469	509202	1753.P23.gz43_222611	F	M00056280D:C06	UC2-NormColon
1470	459914	1753.A24.gz43_222612	F	M00056259C:E03	UC2-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
1471	466894	1753.I24.gz43_222620	F	M00056271A:G04	UC2-NormColon
1472	647839	1754.D07.gz43_222727	F	M00056285B:B01	UC2-NormColon
1473	644862	1754.I07.gz43_222732	F	M00056292D:C06	UC2-NormColon
1474	492587	1754.K07.gz43_222734	F	M00056295C:F12	UC2-NormColon
1475	651057	1754.M07.gz43_222736	F	M00056298A:H02	UC2-NormColon
1476	554276	1754.E10.gz43_222776	F	M00056286C:H08	UC2-NormColon
1477	643984	1754.N10.gz43_222785	F	M00056299C:F06	UC2-NormColon
1478	646060	1754.H12.gz43_222811	F	M00056291B:G01	UC2-NormColon
1479	646387	1754.K12.gz43_222814	F	M00056296A:A07	UC2-NormColon
1480	462986	1754.N12.gz43_222817	F	M00056299D:A02	UC2-NormColon
1481	598471	1754.H19.gz43_222923	F	M00056291C:C11	UC2-NormColon
1482	449882	1754.I19.gz43_222924	F	M00056293B:F02	UC2-NormColon
1483	555998	1754.F20.gz43_222937	F	M00056289B:E05	UC2-NormColon
1484	419801	1754.J20.gz43_222941	F	M00056294B:G06	UC2-NormColon
1485	647462	1754.E21.gz43_222952	F	M00056287C:H08	UC2-NormColon
1486	648524	1754.F21.gz43_222953	F	M00056289B:F09	UC2-NormColon
1487	462865	1754.M22.gz43_222976	F	M00056298D:G01	UC2-NormColon
1488	645844	1754.O22.gz43_222978	F	M00056301C:H08	UC2-NormColon
1489	556497	1754.C23.gz43_222982	F	M00056284C:A11	UC2-NormColon
1490	467709	1754.L23.gz43_222991	F	M00056297D:B10	UC2-NormColon
1491	559857	1754.D24.gz43_222999	F	M00056286B:A04	UC2-NormColon
1492	651115	1754.N24.gz43_223009	F	M00056300B:A11	UC2-NormColon
1493	644660	1755.D05.gz43_223079	F	M00056307A:F07	UC2-NormColon
1494	647248	1755.N05.gz43_223089	F	M00056329C:B09	UC2-NormColon
1495	524261	1755.B06.gz43_223093	F	M00056305A:A02	UC2-NormColon
1496	556444	1755.K06.gz43_223102	F	M00056320C:E08	UC2-NormColon
1497	639378	1755.M08.gz43_223136	F	M00056326C:G07	UC2-NormColon
1498	460929	1755.O09.gz43_223154	F	M00056333A:E09	UC2-NormColon
1499	642260	1755.K10.gz43_223166	F	M00056320D:F07	UC2-NormColon
1500	635062	1755.I11.gz43_223180	F	M00056319A:A11	UC2-NormColon
1501	644880	1755.B14.gz43_223221	F	M00056305B:F09	UC2-NormColon
1502	452075	1755.N14.gz43_223233	F	M00056330B:C02	UC2-NormColon
1503	557052	1755.E15.gz43_223240	F	M00056310A:C10	UC2-NormColon
1504	569195	1755.K15.gz43_223246	F	M00056323A:G03	UC2-NormColon
1505	444222	1755.M16.gz43_223264	F	M00056328B:E07	UC2-NormColon
1506	467364	1755.A17.gz43_223268	F	M00056304A:H04	UC2-NormColon
1507	446910	1755.A18.gz43_223284	F	M00056304B:C05	UC2-NormColon
1508	447126	1755.M19.gz43_223312	F	M00056328D:B01	UC2-NormColon
1509	650639	1755.D20.gz43_223319	F	M00056308A:C01	UC2-NormColon
1510	641681	1755.B22.gz43_223349	F	M00056305D:E08	UC2-NormColon
1511	606129	1755.P24.gz43_223395	F	M00056338B:B08	UC2-NormColon
1512	448412	1766.A01.gz43_224099	F	M00042346A:B04	UC2-PrimColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
1513	485237	1766.E01.gz43_224103	F	M00042432D:G02	UC2-PrimColon
1514	479131	1766.G01.gz43_224105	F	M00042437B:A11	UC2-PrimColon
1515	481457	1766.H03.gz43_224138	F	M00042439A:D09	UC2-PrimColon
1516	448892	1766.A09.gz43_224227	F	M00042346C:G12	UC2-PrimColon
1517	477797	1766.E13.gz43_224295	F	M00042433C:H05	UC2-PrimColon
1518	450212	1766.I19.gz43_224395	F	M00042462A:F12	UC2-PrimColon
1519	3781	1766.J21.gz43_224428	F	M00042464A:F06	UC2-PrimColon
1520	447377	1766.M22.gz43_224447	F	M00042470B:H11	UC2-PrimColon
1521	453606	1767.H01.gz43_224490	F	M00042764B:B10	UC2-PrimColon
1522	472101	1767.O02.gz43_224513	F	M00042777B:B05	UC2-PrimColon
1523	284586	1767.D03.gz43_224518	F	M00042756B:B01	UC2-PrimColon
1524	449689	1767.M03.gz43_224527	F	M00042773A:H11	UC2-PrimColon
1525	449215	1767.A04.gz43_224531	F	M00042515D:B11	UC2-PrimColon
1526	128749	1767.I04.gz43_224539	F	M00042766A:D07	UC2-PrimColon
1527	451982	1767.A05.gz43_224547	F	M00042515D:G01	UC2-PrimColon
1528	448251	1767.H05.gz43_224554	F	M00042764C:B10	UC2-PrimColon
1529	449437	1767.J05.gz43_224556	F	M00042767D:D02	UC2-PrimColon
1530	482876	1767.K05.gz43_224557	F	M00042769B:E12	UC2-PrimColon
1531	481614	1767.C06.gz43_224565	F	M00042755A:D09	UC2-PrimColon
1532	486547	1767.M06.gz43_224575	F	M00042773B:H08	UC2-PrimColon
1533	179760	1767.A07.gz43_224579	F	M00042751B:C07	UC2-PrimColon
1534	484633	1767.I08.gz43_224603	F	M00042766B:G11	UC2-PrimColon
1535	479851	1767.K08.gz43_224605	F	M00042769C:B01	UC2-PrimColon
1536	470801	1767.G09.gz43_224617	F	M00042763B:A03	UC2-PrimColon
1537	486452	1767.J09.gz43_224620	F	M00042768A:H09	UC2-PrimColon
1538	479868	1767.K09.gz43_224621	F	M00042769C:B06	UC2-PrimColon
1539	485880	1767.C10.gz43_224629	F	M00042755A:H04	UC2-PrimColon
1540	456513	1767.J11.gz43_224652	F	M00042768B:F02	UC2-PrimColon
1541	473433	1767.O11.gz43_224657	F	M00042778A:C04	UC2-PrimColon
1542	481594	1767.C12.gz43_224661	F	M00042755B:D01	UC2-PrimColon
1543	477521	1767.F12.gz43_224664	F	M00042761C:G11	UC2-PrimColon
1544	485073	1767.L12.gz43_224670	F	M00042771B:G05	UC2-PrimColon
1545	480960	1767.B13.gz43_224676	F	M00042753B:C08	UC2-PrimColon
1546	449215	1767.A14.gz43_224691	F	M00042751D:D03	UC2-PrimColon
1547	450551	1767.I14.gz43_224699	F	M00042766D:C05	UC2-PrimColon
1548	481057	1767.M14.gz43_224703	F	M00042774B:C01	UC2-PrimColon
1549	449076	1767.D15.gz43_224710	F	M00042757A:H07	UC2-PrimColon
1550	477098	1767.E15.gz43_224711	F	M00042760A:G12	UC2-PrimColon
1551	482486	1767.J15.gz43_224716	F	M00042768C:E06	UC2-PrimColon
1552	449438	1767.K15.gz43_224717	F	M00042770A:D02	UC2-PrimColon
1553	448260	1767.O15.gz43_224721	F	M00042778B:B07	UC2-PrimColon
1554	453385	1767.P15.gz43_224722	F	M00042779D:D04	UC2-PrimColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
1555	484355	1767.A16.gz43_224723	F	M00042751D:F09	UC2-PrimColon
1556	485882	1767.C16.gz43_224725	F	M00042755B:H04	UC2-PrimColon
1557	449592	1767.L16.gz43_224734	F	M00042771D:F02	UC2-PrimColon
1558	449261	1767.M16.gz43_224735	F	M00042774C:B09	UC2-PrimColon
1559	485907	1767.C17.gz43_224741	F	M00042755B:H11	UC2-PrimColon
1560	474580	1767.F17.gz43_224744	F	M00042761D:D12	UC2-PrimColon
1561	448152	1767.N17.gz43_224752	F	M00042776D:D01	UC2-PrimColon
1562	474823	1767.P17.gz43_224754	F	M00042779D:E06	UC2-PrimColon
1563	453024	1767.E18.gz43_224759	F	M00042760B:E12	UC2-PrimColon
1564	479880	1767.I18.gz43_224763	F	M00042767A:B10	UC2-PrimColon
1565	477399	1767.N18.gz43_224768	F	M00042776D:G10	UC2-PrimColon
1566	485441	1767.A19.gz43_224771	F	M00042751D:G09	UC2-PrimColon
1567	485183	1767.B19.gz43_224772	F	M00042753C:G12	UC2-PrimColon
1568	452104	1767.C19.gz43_224773	F	M00042755C:A10	UC2-PrimColon
1569	449275	1767.A20.gz43_224787	F	M00042752A:B04	UC2-PrimColon
1570	447218	1767.L20.gz43_224798	F	M00042772C:C12	UC2-PrimColon
1571	472119	1767.N20.gz43_224800	F	M00042777A:B10	UC2-PrimColon
1572	482868	1767.I21.gz43_224811	F	M00042767B:E10	UC2-PrimColon
1573	455143	1767.F22.gz43_224824	F	M00042762A:G02	UC2-PrimColon
1574	484964	1767.I22.gz43_224827	F	M00042767B:G04	UC2-PrimColon
1575	448325	1767.D23.gz43_224838	F	M00042758B:C06	UC2-PrimColon
1576	484987	1767.I23.gz43_224843	F	M00042767B:G09	UC2-PrimColon
1577	475797	1767.O23.gz43_224849	F	M00042778D:F11	UC2-PrimColon
1578	477757	1767.P24.gz43_224866	F	M00042780A:H05	UC2-PrimColon
1579	448233	1778.D01.gz43_225254	F	M00042842A:B12	UC2-PrimColon
1580	475111	1778.B02.gz43_225268	F	M00042838A:E02	UC2-PrimColon
1581	449403	1778.N02.gz43_225280	F	M00042859B:D06	UC2-PrimColon
1582	449604	1778.O02.gz43_225281	F	M00042860D:F02	UC2-PrimColon
1583	447983	1778.F03.gz43_225288	F	M00042845C:A09	UC2-PrimColon
1584	484091	1778.O03.gz43_225297	F	M00042860D:F05	UC2-PrimColon
1585	480900	1778.J04.gz43_225308	F	M00042852B:C06	UC2-PrimColon
1586	551811	1778.K04.gz43_225309	F	M00042854A:B11	UC2-PrimColon
1587	485841	1778.L05.gz43_225326	F	M00042855B:H06	UC2-PrimColon
1588	476256	1778.C07.gz43_225349	F	M00042839D:F02	UC2-PrimColon
1589	447983	1778.E07.gz43_225351	F	M00042844A:D02	UC2-PrimColon
1590	725641	1778.K07.gz43_225357	F	M00042854A:D05	UC2-PrimColon
1591	484789	1778.L08.gz43_225374	F	M00042855C:G11	UC2-PrimColon
1592	449110	1778.L09.gz43_225390	F	M00042855D:A12	UC2-PrimColon
1593	451368	1778.O09.gz43_225393	F	M00042861A:F04	UC2-PrimColon
1594	449521	1778.P09.gz43_225394	F	M00042862C:E02	UC2-PrimColon
1595	727875	1778.G10.gz43_225401	F	M00042847A:F04	UC2-PrimColon
1596	449273	1778.I11.gz43_225419	F	M00042851A:B08	UC2-PrimColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
1597	449652	1778.M11.gz43_225423	F	M00042857C:G04	UC2-PrimColon
1598	481664	1778.N11.gz43_225424	F	M00042859D:D12	UC2-PrimColon
1599	448230	1778.E12.gz43_225431	F	M00042844C:B03	UC2-PrimColon
1600	485029	1778.H12.gz43_225434	F	M00042849B:G06	UC2-PrimColon
1601	483274	1778.I12.gz43_225435	F	M00042851A:E11	UC2-PrimColon
1602	644190	1778.J12.gz43_225436	F	M00042853A:G03	UC2-PrimColon
1603	725266	1778.K12.gz43_225437	F	M00042854B:F05	UC2-PrimColon
1604	480005	1778.L12.gz43_225438	F	M00042855D:B12	UC2-PrimColon
1605	484841	1778.M12.gz43_225439	F	M00042857C:G05	UC2-PrimColon
1606	480641	1778.N12.gz43_225440	F	M00042860A:C01	UC2-PrimColon
1607	481319	1778.O13.gz43_225457	F	M00042861C:C03	UC2-PrimColon
1608	387077	1778.C14.gz43_225461	F	M00042840C:B12	UC2-PrimColon
1609	456737	1778.L14.gz43_225470	F	M00042855D:D06	UC2-PrimColon
1610	479084	1778.M14.gz43_225471	F	M00042858A:A08	UC2-PrimColon
1611	484468	1778.O15.gz43_225489	F	M00042861C:F07	UC2-PrimColon
1612	450673	1778.C18.gz43_225525	F	M00042841B:H05	UC2-PrimColon
1613	474597	1778.D18.gz43_225526	F	M00042843A:E07	UC2-PrimColon
1614	477593	1778.E18.gz43_225527	F	M00042844D:H02	UC2-PrimColon
1615	452990	1778.I18.gz43_225531	F	M00042851D:B08	UC2-PrimColon
1616	449407	1778.O18.gz43_225537	F	M00042861D:D09	UC2-PrimColon
1617	448104	1778.E19.gz43_225543	F	M00042845A:B05	UC2-PrimColon
1618	453856	1778.D22.gz43_225590	F	M00042843B:F05	UC2-PrimColon
1619	475942	1778.B23.gz43_225604	F	M00042839B:F05	UC2-PrimColon
1620	639991	1778.F23.gz43_225608	F	M00042846C:D09	UC2-PrimColon
1621	480640	1778.O23.gz43_225617	F	M00042862A:C01	UC2-PrimColon
1622	472307	1778.C24.gz43_225621	F	M00042842A:B04	UC2-PrimColon
1623	733806	1780.I01.gz43_226027	F	M00056361A:C01	UC2-PrimColon
1624	732150	1780.E02.gz43_226039	F	M00056356C:H07	UC2-PrimColon
1625	724907	1780.K02.gz43_226045	F	M00056363A:C06	UC2-PrimColon
1626	724792	1780.L02.gz43_226046	F	M00056364A:B04	UC2-PrimColon
1627	736210	1780.B04.gz43_226068	F	M00056353C:E12	UC2-PrimColon
1628	623978	1780.G05.gz43_226089	F	M00056359A:C08	UC2-PrimColon
1629	600856	1780.I05.gz43_226091	F	M00056361A:H06	UC2-PrimColon
1630	364334	1780.K05.gz43_226093	F	M00056363A:E10	UC2-PrimColon
1631	661194	1780.P05.gz43_226098	F	M00056368B:H09	UC2-PrimColon
1632	416326	1780.G06.gz43_226105	F	M00056359A:F06	UC2-PrimColon
1633	727129	1780.D07.gz43_226118	F	M00056355D:A05	UC2-PrimColon
1634	560859	1780.O07.gz43_226129	F	M00056367C:D06	UC2-PrimColon
1635	482831	1780.P07.gz43_226130	F	M00056368C:E07	UC2-PrimColon
1636	503862	1780.L08.gz43_226142	F	M00056364C:B01	UC2-PrimColon
1637	468467	1780.D09.gz43_226150	F	M00056355D:B08	UC2-PrimColon
1638	594994	1780.A10.gz43_226163	F	M00056352D:H02	UC2-PrimColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
1639	463966	1780.C10.gz43_226165	F	M00056355A:C10	UC2-PrimColon
1640	471646	1780.I10.gz43_226171	F	M00056361B:E02	UC2-PrimColon
1641	731925	1780.B11.gz43_226180	F	M00056353D:D10	UC2-PrimColon
1642	480924	1780.M11.gz43_226191	F	M00056365B:G10	UC2-PrimColon
1643	517298	1780.P11.gz43_226194	F	M00056368D:D03	UC2-PrimColon
1644	734150	1780.F12.gz43_226200	F	M00056358A:G05	UC2-PrimColon
1645	528981	1780.H12.gz43_226202	F	M00056360B:D09	UC2-PrimColon
1646	135364	1780.I12.gz43_226203	F	M00056361C:C06	UC2-PrimColon
1647	511606	1780.J12.gz43_226204	F	M00056362C:C02	UC2-PrimColon
1648	552891	1780.K14.gz43_226237	F	M00056363C:C12	UC2-PrimColon
1649	730301	1780.P14.gz43_226242	F	M00056368D:G05	UC2-PrimColon
1650	480005	1780.H15.gz43_226250	F	M00056360C:B01	UC2-PrimColon
1651	588959	1780.L15.gz43_226254	F	M00056364C:H08	UC2-PrimColon
1652	557029	1780.C16.gz43_226261	F	M00056355B:D02	UC2-PrimColon
1653	553244	1780.L17.gz43_226286	F	M00056364D:C05	UC2-PrimColon
1654	456535	1780.O20.gz43_226337	F	M00056368A:C11	UC2-PrimColon
1655	728774	1780.K22.gz43_226365	F	M00056363D:H03	UC2-PrimColon
1656	724039	1780.E23.gz43_226375	F	M00056357C:C06	UC2-PrimColon
1657	732144	1780.H23.gz43_226378	F	M00056360D:H10	UC2-PrimColon
1658	724257	1789.G01.gz43_226409	F	M00056375D:D12	UC2-PrimColon
1659	474346	1789.M01.gz43_226415	F	M00056384C:H04	UC2-PrimColon
1660	376342	1789.N01.gz43_226416	F	M00056386A:F08	UC2-PrimColon
1661	475682	1789.P01.gz43_226418	F	M00056388B:A05	UC2-PrimColon
1662	734646	1789.B02.gz43_226420	F	M00056370B:C10	UC2-PrimColon
1663	186372	1789.M02.gz43_226431	F	M00056384D:A04	UC2-PrimColon
1664	736001	1789.A03.gz43_226435	F	M00056369B:E03	UC2-PrimColon
1665	487079	1789.F03.gz43_226440	F	M00056374C:G08	UC2-PrimColon
1666	460284	1789.H03.gz43_226442	F	M00056377A:C01	UC2-PrimColon
1667	725274	1789.I03.gz43_226443	F	M00056377D:F08	UC2-PrimColon
1668	553035	1789.N03.gz43_226448	F	M00056386A:G01	UC2-PrimColon
1669	724009	1789.P03.gz43_226450	F	M00056388B:B03	UC2-PrimColon
1670	568484	1789.B04.gz43_226452	F	M00056370B:E07	UC2-PrimColon
1671	725321	1789.L04.gz43_226462	F	M00056383B:F08	UC2-PrimColon
1672	731542	1789.K05.gz43_226477	F	M00056382C:F11	UC2-PrimColon
1673	725448	1789.L06.gz43_226494	F	M00056383B:G08	UC2-PrimColon
1674	452806	1789.N06.gz43_226496	F	M00056386B:A07	UC2-PrimColon
1675	549790	1789.L07.gz43_226510	F	M00056383C:E07	UC2-PrimColon
1676	730660	1789.N07.gz43_226512	F	M00056386B:A11	UC2-PrimColon
1677	503625	1789.B08.gz43_226516	F	M00056370C:F01	UC2-PrimColon
1678	725381	1789.E09.gz43_226535	F	M00056373D:G01	UC2-PrimColon
1679	649411	1789.G09.gz43_226537	F	M00056376A:C10	UC2-PrimColon
1680	729993	1789.I09.gz43_226539	F	M00056378C:E10	UC2-PrimColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
1681	727523	1789.M10.gz43_226559	F	M00056385A:A07	UC2-PrimColon
1682	459918	1789.N10.gz43_226560	F	M00056386B:D07	UC2-PrimColon
1683	735649	1789.B11.gz43_226564	F	M00056370D:C06	UC2-PrimColon
1684	734348	1789.F11.gz43_226568	F	M00056375A:D11	UC2-PrimColon
1685	558412	1789.O11.gz43_226577	F	M00056387C:D01	UC2-PrimColon
1686	724694	1789.H12.gz43_226586	F	M00056377C:A01	UC2-PrimColon
1687	723972	1789.J12.gz43_226588	F	M00056382A:A12	UC2-PrimColon
1688	623408	1789.N12.gz43_226592	F	M00056386B:E09	UC2-PrimColon
1689	640158	1790.F01.gz43_226792	F	M00056394C:D07	UC2-PrimColon
1690	725095	1790.J02.gz43_226812	F	M00056398C:D10	UC2-PrimColon
1691	562769	1790.O02.gz43_226817	F	M00056404D:G03	UC2-PrimColon
1692	479851	1790.L03.gz43_226830	F	M00056400C:G04	UC2-PrimColon
1693	481077	1790.N03.gz43_226832	F	M00056403C:F02	UC2-PrimColon
1694	656268	1790.K04.gz43_226845	F	M00056399D:C11	UC2-PrimColon
1695	724411	1790.N04.gz43_226848	F	M00056403C:F03	UC2-PrimColon
1696	640261	1790.N05.gz43_226864	F	M00056403C:F12	UC2-PrimColon
1697	426297	1790.D07.gz43_226886	F	M00056392D:C05	UC2-PrimColon
1698	649591	1790.M07.gz43_226895	F	M00056402C:B09	UC2-PrimColon
1699	729111	1790.D08.gz43_226902	F	M00056392D:H02	UC2-PrimColon
1700	733563	1790.G08.gz43_226905	F	M00056396A:D03	UC2-PrimColon
1701	729637	1790.A10.gz43_226931	F	M00056389B:H03	UC2-PrimColon
1702	726494	1790.K10.gz43_226941	F	M00056400A:D08	UC2-PrimColon
1703	724714	1790.M10.gz43_226943	F	M00056402D:A01	UC2-PrimColon
1704	543323	1790.P10.gz43_226946	F	M00056406C:D09	UC2-PrimColon
1705	556769	1790.B11.gz43_226948	F	M00056390C:B08	UC2-PrimColon
1706	209	1790.M11.gz43_226959	F	M00056402D:B07	UC2-PrimColon
1707	724914	1790.B12.gz43_226964	F	M00056390C:C04	UC2-PrimColon
1708	614463	1790.D12.gz43_226966	F	M00056393A:G06	UC2-PrimColon
1709	474981	1790.G12.gz43_226969	F	M00056396A:G10	UC2-PrimColon
1710	729950	1790.L12.gz43_226974	F	M00056401A:F09	UC2-PrimColon
1711	640756	1790.N12.gz43_226976	F	M00056404A:G03	UC2-PrimColon
1712	449228	1790.O13.gz43_226993	F	M00056405C:H04	UC2-PrimColon
1713	423420	1790.P13.gz43_226994	F	M00056406C:F12	UC2-PrimColon
1714	727150	1790.C14.gz43_226997	F	M00056391C:H12	UC2-PrimColon
1715	503173	1790.E14.gz43_226999	F	M00056394B:C11	UC2-PrimColon
1716	188309	1790.N14.gz43_227008	F	M00056404B:B06	UC2-PrimColon
1717	448758	1790.J15.gz43_227020	F	M00056399B:G09	UC2-PrimColon
1718	735234	1790.L15.gz43_227022	F	M00056401B:B01	UC2-PrimColon
1719	483147	1790.P15.gz43_227026	F	M00056407A:D10	UC2-PrimColon
1720	642985	1790.G16.gz43_227033	F	M00056396B:E10	UC2-PrimColon
1721	725451	1790.K16.gz43_227037	F	M00056400A:G10	UC2-PrimColon
1722	729809	1790.P16.gz43_227042	F	M00056407A:G03	UC2-PrimColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
1723	495712	1790.A17.gz43_227043	F	M00056389D:F01	UC2-PrimColon
1724	730948	1790.O17.gz43_227057	F	M00056405D:E05	UC2-PrimColon
1725	457508	1790.C18.gz43_227061	F	M00056391D:E06	UC2-PrimColon
1726	417549	1790.M18.gz43_227071	F	M00056403A:E09	UC2-PrimColon
1727	725454	1790.E19.gz43_227079	F	M00056394B:G05	UC2-PrimColon
1728	448817	1790.C20.gz43_227093	F	M00056392A:F06	UC2-PrimColon
1729	726411	1790.O20.gz43_227105	F	M00056406A:C02	UC2-PrimColon
1730	558794	1790.D21.gz43_227110	F	M00056393D:A09	UC2-PrimColon
1731	641687	1790.P21.gz43_227122	F	M00056409A:C03	UC2-PrimColon
1732	733643	1790.N22.gz43_227136	F	M00056404C:C12	UC2-PrimColon
1733	523364	1790.F23.gz43_227144	F	M00056395C:H03	UC2-PrimColon
1734	468467	1790.M23.gz43_227151	F	M00056403B:D09	UC2-PrimColon
1735	402799	1790.O23.gz43_227153	F	M00056406A:E01	UC2-PrimColon
1736	470462	1790.P23.gz43_227154	F	M00056409A:D03	UC2-PrimColon
1737	118514	1790.D24.gz43_227158	F	M00056393D:C12	UC2-PrimColon
1738	732821	1790.F24.gz43_227160	F	M00056395D:B01	UC2-PrimColon
1739	447222	1790.K24.gz43_227165	F	M00056400C:B11	UC2-PrimColon
1740	729779	1790.M24.gz43_227167	F	M00056403B:G12	UC2-PrimColon
1741	727633	1790.P24.gz43_227170	F	M00056409A:D06	UC2-PrimColon
1742	475797	1791.F01.gz43_227176	F	M00056415A:D03	UC2-PrimColon
1743	648170	1791.G01.gz43_227177	F	M00056416B:B11	UC2-PrimColon
1744	472684	1791.I01.gz43_227179	F	M00056418A:G09	UC2-PrimColon
1745	477718	1791.O02.gz43_227201	F	M00056423D:H07	UC2-PrimColon
1746	729784	1791.A03.gz43_227203	F	M00056409B:C12	UC2-PrimColon
1747	402471	1791.F03.gz43_227208	F	M00056415B:B10	UC2-PrimColon
1748	453762	1791.K03.gz43_227213	F	M00056419D:G04	UC2-PrimColon
1749	511149	1791.M03.gz43_227215	F	M00056422B:A08	UC2-PrimColon
1750	727090	1791.G04.gz43_227225	F	M00056416B:H01	UC2-PrimColon
1751	560957	1791.K04.gz43_227229	F	M00056420A:C01	UC2-PrimColon
1752	727845	1791.M04.gz43_227231	F	M00056422B:C12	UC2-PrimColon
1753	642170	1791.H05.gz43_227242	F	M00056417B:D05	UC2-PrimColon
1754	128749	1791.K05.gz43_227245	F	M00056420A:C12	UC2-PrimColon
1755	736632	1791.P05.gz43_227250	F	M00056424D:C08	UC2-PrimColon
1756	542957	1791.J07.gz43_227276	F	M00056419A:F08	UC2-PrimColon
1757	733490	1791.O08.gz43_227297	F	M00056424A:F05	UC2-PrimColon
1758	649722	1791.O09.gz43_227313	F	M00056424A:F12	UC2-PrimColon
1759	562137	1791.L11.gz43_227342	F	M00056421C:E06	UC2-PrimColon
1760	729199	1791.G12.gz43_227353	F	M00056416D:C08	UC2-PrimColon
1761	730178	1791.L12.gz43_227358	F	M00056421C:E12	UC2-PrimColon
1762	435349	1791.G13.gz43_227369	F	M00056416D:D12	UC2-PrimColon
1763	723963	1791.P13.gz43_227378	F	M00056425B:B02	UC2-PrimColon
1764	725408	1791.H14.gz43_227386	F	M00056417C:G10	UC2-PrimColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
1765	500253	1791.L14.gz43_227390	F	M00056421C:H01	UC2-PrimColon
1766	644723	1791.N14.gz43_227392	F	M00056423C:G05	UC2-PrimColon
1767	474965	1791.M15.gz43_227407	F	M00056422C:B10	UC2-PrimColon
1768	724024	1791.N17.gz43_227440	F	M00056423D:B06	UC2-PrimColon
1769	27083	1791.D18.gz43_227446	F	M00056413B:D07	UC2-PrimColon
1770	729899	1791.E18.gz43_227447	F	M00056414C:H08	UC2-PrimColon
1771	728986	1791.G18.gz43_227449	F	M00056416D:H10	UC2-PrimColon
1772	640744	1791.A19.gz43_227459	F	M00056410A:A04	UC2-PrimColon
1773	703978	1791.B19.gz43_227460	F	M00056411B:D01	UC2-PrimColon
1774	725408	1791.O19.gz43_227473	F	M00056424C:B10	UC2-PrimColon
1775	725407	1791.H20.gz43_227482	F	M00056417D:G09	UC2-PrimColon
1776	736507	1791.K21.gz43_227501	F	M00056420C:E08	UC2-PrimColon
1777	555359	1791.O21.gz43_227505	F	M00056424C:F02	UC2-PrimColon
1778	724773	1791.C22.gz43_227509	F	M00056412B:B08	UC2-PrimColon
1779	724220	1791.P22.gz43_227522	F	M00056425D:D08	UC2-PrimColon
1780	641383	1791.A23.gz43_227523	F	M00056410B:A09	UC2-PrimColon
1781	562581	1791.K23.gz43_227533	F	M00056420D:A09	UC2-PrimColon
1782	726768	1791.P23.gz43_227538	F	M00056425D:H01	UC2-PrimColon
1783	729579	1791.H24.gz43_227546	F	M00056418A:G01	UC2-PrimColon
1784	498194	1791.L24.gz43_227550	F	M00056422A:F07	UC2-PrimColon
1785	288134	1791.N24.gz43_227552	F	M00056423D:F10	UC2-PrimColon
1786	553983	1792.P01.gz43_227582	F	M00056486B:G02	UC2-PrimColon
1787	724400	1792.E03.gz43_227603	F	M00056433B:A09	UC2-PrimColon
1788	645476	1792.J05.gz43_227640	F	M00056479C:E04	UC2-PrimColon
1789	556115	1792.D06.gz43_227650	F	M00056432A:A01	UC2-PrimColon
1790	734287	1792.F06.gz43_227652	F	M00056434C:B01	UC2-PrimColon
1791	725584	1792.I07.gz43_227671	F	M00056478C:H01	UC2-PrimColon
1792	725006	1792.P07.gz43_227678	F	M00056486D:A12	UC2-PrimColon
1793	731158	1792.A09.gz43_227695	F	M00056426B:G12	UC2-PrimColon
1794	592186	1792.B09.gz43_227696	F	M00056428A:F10	UC2-PrimColon
1795	452618	1792.M09.gz43_227707	F	M00056483A:F10	UC2-PrimColon
1796	725238	1792.G10.gz43_227717	F	M00056476C:E05	UC2-PrimColon
1797	727948	1792.P10.gz43_227726	F	M00056486D:F04	UC2-PrimColon
1798	452981	1792.A11.gz43_227727	F	M00056426C:G05	UC2-PrimColon
1799	710362	1792.B11.gz43_227728	F	M00056428B:B01	UC2-PrimColon
1800	480005	1792.C11.gz43_227729	F	M00056429D:E02	UC2-PrimColon
1801	471931	1792.P11.gz43_227742	F	M00056487A:C10	UC2-PrimColon
1802	725454	1792.H12.gz43_227750	F	M00056477C:G09	UC2-PrimColon
1803	729584	1792.I12.gz43_227751	F	M00056478D:G02	UC2-PrimColon
1804	725210	1792.N12.gz43_227756	F	M00056484B:E11	UC2-PrimColon
1805	462687	1792.P12.gz43_227758	F	M00056487A:D01	UC2-PrimColon
1806	724183	1792.M13.gz43_227771	F	M00056483B:E04	UC2-PrimColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
1807	724390	1792.M14.gz43_227787	F	M00056483B:F04	UC2-PrimColon
1808	647375	1792.G16.gz43_227813	F	M00056476D:H11	UC2-PrimColon
1809	736751	1792.G17.gz43_227829	F	M00056477A:B11	UC2-PrimColon
1810	725348	1792.P17.gz43_227838	F	M00056487A:F05	UC2-PrimColon
1811	481594	1792.L18.gz43_227850	F	M00056482B:B11	UC2-PrimColon
1812	675299	1792.N18.gz43_227852	F	M00056484D:D01	UC2-PrimColon
1813	734646	1792.K19.gz43_227865	F	M00056481A:F02	UC2-PrimColon
1814	453713	1792.L20.gz43_227882	F	M00056482B:C09	UC2-PrimColon
1815	724183	1792.M20.gz43_227883	F	M00056483C:D06	UC2-PrimColon
1816	730282	1792.M24.gz43_227947	F	M00056483D:F06	UC2-PrimColon
1817	733006	1801.D01.gz43_227954	F	M00056491B:B09	UC2-PrimColon
1818	733151	1801.I01.gz43_227959	F	M00056496D:B12	UC2-PrimColon
1819	734261	1801.J01.gz43_227960	F	M00056497C:D05	UC2-PrimColon
1820	514142	1801.K01.gz43_227961	F	M00056498D:C01	UC2-PrimColon
1821	471232	1801.M01.gz43_227963	F	M00056501B:B09	UC2-PrimColon
1822	447785	1801.D02.gz43_227970	F	M00056491B:E02	UC2-PrimColon
1823	523753	1801.J02.gz43_227976	F	M00056497C:E01	UC2-PrimColon
1824	451383	1801.M02.gz43_227979	F	M00056501B:C07	UC2-PrimColon
1825	635951	1801.K03.gz43_227993	F	M00056499A:A04	UC2-PrimColon
1826	731820	1801.A04.gz43_227999	F	M00056487C:E03	UC2-PrimColon
1827	446928	1801.E04.gz43_228003	F	M00056492B:D06	UC2-PrimColon
1828	732598	1801.P04.gz43_228014	F	M00056504B:B01	UC2-PrimColon
1829	725434	1801.B05.gz43_228016	F	M00056488B:G10	UC2-PrimColon
1830	460690	1801.G05.gz43_228021	F	M00056495A:C02	UC2-PrimColon
1831	611604	1801.J05.gz43_228024	F	M00056497D:C11	UC2-PrimColon
1832	635951	1801.L05.gz43_228026	F	M00056500A:G12	UC2-PrimColon
1833	429191	1801.B06.gz43_228032	F	M00056488B:H04	UC2-PrimColon
1834	640116	1801.O06.gz43_228045	F	M00056503B:G11	UC2-PrimColon
1835	734043	1813.H05.gz43_229558	F	M00056576A:A04	UC2-PrimColon
1836	508210	1813.I06.gz43_229575	F	M00056577A:F10	UC2-PrimColon
1837	11632	1813.O07.gz43_229597	F	M00056585C:C08	UC2-PrimColon
1838	475757	1813.H08.gz43_229606	F	M00056576A:E01	UC2-PrimColon
1839	729281	1813.J10.gz43_229640	F	M00056578D:A02	UC2-PrimColon
1840	733970	1813.N10.gz43_229644	F	M00056584C:A06	UC2-PrimColon
1841	727410	1813.A13.gz43_229679	F	M00056567A:H06	UC2-PrimColon
1842	465446	1813.L13.gz43_229690	F	M00056581D:A08	UC2-PrimColon
1843	511351	1813.M13.gz43_229691	F	M00056583C:A05	UC2-PrimColon
1844	733664	1813.I20.gz43_229799	F	M00056577D:F08	UC2-PrimColon
1845	548893	1813.C22.gz43_229825	F	M00056570A:D09	UC2-PrimColon
1846	513540	1813.H22.gz43_229830	F	M00056576C:G01	UC2-PrimColon
1847	725759	1813.I22.gz43_229831	F	M00056578A:B05	UC2-PrimColon
1848	726104	1816.C19.gz43_230929	F	M00056633D:E05	UC2-PrimColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
1849	482868	1816.E19.gz43_230931	F	M00056636C:H05	UC2-PrimColon
1850	727332	1816.I19.gz43_230935	F	M00056641C:G09	UC2-PrimColon
1851	727078	1816.K19.gz43_230937	F	M00056644C:B03	UC2-PrimColon
1852	727108	1816.L19.gz43_230938	F	M00056645D:E06	UC2-PrimColon
1853	736325	1816.B20.gz43_230944	F	M00056632C:E03	UC2-PrimColon
1854	726818	1816.J20.gz43_230952	F	M00056642D:C05	UC2-PrimColon
1855	724083	1816.M20.gz43_230955	F	M00056646D:E03	UC2-PrimColon
1856	724565	1816.N20.gz43_230956	F	M00056648B:C08	UC2-PrimColon
1857	207530	1816.O20.gz43_230957	F	M00056650A:E01	UC2-PrimColon
1858	736778	1816.C21.gz43_230961	F	M00056634A:C06	UC2-PrimColon
1859	559684	1816.E21.gz43_230963	F	M00056636D:F03	UC2-PrimColon
1860	726494	1816.B22.gz43_230976	F	M00056632C:H08	UC2-PrimColon
1861	419711	1816.G22.gz43_230981	F	M00056639A:F11	UC2-PrimColon
1862	377935	1816.M22.gz43_230987	F	M00056646D:F07	UC2-PrimColon
1863	726448	1816.C23.gz43_230993	F	M00056634A:G11	UC2-PrimColon
1864	215249	1816.G23.gz43_230997	F	M00056639A:H12	UC2-PrimColon
1865	735322	1816.N23.gz43_231004	F	M00056648B:E09	UC2-PrimColon
1866	727175	1816.O23.gz43_231005	F	M00056650B:C11	UC2-PrimColon
1867	731966	1816.P23.gz43_231006	F	M00056651B:E12	UC2-PrimColon
1868	727944	1816.B24.gz43_231008	F	M00056632D:E02	UC2-PrimColon
1869	730596	1816.M24.gz43_231019	F	M00056647A:F06	UC2-PrimColon
1870	725607	1825.N13.gz43_231228	F	M00056667A:A12	UC2-PrimColon
1871	45934	1825.P13.gz43_231230	F	M00056670A:G02	UC2-PrimColon
1872	484987	1825.F14.gz43_231236	F	M00056658A:E11	UC2-PrimColon
1873	481592	1825.M14.gz43_231243	F	M00056666A:C04	UC2-PrimColon
1874	735605	1825.O14.gz43_231245	F	M00056668D:E03	UC2-PrimColon
1875	734184	1825.P14.gz43_231246	F	M00056670B:A12	UC2-PrimColon
1876	477718	1825.E16.gz43_231267	F	M00056657A:F06	UC2-PrimColon
1877	552927	1825.F16.gz43_231268	F	M00056658B:C03	UC2-PrimColon
1878	719620	1825.J16.gz43_231272	F	M00056663A:B02	UC2-PrimColon
1879	27083	1825.M16.gz43_231275	F	M00056666A:D09	UC2-PrimColon
1880	478458	1825.P17.gz43_231294	F	M00056670B:G05	UC2-PrimColon
1881	448104	1825.L19.gz43_231322	F	M00056664D:H06	UC2-PrimColon
1882	729675	1825.J20.gz43_231336	F	M00056663A:H09	UC2-PrimColon
1883	730570	1825.B21.gz43_231344	F	M00056653D:F07	UC2-PrimColon
1884	727108	1825.D21.gz43_231346	F	M00056656A:E01	UC2-PrimColon
1885	447074	1825.I21.gz43_231351	F	M00056661D:D06	UC2-PrimColon
1886	463741	1825.F22.gz43_231364	F	M00056658C:B12	UC2-PrimColon
1887	732351	1825.N22.gz43_231372	F	M00056667D:E05	UC2-PrimColon
1888	727343	1825.L23.gz43_231386	F	M00056665A:G08	UC2-PrimColon
1889	736415	1825.B24.gz43_231392	F	M00056654A:A07	UC2-PrimColon
1890	554597	1825.O24.gz43_231405	F	M00056669B:E10	UC2-PrimColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
1891	723914	1826.A13.gz43_231599	F	M00056672A:E05	UC2-PrimColon
1892	734622	1826.C14.gz43_231617	F	M00056674D:E09	UC2-PrimColon
1893	645925	1826.I14.gz43_231623	F	M00056683B:H04	UC2-PrimColon
1894	641777	1826.D16.gz43_231650	F	M00056676B:G12	UC2-PrimColon
1895	734828	1826.E17.gz43_231667	F	M00056678B:E11	UC2-PrimColon
1896	381623	1826.I17.gz43_231671	F	M00056683C:H10	UC2-PrimColon
1897	517274	1826.J17.gz43_231672	F	M00056685A:H11	UC2-PrimColon
1898	446575	1826.C18.gz43_231681	F	M00056675A:C02	UC2-PrimColon
1899	725899	1826.D18.gz43_231682	F	M00056676C:B04	UC2-PrimColon
1900	492094	1826.M19.gz43_231707	F	M00056689B:F03	UC2-PrimColon
1901	736246	1826.E20.gz43_231715	F	M00056678B:H02	UC2-PrimColon
1902	473238	1826.J20.gz43_231720	F	M00056685B:G04	UC2-PrimColon
1903	730829	1826.K20.gz43_231721	F	M00056686D:E04	UC2-PrimColon
1904	726722	1826.A21.gz43_231727	F	M00056672D:B08	UC2-PrimColon
1905	492629	1826.O21.gz43_231741	F	M00056692A:A05	UC2-PrimColon
1906	730664	1826.E22.gz43_231747	F	M00056678C:A12	UC2-PrimColon
1907	729387	1826.G22.gz43_231749	F	M00056681A:E06	UC2-PrimColon
1908	546121	1826.A23.gz43_231759	F	M00056672D:E04	UC2-PrimColon
1909	513156	1826.C23.gz43_231761	F	M00056675A:G02	UC2-PrimColon
1910	728791	1826.G24.gz43_231781	F	M00056681B:A11	UC2-PrimColon
1911	559610	1826.I24.gz43_231783	F	M00056684B:B12	UC2-PrimColon
1912	729205	1826.J24.gz43_231784	F	M00056685C:G07	UC2-PrimColon
1913	561301	1827.C01.gz43_231793	F	M00056695C:C04	UC2-PrimColon
1914	728556	1827.E01.gz43_231795	F	M00056697C:H10	UC2-PrimColon
1915	640458	1827.I01.gz43_231799	F	M00056701C:G09	UC2-PrimColon
1916	650136	1827.K01.gz43_231801	F	M00056703C:F04	UC2-PrimColon
1917	288801	1827.L01.gz43_231802	F	M00056704D:H10	UC2-PrimColon
1918	648777	1827.M01.gz43_231803	F	M00056706A:B05	UC2-PrimColon
1919	728196	1827.G02.gz43_231813	F	M00056699C:F09	UC2-PrimColon
1920	644354	1827.I02.gz43_231815	F	M00056701D:C03	UC2-PrimColon
1921	419465	1827.M02.gz43_231819	F	M00056706A:E09	UC2-PrimColon
1922	558317	1827.P02.gz43_231822	F	M00056708C:F11	UC2-PrimColon
1923	693869	1827.B03.gz43_231824	F	M00056694A:G03	UC2-PrimColon
1924	553805	1827.L03.gz43_231834	F	M00056705A:B12	UC2-PrimColon
1925	626791	1827.N03.gz43_231836	F	M00056707A:G11	UC2-PrimColon
1926	580601	1827.A04.gz43_231839	F	M00056693B:D11	UC2-PrimColon
1927	493830	1827.B04.gz43_231840	F	M00056694A:G11	UC2-PrimColon
1928	724714	1827.E04.gz43_231843	F	M00056697D:B09	UC2-PrimColon
1929	737109	1827.F04.gz43_231844	F	M00056698D:E11	UC2-PrimColon
1930	395604	1827.G04.gz43_231845	F	M00056699C:G11	UC2-PrimColon
1931	735834	1827.J04.gz43_231848	F	M00056702D:G03	UC2-PrimColon
1932	726852	1827.L04.gz43_231850	F	M00056705A:D02	UC2-PrimColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
1933	728892	1827.P05.gz43_231870	F	M00056708D:B03	UC2-PrimColon
1934	540618	1827.C06.gz43_231873	F	M00056695C:H08	UC2-PrimColon
1935	501030	1827.E06.gz43_231875	F	M00056697D:C09	UC2-PrimColon
1936	477366	1827.F06.gz43_231876	F	M00056698D:G09	UC2-PrimColon
1937	727948	1827.I06.gz43_231879	F	M00056701D:D04	UC2-PrimColon
1938	649927	1827.K06.gz43_231881	F	M00056703D:F08	UC2-PrimColon
1939	449752	1827.M06.gz43_231883	F	M00056706B:C02	UC2-PrimColon
1940	649106	1827.N06.gz43_231884	F	M00056707B:E02	UC2-PrimColon
1941	730463	1827.P06.gz43_231886	F	M00056708D:D10	UC2-PrimColon
1942	462687	1827.E07.gz43_231891	F	M00056697D:C12	UC2-PrimColon
1943	553140	1827.I07.gz43_231895	F	M00056701D:G03	UC2-PrimColon
1944	736100	1827.M07.gz43_231899	F	M00056706B:C07	UC2-PrimColon
1945	730375	1827.B08.gz43_231904	F	M00056694B:H10	UC2-PrimColon
1946	403671	1827.K08.gz43_231913	F	M00056704A:B05	UC2-PrimColon
1947	595181	1827.M08.gz43_231915	F	M00056706B:D04	UC2-PrimColon
1948	573733	1827.A09.gz43_231919	F	M00056693B:H03	UC2-PrimColon
1949	550454	1827.I09.gz43_231927	F	M00056701D:H12	UC2-PrimColon
1950	651050	1827.J09.gz43_231928	F	M00056703A:G01	UC2-PrimColon
1951	728768	1827.L09.gz43_231930	F	M00056705B:A12	UC2-PrimColon
1952	736276	1827.N09.gz43_231932	F	M00056707B:F06	UC2-PrimColon
1953	472837	1827.C10.gz43_231937	F	M00056695D:E05	UC2-PrimColon
1954	732770	1827.H10.gz43_231942	F	M00056700D:H07	UC2-PrimColon
1955	83388	1827.L10.gz43_231946	F	M00056705B:D10	UC2-PrimColon
1956	584693	1827.M10.gz43_231947	F	M00056706C:A07	UC2-PrimColon
1957	588059	1827.D11.gz43_231954	F	M00056697A:D02	UC2-PrimColon
1958	452662	1827.F11.gz43_231956	F	M00056699A:D08	UC2-PrimColon
1959	728898	1827.M11.gz43_231963	F	M00056706C:B12	UC2-PrimColon
1960	672032	1827.F12.gz43_231972	F	M00056699A:E08	UC2-PrimColon
1961	496084	1827.H12.gz43_231974	F	M00056701A:A02	UC2-PrimColon
1962	736579	1827.O12.gz43_231981	F	M00056708B:B09	UC2-PrimColon
1963	727968	1827.A13.gz43_231983	F	M00056693C:D12	UC2-PrimColon
1964	447624	1827.J13.gz43_231992	F	M00056703B:A04	UC2-PrimColon
1965	728552	1827.K13.gz43_231993	F	M00056704A:H08	UC2-PrimColon
1966	733064	1827.M13.gz43_231995	F	M00056706C:D05	UC2-PrimColon
1967	607202	1827.O13.gz43_231997	F	M00056708B:D03	UC2-PrimColon
1968	473433	1827.P13.gz43_231998	F	M00056708D:H06	UC2-PrimColon
1969	617813	1827.A14.gz43_231999	F	M00056693C:G06	UC2-PrimColon
1970	728300	1827.G14.gz43_232005	F	M00056700A:F12	UC2-PrimColon
1971	727760	1827.K14.gz43_232009	F	M00056704B:C02	UC2-PrimColon
1972	454087	1827.P14.gz43_232014	F	M00056709A:A05	UC2-PrimColon
1973	425396	1827.A15.gz43_232015	F	M00056693D:B02	UC2-PrimColon
1974	552430	1827.N15.gz43_232028	F	M00056707C:E01	UC2-PrimColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
1975	650542	1827.C16.gz43_232033	F	M00056696A:G12	UC2-PrimColon
1976	725084	1827.D16.gz43_232034	F	M00056697A:H10	UC2-PrimColon
1977	446607	1827.G16.gz43_232037	F	M00056700A:G05	UC2-PrimColon
1978	4584	1827.H16.gz43_232038	F	M00056701A:G09	UC2-PrimColon
1979	560678	1827.J16.gz43_232040	F	M00056703B:D07	UC2-PrimColon
1980	730639	1827.N16.gz43_232044	F	M00056707C:E03	UC2-PrimColon
1981	727506	1827.C17.gz43_232049	F	M00056696B:B03	UC2-PrimColon
1982	540618	1827.E17.gz43_232051	F	M00056698B:E10	UC2-PrimColon
1983	735676	1827.I17.gz43_232055	F	M00056702C:A10	UC2-PrimColon
1984	728768	1827.N17.gz43_232060	F	M00056707C:F10	UC2-PrimColon
1985	475942	1827.A18.gz43_232063	F	M00056693D:E12	UC2-PrimColon
1986	631056	1827.H18.gz43_232070	F	M00056701B:D02	UC2-PrimColon
1987	259218	1827.P18.gz43_232078	F	M00056709A:H11	UC2-PrimColon
1988	724489	1827.H19.gz43_232086	F	M00056701B:D06	UC2-PrimColon
1989	727845	1827.D21.gz43_232114	F	M00056697C:D11	UC2-PrimColon
1990	641072	1827.F21.gz43_232116	F	M00056699B:G04	UC2-PrimColon
1991	553483	1827.A22.gz43_232127	F	M00056694A:C05	UC2-PrimColon
1992	551096	1827.C24.gz43_232161	F	M00056696B:H01	UC2-PrimColon
1993	727649	1827.F24.gz43_232164	F	M00056699C:C02	UC2-PrimColon
1994	728196	1827.H24.gz43_232166	F	M00056701C:F08	UC2-PrimColon
1995	729428	1828.A01.gz43_232175	F	M00056709C:F06	UC2-PrimColon
1996	724050	1828.F01.gz43_232180	F	M00056714B:C12	UC2-PrimColon
1997	732351	1828.L01.gz43_232186	F	M00056721C:E05	UC2-PrimColon
1998	730627	1828.M01.gz43_232187	F	M00056722C:C09	UC2-PrimColon
1999	728182	1828.H02.gz43_232198	F	M00056716B:F12	UC2-PrimColon
2000	727878	1828.M02.gz43_232203	F	M00056722C:D11	UC2-PrimColon
2001	462687	1828.N02.gz43_232204	F	M00056723C:C09	UC2-PrimColon
2002	555763	1828.L03.gz43_232218	F	M00056721C:H01	UC2-PrimColon
2003	728627	1828.P03.gz43_232222	F	M00056725C:H06	UC2-PrimColon
2004	630516	1828.H04.gz43_232230	F	M00056716C:B06	UC2-PrimColon
2005	584179	1828.A05.gz43_232239	F	M00056709D:D05	UC2-PrimColon
2006	558544	1828.G05.gz43_232245	F	M00056715C:B07	UC2-PrimColon
2007	553294	1828.N05.gz43_232252	F	M00056723C:E01	UC2-PrimColon
2008	726576	1828.O05.gz43_232253	F	M00056724C:H11	UC2-PrimColon
2009	734622	1828.L07.gz43_232282	F	M00056721D:D01	UC2-PrimColon
2010	735362	1828.P07.gz43_232286	F	M00056726A:C12	UC2-PrimColon
2011	455297	1828.A08.gz43_232287	F	M00056709D:E12	UC2-PrimColon
2012	734990	1828.N08.gz43_232300	F	M00056723C:G03	UC2-PrimColon
2013	707609	1828.B10.gz43_232320	F	M00056710D:C05	UC2-PrimColon
2014	728178	1828.L10.gz43_232330	F	M00056721D:F12	UC2-PrimColon
2015	447634	1828.P10.gz43_232334	F	M00056726B:H06	UC2-PrimColon
2016	729813	1828.F11.gz43_232340	F	M00056714D:A11	UC2-PrimColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
2017	728528	1828.I11.gz43_232343	F	M00056718A:H05	UC2-PrimColon
2018	732770	1828.J11.gz43_232344	F	M00056719B:G04	UC2-PrimColon
2019	505858	1828.F12.gz43_232356	F	M00056714D:E08	UC2-PrimColon
2020	735047	1828.E13.gz43_232371	F	M00056714A:B02	UC2-PrimColon
2021	727749	1828.K13.gz43_232377	F	M00056721A:C07	UC2-PrimColon
2022	598746	1828.L13.gz43_232378	F	M00056722A:E10	UC2-PrimColon
2023	728061	1828.O13.gz43_232381	F	M00056725A:E02	UC2-PrimColon
2024	448217	1828.F14.gz43_232388	F	M00056714D:H07	UC2-PrimColon
2025	485899	1828.L14.gz43_232394	F	M00056722A:F08	UC2-PrimColon
2026	641287	1828.B15.gz43_232400	F	M00056711A:A09	UC2-PrimColon
2027	48619	1828.D15.gz43_232402	F	M00056713A:F05	UC2-PrimColon
2028	728929	1828.E15.gz43_232403	F	M00056714A:B09	UC2-PrimColon
2029	451972	1828.I15.gz43_232407	F	M00056718B:C02	UC2-PrimColon
2030	486363	1828.J18.gz43_232456	F	M00056719C:B10	UC2-PrimColon
2031	728897	1828.C19.gz43_232465	F	M00056712B:B11	UC2-PrimColon
2032	448217	1828.E19.gz43_232467	F	M00056714A:E12	UC2-PrimColon
2033	646309	1828.I19.gz43_232471	F	M00056718C:B01	UC2-PrimColon
2034	728303	1828.J19.gz43_232472	F	M00056719C:F06	UC2-PrimColon
2035	728002	1828.K19.gz43_232473	F	M00056721B:D03	UC2-PrimColon
2036	473640	1828.N20.gz43_232492	F	M00056724B:E11	UC2-PrimColon
2037	727480	1828.O21.gz43_232509	F	M00056725C:A03	UC2-PrimColon
2038	509678	1828.P21.gz43_232510	F	M00056726D:G08	UC2-PrimColon
2039	728445	1828.E22.gz43_232515	F	M00056714A:H06	UC2-PrimColon
2040	447150	1828.N22.gz43_232524	F	M00056724B:G03	UC2-PrimColon
2041	728273	1828.A23.gz43_232527	F	M00056710B:F05	UC2-PrimColon
2042	734453	1828.C23.gz43_232529	F	M00056712B:F02	UC2-PrimColon
2043	732006	1828.D23.gz43_232530	F	M00056713C:A10	UC2-PrimColon
2044	449585	1828.I23.gz43_232535	F	M00056718D:D12	UC2-PrimColon
2045	728966	1828.E24.gz43_232547	F	M00056714B:B06	UC2-PrimColon
2046	529356	1838.C01.gz43_232945	F	M00056747D:A03	UC2-PrimColon
2047	551693	1838.P01.gz43_232958	F	M00056764C:A02	UC2-PrimColon
2048	438663	1838.B03.gz43_232976	F	M00056746D:D06	UC2-PrimColon
2049	735464	1838.E03.gz43_232979	F	M00056750B:H03	UC2-PrimColon
2050	736035	1838.J03.gz43_232984	F	M00056756C:D06	UC2-PrimColon
2051	736210	1838.L03.gz43_232986	F	M00056759C:C04	UC2-PrimColon
2052	728464	1838.I05.gz43_233015	F	M00056755B:E07	UC2-PrimColon
2053	730178	1838.K05.gz43_233017	F	M00056758C:B08	UC2-PrimColon
2054	481614	1838.N05.gz43_233020	F	M00056762B:D06	UC2-PrimColon
2055	402799	1839.A01.gz43_233327	F	M00056766D:G09	UC2-PrimColon
2056	675768	1839.N01.gz43_233340	F	M00056784D:C06	UC2-PrimColon
2057	577305	1839.P01.gz43_233342	F	M00056787B:C07	UC2-PrimColon
2058	730505	1839.K02.gz43_233353	F	M00056781A:E06	UC2-PrimColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
2059	349977	1839.B03.gz43_233360	F	M00056768D:A09	UC2-PrimColon
2060	726344	1839.N03.gz43_233372	F	M00056784D:G10	UC2-PrimColon
2061	724183	1839.J04.gz43_233384	F	M00056780B:E06	UC2-PrimColon
2062	730352	1839.M04.gz43_233387	F	M00056783C:E03	UC2-PrimColon
2063	510596	1839.E05.gz43_233395	F	M00056773C:C09	UC2-PrimColon
2064	128773	1839.F05.gz43_233396	F	M00056775A:A05	UC2-PrimColon
2065	728464	1839.G06.gz43_233413	F	M00056776A:G04	UC2-PrimColon
2066	449010	1839.L06.gz43_233418	F	M00056782B:G05	UC2-PrimColon
2067	460023	1839.M06.gz43_233419	F	M00056783D:A02	UC2-PrimColon
2068	733744	1839.K07.gz43_233433	F	M00056781B:C03	UC2-PrimColon
2069	2180	1839.L07.gz43_233434	F	M00056782B:H11	UC2-PrimColon
2070	556458	1839.M07.gz43_233435	F	M00056783D:B07	UC2-PrimColon
2071	711325	1839.A08.gz43_233439	F	M00056767A:F12	UC2-PrimColon
2072	135593	1839.E08.gz43_233443	F	M00056773C:F12	UC2-PrimColon
2073	639178	1839.K08.gz43_233449	F	M00056781B:C05	UC2-PrimColon
2074	504513	1839.B09.gz43_233456	F	M00056769C:C03	UC2-PrimColon
2075	493193	1839.J09.gz43_233464	F	M00056780B:H04	UC2-PrimColon
2076	728133	1839.K09.gz43_233465	F	M00056781B:E01	UC2-PrimColon
2077	727737	1839.A11.gz43_233487	F	M00056767B:C01	UC2-PrimColon
2078	477053	1839.F12.gz43_233508	F	M00056775B:H07	UC2-PrimColon
2079	726384	1839.P12.gz43_233518	F	M00056787C:G01	UC2-PrimColon
2080	736686	1839.A13.gz43_233519	F	M00056767B:G08	UC2-PrimColon
2081	483549	1839.L13.gz43_233530	F	M00056782D:F02	UC2-PrimColon
2082	549801	1839.A14.gz43_233535	F	M00056767C:A09	UC2-PrimColon
2083	730484	1839.H14.gz43_233542	F	M00056777D:D04	UC2-PrimColon
2084	647991	1839.J14.gz43_233544	F	M00056780C:H12	UC2-PrimColon
2085	490393	1839.L14.gz43_233546	F	M00056782D:F08	UC2-PrimColon
2086	643968	1839.N14.gz43_233548	F	M00056785C:B09	UC2-PrimColon
2087	641968	1839.B15.gz43_233552	F	M00056770C:A07	UC2-PrimColon
2088	726261	1839.L15.gz43_233562	F	M00056782D:F10	UC2-PrimColon
2089	733891	1839.M15.gz43_233563	F	M00056784B:A01	UC2-PrimColon
2090	730022	1839.O15.gz43_233565	F	M00056786D:A03	UC2-PrimColon
2091	730296	1839.M16.gz43_233579	F	M00056784B:C02	UC2-PrimColon
2092	733149	1839.M17.gz43_233595	F	M00056784B:D06	UC2-PrimColon
2093	728487	1839.A18.gz43_233599	F	M00056768A:C10	UC2-PrimColon
2094	726229	1839.C18.gz43_233601	F	M00056771D:D10	UC2-PrimColon
2095	523868	1839.G18.gz43_233605	F	M00056776D:B02	UC2-PrimColon
2096	577305	1839.L18.gz43_233610	F	M00056783A:C08	UC2-PrimColon
2097	727216	1839.J19.gz43_233624	F	M00056780D:G05	UC2-PrimColon
2098	47461	1839.L19.gz43_233626	F	M00056783B:B01	UC2-PrimColon
2099	550780	1839.N19.gz43_233628	F	M00056785D:C09	UC2-PrimColon
2100	606076	1839.P21.gz43_233662	F	M00056788A:D06	UC2-PrimColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
2101	691229	1839.C22.gz43_233665	F	M00056772A:C08	UC2-PrimColon
2102	727366	1839.D22.gz43_233666	F	M00056773A:G10	UC2-PrimColon
2103	724722	1839.J22.gz43_233672	F	M00056780D:H10	UC2-PrimColon
2104	725784	1839.M22.gz43_233675	F	M00056784C:C06	UC2-PrimColon
2105	732345	1839.B23.gz43_233680	F	M00056771A:F03	UC2-PrimColon
2106	726699	1839.C23.gz43_233681	F	M00056772A:D03	UC2-PrimColon
2107	513156	1839.J23.gz43_233688	F	M00056781A:C05	UC2-PrimColon
2108	631038	1839.E24.gz43_233699	F	M00056774D:B02	UC2-PrimColon
2109	609459	1839.H24.gz43_233702	F	M00056778C:G08	UC2-PrimColon
2110	482788	1839.J24.gz43_233704	F	M00056781A:D02	UC2-PrimColon
2111	730592	1839.N24.gz43_233708	F	M00056785D:G07	UC2-PrimColon
2112	735801	1852.A13.gz43_235742	F	M00056871C:D05	UC2-PrimColon
2113	472704	1852.H13.gz43_235749	F	M00056879D:D01	UC2-PrimColon
2114	649299	1852.I13.gz43_235750	F	M00056881A:A10	UC2-PrimColon
2115	650944	1852.N13.gz43_235755	F	M00056886B:B10	UC2-PrimColon
2116	481641	1852.E14.gz43_235762	F	M00056876C:B02	UC2-PrimColon
2117	488349	1852.F14.gz43_235763	F	M00056877B:H09	UC2-PrimColon
2118	735096	1852.I14.gz43_235766	F	M00056881A:C02	UC2-PrimColon
2119	594434	1852.J14.gz43_235767	F	M00056882B:E12	UC2-PrimColon
2120	550673	1852.L14.gz43_235769	F	M00056884C:H08	UC2-PrimColon
2121	735672	1852.N14.gz43_235771	F	M00056886B:C05	UC2-PrimColon
2122	732712	1852.K15.gz43_235784	F	M00056883D:A07	UC2-PrimColon
2123	472307	1852.L15.gz43_235785	F	M00056884C:H11	UC2-PrimColon
2124	729981	1852.D16.gz43_235793	F	M00056875D:C04	UC2-PrimColon
2125	639950	1852.I16.gz43_235798	F	M00056881A:H02	UC2-PrimColon
2126	724517	1852.L16.gz43_235801	F	M00056884D:C07	UC2-PrimColon
2127	735412	1852.B17.gz43_235807	F	M00056873A:H06	UC2-PrimColon
2128	724223	1852.N17.gz43_235819	F	M00056886B:H02	UC2-PrimColon
2129	727602	1852.D18.gz43_235825	F	M00056875D:E09	UC2-PrimColon
2130	561396	1852.L18.gz43_235833	F	M00056884D:D06	UC2-PrimColon
2131	726408	1852.B19.gz43_235839	F	M00056873B:C09	UC2-PrimColon
2132	730059	1852.C19.gz43_235840	F	M00056874C:D05	UC2-PrimColon
2133	655327	1852.F19.gz43_235843	F	M00056877C:G12	UC2-PrimColon
2134	732872	1852.M19.gz43_235850	F	M00056886A:A09	UC2-PrimColon
2135	473512	1852.N19.gz43_235851	F	M00056886C:D02	UC2-PrimColon
2136	730441	1852.F20.gz43_235859	F	M00056877C:H03	UC2-PrimColon
2137	451184	1852.N20.gz43_235867	F	M00056886C:D11	UC2-PrimColon
2138	733040	1852.D21.gz43_235873	F	M00056875D:H12	UC2-PrimColon
2139	732872	1852.K21.gz43_235880	F	M00056883D:F07	UC2-PrimColon
2140	152	1852.M21.gz43_235882	F	M00056886A:C11	UC2-PrimColon
2141	730301	1852.I22.gz43_235894	F	M00056881B:G04	UC2-PrimColon
2142	471931	1852.J22.gz43_235895	F	M00056882D:A06	UC2-PrimColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
2143	730106	1852.L23.gz43_235913	F	M00056885A:D12	UC2-PrimColon
2144	649030	1852.O24.gz43_235932	F	M00056888A:H04	UC2-PrimColon
2145	562345	1861.I04.gz43_235990	F	M00056900C:B12	UC2-PrimColon
2146	472226	1861.P04.gz43_235997	F	M00056910B:F01	UC2-PrimColon
2147	494393	1861.E07.gz43_236034	F	M00056895C:E11	UC2-PrimColon
2148	730393	1861.B08.gz43_236047	F	M00056891C:H08	UC2-PrimColon
2149	676221	1861.G10.gz43_236084	F	M00056898C:B06	UC2-PrimColon
2150	648774	1861.O11.gz43_236108	F	M00056909B:E11	UC2-PrimColon
2151	448368	1861.H12.gz43_236117	F	M00056899D:B06	UC2-PrimColon
2152	489001	1861.K12.gz43_236120	F	M00056902D:H09	UC2-PrimColon
2153	557525	1861.J14.gz43_236151	F	M00056902A:G12	UC2-PrimColon
2154	724773	1861.C16.gz43_236176	F	M00056893B:G12	UC2-PrimColon
2155	730608	1861.I16.gz43_236182	F	M00056901B:C03	UC2-PrimColon
2156	642897	1861.K16.gz43_236184	F	M00056903A:C08	UC2-PrimColon
2157	548275	1861.N16.gz43_236187	F	M00056908B:D02	UC2-PrimColon
2158	728640	1861.C17.gz43_236192	F	M00056893C:A02	UC2-PrimColon
2159	479572	1861.B18.gz43_236207	F	M00056892B:C09	UC2-PrimColon
2160	735834	1861.E18.gz43_236210	F	M00056896A:C01	UC2-PrimColon
2161	733425	1861.K18.gz43_236216	F	M00056903A:F03	UC2-PrimColon
2162	732653	1861.P19.gz43_236237	F	M00056911B:A01	UC2-PrimColon
2163	729060	1861.G20.gz43_236244	F	M00056898D:H09	UC2-PrimColon
2164	656667	1861.H21.gz43_236261	F	M00056900B:D01	UC2-PrimColon
2165	732676	1861.G22.gz43_236276	F	M00056899A:A11	UC2-PrimColon
2166	730296	1861.H24.gz43_236309	F	M00056900B:F07	UC2-PrimColon
2167	453001	1861.K24.gz43_236312	F	M00056903B:D09	UC2-PrimColon
2168	725451	1861.N24.gz43_236315	F	M00056908D:A11	UC2-PrimColon
2169	730851	1863.C01.gz43_236704	F	M00056936C:E04	UC2-PrimColon
2170	727596	1863.H01.gz43_236709	F	M00056941D:D07	UC2-PrimColon
2171	736293	1863.L01.gz43_236713	F	M00056946A:F07	UC2-PrimColon
2172	733910	1863.N01.gz43_236715	F	M00056948C:F03	UC2-PrimColon
2173	77737	1863.C02.gz43_236720	F	M00056936C:F11	UC2-PrimColon
2174	638983	1863.L02.gz43_236729	F	M00056946A:G06	UC2-PrimColon
2175	736001	1863.M02.gz43_236730	F	M00056947C:B04	UC2-PrimColon
2176	731196	1863.P02.gz43_236733	F	M00056950D:F12	UC2-PrimColon
2177	446820	1863.A03.gz43_236734	F	M00056934A:E07	UC2-PrimColon
2178	734151	1863.E03.gz43_236738	F	M00056939A:C01	UC2-PrimColon
2179	456183	1863.H03.gz43_236741	F	M00056941D:G05	UC2-PrimColon
2180	734629	1863.I03.gz43_236742	F	M00056943A:B04	UC2-PrimColon
2181	733623	1863.J03.gz43_236743	F	M00056944A:D09	UC2-PrimColon
2182	733856	1863.N03.gz43_236747	F	M00056948D:A11	UC2-PrimColon
2183	727480	1863.P03.gz43_236749	F	M00056950D:H09	UC2-PrimColon
2184	448233	1863.J04.gz43_236759	F	M00056944B:C02	UC2-PrimColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
2185	729691	1863.I05.gz43_236774	F	M00056943A:F01	UC2-PrimColon
2186	500239	1863.N05.gz43_236779	F	M00056949A:A04	UC2-PrimColon
2187	646314	1863.K06.gz43_236792	F	M00056945A:F02	UC2-PrimColon
2188	492893	1863.A08.gz43_236814	F	M00056934C:C04	UC2-PrimColon
2189	451624	1863.D08.gz43_236817	F	M00056938A:H09	UC2-PrimColon
2190	552416	1863.L08.gz43_236825	F	M00056946C:B08	UC2-PrimColon
2191	555478	1863.A10.gz43_236846	F	M00056934C:G09	UC2-PrimColon
2192	616541	1863.G10.gz43_236852	F	M00056941B:B02	UC2-PrimColon
2193	410487	1863.O10.gz43_236860	F	M00056950A:H03	UC2-PrimColon
2194	726825	1863.B11.gz43_236863	F	M00056935C:G08	UC2-PrimColon
2195	733144	1863.D12.gz43_236881	F	M00056938B:C09	UC2-PrimColon
2196	642528	1863.E12.gz43_236882	F	M00056939B:E05	UC2-PrimColon
2197	735994	1863.J12.gz43_236887	F	M00056944C:B03	UC2-PrimColon
2198	724401	1863.K12.gz43_236888	F	M00056945C:A11	UC2-PrimColon
2199	736129	1863.M12.gz43_236890	F	M00056948A:D09	UC2-PrimColon
2200	448046	1863.P13.gz43_236909	F	M00056951B:F09	UC2-PrimColon
2201	731216	1863.D15.gz43_236929	F	M00056938B:H08	UC2-PrimColon
2202	449061	1863.M15.gz43_236938	F	M00056948B:B03	UC2-PrimColon
2203	730815	1863.F17.gz43_236963	F	M00056940C:E05	UC2-PrimColon
2204	732756	1863.H17.gz43_236965	F	M00056942C:F11	UC2-PrimColon
2205	468015	1863.I17.gz43_236966	F	M00056943C:A01	UC2-PrimColon
2206	733081	1863.J17.gz43_236967	F	M00056944D:A06	UC2-PrimColon
2207	555484	1863.L17.gz43_236969	F	M00056946D:G09	UC2-PrimColon
2208	731355	1863.A18.gz43_236974	F	M00056935A:C02	UC2-PrimColon
2209	730375	1863.G18.gz43_236980	F	M00056941B:G08	UC2-PrimColon
2210	467803	1863.M18.gz43_236986	F	M00056948B:G05	UC2-PrimColon
2211	735306	1863.D20.gz43_237009	F	M00056938C:F10	UC2-PrimColon
2212	729316	1863.I20.gz43_237014	F	M00056943D:B02	UC2-PrimColon
2213	551441	1863.L20.gz43_237017	F	M00056947A:C05	UC2-PrimColon
2214	735484	1863.A21.gz43_237022	F	M00056935A:F04	UC2-PrimColon
2215	171511	1863.E21.gz43_237026	F	M00056939D:B02	UC2-PrimColon
2216	728076	1863.H21.gz43_237029	F	M00056942D:D07	UC2-PrimColon
2217	511351	1863.H22.gz43_237045	F	M00056942D:D11	UC2-PrimColon
2218	731125	1863.I22.gz43_237046	F	M00056943D:H08	UC2-PrimColon
2219	524706	1863.B24.gz43_237071	F	M00056936C:C06	UC2-PrimColon
2220	485880	1863.C24.gz43_237072	F	M00056937C:H08	UC2-PrimColon
2221	736197	1864.I03.gz43_237126	F	M00056961C:C07	UC2-PrimColon
2222	731089	1864.M04.gz43_237146	F	M00056968C:C06	UC2-PrimColon
2223	642781	1864.G12.gz43_237268	F	M00056959C:B10	UC2-PrimColon
2224	731947	1864.M14.gz43_237306	F	M00056969A:B07	UC2-PrimColon
2225	448712	1864.M16.gz43_237338	F	M00056969A:C07	UC2-PrimColon
2226	736289	1864.I17.gz43_237350	F	M00056962D:F09	UC2-PrimColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
2227	735123	1873.E02.gz43_237490	F	M00056978D:B07	UC2-PrimColon
2228	724411	1873.H02.gz43_237493	F	M00056982D:B12	UC2-PrimColon
2229	662617	1873.P02.gz43_237501	F	M00056993D:C05	UC2-PrimColon
2230	639934	1873.M03.gz43_237514	F	M00056989C:H09	UC2-PrimColon
2231	733563	1873.C04.gz43_237520	F	M00056977A:C02	UC2-PrimColon
2232	203793	1873.K04.gz43_237528	F	M00056987C:D08	UC2-PrimColon
2233	703978	1873.L04.gz43_237529	F	M00056988C:D05	UC2-PrimColon
2234	732114	1873.P05.gz43_237549	F	M00056993D:F05	UC2-PrimColon
2235	732213	1873.J06.gz43_237559	F	M00056986A:E09	UC2-PrimColon
2236	725825	1873.N06.gz43_237563	F	M00056990D:C11	UC2-PrimColon
2237	734936	1873.D08.gz43_237585	F	M00056978A:A03	UC2-PrimColon
2238	731607	1873.E08.gz43_237586	F	M00056979B:D03	UC2-PrimColon
2239	731302	1873.K10.gz43_237624	F	M00056987D:A09	UC2-PrimColon
2240	732113	1873.L10.gz43_237625	F	M00056988D:F05	UC2-PrimColon
2241	728013	1873.M10.gz43_237626	F	M00056989D:F07	UC2-PrimColon
2242	730089	1873.D11.gz43_237633	F	M00056978A:H04	UC2-PrimColon
2243	648034	1873.E12.gz43_237650	F	M00056979C:D11	UC2-PrimColon
2244	729623	1873.I12.gz43_237654	F	M00056985A:D06	UC2-PrimColon
2245	731317	1873.M12.gz43_237658	F	M00056989D:H11	UC2-PrimColon
2246	728249	1873.A13.gz43_237662	F	M00056975A:H11	UC2-PrimColon
2247	613029	1873.C13.gz43_237664	F	M00056977B:B06	UC2-PrimColon
2248	731542	1873.O13.gz43_237676	F	M00056993A:B08	UC2-PrimColon
2249	732535	1873.G14.gz43_237684	F	M00056981D:H02	UC2-PrimColon
2250	735440	1873.A16.gz43_237710	F	M00056975B:E04	UC2-PrimColon
2251	641658	1873.D16.gz43_237713	F	M00056978B:G02	UC2-PrimColon
2252	406931	1873.N18.gz43_237755	F	M00056991C:H11	UC2-PrimColon
2253	736401	1873.P18.gz43_237757	F	M00056994B:H05	UC2-PrimColon
2254	734561	1873.B20.gz43_237775	F	M00056976C:F05	UC2-PrimColon
2255	727151	1873.F20.gz43_237779	F	M00056980D:E07	UC2-PrimColon
2256	731453	1873.I20.gz43_237782	F	M00056985C:C06	UC2-PrimColon
2257	642649	1873.K20.gz43_237784	F	M00056988A:F06	UC2-PrimColon
2258	642288	1873.M20.gz43_237786	F	M00056990B:H07	UC2-PrimColon
2259	572426	1873.P20.gz43_237789	F	M00056994C:B04	UC2-PrimColon
2260	731358	1873.K22.gz43_237816	F	M00056988B:A06	UC2-PrimColon
2261	471883	1873.N22.gz43_237819	F	M00056992A:E01	UC2-PrimColon
2262	733778	1873.D24.gz43_237841	F	M00056978D:A01	UC2-PrimColon
2263	731592	1873.J24.gz43_237847	F	M00056987A:C02	UC2-PrimColon
2264	456236	1874.D01.gz43_237857	F	M00056998C:B10	UC2-PrimColon
2265	732792	1874.N01.gz43_237867	F	M00057009C:B02	UC2-PrimColon
2266	733932	1874.E03.gz43_237890	F	M00057000A:A05	UC2-PrimColon
2267	724810	1874.P07.gz43_237965	F	M00057011C:H03	UC2-PrimColon
2268	731317	1874.B08.gz43_237967	F	M00056996D:A02	UC2-PrimColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
2269	726408	1874.D08.gz43_237969	F	M00056998D:H08	UC2-PrimColon
2270	734708	1874.D12.gz43_238033	F	M00056999A:G12	UC2-PrimColon
2271	631251	1874.A15.gz43_238078	F	M00056995C:H06	UC2-PrimColon
2272	726696	1874.D16.gz43_238097	F	M00056999B:D07	UC2-PrimColon
2273	448202	1874.F16.gz43_238099	F	M00057001D:F02	UC2-PrimColon
2274	734629	1874.H16.gz43_238101	F	M00057003D:F02	UC2-PrimColon
2275	561993	1874.K16.gz43_238104	F	M00057007B:G02	UC2-PrimColon
2276	407723	1874.J17.gz43_238119	F	M00057006A:G10	UC2-PrimColon
2277	736413	1874.K17.gz43_238120	F	M00057007C:A06	UC2-PrimColon
2278	556637	1874.P17.gz43_238125	F	M00057012A:D12	UC2-PrimColon
2279	731686	1874.A19.gz43_238142	F	M00056995D:C11	UC2-PrimColon
2280	559053	1874.B20.gz43_238159	F	M00056997B:C11	UC2-PrimColon
2281	733625	1875.J01.gz43_238247	F	M00057024B:F07	UC2-PrimColon
2282	461486	1875.O01.gz43_238252	F	M00057030C:B03	UC2-PrimColon
2283	556019	1875.B02.gz43_238255	F	M00057014B:A02	UC2-PrimColon
2284	732119	1875.F02.gz43_238259	F	M00057018C:F02	UC2-PrimColon
2285	411128	1875.K02.gz43_238264	F	M00057025C:A08	UC2-PrimColon
2286	732441	1875.A03.gz43_238270	F	M00057012D:G03	UC2-PrimColon
2287	478448	1875.B03.gz43_238271	F	M00057014B:B01	UC2-PrimColon
2288	733723	1875.D03.gz43_238273	F	M00057016B:A09	UC2-PrimColon
2289	726173	1875.I03.gz43_238278	F	M00057023A:H09	UC2-PrimColon
2290	451351	1875.B04.gz43_238287	F	M00057014B:B06	UC2-PrimColon
2291	570573	1875.E04.gz43_238290	F	M00057017A:F11	UC2-PrimColon
2292	655312	1875.K04.gz43_238296	F	M00057025C:D11	UC2-PrimColon
2293	732047	1875.C05.gz43_238304	F	M00057015A:E02	UC2-PrimColon
2294	734091	1875.F05.gz43_238307	F	M00057018D:B10	UC2-PrimColon
2295	538582	1875.E06.gz43_238322	F	M00057017A:G04	UC2-PrimColon
2296	487183	1875.C07.gz43_238336	F	M00057015A:G06	UC2-PrimColon
2297	483919	1875.G07.gz43_238340	F	M00057020D:A05	UC2-PrimColon
2298	651049	1875.L07.gz43_238345	F	M00057027B:B11	UC2-PrimColon
2299	734392	1875.D08.gz43_238353	F	M00057016B:E06	UC2-PrimColon
2300	557896	1875.F08.gz43_238355	F	M00057018D:E05	UC2-PrimColon
2301	89082	1875.L08.gz43_238361	F	M00057027B:E04	UC2-PrimColon
2302	512863	1875.P08.gz43_238365	F	M00057032A:C01	UC2-PrimColon
2303	474009	1875.D09.gz43_238369	F	M00057016B:H08	UC2-PrimColon
2304	729731	1875.H09.gz43_238373	F	M00057022B:A04	UC2-PrimColon
2305	481581	1875.A10.gz43_238382	F	M00057013B:H07	UC2-PrimColon
2306	732550	1875.C10.gz43_238384	F	M00057015A:H12	UC2-PrimColon
2307	735396	1875.J10.gz43_238391	F	M00057024D:D12	UC2-PrimColon
2308	642693	1875.P10.gz43_238397	F	M00057032A:F12	UC2-PrimColon
2309	733970	1875.D11.gz43_238401	F	M00057016C:B05	UC2-PrimColon
2310	639629	1875.H11.gz43_238405	F	M00057022B:F03	UC2-PrimColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
2311	731577	1875.L11.gz43_238409	F	M00057027B:F06	UC2-PrimColon
2312	733354	1875.B12.gz43_238415	F	M00057014C:E01	UC2-PrimColon
2313	626791	1875.F12.gz43_238419	F	M00057019A:G04	UC2-PrimColon
2314	559699	1875.H12.gz43_238421	F	M00057022B:H04	UC2-PrimColon
2315	726208	1875.A13.gz43_238430	F	M00057013C:E09	UC2-PrimColon
2316	730828	1875.B13.gz43_238431	F	M00057014C:E03	UC2-PrimColon
2317	390968	1875.I13.gz43_238438	F	M00057023D:D05	UC2-PrimColon
2318	471522	1875.O13.gz43_238444	F	M00057031A:H02	UC2-PrimColon
2319	731838	1875.D14.gz43_238449	F	M00057016C:E04	UC2-PrimColon
2320	726476	1875.H14.gz43_238453	F	M00057022C:D12	UC2-PrimColon
2321	466920	1875.I14.gz43_238454	F	M00057023D:D08	UC2-PrimColon
2322	732712	1875.N14.gz43_238459	F	M00057029D:A06	UC2-PrimColon
2323	561338	1875.O14.gz43_238460	F	M00057031B:A01	UC2-PrimColon
2324	733756	1875.A15.gz43_238462	F	M00057013C:H01	UC2-PrimColon
2325	484023	1875.C15.gz43_238464	F	M00057015B:E01	UC2-PrimColon
2326	557262	1875.D15.gz43_238465	F	M00057016C:E11	UC2-PrimColon
2327	559096	1875.E15.gz43_238466	F	M00057017C:E03	UC2-PrimColon
2328	455148	1875.F15.gz43_238467	F	M00057019C:C08	UC2-PrimColon
2329	616985	1875.I15.gz43_238470	F	M00057023D:E11	UC2-PrimColon
2330	733479	1875.N15.gz43_238475	F	M00057029D:F01	UC2-PrimColon
2331	558134	1875.F16.gz43_238483	F	M00057019C:E03	UC2-PrimColon
2332	703298	1875.D17.gz43_238497	F	M00057016D:B07	UC2-PrimColon
2333	477797	1875.G18.gz43_238516	F	M00057021B:B07	UC2-PrimColon
2334	432159	1875.L18.gz43_238521	F	M00057027D:A12	UC2-PrimColon
2335	736385	1875.P18.gz43_238525	F	M00057032D:A04	UC2-PrimColon
2336	619265	1875.B19.gz43_238527	F	M00057014D:E05	UC2-PrimColon
2337	4255	1875.F19.gz43_238531	F	M00057019D:C02	UC2-PrimColon
2338	554080	1875.M19.gz43_238538	F	M00057028D:D09	UC2-PrimColon
2339	734074	1875.C21.gz43_238560	F	M00057016A:B04	UC2-PrimColon
2340	734177	1875.E21.gz43_238562	F	M00057018A:C05	UC2-PrimColon
2341	727761	1875.I21.gz43_238566	F	M00057024A:D08	UC2-PrimColon
2342	733209	1875.L21.gz43_238569	F	M00057027D:D07	UC2-PrimColon
2343	512377	1875.A22.gz43_238574	F	M00057014A:B11	UC2-PrimColon
2344	733664	1875.B22.gz43_238575	F	M00057014D:G10	UC2-PrimColon
2345	640904	1875.D22.gz43_238577	F	M00057016D:H03	UC2-PrimColon
2346	425203	1875.N22.gz43_238587	F	M00057030B:B03	UC2-PrimColon
2347	557164	1875.B23.gz43_238591	F	M00057014D:H01	UC2-PrimColon
2348	494450	1875.C23.gz43_238592	F	M00057016A:G01	UC2-PrimColon
2349	639427	1875.F23.gz43_238595	F	M00057020A:F09	UC2-PrimColon
2350	554693	1875.H23.gz43_238597	F	M00057022D:E10	UC2-PrimColon
2351	732598	1875.K23.gz43_238600	F	M00057026D:A05	UC2-PrimColon
2352	495241	1875.M23.gz43_238602	F	M00057029A:C08	UC2-PrimColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
2353	735989	1875.N23.gz43_238603	F	M00057030B:F01	UC2-PrimColon
2354	726044	1875.I24.gz43_238614	F	M00057024B:A11	UC2-PrimColon
2355	728791	1875.L24.gz43_238617	F	M00057027D:G03	UC2-PrimColon
2356	562769	1875.N24.gz43_238619	F	M00057030C:A05	UC2-PrimColon
2357	479208	1875.P24.gz43_238621	F	M00057033A:D08	UC2-PrimColon
2358	4244	1876.C03.gz43_238656	F	M00057035C:E10	UC2-PrimColon
2359	732159	1876.K03.gz43_238664	F	M00057046A:F02	UC2-PrimColon
2360	473026	1876.E04.gz43_238674	F	M00057038A:H07	UC2-PrimColon
2361	736385	1876.B05.gz43_238687	F	M00057034C:G12	UC2-PrimColon
2362	734466	1876.J05.gz43_238695	F	M00057045A:C04	UC2-PrimColon
2363	668731	1876.K05.gz43_238696	F	M00057046A:G05	UC2-PrimColon
2364	736881	1876.H06.gz43_238709	F	M00057042D:E06	UC2-PrimColon
2365	466920	1876.O06.gz43_238716	F	M00057051B:E09	UC2-PrimColon
2366	728353	1876.E07.gz43_238722	F	M00057038C:B06	UC2-PrimColon
2367	732246	1876.N07.gz43_238731	F	M00057049D:F12	UC2-PrimColon
2368	468296	1876.A08.gz43_238734	F	M00057033C:B03	UC2-PrimColon
2369	454819	1876.E09.gz43_238754	F	M00057038C:G08	UC2-PrimColon
2370	481293	1876.M10.gz43_238778	F	M00057048C:E04	UC2-PrimColon
2371	735815	1876.E11.gz43_238786	F	M00057038D:A12	UC2-PrimColon
2372	732315	1876.H12.gz43_238805	F	M00057043A:G07	UC2-PrimColon
2373	558573	1876.M12.gz43_238810	F	M00057048C:H11	UC2-PrimColon
2374	492627	1876.G13.gz43_238820	F	M00057041D:C08	UC2-PrimColon
2375	732042	1876.K14.gz43_238840	F	M00057046C:E05	UC2-PrimColon
2376	737087	1876.N14.gz43_238843	F	M00057050B:F06	UC2-PrimColon
2377	456469	1876.A16.gz43_238862	F	M00057033D:F10	UC2-PrimColon
2378	735871	1876.I16.gz43_238870	F	M00057044C:B05	UC2-PrimColon
2379	736855	1876.F18.gz43_238899	F	M00057040D:H04	UC2-PrimColon
2380	732562	1876.M20.gz43_238938	F	M00057048D:H10	UC2-PrimColon
2381	727321	1876.G22.gz43_238964	F	M00057042B:A10	UC2-PrimColon
2382	638857	1876.H22.gz43_238965	F	M00057043C:H11	UC2-PrimColon
2383	735972	1876.A23.gz43_238974	F	M00057034B:B01	UC2-PrimColon
2384	735054	1876.L23.gz43_238985	F	M00057047D:H04	UC2-PrimColon
2385	554854	1885.M01.gz43_239018	F	M00057068D:F04	UC2-PrimColon
2386	731262	1885.O01.gz43_239020	F	M00057071A:A10	UC2-PrimColon
2387	729981	1885.C02.gz43_239024	F	M00057055C:F01	UC2-PrimColon
2388	735292	1885.F02.gz43_239027	F	M00057059D:H09	UC2-PrimColon
2389	726699	1885.L02.gz43_239033	F	M00057067D:H06	UC2-PrimColon
2390	624133	1885.O02.gz43_239036	F	M00057071A:B04	UC2-PrimColon
2391	645262	1885.A03.gz43_239038	F	M00057053A:A02	UC2-PrimColon
2392	558549	1885.K03.gz43_239048	F	M00057066D:B03	UC2-PrimColon
2393	736093	1885.L03.gz43_239049	F	M00057068A:C10	UC2-PrimColon
2394	733573	1885.G04.gz43_239060	F	M00057061B:H02	UC2-PrimColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
2395	481366	1885.I04.gz43_239062	F	M00057064B:H10	UC2-PrimColon
2396	556385	1885.N04.gz43_239067	F	M00057070A:B07	UC2-PrimColon
2397	559656	1885.L05.gz43_239081	F	M00057068A:F05	UC2-PrimColon
2398	446616	1885.A06.gz43_239086	F	M00057053A:D11	UC2-PrimColon
2399	728445	1885.C06.gz43_239088	F	M00057055C:H07	UC2-PrimColon
2400	732223	1885.D06.gz43_239089	F	M00057056D:F11	UC2-PrimColon
2401	595506	1885.G06.gz43_239092	F	M00057061C:D04	UC2-PrimColon
2402	627515	1885.K06.gz43_239096	F	M00057066D:E01	UC2-PrimColon
2403	730528	1885.L06.gz43_239097	F	M00057068A:F07	UC2-PrimColon
2404	451233	1885.E07.gz43_239106	F	M00057058D:G08	UC2-PrimColon
2405	728884	1885.H07.gz43_239109	F	M00057063A:C08	UC2-PrimColon
2406	541793	1885.I07.gz43_239110	F	M00057064C:F11	UC2-PrimColon
2407	736415	1885.L08.gz43_239129	F	M00057068A:G05	UC2-PrimColon
2408	552641	1885.F09.gz43_239139	F	M00057060B:D07	UC2-PrimColon
2409	736156	1885.G09.gz43_239140	F	M00057061D:D03	UC2-PrimColon
2410	560581	1885.M09.gz43_239146	F	M00057069A:F09	UC2-PrimColon
2411	654723	1885.D10.gz43_239153	F	M00057057A:G01	UC2-PrimColon
2412	731449	1885.E10.gz43_239154	F	M00057059A:B04	UC2-PrimColon
2413	452623	1885.G10.gz43_239156	F	M00057061D:F05	UC2-PrimColon
2414	732072	1885.M10.gz43_239162	F	M00057069A:H08	UC2-PrimColon
2415	452224	1885.P10.gz43_239165	F	M00057072C:A03	UC2-PrimColon
2416	550637	1885.K11.gz43_239176	F	M00057067B:C11	UC2-PrimColon
2417	453508	1885.M11.gz43_239178	F	M00057069B:A08	UC2-PrimColon
2418	732872	1885.A12.gz43_239182	F	M00057053C:B10	UC2-PrimColon
2419	735283	1885.P12.gz43_239197	F	M00057072C:A09	UC2-PrimColon
2420	422590	1885.D13.gz43_239201	F	M00057057B:E06	UC2-PrimColon
2421	422242	1885.J13.gz43_239207	F	M00057066A:A09	UC2-PrimColon
2422	471982	1885.D14.gz43_239217	F	M00057057B:E07	UC2-PrimColon
2423	736285	1885.H14.gz43_239221	F	M00057063B:F06	UC2-PrimColon
2424	734787	1885.P14.gz43_239229	F	M00057072C:C02	UC2-PrimColon
2425	733623	1885.A15.gz43_239230	F	M00057053C:G04	UC2-PrimColon
2426	736318	1885.D15.gz43_239233	F	M00057057B:G03	UC2-PrimColon
2427	677769	1885.A16.gz43_239246	F	M00057053D:D01	UC2-PrimColon
2428	726380	1885.B16.gz43_239247	F	M00057055B:D07	UC2-PrimColon
2429	134501	1885.C16.gz43_239248	F	M00057056B:C06	UC2-PrimColon
2430	731844	1885.F16.gz43_239251	F	M00057060C:D05	UC2-PrimColon
2431	730472	1885.B17.gz43_239263	F	M00057055B:E10	UC2-PrimColon
2432	455884	1885.C17.gz43_239264	F	M00057056B:D05	UC2-PrimColon
2433	669159	1885.H17.gz43_239269	F	M00057063C:C04	UC2-PrimColon
2434	736146	1885.K17.gz43_239272	F	M00057067C:D04	UC2-PrimColon
2435	729502	1885.A18.gz43_239278	F	M00057054A:B12	UC2-PrimColon
2436	731830	1885.C18.gz43_239280	F	M00057056B:D11	UC2-PrimColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
2437	706245	1885.N18.gz43_239291	F	M00057070C:H10	UC2-PrimColon
2438	631526	1885.P18.gz43_239293	F	M00057072C:H01	UC2-PrimColon
2439	736113	1885.A19.gz43_239294	F	M00057054A:D01	UC2-PrimColon
2440	567005	1885.B19.gz43_239295	F	M00057055B:F05	UC2-PrimColon
2441	730128	1885.K19.gz43_239304	F	M00057067C:H09	UC2-PrimColon
2442	620462	1885.E20.gz43_239314	F	M00057059C:H02	UC2-PrimColon
2443	450551	1885.F20.gz43_239315	F	M00057060D:C09	UC2-PrimColon
2444	724773	1885.L20.gz43_239321	F	M00057068D:B03	UC2-PrimColon
2445	735028	1885.N20.gz43_239323	F	M00057070D:B08	UC2-PrimColon
2446	476947	1885.E21.gz43_239330	F	M00057059D:A09	UC2-PrimColon
2447	420958	1885.I21.gz43_239334	F	M00057065C:B07	UC2-PrimColon
2448	447758	1885.O21.gz43_239340	F	M00057071D:E01	UC2-PrimColon
2449	447075	1885.G22.gz43_239348	F	M00057062B:H04	UC2-PrimColon
2450	455248	1885.L22.gz43_239353	F	M00057068D:C09	UC2-PrimColon
2451	732351	1885.O22.gz43_239356	F	M00057071D:G01	UC2-PrimColon
2452	620159	1885.P22.gz43_239357	F	M00057073A:B12	UC2-PrimColon
2453	472704	1885.K23.gz43_239368	F	M00057067D:F03	UC2-PrimColon
2454	649349	1885.N23.gz43_239371	F	M00057070D:G03	UC2-PrimColon
2455	735216	1885.F24.gz43_239379	F	M00057061A:F09	UC2-PrimColon
2456	572273	1885.J24.gz43_239383	F	M00057066C:B02	UC2-PrimColon
2457	736210	1885.L24.gz43_239385	F	M00057068D:E05	UC2-PrimColon
2458	731358	1886.M02.gz43_239418	F	M00057088B:E02	UC2-PrimColon
2459	639629	1886.D03.gz43_239425	F	M00057077B:B06	UC2-PrimColon
2460	733910	1886.L03.gz43_239433	F	M00057087B:A07	UC2-PrimColon
2461	473588	1886.N04.gz43_239451	F	M00057090A:B02	UC2-PrimColon
2462	727407	1886.N05.gz43_239467	F	M00057090A:C03	UC2-PrimColon
2463	368965	1886.H07.gz43_239493	F	M00057082C:G03	UC2-PrimColon
2464	734059	1886.L13.gz43_239593	F	M00057087D:B04	UC2-PrimColon
2465	419465	1886.P15.gz43_239629	F	M00057092C:A05	UC2-PrimColon
2466	732487	1886.A18.gz43_239662	F	M00057073D:H05	UC2-PrimColon
2467	538582	1886.M20.gz43_239706	F	M00057089B:D01	UC2-PrimColon
2468	732131	1886.O22.gz43_239740	F	M00057091D:F11	UC2-PrimColon
2469	556212	1886.E23.gz43_239746	F	M00057079A:F05	UC2-PrimColon
2470	731966	1886.M24.gz43_239770	F	M00057089D:E03	UC2-PrimColon
2471	732873	1887.C02.gz43_239809	F	M00057095B:G03	UC2-PrimColon
2472	732550	1887.G02.gz43_239813	F	M00057099D:D11	UC2-PrimColon
2473	731477	1887.D04.gz43_239842	F	M00057096C:B08	UC2-PrimColon
2474	485441	1887.I04.gz43_239847	F	M00057102A:F12	UC2-PrimColon
2475	533689	1887.B05.gz43_239856	F	M00057094B:D07	UC2-PrimColon
2476	735515	1887.H05.gz43_239862	F	M00057100D:E09	UC2-PrimColon
2477	678846	1887.M06.gz43_239883	F	M00057106A:H04	UC2-PrimColon
2478	638908	1887.P06.gz43_239886	F	M00057110C:A04	UC2-PrimColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
2479	516799	1887.L07.gz43_239898	F	M00057105C:C06	UC2-PrimColon
2480	553898	1887.A08.gz43_239903	F	M00057093C:A02	UC2-PrimColon
2481	644354	1887.F09.gz43_239924	F	M00057099A:C04	UC2-PrimColon
2482	731697	1887.K09.gz43_239929	F	M00057104D:A02	UC2-PrimColon
2483	645139	1887.F10.gz43_239940	F	M00057099A:H12	UC2-PrimColon
2484	732885	1887.O10.gz43_239949	F	M00057109A:F11	UC2-PrimColon
2485	736634	1887.A11.gz43_239951	F	M00057093C:E01	UC2-PrimColon
2486	457842	1887.D11.gz43_239954	F	M00057096D:H05	UC2-PrimColon
2487	654475	1887.F11.gz43_239956	F	M00057099B:A06	UC2-PrimColon
2488	543772	1887.I12.gz43_239975	F	M00057102B:E12	UC2-PrimColon
2489	734344	1887.L12.gz43_239978	F	M00057105C:G02	UC2-PrimColon
2490	693869	1887.N12.gz43_239980	F	M00057108B:A12	UC2-PrimColon
2491	733348	1887.O12.gz43_239981	F	M00057109A:H09	UC2-PrimColon
2492	733209	1887.L14.gz43_240010	F	M00057105D:C10	UC2-PrimColon
2493	401368	1887.F15.gz43_240020	F	M00057099B:D02	UC2-PrimColon
2494	452276	1887.I17.gz43_240055	F	M00057102D:C11	UC2-PrimColon
2495	736220	1887.P17.gz43_240062	F	M00057110D:E12	UC2-PrimColon
2496	735584	1887.G18.gz43_240069	F	M00057100C:F02	UC2-PrimColon
2497	448325	1887.J19.gz43_240088	F	M00057104A:H06	UC2-PrimColon
2498	732312	1887.O19.gz43_240093	F	M00057109C:D10	UC2-PrimColon
2499	477387	1887.C20.gz43_240097	F	M00057096B:C05	UC2-PrimColon
2500	729222	1887.D20.gz43_240098	F	M00057097B:E02	UC2-PrimColon
2501	733972	1887.F20.gz43_240100	F	M00057099C:A06	UC2-PrimColon
2502	735113	1887.B21.gz43_240112	F	M00057095A:F11	UC2-PrimColon
2503	650920	1887.I21.gz43_240119	F	M00057103A:F11	UC2-PrimColon
2504	729560	1887.O24.gz43_240173	F	M00057110A:A03	UC2-PrimColon
2505	415825	1888.A01.gz43_240175	F	M00057112A:C12	UC2-PrimColon
2506	733225	1888.D01.gz43_240178	F	M00057115D:C10	UC2-PrimColon
2507	732113	1888.D02.gz43_240194	F	M00057115D:D06	UC2-PrimColon
2508	568632	1888.L03.gz43_240218	F	M00057126D:A04	UC2-PrimColon
2509	736539	1888.J04.gz43_240232	F	M00057124A:G08	UC2-PrimColon
2510	602673	1888.D05.gz43_240242	F	M00057115D:F06	UC2-PrimColon
2511	553264	1888.F06.gz43_240260	F	M00057118B:E10	UC2-PrimColon
2512	555655	1888.G06.gz43_240261	F	M00057120A:D01	UC2-PrimColon
2513	736534	1888.K06.gz43_240265	F	M00057125C:B11	UC2-PrimColon
2514	451764	1888.O06.gz43_240269	F	M00057129D:F03	UC2-PrimColon
2515	732896	1888.D07.gz43_240274	F	M00057116A:B06	UC2-PrimColon
2516	733365	1888.I07.gz43_240279	F	M00057122D:A01	UC2-PrimColon
2517	736548	1888.O08.gz43_240301	F	M00057130A:A02	UC2-PrimColon
2518	553338	1888.H09.gz43_240310	F	M00057121B:H10	UC2-PrimColon
2519	105056	1888.K10.gz43_240329	F	M00057125C:E02	UC2-PrimColon
2520	288535	1888.O10.gz43_240333	F	M00057130A:A11	UC2-PrimColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
2521	453733	1888.G12.gz43_240357	F	M00057120C:B09	UC2-PrimColon
2522	552783	1888.H12.gz43_240358	F	M00057121C:E08	UC2-PrimColon
2523	732937	1888.I12.gz43_240359	F	M00057123A:F09	UC2-PrimColon
2524	542490	1888.K12.gz43_240361	F	M00057125D:B02	UC2-PrimColon
2525	553087	1888.L12.gz43_240362	F	M00057127A:E10	UC2-PrimColon
2526	609459	1888.G14.gz43_240389	F	M00057120C:F08	UC2-PrimColon
2527	736810	1888.O14.gz43_240397	F	M00057130A:D10	UC2-PrimColon
2528	735959	1888.L15.gz43_240410	F	M00057127A:H10	UC2-PrimColon
2529	560868	1888.H17.gz43_240438	F	M00057122A:A07	UC2-PrimColon
2530	726176	1888.P17.gz43_240446	F	M00057131D:D02	UC2-PrimColon
2531	724952	1888.A18.gz43_240447	F	M00057112D:G08	UC2-PrimColon
2532	1030	1888.H18.gz43_240454	F	M00057122A:C04	UC2-PrimColon
2533	454961	1888.L18.gz43_240458	F	M00057127B:D10	UC2-PrimColon
2534	643517	1888.C19.gz43_240465	F	M00057115C:B11	UC2-PrimColon
2535	733006	1888.H19.gz43_240470	F	M00057122A:C11	UC2-PrimColon
2536	733171	1888.A20.gz43_240479	F	M00057113A:A08	UC2-PrimColon
2537	735018	1888.B20.gz43_240480	F	M00057114C:E07	UC2-PrimColon
2538	728479	1888.B21.gz43_240496	F	M00057114C:F08	UC2-PrimColon
2539	726575	1888.J21.gz43_240504	F	M00057125A:A07	UC2-PrimColon
2540	734606	1888.I22.gz43_240519	F	M00057123D:F07	UC2-PrimColon
2541	732476	1888.D23.gz43_240530	F	M00057116C:H09	UC2-PrimColon
2542	656263	1888.H23.gz43_240534	F	M00057122B:F04	UC2-PrimColon
2543	662617	1888.K23.gz43_240537	F	M00057126C:C05	UC2-PrimColon
2544	474108	1888.D24.gz43_240546	F	M00057116D:B10	UC2-PrimColon
2545	455581	1888.J24.gz43_240552	F	M00057125A:F07	UC2-PrimColon
2546	447692	1888.L24.gz43_240554	F	M00057127C:F03	UC2-PrimColon
2547	735514	1888.M24.gz43_240555	F	M00057128C:H02	UC2-PrimColon
2548	440284	1888.N24.gz43_240556	F	M00057129D:D07	UC2-PrimColon
2549	639644	1897.A02.gz43_240575	F	M00057132B:H05	UC2-PrimColon
2550	568031	1897.G02.gz43_240581	F	M00057139A:G08	UC2-PrimColon
2551	555960	1897.L02.gz43_240586	F	M00057144D:D03	UC2-PrimColon
2552	462779	1897.M02.gz43_240587	F	M00057145D:E01	UC2-PrimColon
2553	472068	1897.C03.gz43_240593	F	M00057134B:D06	UC2-PrimColon
2554	728413	1897.N03.gz43_240604	F	M00057147A:B07	UC2-PrimColon
2555	519378	1897.P03.gz43_240606	F	M00057149B:B07	UC2-PrimColon
2556	733951	1897.A04.gz43_240607	F	M00057132C:C04	UC2-PrimColon
2557	448212	1897.P04.gz43_240622	F	M00057149B:B08	UC2-PrimColon
2558	536225	1897.B05.gz43_240624	F	M00057133C:B02	UC2-PrimColon
2559	736288	1897.F05.gz43_240628	F	M00057138A:F02	UC2-PrimColon
2560	225960	1897.E06.gz43_240643	F	M00057137A:H12	UC2-PrimColon
2561	655327	1897.H08.gz43_240678	F	M00057140B:H01	UC2-PrimColon
2562	735729	1897.N08.gz43_240684	F	M00057147A:H07	UC2-PrimColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
2563	642273	1897.F09.gz43_240692	F	M00057138B:B02	UC2-PrimColon
2564	549285	1897.O09.gz43_240701	F	M00057148C:B02	UC2-PrimColon
2565	735756	1897.P11.gz43_240734	F	M00057149C:H01	UC2-PrimColon
2566	640662	1897.E12.gz43_240739	F	M00057137B:C07	UC2-PrimColon
2567	543772	1897.F12.gz43_240740	F	M00057138B:H02	UC2-PrimColon
2568	735801	1897.M12.gz43_240747	F	M00057146A:H05	UC2-PrimColon
2569	457846	1897.N12.gz43_240748	F	M00057147C:B01	UC2-PrimColon
2570	736318	1897.O12.gz43_240749	F	M00057148C:C09	UC2-PrimColon
2571	658271	1897.K13.gz43_240761	F	M00057144B:D04	UC2-PrimColon
2572	735283	1897.M13.gz43_240763	F	M00057146B:C06	UC2-PrimColon
2573	447550	1897.A15.gz43_240783	F	M00057133A:B07	UC2-PrimColon
2574	500758	1897.H15.gz43_240790	F	M00057140D:B03	UC2-PrimColon
2575	567005	1897.H17.gz43_240822	F	M00057140D:F02	UC2-PrimColon
2576	523171	1897.K17.gz43_240825	F	M00057144B:H10	UC2-PrimColon
2577	397515	1897.M17.gz43_240827	F	M00057146B:H12	UC2-PrimColon
2578	736318	1897.F18.gz43_240836	F	M00057138D:F03	UC2-PrimColon
2579	449035	1897.I18.gz43_240839	F	M00057142A:H07	UC2-PrimColon
2580	486076	1897.K18.gz43_240841	F	M00057144C:A02	UC2-PrimColon
2581	729843	1897.O18.gz43_240845	F	M00057149A:A04	UC2-PrimColon
2582	726440	1897.F19.gz43_240852	F	M00057138D:F10	UC2-PrimColon
2583	731317	1897.G19.gz43_240853	F	M00057139D:G07	UC2-PrimColon
2584	559004	1897.I22.gz43_240903	F	M00057142B:F06	UC2-PrimColon
2585	448202	1897.L22.gz43_240906	F	M00057145C:H03	UC2-PrimColon
2586	718314	1897.N22.gz43_240908	F	M00057147D:H09	UC2-PrimColon
2587	735989	1897.C23.gz43_240913	F	M00057135A:B02	UC2-PrimColon
2588	489001	1897.F23.gz43_240916	F	M00057139A:B10	UC2-PrimColon
2589	462779	1897.H23.gz43_240918	F	M00057141A:G06	UC2-PrimColon
2590	596809	1898.C02.gz43_242213	F	M00057153B:G07	UC2-PrimColon
2591	447003	1898.A03.gz43_242227	F	M00057150D:C04	UC2-PrimColon
2592	730661	1898.D04.gz43_242246	F	M00057155A:E11	UC2-PrimColon
2593	461316	1898.H04.gz43_242250	F	M00057160D:A11	UC2-PrimColon
2594	450724	1898.A05.gz43_242259	F	M00057150D:F08	UC2-PrimColon
2595	480307	1898.B05.gz43_242260	F	M00057152B:H02	UC2-PrimColon
2596	727608	1898.F05.gz43_242264	F	M00057157D:H08	UC2-PrimColon
2597	649852	1898.P05.gz43_242274	F	M00057169A:F05	UC2-PrimColon
2598	650297	1898.A06.gz43_242275	F	M00057151A:B04	UC2-PrimColon
2599	491933	1898.E06.gz43_242279	F	M00057156B:D10	UC2-PrimColon
2600	733552	1898.P06.gz43_242290	F	M00057169A:F06	UC2-PrimColon
2601	730341	1898.D07.gz43_242294	F	M00057155A:G11	UC2-PrimColon
2602	640563	1898.D08.gz43_242310	F	M00057155A:H07	UC2-PrimColon
2603	640603	1898.B10.gz43_242340	F	M00057152C:C10	UC2-PrimColon
2604	552972	1898.E10.gz43_242343	F	M00057156C:E08	UC2-PrimColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
2605	736030	1898.F10.gz43_242344	F	M00057158B:C02	UC2-PrimColon
2606	736228	1898.G11.gz43_242361	F	M00057159C:E11	UC2-PrimColon
2607	648820	1898.M11.gz43_242367	F	M00057165D:H05	UC2-PrimColon
2608	735993	1898.D12.gz43_242374	F	M00057155C:B07	UC2-PrimColon
2609	402516	1898.H12.gz43_242378	F	M00057161B:D02	UC2-PrimColon
2610	583625	1898.O12.gz43_242385	F	M00057168B:D02	UC2-PrimColon
2611	726448	1898.N13.gz43_242400	F	M00057167A:D08	UC2-PrimColon
2612	735756	1898.H14.gz43_242410	F	M00057161B:E07	UC2-PrimColon
2613	551654	1898.C15.gz43_242421	F	M00057153D:H01	UC2-PrimColon
2614	558477	1898.D15.gz43_242422	F	M00057155C:G04	UC2-PrimColon
2615	728353	1898.I15.gz43_242427	F	M00057162B:E10	UC2-PrimColon
2616	736634	1898.M15.gz43_242431	F	M00057166B:B07	UC2-PrimColon
2617	737006	1898.P15.gz43_242434	F	M00057169C:H10	UC2-PrimColon
2618	736288	1898.J16.gz43_242444	F	M00057163C:D06	UC2-PrimColon
2619	734794	1898.P16.gz43_242450	F	M00057169C:H12	UC2-PrimColon
2620	734928	1898.E17.gz43_242455	F	M00057156D:F02	UC2-PrimColon
2621	727976	1898.F17.gz43_242456	F	M00057158C:C10	UC2-PrimColon
2622	736790	1898.F19.gz43_242488	F	M00057158C:G05	UC2-PrimColon
2623	735633	1898.I21.gz43_242523	F	M00057162C:C01	UC2-PrimColon
2624	734484	1898.B22.gz43_242532	F	M00057153B:A04	UC2-PrimColon
2625	480142	1898.D22.gz43_242534	F	M00057155D:E12	UC2-PrimColon
2626	454073	1898.G22.gz43_242537	F	M00057160B:G08	UC2-PrimColon
2627	599714	1898.L22.gz43_242542	F	M00057165C:E08	UC2-PrimColon
2628	737042	1898.M22.gz43_242543	F	M00057166B:G06	UC2-PrimColon
2629	405016	1898.N22.gz43_242544	F	M00057167C:A05	UC2-PrimColon
2630	723915	1898.L23.gz43_242558	F	M00057165C:F05	UC2-PrimColon
2631	737006	1898.O23.gz43_242561	F	M00057168C:D03	UC2-PrimColon
2632	734808	1898.B24.gz43_242564	F	M00057153B:D02	UC2-PrimColon
2633	471887	1898.P24.gz43_242578	F	M00057170A:D11	UC2-PrimColon
2634	733972	1899.A01.gz43_242579	F	M00057170A:D06	UC2-PrimColon
2635	554221	1899.J01.gz43_242588	F	M00057181C:D10	UC2-PrimColon
2636	735426	1899.N01.gz43_242592	F	M00057192A:D12	UC2-PrimColon
2637	454812	1899.P01.gz43_242594	F	M00057194C:A03	UC2-PrimColon
2638	562453	1899.D02.gz43_242598	F	M00057173D:B12	UC2-PrimColon
2639	554683	1899.M02.gz43_242607	F	M00057189D:G08	UC2-PrimColon
2640	474346	1899.N02.gz43_242608	F	M00057192A:F01	UC2-PrimColon
2641	729039	1899.D03.gz43_242614	F	M00057173D:C07	UC2-PrimColon
2642	560183	1899.J03.gz43_242620	F	M00057181C:G07	UC2-PrimColon
2643	422590	1899.D04.gz43_242630	F	M00057173D:E04	UC2-PrimColon
2644	642936	1899.K04.gz43_242637	F	M00057182C:C03	UC2-PrimColon
2645	730106	1899.N04.gz43_242640	F	M00057192A:H05	UC2-PrimColon
2646	449548	1899.H05.gz43_242650	F	M00057179C:B05	UC2-PrimColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
2647	736861	1899.P05.gz43_242658	F	M00057194C:F02	UC2-PrimColon
2648	730220	1899.A06.gz43_242659	F	M00057170A:H04	UC2-PrimColon
2649	736309	1899.I06.gz43_242667	F	M00057180C:F09	UC2-PrimColon
2650	373615	1899.K06.gz43_242669	F	M00057182C:C11	UC2-PrimColon
2651	640635	1899.O06.gz43_242673	F	M00057193C:F11	UC2-PrimColon
2652	735764	1899.F07.gz43_242680	F	M00057176A:H10	UC2-PrimColon
2653	735801	1899.J07.gz43_242684	F	M00057181D:C09	UC2-PrimColon
2654	477098	1899.K07.gz43_242685	F	M00057182D:A08	UC2-PrimColon
2655	734031	1899.M07.gz43_242687	F	M00057191A:H09	UC2-PrimColon
2656	419711	1899.N07.gz43_242688	F	M00057192B:D10	UC2-PrimColon
2657	390968	1899.P07.gz43_242690	F	M00057194C:F10	UC2-PrimColon
2658	732625	1899.E08.gz43_242695	F	M00057175B:G12	UC2-PrimColon
2659	462986	1899.F08.gz43_242696	F	M00057176A:H12	UC2-PrimColon
2660	482512	1899.H08.gz43_242698	F	M00057179C:G10	UC2-PrimColon
2661	473238	1899.C09.gz43_242709	F	M00057172D:F08	UC2-PrimColon
2662	735789	1899.I09.gz43_242715	F	M00057180D:C10	UC2-PrimColon
2663	736595	1899.K09.gz43_242717	F	M00057182D:B11	UC2-PrimColon
2664	735514	1899.M09.gz43_242719	F	M00057191B:C06	UC2-PrimColon
2665	630516	1899.O09.gz43_242721	F	M00057193D:F06	UC2-PrimColon
2666	730899	1899.N10.gz43_242736	F	M00057192C:B11	UC2-PrimColon
2667	552055	1899.P10.gz43_242738	F	M00057194D:C12	UC2-PrimColon
2668	528404	1899.C11.gz43_242741	F	M00057173A:C07	UC2-PrimColon
2669	734209	1899.D11.gz43_242742	F	M00057174B:C06	UC2-PrimColon
2670	452243	1899.J11.gz43_242748	F	M00057181D:H07	UC2-PrimColon
2671	734061	1899.O11.gz43_242753	F	M00057194A:B07	UC2-PrimColon
2672	625988	1899.G12.gz43_242761	F	M00057177C:D07	UC2-PrimColon
2673	561632	1899.D13.gz43_242774	F	M00057174B:C11	UC2-PrimColon
2674	731370	1899.E13.gz43_242775	F	M00057175C:D02	UC2-PrimColon
2675	480142	1899.G13.gz43_242777	F	M00057177C:G11	UC2-PrimColon
2676	736049	1899.O13.gz43_242785	F	M00057194A:C06	UC2-PrimColon
2677	725691	1899.A14.gz43_242787	F	M00057170C:C01	UC2-PrimColon
2678	727523	1899.M14.gz43_242799	F	M00057191C:D02	UC2-PrimColon
2679	421794	1899.D15.gz43_242806	F	M00057174B:F11	UC2-PrimColon
2680	732429	1899.G15.gz43_242809	F	M00057177C:H04	UC2-PrimColon
2681	530883	1899.H15.gz43_242810	F	M00057180A:H11	UC2-PrimColon
2682	729173	1899.P15.gz43_242818	F	M00057196A:E03	UC2-PrimColon
2683	734744	1899.D16.gz43_242822	F	M00057174B:G03	UC2-PrimColon
2684	735605	1899.F16.gz43_242824	F	M00057176B:F10	UC2-PrimColon
2685	726786	1899.N16.gz43_242832	F	M00057192D:G02	UC2-PrimColon
2686	725089	1899.O16.gz43_242833	F	M00057194A:F01	UC2-PrimColon
2687	448770	1899.D17.gz43_242838	F	M00057174B:G12	UC2-PrimColon
2688	532904	1899.E17.gz43_242839	F	M00057175D:A12	UC2-PrimColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
2689	560568	1899.K17.gz43_242845	F	M00057186A:E12	UC2-PrimColon
2690	736402	1899.N17.gz43_242848	F	M00057192D:G04	UC2-PrimColon
2691	516729	1899.P17.gz43_242850	F	M00057196B:H10	UC2-PrimColon
2692	718314	1899.H18.gz43_242858	F	M00057180B:C06	UC2-PrimColon
2693	737116	1899.J18.gz43_242860	F	M00057182A:H07	UC2-PrimColon
2694	723985	1899.B19.gz43_242868	F	M00057172A:B02	UC2-PrimColon
2695	573733	1899.F19.gz43_242872	F	M00057176C:H08	UC2-PrimColon
2696	475872	1899.H19.gz43_242874	F	M00057180B:D01	UC2-PrimColon
2697	625988	1899.F20.gz43_242888	F	M00057176D:A03	UC2-PrimColon
2698	736354	1899.L20.gz43_242894	F	M00057189C:G11	UC2-PrimColon
2699	535866	1899.C21.gz43_242901	F	M00057173C:C07	UC2-PrimColon
2700	648221	1899.D21.gz43_242902	F	M00057174C:G07	UC2-PrimColon
2701	736280	1899.H21.gz43_242906	F	M00057180B:F05	UC2-PrimColon
2702	156329	1899.N21.gz43_242912	F	M00057193B:C11	UC2-PrimColon
2703	721768	1899.O21.gz43_242913	F	M00057194B:E05	UC2-PrimColon
2704	639507	1899.B22.gz43_242916	F	M00057172A:H06	UC2-PrimColon
2705	451383	1899.E22.gz43_242919	F	M00057175D:E12	UC2-PrimColon
2706	349977	1899.J22.gz43_242924	F	M00057182B:D09	UC2-PrimColon
2707	734928	1899.M22.gz43_242927	F	M00057191D:G10	UC2-PrimColon
2708	480623	1899.A23.gz43_242931	F	M00057170D:B08	UC2-PrimColon
2709	674526	1899.H23.gz43_242938	F	M00057180B:G06	UC2-PrimColon
2710	730805	1899.M23.gz43_242943	F	M00057192A:B04	UC2-PrimColon
2711	640350	1900.G01.gz43_242969	F	M00057206A:C06	UC2-PrimColon
2712	726449	1900.K01.gz43_242973	F	M00057210A:C12	UC2-PrimColon
2713	552457	1900.E02.gz43_242983	F	M00057203B:F08	UC2-PrimColon
2714	730308	1900.C04.gz43_243013	F	M00057200D:E03	UC2-PrimColon
2715	734993	1900.E04.gz43_243015	F	M00057203C:A09	UC2-PrimColon
2716	562320	1900.H04.gz43_243018	F	M00057207B:F06	UC2-PrimColon
2717	556656	1900.O04.gz43_243025	F	M00057216D:D05	UC2-PrimColon
2718	446752	1900.D06.gz43_243046	F	M00057202A:D05	UC2-PrimColon
2719	736738	1900.L06.gz43_243054	F	M00057211C:C06	UC2-PrimColon
2720	639395	1900.O07.gz43_243073	F	M00057216D:F10	UC2-PrimColon
2721	516729	1900.B08.gz43_243076	F	M00057199B:B06	UC2-PrimColon
2722	557262	1900.E08.gz43_243079	F	M00057203D:A09	UC2-PrimColon
2723	731531	1900.I08.gz43_243083	F	M00057208B:H08	UC2-PrimColon
2724	736778	1900.K08.gz43_243085	F	M00057210C:D09	UC2-PrimColon
2725	724638	1900.O10.gz43_243121	F	M00057217A:A12	UC2-PrimColon
2726	483061	1900.B12.gz43_243140	F	M00057199C:H08	UC2-PrimColon
2727	725905	1900.C12.gz43_243141	F	M00057201A:H03	UC2-PrimColon
2728	648757	1900.M12.gz43_243151	F	M00057213C:D06	UC2-PrimColon
2729	735797	1900.A14.gz43_243171	F	M00057197D:H10	UC2-PrimColon
2730	732771	1900.I14.gz43_243179	F	M00057208C:E12	UC2-PrimColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
2731	736276	1900.E15.gz43_243191	F	M00057204A:F11	UC2-PrimColon
2732	449078	1900.O19.gz43_243265	F	M00057217B:F12	UC2-PrimColon
2733	161489	1900.A20.gz43_243267	F	M00057198B:C02	UC2-PrimColon
2734	734226	1900.F20.gz43_243272	F	M00057205D:G06	UC2-PrimColon
2735	736500	1900.G20.gz43_243273	F	M00057207A:A07	UC2-PrimColon
2736	733272	1900.K20.gz43_243277	F	M00057211A:D01	UC2-PrimColon
2737	532904	1900.B22.gz43_243300	F	M00057200B:D04	UC2-PrimColon
2738	648379	1900.K22.gz43_243309	F	M00057211B:A08	UC2-PrimColon
2739	649490	1900.M22.gz43_243311	F	M00057214B:B12	UC2-PrimColon
2740	186522	1900.N22.gz43_243312	F	M00057216C:D12	UC2-PrimColon
2741	561626	1900.E24.gz43_243335	F	M00057204C:G06	UC2-PrimColon
2742	653616	1900.K24.gz43_243341	F	M00057211B:C09	UC2-PrimColon
2743	734828	1909.G01.gz43_243353	F	M00057225C:H07	UC2-PrimColon
2744	427113	1909.H01.gz43_243354	F	M00057226C:E05	UC2-PrimColon
2745	561877	1909.K01.gz43_243357	F	M00057231B:A01	UC2-PrimColon
2746	454563	1909.M01.gz43_243359	F	M00057233B:G04	UC2-PrimColon
2747	625810	1909.P01.gz43_243362	F	M00057236D:H09	UC2-PrimColon
2748	475562	1909.F02.gz43_243368	F	M00057224C:B02	UC2-PrimColon
2749	735749	1909.K02.gz43_243373	F	M00057231C:B04	UC2-PrimColon
2750	289328	1909.B03.gz43_243380	F	M00057219D:G11	UC2-PrimColon
2751	465697	1909.C03.gz43_243381	F	M00057220D:E06	UC2-PrimColon
2752	726892	1909.E03.gz43_243383	F	M00057223B:G01	UC2-PrimColon
2753	723959	1909.J03.gz43_243388	F	M00057230C:C05	UC2-PrimColon
2754	733874	1909.N03.gz43_243392	F	M00057234D:A12	UC2-PrimColon
2755	454129	1909.A04.gz43_243395	F	M00057218C:F10	UC2-PrimColon
2756	733868	1909.B04.gz43_243396	F	M00057219D:H04	UC2-PrimColon
2757	642940	1909.H04.gz43_243402	F	M00057226C:F12	UC2-PrimColon
2758	398061	1909.D05.gz43_243414	F	M00057222B:A06	UC2-PrimColon
2759	734690	1909.G05.gz43_243417	F	M00057225D:E01	UC2-PrimColon
2760	601051	1909.N05.gz43_243424	F	M00057234D:E04	UC2-PrimColon
2761	727255	1909.E06.gz43_243431	F	M00057223C:B01	UC2-PrimColon
2762	632499	1909.I06.gz43_243435	F	M00057229A:B03	UC2-PrimColon
2763	737010	1909.K06.gz43_243437	F	M00057231C:E06	UC2-PrimColon
2764	728121	1909.L06.gz43_243438	F	M00057232B:G02	UC2-PrimColon
2765	472811	1909.B08.gz43_243460	F	M00057220A:C06	UC2-PrimColon
2766	648140	1909.H08.gz43_243466	F	M00057226C:H10	UC2-PrimColon
2767	726251	1909.A09.gz43_243475	F	M00057219A:D05	UC2-PrimColon
2768	642631	1909.B09.gz43_243476	F	M00057220A:D09	UC2-PrimColon
2769	598087	1909.J09.gz43_243484	F	M00057230C:G12	UC2-PrimColon
2770	398061	1909.K09.gz43_243485	F	M00057231C:F12	UC2-PrimColon
2771	463513	1909.M09.gz43_243487	F	M00057233D:G12	UC2-PrimColon
2772	81	1909.F10.gz43_243496	F	M00057225A:C08	UC2-PrimColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
2773	735050	1909.H10.gz43_243498	F	M00057226D:B03	UC2-PrimColon
2774	735140	1909.K10.gz43_243501	F	M00057231C:G04	UC2-PrimColon
2775	220107	1909.O10.gz43_243505	F	M00057236A:F08	UC2-PrimColon
2776	735817	1909.P10.gz43_243506	F	M00057237B:D10	UC2-PrimColon
2777	735514	1909.D11.gz43_243510	F	M00057222D:C10	UC2-PrimColon
2778	602673	1909.F11.gz43_243512	F	M00057225A:E03	UC2-PrimColon
2779	647815	1909.I11.gz43_243515	F	M00057229B:F11	UC2-PrimColon
2780	402024	1909.A12.gz43_243523	F	M00057219A:E11	UC2-PrimColon
2781	631111	1909.C12.gz43_243525	F	M00057221B:B01	UC2-PrimColon
2782	451888	1909.I12.gz43_243531	F	M00057229B:G11	UC2-PrimColon
2783	456224	1909.J12.gz43_243532	F	M00057230D:C05	UC2-PrimColon
2784	555336	1909.L12.gz43_243534	F	M00057232D:B03	UC2-PrimColon
2785	736988	1909.A13.gz43_243539	F	M00057219A:H11	UC2-PrimColon
2786	613067	1909.B13.gz43_243540	F	M00057220B:A06	UC2-PrimColon
2787	736738	1909.E13.gz43_243543	F	M00057223D:H03	UC2-PrimColon
2788	646552	1909.G13.gz43_243545	F	M00057226A:B04	UC2-PrimColon
2789	725120	1909.O13.gz43_243553	F	M00057236B:D11	UC2-PrimColon
2790	591979	1909.A14.gz43_243555	F	M00057219B:B10	UC2-PrimColon
2791	731467	1909.N14.gz43_243568	F	M00057235B:A07	UC2-PrimColon
2792	474869	1909.A15.gz43_243571	F	M00057219B:C06	UC2-PrimColon
2793	735306	1909.C15.gz43_243573	F	M00057221B:E11	UC2-PrimColon
2794	732736	1909.K15.gz43_243581	F	M00057231D:A05	UC2-PrimColon
2795	724417	1909.L15.gz43_243582	F	M00057233A:C04	UC2-PrimColon
2796	454355	1909.E16.gz43_243591	F	M00057224A:D07	UC2-PrimColon
2797	732899	1909.D17.gz43_243606	F	M00057223A:F06	UC2-PrimColon
2798	733149	1909.J17.gz43_243612	F	M00057231A:D04	UC2-PrimColon
2799	735622	1909.B18.gz43_243620	F	M00057220B:G10	UC2-PrimColon
2800	453132	1909.O19.gz43_243649	F	M00057236C:C07	UC2-PrimColon
2801	724781	1909.P19.gz43_243650	F	M00057237D:C11	UC2-PrimColon
2802	556852	1909.B20.gz43_243652	F	M00057220C:A08	UC2-PrimColon
2803	732159	1909.H20.gz43_243658	F	M00057227B:A05	UC2-PrimColon
2804	734609	1909.D21.gz43_243670	F	M00057223B:A07	UC2-PrimColon
2805	616985	1909.I21.gz43_243675	F	M00057230B:B07	UC2-PrimColon
2806	734151	1909.N21.gz43_243680	F	M00057235C:C08	UC2-PrimColon
2807	553850	1909.C22.gz43_243685	F	M00057221C:E07	UC2-PrimColon
2808	736894	1909.D22.gz43_243686	F	M00057223B:B04	UC2-PrimColon
2809	486051	1909.K22.gz43_243693	F	M00057231D:F10	UC2-PrimColon
2810	734553	1909.N22.gz43_243696	F	M00057235C:F03	UC2-PrimColon
2811	473578	1909.P22.gz43_243698	F	M00057237D:D09	UC2-PrimColon
2812	737010	1909.A23.gz43_243699	F	M00057219D:C02	UC2-PrimColon
2813	735514	1909.B23.gz43_243700	F	M00057220C:F08	UC2-PrimColon
2814	418682	1909.C23.gz43_243701	F	M00057221C:F02	UC2-PrimColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
2815	734562	1909.F23.gz43_243704	F	M00057225C:F09	UC2-PrimColon
2816	664711	1909.M23.gz43_243711	F	M00057234C:D11	UC2-PrimColon
2817	727558	1909.E24.gz43_243719	F	M00057224B:H02	UC2-PrimColon
2818	730028	1910.C01.gz43_243733	F	M00057240A:F03	UC2-PrimColon
2819	611604	1910.E01.gz43_243735	F	M00057242C:G12	UC2-PrimColon
2820	558617	1910.H01.gz43_243738	F	M00057246A:G11	UC2-PrimColon
2821	733144	1910.J01.gz43_243740	F	M00057248B:D11	UC2-PrimColon
2822	647242	1910.M01.gz43_243743	F	M00057252B:E04	UC2-PrimColon
2823	733552	1910.F02.gz43_243752	F	M00057243C:D01	UC2-PrimColon
2824	729428	1910.N02.gz43_243760	F	M00057253C:A06	UC2-PrimColon
2825	641680	1910.A03.gz43_243763	F	M00057238A:D07	UC2-PrimColon
2826	514838	1910.L03.gz43_243774	F	M00057251A:F02	UC2-PrimColon
2827	735403	1910.N03.gz43_243776	F	M00057253C:D11	UC2-PrimColon
2828	732859	1910.I04.gz43_243787	F	M00057247C:C11	UC2-PrimColon
2829	730046	1910.C06.gz43_243813	F	M00057240B:C01	UC2-PrimColon
2830	650067	1910.E06.gz43_243815	F	M00057242D:C07	UC2-PrimColon
2831	734884	1910.F06.gz43_243816	F	M00057243C:H11	UC2-PrimColon
2832	550730	1910.I06.gz43_243819	F	M00057247C:F10	UC2-PrimColon
2833	449042	1910.K06.gz43_243821	F	M00057249D:H09	UC2-PrimColon
2834	647704	1910.B07.gz43_243828	F	M00057239B:F05	UC2-PrimColon
2835	555641	1910.G07.gz43_243833	F	M00057245A:F03	UC2-PrimColon
2836	734226	1910.D08.gz43_243846	F	M00057241D:C04	UC2-PrimColon
2837	551437	1910.A09.gz43_243859	F	M00057238B:F05	UC2-PrimColon
2838	639494	1910.M09.gz43_243871	F	M00057252D:B10	UC2-PrimColon
2839	661194	1910.P09.gz43_243874	F	M00057256B:A05	UC2-PrimColon
2840	734466	1910.B10.gz43_243876	F	M00057239C:E05	UC2-PrimColon
2841	734371	1910.I10.gz43_243883	F	M00057247D:D10	UC2-PrimColon
2842	731392	1910.K11.gz43_243901	F	M00057250B:A03	UC2-PrimColon
2843	484964	1910.G12.gz43_243913	F	M00057245B:E02	UC2-PrimColon
2844	733991	1910.H12.gz43_243914	F	M00057246C:B12	UC2-PrimColon
2845	585976	1910.M12.gz43_243919	F	M00057252D:D04	UC2-PrimColon
2846	729125	1910.B13.gz43_243924	F	M00057239C:G07	UC2-PrimColon
2847	733855	1910.C13.gz43_243925	F	M00057240C:A06	UC2-PrimColon
2848	733945	1910.D14.gz43_243942	F	M00057241D:G01	UC2-PrimColon
2849	555103	1910.J14.gz43_243948	F	M00057249A:C06	UC2-PrimColon
2850	726011	1910.K14.gz43_243949	F	M00057250B:D04	UC2-PrimColon
2851	557353	1910.N14.gz43_243952	F	M00057254A:G07	UC2-PrimColon
2852	457846	1910.E15.gz43_243959	F	M00057243A:H03	UC2-PrimColon
2853	456753	1910.B16.gz43_243972	F	M00057239D:D01	UC2-PrimColon
2854	731238	1910.M17.gz43_243999	F	M00057253A:C05	UC2-PrimColon
2855	558332	1910.O17.gz43_244001	F	M00057255C:A07	UC2-PrimColon
2856	649390	1910.P17.gz43_244002	F	M00057256D:A11	UC2-PrimColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
2857	734808	1910.D19.gz43_244022	F	M00057242A:H11	UC2-PrimColon
2858	731125	1910.L19.gz43_244030	F	M00057252A:D10	UC2-PrimColon
2859	476455	1910.G20.gz43_244041	F	M00057245D:G02	UC2-PrimColon
2860	735754	1910.M20.gz43_244047	F	M00057253A:H10	UC2-PrimColon
2861	735477	1910.D21.gz43_244054	F	M00057242B:F07	UC2-PrimColon
2862	734894	1910.I21.gz43_244059	F	M00057248A:H10	UC2-PrimColon
2863	473588	1910.J21.gz43_244060	F	M00057249C:C07	UC2-PrimColon
2864	735665	1910.K21.gz43_244061	F	M00057250C:G02	UC2-PrimColon
2865	725095	1910.M22.gz43_244079	F	M00057253B:C06	UC2-PrimColon
2866	726081	1910.P23.gz43_244098	F	M00057257A:H10	UC2-PrimColon
2867	455821	1910.F24.gz43_244104	F	M00057244C:E06	UC2-PrimColon
2868	449537	1910.O24.gz43_244113	F	M00057255D:E02	UC2-PrimColon
2869	514697	1910.P24.gz43_244114	F	M00057257B:C11	UC2-PrimColon
2870	586794	1911.I01.gz43_244123	F	M00057269D:F02	UC2-PrimColon
2871	648710	1911.M01.gz43_244127	F	M00057275B:B02	UC2-PrimColon
2872	630348	1911.C02.gz43_244133	F	M00057260A:E05	UC2-PrimColon
2873	733570	1911.F02.gz43_244136	F	M00057266D:B12	UC2-PrimColon
2874	480723	1911.J02.gz43_244140	F	M00057271A:E04	UC2-PrimColon
2875	728756	1911.C03.gz43_244149	F	M00057260A:E11	UC2-PrimColon
2876	735071	1911.E04.gz43_244167	F	M00057265D:B12	UC2-PrimColon
2877	630655	1911.K04.gz43_244173	F	M00057273A:C08	UC2-PrimColon
2878	736014	1911.N04.gz43_244176	F	M00057279A:G02	UC2-PrimColon
2879	42	1911.P04.gz43_244178	F	M00057283A:E06	UC2-PrimColon
2880	482145	1911.D07.gz43_244214	F	M00057262B:C03	UC2-PrimColon
2881	735834	1911.K10.gz43_244269	F	M00057273B:A12	UC2-PrimColon
2882	42	1911.P10.gz43_244274	F	M00057283B:D09	UC2-PrimColon
2883	736014	1911.M11.gz43_244287	F	M00057277B:C09	UC2-PrimColon
2884	450692	1911.O11.gz43_244289	F	M00057281A:D08	UC2-PrimColon
2885	4470	1911.M12.gz43_244303	F	M00057277B:E10	UC2-PrimColon
2886	456065	1911.O12.gz43_244305	F	M00057281A:H02	UC2-PrimColon
2887	482985	1911.K15.gz43_244349	F	M00057273C:F11	UC2-PrimColon
2888	652782	1911.G18.gz43_244393	F	M00057268B:B03	UC2-PrimColon
2889	725784	1911.H18.gz43_244394	F	M00057269C:E01	UC2-PrimColon
2890	729321	1911.K19.gz43_244413	F	M00057273D:A06	UC2-PrimColon
2891	732213	1911.H22.gz43_244458	F	M00057269C:H06	UC2-PrimColon
2892	420504	1911.B23.gz43_244468	F	M00057259D:D11	UC2-PrimColon
2893	735687	1911.F23.gz43_244472	F	M00057267C:G09	UC2-PrimColon
2894	728790	1911.J23.gz43_244476	F	M00057272C:D08	UC2-PrimColon
2895	734131	1911.P23.gz43_244482	F	M00057283D:B12	UC2-PrimColon
2896	725951	1911.D24.gz43_244486	F	M00057265C:F03	UC2-PrimColon
2897	554703	1911.E24.gz43_244487	F	M00057266C:G12	UC2-PrimColon
2898	546642	1911.L24.gz43_244494	F	M00057275B:A12	UC2-PrimColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
2899	730189	1912.E03.gz43_244535	F	M00057291B:H08	UC2-PrimColon
2900	728768	1912.D08.gz43_244614	F	M00057290B:A02	UC2-PrimColon
2901	420402	1912.H10.gz43_244650	F	M00057299C:A08	UC2-PrimColon
2902	737109	1912.F12.gz43_244680	F	M00057293A:H03	UC2-PrimColon
2903	424672	1912.H15.gz43_244730	F	M00057299D:E04	UC2-PrimColon
2904	558045	1912.D16.gz43_244742	F	M00057290D:G03	UC2-PrimColon
2905	733856	1912.F16.gz43_244744	F	M00057293B:H04	UC2-PrimColon
2906	736449	1912.H17.gz43_244762	F	M00057300A:A08	UC2-PrimColon
2907	148201	1912.H18.gz43_244778	F	M00057300A:B06	UC2-PrimColon
2908	639427	1912.E19.gz43_244791	F	M00057292A:B08	UC2-PrimColon
2909	730187	1912.B21.gz43_244820	F	M00057287A:H06	UC2-PrimColon
2910	732300	1912.D24.gz43_244870	F	M00057291B:D08	UC2-PrimColon
2911	465528	1921.A01.gz43_244883	F	M00057314A:A10	UC2-PrimColon
2912	549552	1921.J01.gz43_244892	F	M00057331D:D08	UC2-PrimColon
2913	470199	1921.E02.gz43_244903	F	M00057320A:G08	UC2-PrimColon
2914	729125	1921.F03.gz43_244920	F	M00057323B:G04	UC2-PrimColon
2915	640341	1921.C04.gz43_244933	F	M00057316D:D02	UC2-PrimColon
2916	77737	1921.F04.gz43_244936	F	M00057323B:H08	UC2-PrimColon
2917	735469	1921.G04.gz43_244937	F	M00057324B:E04	UC2-PrimColon
2918	736733	1921.B06.gz43_244964	F	M00057315D:C06	UC2-PrimColon
2919	732969	1921.I06.gz43_244971	F	M00057328C:F11	UC2-PrimColon
2920	635849	1921.J06.gz43_244972	F	M00057332A:C06	UC2-PrimColon
2921	733146	1921.O06.gz43_244977	F	M00057339D:H09	UC2-PrimColon
2922	737114	1921.A07.gz43_244979	F	M00057314B:H06	UC2-PrimColon
2923	732114	1921.L07.gz43_244990	F	M00057334D:E03	UC2-PrimColon
2924	482788	1921.P08.gz43_245010	F	M00057341D:B09	UC2-PrimColon
2925	554647	1921.M10.gz43_245039	F	M00057337C:G12	UC2-PrimColon
2926	552623	1921.B11.gz43_245044	F	M00057316A:B04	UC2-PrimColon
2927	447705	1921.E11.gz43_245047	F	M00057320D:C02	UC2-PrimColon
2928	731748	1921.G11.gz43_245049	F	M00057324C:G05	UC2-PrimColon
2929	727093	1921.B12.gz43_245060	F	M00057316A:D09	UC2-PrimColon
2930	551607	1921.N12.gz43_245072	F	M00057339A:E08	UC2-PrimColon
2931	727013	1921.G13.gz43_245081	F	M00057324D:E10	UC2-PrimColon
2932	727018	1921.L13.gz43_245086	F	M00057336B:E01	UC2-PrimColon
2933	548635	1921.G14.gz43_245097	F	M00057324D:H03	UC2-PrimColon
2934	726692	1921.J14.gz43_245100	F	M00057332C:F12	UC2-PrimColon
2935	556430	1921.D15.gz43_245110	F	M00057319D:E06	UC2-PrimColon
2936	726692	1921.A16.gz43_245123	F	M00057314D:E09	UC2-PrimColon
2937	473225	1921.F16.gz43_245128	F	M00057323D:E10	UC2-PrimColon
2938	892	1921.K16.gz43_245133	F	M00057334A:C12	UC2-PrimColon
2939	730997	1921.C17.gz43_245141	F	M00057318B:H05	UC2-PrimColon
2940	51616	1921.E18.gz43_245159	F	M00057323A:F01	UC2-PrimColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
2941	546642	1921.F18.gz43_245160	F	M00057324A:A09	UC2-PrimColon
2942	643005	1921.G18.gz43_245161	F	M00057325B:D06	UC2-PrimColon
2943	735054	1921.H18.gz43_245162	F	M00057326D:B10	UC2-PrimColon
2944	727231	1921.F19.gz43_245176	F	M00057324A:C08	UC2-PrimColon
2945	733464	1921.J19.gz43_245180	F	M00057333A:D08	UC2-PrimColon
2946	457092	1921.B20.gz43_245188	F	M00057316C:A06	UC2-PrimColon
2947	733723	1921.H21.gz43_245210	F	M00057328A:F02	UC2-PrimColon
2948	557177	1921.I21.gz43_245211	F	M00057331C:E10	UC2-PrimColon
2949	734582	1921.K21.gz43_245213	F	M00057334B:F01	UC2-PrimColon
2950	448431	1921.L21.gz43_245214	F	M00057336D:F07	UC2-PrimColon
2951	697006	1921.H22.gz43_245226	F	M00057328A:F10	UC2-PrimColon
2952	452936	1921.I22.gz43_245227	F	M00057331C:F10	UC2-PrimColon
2953	727132	1921.L22.gz43_245230	F	M00057337A:A06	UC2-PrimColon
2954	513306	1921.F23.gz43_245240	F	M00057324B:A06	UC2-PrimColon
2955	642986	1921.P24.gz43_245266	F	M00057344A:G07	UC2-PrimColon
2956	496752	1924.G03.gz43_245338	F	M00043308A:D09	UC2-ColonMetLiver
2957	498509	1924.H03.gz43_245339	F	M00043310A:F01	UC2-ColonMetLiver
2958	450805	1924.E04.gz43_245352	F	M00043304B:A10	UC2-ColonMetLiver
2959	451456	1924.G04.gz43_245354	F	M00043308A:F06	UC2-ColonMetLiver
2960	494625	1924.M04.gz43_245360	F	M00043317B:B12	UC2-ColonMetLiver
2961	490401	1924.P05.gz43_245379	F	M00043321B:E05	UC2-ColonMetLiver
2962	495105	1924.H08.gz43_245419	F	M00043310C:B04	UC2-ColonMetLiver
2963	496957	1924.E09.gz43_245432	F	M00043304C:E01	UC2-ColonMetLiver
2964	494306	1924.I10.gz43_245452	F	M00043312D:A02	UC2-ColonMetLiver
2965	492544	1924.J11.gz43_245469	F	M00043313D:B04	UC2-ColonMetLiver
2966	451081	1924.M11.gz43_245472	F	M00043317D:C02	UC2-ColonMetLiver
2967	495951	1924.K14.gz43_245518	F	M00043315C:D05	UC2-ColonMetLiver
2968	450349	1924.D15.gz43_245527	F	M00043303B:E11	UC2-ColonMetLiver
2969	498951	1924.L15.gz43_245535	F	M00043316C:F06	UC2-ColonMetLiver
2970	450999	1924.C17.gz43_245558	F	M00043301D:B12	UC2-ColonMetLiver
2971	499693	1924.G17.gz43_245562	F	M00043309A:H06	UC2-ColonMetLiver
2972	498242	1924.F18.gz43_245577	F	M00043307B:F11	UC2-ColonMetLiver
2973	499700	1924.H18.gz43_245579	F	M00043311B:H08	UC2-ColonMetLiver
2974	479604	1924.L19.gz43_245599	F	M00043316D:F04	UC2-ColonMetLiver
2975	562516	1924.N19.gz43_245601	F	M00043319A:D01	UC2-ColonMetLiver
2976	553779	1924.L21.gz43_245631	F	M00043316D:F09	UC2-ColonMetLiver
2977	493746	1924.E24.gz43_245672	F	M00043306B:A09	UC2-ColonMetLiver
2978	494325	1924.H24.gz43_245675	F	M00043312B:A10	UC2-ColonMetLiver
2979	453078	1933.H03.gz43_245723	F	M00043340B:B04	UC2-ColonMetLiver
2980	492887	1933.J04.gz43_245741	F	M00043343D:H03	UC2-ColonMetLiver
2981	450283	1933.F05.gz43_245753	F	M00043335D:E02	UC2-ColonMetLiver
2982	494271	1933.M05.gz43_245760	F	M00043351C:A07	UC2-ColonMetLiver

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
2983	448110	1933.O05.gz43_245762	F	M00043354D:C01	UC2-ColonMetLiver
2984	412621	1933.D06.gz43_245767	F	M00043330D:G05	UC2-ColonMetLiver
2985	492629	1933.I06.gz43_245772	F	M00043342C:G02	UC2-ColonMetLiver
2986	491212	1933.E07.gz43_245784	F	M00043334A:F10	UC2-ColonMetLiver
2987	447057	1933.H09.gz43_245819	F	M00043340D:C03	UC2-ColonMetLiver
2988	496909	1933.C10.gz43_245830	F	M00043328A:E12	UC2-ColonMetLiver
2989	491933	1933.D10.gz43_245831	F	M00043331C:G01	UC2-ColonMetLiver
2990	496870	1933.N10.gz43_245841	F	M00043353D:E12	UC2-ColonMetLiver
2991	500040	1933.B12.gz43_245861	F	M00043326A:H06	UC2-ColonMetLiver
2992	553594	1933.O12.gz43_245874	F	M00043354D:H08	UC2-ColonMetLiver
2993	561712	1933.N14.gz43_245905	F	M00043354A:E06	UC2-ColonMetLiver
2994	450027	1933.J15.gz43_245917	F	M00043344C:C11	UC2-ColonMetLiver
2995	450129	1933.K16.gz43_245934	F	M00043348A:D02	UC2-ColonMetLiver
2996	492779	1933.C17.gz43_245942	F	M00043329B:H07	UC2-ColonMetLiver
2997	453068	1933.C18.gz43_245958	F	M00043329C:D12	UC2-ColonMetLiver
2998	450804	1933.F18.gz43_245961	F	M00043336C:A04	UC2-ColonMetLiver
2999	1015	1933.N18.gz43_245969	F	M00043354B:C04	UC2-ColonMetLiver
3000	561834	1933.N20.gz43_246001	F	M00043354B:F12	UC2-ColonMetLiver
3001	552687	1933.O23.gz43_246050	F	M00043355B:B01	UC2-ColonMetLiver
3002	517346	1933.O24.gz43_246066	F	M00043355B:D12	UC2-ColonMetLiver
3003	491448	1935.B05.gz43_246289	F	M00043392C:F02	UC2-ColonMetLiver
3004	553890	1935.K06.gz43_246314	F	M00043501A:D07	UC2-ColonMetLiver
3005	635439	1935.N06.gz43_246317	F	M00043504B:C02	UC2-ColonMetLiver
3006	402070	1935.I07.gz43_246328	F	M00043409C:C07	UC2-ColonMetLiver
3007	448924	1935.H08.gz43_246343	F	M00043406D:C04	UC2-ColonMetLiver
3008	562886	1935.O08.gz43_246350	F	M00043505B:G03	UC2-ColonMetLiver
3009	558055	1935.O09.gz43_246366	F	M00043505B:G07	UC2-ColonMetLiver
3010	451456	1935.H15.gz43_246455	F	M00043407C:H08	UC2-ColonMetLiver
3011	555399	1935.N16.gz43_246477	F	M00043504C:E03	UC2-ColonMetLiver
3012	498629	1935.H17.gz43_246487	F	M00043407D:G06	UC2-ColonMetLiver
3013	490805	1935.E18.gz43_246500	F	M00043401A:E09	UC2-ColonMetLiver
3014	450335	1935.F18.gz43_246501	F	M00043403B:A12	UC2-ColonMetLiver
3015	446964	1935.N22.gz43_246573	F	M00043504D:G08	UC2-ColonMetLiver
3016	522703	1935.P24.gz43_246607	F	M00043506D:F06	UC2-ColonMetLiver
3017	549853	1936.K05.gz43_246682	F	M00054494A:H04	UC2-ColonMetLiver
3018	560275	1936.M05.gz43_246684	F	M00054497B:C10	UC2-ColonMetLiver
3019	481057	1936.P05.gz43_246687	F	M00054501C:E08	UC2-ColonMetLiver
3020	414739	1936.C08.gz43_246722	F	M00043508D:C01	UC2-ColonMetLiver
3021	559720	1936.O08.gz43_246734	F	M00054500A:F04	UC2-ColonMetLiver
3022	554908	1936.M11.gz43_246780	F	M00054497D:A04	UC2-ColonMetLiver
3023	449000	1936.N11.gz43_246781	F	M00054498D:F01	UC2-ColonMetLiver
3024	556768	1936.F13.gz43_246805	F	M00054488A:F01	UC2-ColonMetLiver

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SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
3025	449978	1936.I15.gz43_246840	F	M00054492A:D04	UC2-ColonMetLiver
3026	489368	1936.J16.gz43_246857	F	M00054493C:E04	UC2-ColonMetLiver
3027	562823	1936.B18.gz43_246881	F	M00043508B:G11	UC2-ColonMetLiver
3028	559574	1936.E21.gz43_246932	F	M00054487C:A01	UC2-ColonMetLiver
3029	552920	1936.O23.gz43_246974	F	M00054501A:E11	UC2-ColonMetLiver
3030	552086	1971.A01.gz43_246992	F	M00054717A:A03	UC2-ColonMetLiver
3031	553123	1971.D01.gz43_246995	F	M00054720C:A01	UC2-ColonMetLiver
3032	561636	1971.H01.gz43_246999	F	M00054724D:C05	UC2-ColonMetLiver
3033	496772	1971.K01.gz43_247002	F	M00054727D:C06	UC2-ColonMetLiver
3034	549550	1971.A03.gz43_247024	F	M00054717A:C07	UC2-ColonMetLiver
3035	555837	1971.B05.gz43_247057	F	M00054718B:D03	UC2-ColonMetLiver
3036	557714	1971.D05.gz43_247059	F	M00054720C:G10	UC2-ColonMetLiver
3037	446999	1971.E05.gz43_247060	F	M00054721C:D11	UC2-ColonMetLiver
3038	450410	1971.F05.gz43_247061	F	M00054722C:D01	UC2-ColonMetLiver
3039	484043	1971.L05.gz43_247067	F	M00054729B:A08	UC2-ColonMetLiver
3040	452488	1971.N05.gz43_247069	F	M00054731A:D07	UC2-ColonMetLiver
3041	450278	1971.A06.gz43_247072	F	M00054717A:G09	UC2-ColonMetLiver
3042	561313	1971.D06.gz43_247075	F	M00054720C:H01	UC2-ColonMetLiver
3043	557426	1971.L06.gz43_247083	F	M00054729B:B03	UC2-ColonMetLiver
3044	553316	1971.F09.gz43_247125	F	M00054722D:C08	UC2-ColonMetLiver
3045	555818	1971.I09.gz43_247128	F	M00054726A:D02	UC2-ColonMetLiver
3046	551096	1971.H10.gz43_247143	F	M00054725A:A05	UC2-ColonMetLiver
3047	556654	1971.P10.gz43_247151	F	M00054734B:C06	UC2-ColonMetLiver
3048	555491	1971.H11.gz43_247159	F	M00054725A:F09	UC2-ColonMetLiver
3049	559380	1971.M11.gz43_247164	F	M00054730B:F11	UC2-ColonMetLiver
3050	86175	1971.H12.gz43_247175	F	M00054725A:H06	UC2-ColonMetLiver
3051	561830	1971.L12.gz43_247179	F	M00054729C:C08	UC2-ColonMetLiver
3052	421959	1971.G14.gz43_247206	F	M00054724A:G02	UC2-ColonMetLiver
3053	448453	1971.N14.gz43_247213	F	M00054731B:D04	UC2-ColonMetLiver
3054	562263	1971.L15.gz43_247227	F	M00054729C:G07	UC2-ColonMetLiver
3055	553739	1971.I16.gz43_247240	F	M00054726B:F08	UC2-ColonMetLiver
3056	557747	1971.I17.gz43_247256	F	M00054726B:F09	UC2-ColonMetLiver
3057	14573	1971.N17.gz43_247261	F	M00054731B:G02	UC2-ColonMetLiver
3058	553108	1971.P17.gz43_247263	F	M00054734C:A07	UC2-ColonMetLiver
3059	554048	1971.K18.gz43_247274	F	M00054728D:B07	UC2-ColonMetLiver
3060	550315	1971.L18.gz43_247275	F	M00054729D:D05	UC2-ColonMetLiver
3061	449035	1971.I21.gz43_247320	F	M00054726C:D10	UC2-ColonMetLiver
3062	524721	1971.I22.gz43_247336	F	M00054726C:E07	UC2-ColonMetLiver
3063	555571	1971.A24.gz43_247360	F	M00054718A:D11	UC2-ColonMetLiver
3064	553869	1971.N24.gz43_247373	F	M00054731C:H12	UC2-ColonMetLiver
3065	552686	1971.P24.gz43_247375	F	M00054735A:G09	UC2-ColonMetLiver
3066	424723	1972.I03.gz43_247416	F	M00054743A:C07	UC2-ColonMetLiver

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SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
3067	499517	1972.P03.gz43_247423	F	M00054750D:H12	UC2-ColonMetLiver
3068	551441	1972.L04.gz43_247435	F	M00054745D:G09	UC2-ColonMetLiver
3069	86145	1972.P04.gz43_247439	F	M00054751A:A05	UC2-ColonMetLiver
3070	556167	1972.C05.gz43_247442	F	M00054737B:H11	UC2-ColonMetLiver
3071	553834	1972.J05.gz43_247449	F	M00054744A:G10	UC2-ColonMetLiver
3072	454186	1972.C06.gz43_247458	F	M00054737C:B01	UC2-ColonMetLiver
3073	466235	1972.E08.gz43_247492	F	M00054739C:B12	UC2-ColonMetLiver
3074	562323	1972.O09.gz43_247518	F	M00054750A:G10	UC2-ColonMetLiver
3075	450142	1972.E12.gz43_247556	F	M00054739C:E05	UC2-ColonMetLiver
3076	557568	1972.O12.gz43_247566	F	M00054750B:F02	UC2-ColonMetLiver
3077	522322	1972.B13.gz43_247569	F	M00054736B:H03	UC2-ColonMetLiver
3078	558679	1972.D13.gz43_247571	F	M00054738D:F01	UC2-ColonMetLiver
3079	452257	1972.I13.gz43_247576	F	M00054743C:E11	UC2-ColonMetLiver
3080	523753	1972.N13.gz43_247581	F	M00054748B:G10	UC2-ColonMetLiver
3081	59202	1972.N14.gz43_247597	F	M00054748B:H09	UC2-ColonMetLiver
3082	553702	1972.P14.gz43_247599	F	M00054751B:F12	UC2-ColonMetLiver
3083	495832	1972.D15.gz43_247603	F	M00054738D:G07	UC2-ColonMetLiver
3084	493122	1972.F15.gz43_247605	F	M00054740C:H08	UC2-ColonMetLiver
3085	493135	1972.G15.gz43_247606	F	M00054741C:D08	UC2-ColonMetLiver
3086	562793	1972.K15.gz43_247610	F	M00054745C:B12	UC2-ColonMetLiver
3087	587854	1972.J16.gz43_247625	F	M00054744C:D02	UC2-ColonMetLiver
3088	553457	1972.O18.gz43_247662	F	M00054750C:D01	UC2-ColonMetLiver
3089	551778	1972.G19.gz43_247670	F	M00054741D:C05	UC2-ColonMetLiver
3090	555077	1972.I19.gz43_247672	F	M00054743D:F04	UC2-ColonMetLiver
3091	557871	1972.K19.gz43_247674	F	M00054745C:H02	UC2-ColonMetLiver
3092	560282	1972.C21.gz43_247698	F	M00054738B:E12	UC2-ColonMetLiver
3093	503452	1972.L22.gz43_247723	F	M00054746D:E05	UC2-ColonMetLiver
3094	555773	1972.D24.gz43_247747	F	M00054739A:F07	UC2-ColonMetLiver
3095	474309	1972.M24.gz43_247756	F	M00054747D:B05	UC2-ColonMetLiver
3096	556019	1981.J01.gz43_247769	F	M00054764D:F01	UC2-ColonMetLiver
3097	472196	1981.I02.gz43_247784	F	M00054763A:A10	UC2-ColonMetLiver
3098	513632	1981.D03.gz43_247795	F	M00054755D:E05	UC2-ColonMetLiver
3099	553158	1981.F03.gz43_247797	F	M00054759A:B08	UC2-ColonMetLiver
3100	498662	1981.L03.gz43_247803	F	M00054766C:B08	UC2-ColonMetLiver
3101	551693	1981.C04.gz43_247810	F	M00054754D:F11	UC2-ColonMetLiver
3102	554021	1981.I04.gz43_247816	F	M00054763C:D07	UC2-ColonMetLiver
3103	550402	1981.O04.gz43_247822	F	M00054769B:D12	UC2-ColonMetLiver
3104	448510	1981.P04.gz43_247823	F	M00054770B:D09	UC2-ColonMetLiver
3105	558900	1981.I05.gz43_247832	F	M00054763C:F10	UC2-ColonMetLiver
3106	554294	1981.K05.gz43_247834	F	M00054765D:D05	UC2-ColonMetLiver
3107	450840	1981.I06.gz43_247848	F	M00054763C:H04	UC2-ColonMetLiver
3108	561487	1981.J07.gz43_247865	F	M00054765B:C03	UC2-ColonMetLiver

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
3109	552541	1981.L07.gz43_247867	F	M00054766C:E01	UC2-ColonMetLiver
3110	528775	1981.P07.gz43_247871	F	M00054770C:A04	UC2-ColonMetLiver
3111	553918	1981.B08.gz43_247873	F	M00054753C:H02	UC2-ColonMetLiver
3112	477046	1981.B09.gz43_247889	F	M00054753D:A03	UC2-ColonMetLiver
3113	551289	1981.D09.gz43_247891	F	M00054756A:C12	UC2-ColonMetLiver
3114	263800	1981.G09.gz43_247894	F	M00054760D:B03	UC2-ColonMetLiver
3115	495942	1981.A10.gz43_247904	F	M00054752B:H06	UC2-ColonMetLiver
3116	556183	1981.H10.gz43_247911	F	M00054762A:D09	UC2-ColonMetLiver
3117	448357	1981.N10.gz43_247917	F	M00054768D:A01	UC2-ColonMetLiver
3118	554161	1981.P10.gz43_247919	F	M00054770C:C04	UC2-ColonMetLiver
3119	256179	1981.B11.gz43_247921	F	M00054753D:C12	UC2-ColonMetLiver
3120	555478	1981.P11.gz43_247935	F	M00054770C:D05	UC2-ColonMetLiver
3121	554581	1981.P12.gz43_247951	F	M00054770C:F10	UC2-ColonMetLiver
3122	553922	1981.B13.gz43_247953	F	M00054753D:H10	UC2-ColonMetLiver
3123	554336	1981.E13.gz43_247956	F	M00054758A:F03	UC2-ColonMetLiver
3124	560529	1981.F13.gz43_247957	F	M00054759C:G10	UC2-ColonMetLiver
3125	558900	1981.H14.gz43_247975	F	M00054762B:F02	UC2-ColonMetLiver
3126	447667	1981.M14.gz43_247980	F	M00054767C:D03	UC2-ColonMetLiver
3127	551288	1981.D15.gz43_247987	F	M00054756C:C08	UC2-ColonMetLiver
3128	122169	1981.E15.gz43_247988	F	M00054758B:C10	UC2-ColonMetLiver
3129	551617	1981.H15.gz43_247991	F	M00054762B:F07	UC2-ColonMetLiver
3130	260558	1981.L15.gz43_247995	F	M00054766D:H02	UC2-ColonMetLiver
3131	558609	1981.B16.gz43_248001	F	M00054754B:F04	UC2-ColonMetLiver
3132	554352	1981.E16.gz43_248004	F	M00054758B:D03	UC2-ColonMetLiver
3133	556064	1981.F17.gz43_248021	F	M00054759D:E01	UC2-ColonMetLiver
3134	508126	1981.K17.gz43_248026	F	M00054766A:H10	UC2-ColonMetLiver
3135	549576	1981.M17.gz43_248028	F	M00054767C:H06	UC2-ColonMetLiver
3136	554000	1981.A18.gz43_248032	F	M00054753A:A05	UC2-ColonMetLiver
3137	554049	1981.E18.gz43_248036	F	M00054758B:H03	UC2-ColonMetLiver
3138	558503	1981.H18.gz43_248039	F	M00054762C:A12	UC2-ColonMetLiver
3139	451993	1981.D19.gz43_248051	F	M00054756D:F05	UC2-ColonMetLiver
3140	558949	1981.O19.gz43_248062	F	M00054770A:C06	UC2-ColonMetLiver
3141	553131	1981.J20.gz43_248073	F	M00054765C:F10	UC2-ColonMetLiver
3142	555343	1981.D21.gz43_248083	F	M00054757A:H07	UC2-ColonMetLiver
3143	512432	1981.N21.gz43_248093	F	M00054769A:G10	UC2-ColonMetLiver
3144	550580	1981.B22.gz43_248097	F	M00054754C:H09	UC2-ColonMetLiver
3145	551117	1981.F22.gz43_248101	F	M00054760A:A12	UC2-ColonMetLiver
3146	556475	1981.L22.gz43_248107	F	M00054767A:F08	UC2-ColonMetLiver
3147	552549	1981.M22.gz43_248108	F	M00054767D:G09	UC2-ColonMetLiver
3148	470351	1981.P23.gz43_248127	F	M00054771A:E01	UC2-ColonMetLiver
3149	561535	1981.F24.gz43_248133	F	M00054760A:D10	UC2-ColonMetLiver
3150	1093	1981.G24.gz43_248134	F	M00054761C:E02	UC2-ColonMetLiver

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
3151	2284	1981.H24.gz43_248135	F	M00054762D:C06	UC2-ColonMetLiver
3152	555958	1982.F01.gz43_248149	F	M00054778A:D01	UC2-ColonMetLiver
3153	492779	1982.A02.gz43_248160	F	M00054771B:F12	UC2-ColonMetLiver
3154	553848	1982.P02.gz43_248175	F	M00054806A:G04	UC2-ColonMetLiver
3155	555686	1982.C03.gz43_248178	F	M00054774B:A07	UC2-ColonMetLiver
3156	555524	1982.H03.gz43_248183	F	M00054780B:B06	UC2-ColonMetLiver
3157	551068	1982.A04.gz43_248192	F	M00054771C:A11	UC2-ColonMetLiver
3158	552183	1982.O04.gz43_248206	F	M00054805A:H04	UC2-ColonMetLiver
3159	551003	1982.F05.gz43_248213	F	M00054778A:F08	UC2-ColonMetLiver
3160	465207	1982.G05.gz43_248214	F	M00054779B:A07	UC2-ColonMetLiver
3161	533991	1982.H05.gz43_248215	F	M00054780B:E03	UC2-ColonMetLiver
3162	553868	1982.K05.gz43_248218	F	M00054786D:F08	UC2-ColonMetLiver
3163	553774	1982.B06.gz43_248225	F	M00054772D:G12	UC2-ColonMetLiver
3164	554072	1982.C06.gz43_248226	F	M00054774B:G08	UC2-ColonMetLiver
3165	554828	1982.E06.gz43_248228	F	M00054776C:G06	UC2-ColonMetLiver
3166	559872	1982.G06.gz43_248230	F	M00054779B:B07	UC2-ColonMetLiver
3167	491570	1982.H06.gz43_248231	F	M00054780B:G10	UC2-ColonMetLiver
3168	275	1982.M06.gz43_248236	F	M00054802C:A07	UC2-ColonMetLiver
3169	552019	1982.C07.gz43_248242	F	M00054774C:A03	UC2-ColonMetLiver
3170	556183	1982.G07.gz43_248246	F	M00054779B:B11	UC2-ColonMetLiver
3171	552535	1982.J07.gz43_248249	F	M00054784C:D11	UC2-ColonMetLiver
3172	551718	1982.A08.gz43_248256	F	M00054771D:G01	UC2-ColonMetLiver
3173	551169	1982.B08.gz43_248257	F	M00054773A:E09	UC2-ColonMetLiver
3174	551080	1982.F08.gz43_248261	F	M00054778B:A02	UC2-ColonMetLiver
3175	517146	1982.P08.gz43_248271	F	M00054806C:C12	UC2-ColonMetLiver
3176	402147	1982.B09.gz43_248273	F	M00054773A:H05	UC2-ColonMetLiver
3177	557269	1982.D09.gz43_248275	F	M00054776A:D10	UC2-ColonMetLiver
3178	539353	1982.N09.gz43_248285	F	M00054804A:H04	UC2-ColonMetLiver
3179	560520	1982.D10.gz43_248291	F	M00054776A:F01	UC2-ColonMetLiver
3180	575924	1982.I10.gz43_248296	F	M00054782D:D12	UC2-ColonMetLiver
3181	554582	1982.J10.gz43_248297	F	M00054784D:B01	UC2-ColonMetLiver
3182	555696	1982.M10.gz43_248300	F	M00054802D:A09	UC2-ColonMetLiver
3183	556856	1982.O10.gz43_248302	F	M00054805B:E06	UC2-ColonMetLiver
3184	447926	1982.D11.gz43_248307	F	M00054776A:F07	UC2-ColonMetLiver
3185	553743	1982.E11.gz43_248308	F	M00054776D:G09	UC2-ColonMetLiver
3186	553979	1982.N11.gz43_248317	F	M00054804B:E07	UC2-ColonMetLiver
3187	497912	1982.O11.gz43_248318	F	M00054805B:E11	UC2-ColonMetLiver
3188	412621	1982.D12.gz43_248323	F	M00054776A:G01	UC2-ColonMetLiver
3189	497477	1982.M12.gz43_248332	F	M00054802D:C02	UC2-ColonMetLiver
3190	552188	1982.J13.gz43_248345	F	M00054785B:B07	UC2-ColonMetLiver
3191	456052	1982.M13.gz43_248348	F	M00054802D:C03	UC2-ColonMetLiver
3192	143346	1982.H14.gz43_248359	F	M00054780C:G11	UC2-ColonMetLiver

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
3193	553237	1982.N14.gz43_248365	F	M00054804C:F04	UC2-ColonMetLiver
3194	556856	1982.O14.gz43_248366	F	M00054805B:G02	UC2-ColonMetLiver
3195	586600	1982.A15.gz43_248368	F	M00054772B:B01	UC2-ColonMetLiver
3196	562263	1982.J15.gz43_248377	F	M00054785C:C02	UC2-ColonMetLiver
3197	555462	1982.C16.gz43_248386	F	M00054775A:D07	UC2-ColonMetLiver
3198	394168	1982.O16.gz43_248398	F	M00054805B:G10	UC2-ColonMetLiver
3199	472672	1982.A17.gz43_248400	F	M00054772B:D04	UC2-ColonMetLiver
3200	595181	1982.C17.gz43_248402	F	M00054775A:G03	UC2-ColonMetLiver
3201	554627	1982.G17.gz43_248406	F	M00054779D:F07	UC2-ColonMetLiver
3202	552325	1982.I17.gz43_248408	F	M00054783C:C03	UC2-ColonMetLiver
3203	462511	1982.J17.gz43_248409	F	M00054785C:G11	UC2-ColonMetLiver
3204	552813	1982.K17.gz43_248410	F	M00054788C:G04	UC2-ColonMetLiver
3205	175758	1982.M17.gz43_248412	F	M00054803A:D08	UC2-ColonMetLiver
3206	493085	1982.A18.gz43_248416	F	M00054772B:F03	UC2-ColonMetLiver
3207	557834	1982.B18.gz43_248417	F	M00054773C:F09	UC2-ColonMetLiver
3208	548998	1982.F18.gz43_248421	F	M00054778C:F09	UC2-ColonMetLiver
3209	551425	1982.G18.gz43_248422	F	M00054779D:F08	UC2-ColonMetLiver
3210	490414	1982.K18.gz43_248426	F	M00054789A:A02	UC2-ColonMetLiver
3211	551553	1982.M18.gz43_248428	F	M00054803A:E10	UC2-ColonMetLiver
3212	555571	1982.N18.gz43_248429	F	M00054804D:D07	UC2-ColonMetLiver
3213	448629	1982.B19.gz43_248433	F	M00054773C:F10	UC2-ColonMetLiver
3214	552005	1982.J19.gz43_248441	F	M00054785D:A07	UC2-ColonMetLiver
3215	554116	1982.M20.gz43_248460	F	M00054803B:B12	UC2-ColonMetLiver
3216	505792	1982.H21.gz43_248471	F	M00054781A:H09	UC2-ColonMetLiver
3217	561422	1982.J21.gz43_248473	F	M00054786A:G11	UC2-ColonMetLiver
3218	551755	1982.M24.gz43_248524	F	M00054803C:G01	UC2-ColonMetLiver
3219	550063	1945.J03.gz43_248963	F	M00054513A:B08	UC2-ColonMetLiver
3220	388055	1945.D04.gz43_248973	F	M00054506B:A07	UC2-ColonMetLiver
3221	572807	1945.C05.gz43_248988	F	M00054505A:G12	UC2-ColonMetLiver
3222	455814	1945.J05.gz43_248995	F	M00054513A:F09	UC2-ColonMetLiver
3223	452471	1945.H07.gz43_249025	F	M00054510C:G07	UC2-ColonMetLiver
3224	551518	1945.J07.gz43_249027	F	M00054513B:E11	UC2-ColonMetLiver
3225	555660	1945.J09.gz43_249059	F	M00054513C:A01	UC2-ColonMetLiver
3226	524721	1945.B11.gz43_249083	F	M00054504B:A04	UC2-ColonMetLiver
3227	550986	1945.D11.gz43_249085	F	M00054506B:H01	UC2-ColonMetLiver
3228	499696	1945.G11.gz43_249088	F	M00054509C:G01	UC2-ColonMetLiver
3229	554611	1945.N11.gz43_249095	F	M00054519A:C04	UC2-ColonMetLiver
3230	557681	1945.F12.gz43_249103	F	M00054508B:E08	UC2-ColonMetLiver
3231	550678	1945.J13.gz43_249123	F	M00054513D:F04	UC2-ColonMetLiver
3232	554246	1945.K13.gz43_249124	F	M00054515B:E11	UC2-ColonMetLiver
3233	550129	1945.F15.gz43_249151	F	M00054508C:B04	UC2-ColonMetLiver
3234	555771	1945.F17.gz43_249183	F	M00054508C:C08	UC2-ColonMetLiver

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
3235	572992	1945.O18.gz43_249208	F	M00054521D:H01	UC2-ColonMetLiver
3236	461313	1945.J21.gz43_249251	F	M00054514C:B01	UC2-ColonMetLiver
3237	554456	1945.L21.gz43_249253	F	M00054516D:F09	UC2-ColonMetLiver
3238	547866	1945.F23.gz43_249279	F	M00054509A:C01	UC2-ColonMetLiver
3239	458974	1945.P23.gz43_249289	F	M00054523C:A11	UC2-ColonMetLiver
3240	554839	1945.C24.gz43_249292	F	M00054506A:D05	UC2-ColonMetLiver
3241	487658	1945.I24.gz43_249298	F	M00054512D:H08	UC2-ColonMetLiver
3242	556940	1946.H01.gz43_249313	F	M00054533C:B04	UC2-ColonMetLiver
3243	493575	1946.N03.gz43_249351	F	M00054541C:C10	UC2-ColonMetLiver
3244	466020	1946.H05.gz43_249377	F	M00054533C:E07	UC2-ColonMetLiver
3245	552006	1946.C06.gz43_249388	F	M00054527B:A07	UC2-ColonMetLiver
3246	551157	1946.E06.gz43_249390	F	M00054529C:D11	UC2-ColonMetLiver
3247	559574	1946.G06.gz43_249392	F	M00054532D:A01	UC2-ColonMetLiver
3248	556216	1946.I06.gz43_249394	F	M00054534D:D02	UC2-ColonMetLiver
3249	559676	1946.B07.gz43_249403	F	M00054525D:H05	UC2-ColonMetLiver
3250	550018	1946.J07.gz43_249411	F	M00054536B:A03	UC2-ColonMetLiver
3251	526984	1946.G08.gz43_249424	F	M00054532D:E07	UC2-ColonMetLiver
3252	481594	1946.N09.gz43_249447	F	M00054541C:F11	UC2-ColonMetLiver
3253	550618	1946.P09.gz43_249449	F	M00054544B:E03	UC2-ColonMetLiver
3254	454336	1946.A10.gz43_249450	F	M00054523D:G09	UC2-ColonMetLiver
3255	550370	1946.J10.gz43_249459	F	M00054536B:D02	UC2-ColonMetLiver
3256	464154	1946.M10.gz43_249462	F	M00054540A:H07	UC2-ColonMetLiver
3257	550475	1946.B11.gz43_249467	F	M00054526A:E04	UC2-ColonMetLiver
3258	584071	1946.F11.gz43_249471	F	M00054531D:F05	UC2-ColonMetLiver
3259	550730	1946.J11.gz43_249475	F	M00054536B:F08	UC2-ColonMetLiver
3260	552638	1946.O12.gz43_249496	F	M00054543B:E06	UC2-ColonMetLiver
3261	560014	1946.L13.gz43_249509	F	M00054538D:H11	UC2-ColonMetLiver
3262	553338	1946.I14.gz43_249522	F	M00054535A:G03	UC2-ColonMetLiver
3263	556809	1946.B15.gz43_249531	F	M00054526B:C09	UC2-ColonMetLiver
3264	498433	1946.H15.gz43_249537	F	M00054534A:B06	UC2-ColonMetLiver
3265	455821	1946.K16.gz43_249556	F	M00054538A:E10	UC2-ColonMetLiver
3266	82864	1946.J17.gz43_249571	F	M00054536C:D12	UC2-ColonMetLiver
3267	560519	1946.L17.gz43_249573	F	M00054539B:D06	UC2-ColonMetLiver
3268	409262	1946.N17.gz43_249575	F	M00054542B:B01	UC2-ColonMetLiver
3269	560717	1946.P17.gz43_249577	F	M00054544C:F04	UC2-ColonMetLiver
3270	550172	1946.K18.gz43_249588	F	M00054538B:B05	UC2-ColonMetLiver
3271	552753	1946.O18.gz43_249592	F	M00054543C:F01	UC2-ColonMetLiver
3272	549734	1946.L19.gz43_249605	F	M00054539B:G03	UC2-ColonMetLiver
3273	550714	1946.G20.gz43_249616	F	M00054533B:F04	UC2-ColonMetLiver
3274	585380	1946.D21.gz43_249629	F	M00054529A:H01	UC2-ColonMetLiver
3275	550204	1946.F21.gz43_249631	F	M00054532B:C05	UC2-ColonMetLiver
3276	560205	1946.I22.gz43_249650	F	M00054535B:H08	UC2-ColonMetLiver

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
3277	312036	1946.E23.gz43_249662	F	M00054530D:C10	UC2-ColonMetLiver
3278	553002	1946.E24.gz43_249678	F	M00054530D:H07	UC2-ColonMetLiver
3279	394567	1948.O01.gz43_249704	F	M00054583D:E04	UC2-ColonMetLiver
3280	468613	1948.C02.gz43_249708	F	M00054569D:E01	UC2-ColonMetLiver
3281	378610	1948.I02.gz43_249714	F	M00054576D:C07	UC2-ColonMetLiver
3282	559752	1948.M02.gz43_249718	F	M00054581B:A01	UC2-ColonMetLiver
3283	550804	1948.K03.gz43_249732	F	M00054579A:G10	UC2-ColonMetLiver
3284	549956	1948.O03.gz43_249736	F	M00054584A:A07	UC2-ColonMetLiver
3285	556065	1948.A04.gz43_249738	F	M00054567C:B03	UC2-ColonMetLiver
3286	550397	1948.M04.gz43_249750	F	M00054581B:D03	UC2-ColonMetLiver
3287	550874	1948.M05.gz43_249766	F	M00054581B:G10	UC2-ColonMetLiver
3288	533812	1948.O05.gz43_249768	F	M00054584A:B03	UC2-ColonMetLiver
3289	549597	1948.C08.gz43_249804	F	M00054570A:F02	UC2-ColonMetLiver
3290	553749	1948.K08.gz43_249812	F	M00054579B:D10	UC2-ColonMetLiver
3291	446814	1948.G10.gz43_249840	F	M00054574D:F11	UC2-ColonMetLiver
3292	555000	1948.M10.gz43_249846	F	M00054581D:C12	UC2-ColonMetLiver
3293	554887	1948.O10.gz43_249848	F	M00054584B:A03	UC2-ColonMetLiver
3294	561876	1948.E11.gz43_249854	F	M00054572C:E09	UC2-ColonMetLiver
3295	556488	1948.M11.gz43_249862	F	M00054581D:D01	UC2-ColonMetLiver
3296	560080	1948.G12.gz43_249872	F	M00054575A:B06	UC2-ColonMetLiver
3297	556336	1948.M12.gz43_249878	F	M00054581D:E04	UC2-ColonMetLiver
3298	558729	1948.I13.gz43_249890	F	M00054577B:A09	UC2-ColonMetLiver
3299	549716	1948.A14.gz43_249898	F	M00054568A:G02	UC2-ColonMetLiver
3300	568467	1948.M14.gz43_249910	F	M00054582A:A05	UC2-ColonMetLiver
3301	550694	1948.N14.gz43_249911	F	M00054583A:F05	UC2-ColonMetLiver
3302	549994	1948.M15.gz43_249926	F	M00054582A:A07	UC2-ColonMetLiver
3303	549858	1948.A16.gz43_249930	F	M00054568A:H03	UC2-ColonMetLiver
3304	554793	1948.A17.gz43_249946	F	M00054568B:A07	UC2-ColonMetLiver
3305	466020	1948.O17.gz43_249960	F	M00054584D:C01	UC2-ColonMetLiver
3306	509202	1948.I19.gz43_249986	F	M00054577B:F01	UC2-ColonMetLiver
3307	450963	1948.A21.gz43_250010	F	M00054568C:D06	UC2-ColonMetLiver
3308	451049	1948.C21.gz43_250012	F	M00054571A:B10	UC2-ColonMetLiver
3309	528404	1948.K21.gz43_250020	F	M00054580A:B11	UC2-ColonMetLiver
3310	160320	1948.O21.gz43_250024	F	M00054585A:E07	UC2-ColonMetLiver
3311	492139	1948.K22.gz43_250036	F	M00054580A:C10	UC2-ColonMetLiver
3312	557656	1948.A23.gz43_250042	F	M00054568C:G12	UC2-ColonMetLiver
3313	570248	1948.K24.gz43_250068	F	M00054580A:D04	UC2-ColonMetLiver
3314	561836	1957.G01.gz43_250080	F	M00054594A:D04	UC2-ColonMetLiver
3315	558332	1957.J01.gz43_250083	F	M00054597A:C11	UC2-ColonMetLiver
3316	558981	1957.J02.gz43_250099	F	M00054597A:D08	UC2-ColonMetLiver
3317	535129	1957.B03.gz43_250107	F	M00054587C:G02	UC2-ColonMetLiver
3318	549781	1957.J03.gz43_250115	F	M00054597A:G08	UC2-ColonMetLiver

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
3319	555920	1957.C04.gz43_250124	F	M00054589A:D09	UC2-ColonMetLiver
3320	550044	1957.E04.gz43_250126	F	M00054591C:A01	UC2-ColonMetLiver
3321	447356	1957.I04.gz43_250130	F	M00054596B:C01	UC2-ColonMetLiver
3322	560751	1957.A05.gz43_250138	F	M00054586C:H02	UC2-ColonMetLiver
3323	550322	1957.B05.gz43_250139	F	M00054587D:D04	UC2-ColonMetLiver
3324	416884	1957.N05.gz43_250151	F	M00054602A:E06	UC2-ColonMetLiver
3325	559857	1957.A06.gz43_250154	F	M00054586D:A03	UC2-ColonMetLiver
3326	446164	1957.C06.gz43_250156	F	M00054589B:A07	UC2-ColonMetLiver
3327	550088	1957.D06.gz43_250157	F	M00054590B:B11	UC2-ColonMetLiver
3328	554764	1957.E06.gz43_250158	F	M00054591C:H09	UC2-ColonMetLiver
3329	552907	1957.O07.gz43_250184	F	M00054603A:G06	UC2-ColonMetLiver
3330	498827	1957.D08.gz43_250189	F	M00054590C:A03	UC2-ColonMetLiver
3331	498777	1957.G08.gz43_250192	F	M00054594C:E06	UC2-ColonMetLiver
3332	559883	1957.L08.gz43_250197	F	M00054599D:B07	UC2-ColonMetLiver
3333	554869	1957.M08.gz43_250198	F	M00054600D:H07	UC2-ColonMetLiver
3334	559419	1957.A09.gz43_250202	F	M00054586D:G01	UC2-ColonMetLiver
3335	473859	1957.F09.gz43_250207	F	M00054593B:B03	UC2-ColonMetLiver
3336	555949	1957.M09.gz43_250214	F	M00054601A:E08	UC2-ColonMetLiver
3337	552913	1957.O09.gz43_250216	F	M00054603A:G12	UC2-ColonMetLiver
3338	551463	1957.C10.gz43_250220	F	M00054589B:F05	UC2-ColonMetLiver
3339	550855	1957.B11.gz43_250235	F	M00054588A:G08	UC2-ColonMetLiver
3340	526733	1957.O11.gz43_250248	F	M00054603B:B04	UC2-ColonMetLiver
3341	557970	1957.F12.gz43_250255	F	M00054593B:E03	UC2-ColonMetLiver
3342	549665	1957.H12.gz43_250257	F	M00054595C:G06	UC2-ColonMetLiver
3343	446503	1957.M12.gz43_250262	F	M00054601B:D08	UC2-ColonMetLiver
3344	549599	1957.P12.gz43_250265	F	M00054604C:F03	UC2-ColonMetLiver
3345	558413	1957.A13.gz43_250266	F	M00054587A:A08	UC2-ColonMetLiver
3346	553331	1957.B13.gz43_250267	F	M00054588B:B12	UC2-ColonMetLiver
3347	549609	1957.I14.gz43_250290	F	M00054596C:F09	UC2-ColonMetLiver
3348	455298	1957.I15.gz43_250306	F	M00054596C:F10	UC2-ColonMetLiver
3349	563514	1957.P15.gz43_250313	F	M00054604D:A04	UC2-ColonMetLiver
3350	471181	1957.A16.gz43_250314	F	M00054587A:F06	UC2-ColonMetLiver
3351	487176	1957.N16.gz43_250327	F	M00054602C:C12	UC2-ColonMetLiver
3352	561130	1957.I17.gz43_250338	F	M00054596C:G09	UC2-ColonMetLiver
3353	461718	1957.J17.gz43_250339	F	M00054597D:E12	UC2-ColonMetLiver
3354	559554	1957.L17.gz43_250341	F	M00054600A:G12	UC2-ColonMetLiver
3355	452506	1957.A18.gz43_250346	F	M00054587A:F09	UC2-ColonMetLiver
3356	551975	1957.D18.gz43_250349	F	M00054590D:C12	UC2-ColonMetLiver
3357	485029	1957.H18.gz43_250353	F	M00054595D:A10	UC2-ColonMetLiver
3358	549816	1957.L18.gz43_250357	F	M00054600A:H03	UC2-ColonMetLiver
3359	408130	1957.O18.gz43_250360	F	M00054603C:G09	UC2-ColonMetLiver
3360	558927	1957.P18.gz43_250361	F	M00054605A:A03	UC2-ColonMetLiver

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
3361	550217	1957.B19.gz43_250363	F	M00054588C:F04	UC2-ColonMetLiver
3362	556376	1957.C20.gz43_250380	F	M00054589D:C06	UC2-ColonMetLiver
3363	549964	1957.E20.gz43_250382	F	M00054592C:A05	UC2-ColonMetLiver
3364	549228	1957.K20.gz43_250388	F	M00054599B:C06	UC2-ColonMetLiver
3365	459581	1957.L20.gz43_250389	F	M00054600C:B10	UC2-ColonMetLiver
3366	562722	1957.N20.gz43_250391	F	M00054602D:A06	UC2-ColonMetLiver
3367	552121	1957.O20.gz43_250392	F	M00054603D:B02	UC2-ColonMetLiver
3368	447311	1957.C23.gz43_250428	F	M00054590A:A01	UC2-ColonMetLiver
3369	467035	1957.I23.gz43_250434	F	M00054597A:A07	UC2-ColonMetLiver
3370	549611	1957.K23.gz43_250436	F	M00054599B:F09	UC2-ColonMetLiver
3371	549731	1957.H24.gz43_250449	F	M00054596A:G11	UC2-ColonMetLiver
3372	380127	1957.P24.gz43_250457	F	M00054605B:F10	UC2-ColonMetLiver
3373	405042	1958.H01.gz43_250465	F	M00054614B:E01	UC2-ColonMetLiver
3374	552418	1958.J01.gz43_250467	F	M00054616D:C10	UC2-ColonMetLiver
3375	558642	1958.N01.gz43_250471	F	M00054621D:C06	UC2-ColonMetLiver
3376	549649	1958.A02.gz43_250474	F	M00054605B:G01	UC2-ColonMetLiver
3377	557190	1958.B02.gz43_250475	F	M00054606D:B05	UC2-ColonMetLiver
3378	549320	1958.N02.gz43_250487	F	M00054621D:D11	UC2-ColonMetLiver
3379	549739	1958.J03.gz43_250499	F	M00054616D:G09	UC2-ColonMetLiver
3380	561116	1958.M03.gz43_250502	F	M00054620D:D06	UC2-ColonMetLiver
3381	473111	1958.M04.gz43_250518	F	M00054620D:D11	UC2-ColonMetLiver
3382	558103	1958.P04.gz43_250521	F	M00054625A:D07	UC2-ColonMetLiver
3383	548864	1958.A05.gz43_250522	F	M00054605C:A04	UC2-ColonMetLiver
3384	560862	1958.B05.gz43_250523	F	M00054607A:B06	UC2-ColonMetLiver
3385	557199	1958.P05.gz43_250537	F	M00054625A:E05	UC2-ColonMetLiver
3386	188753	1958.A06.gz43_250538	F	M00054605C:D03	UC2-ColonMetLiver
3387	550177	1958.G06.gz43_250544	F	M00054613A:D07	UC2-ColonMetLiver
3388	556896	1958.M06.gz43_250550	F	M00054620D:F11	UC2-ColonMetLiver
3389	552823	1958.B07.gz43_250555	F	M00054607A:G02	UC2-ColonMetLiver
3390	395411	1958.M07.gz43_250566	F	M00054620D:G11	UC2-ColonMetLiver
3391	10397	1958.N07.gz43_250567	F	M00054622A:D06	UC2-ColonMetLiver
3392	551250	1958.P07.gz43_250569	F	M00054625B:B02	UC2-ColonMetLiver
3393	561892	1958.C08.gz43_250572	F	M00054609A:F01	UC2-ColonMetLiver
3394	549347	1958.F08.gz43_250575	F	M00054612A:D12	UC2-ColonMetLiver
3395	561068	1958.N08.gz43_250583	F	M00054622A:H01	UC2-ColonMetLiver
3396	549912	1958.C09.gz43_250588	F	M00054609A:H04	UC2-ColonMetLiver
3397	549114	1958.F10.gz43_250607	F	M00054612B:B11	UC2-ColonMetLiver
3398	548965	1958.J10.gz43_250611	F	M00054617B:A09	UC2-ColonMetLiver
3399	491644	1958.N10.gz43_250615	F	M00054622B:F05	UC2-ColonMetLiver
3400	550018	1958.G11.gz43_250624	F	M00054613B:H04	UC2-ColonMetLiver
3401	556530	1958.C12.gz43_250636	F	M00054609B:E01	UC2-ColonMetLiver
3402	562749	1958.L12.gz43_250645	F	M00054619D:C10	UC2-ColonMetLiver

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SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
3403	556308	1958.N12.gz43_250647	F	M00054622B:H09	UC2-ColonMetLiver
3404	551305	1958.O12.gz43_250648	F	M00054623D:C12	UC2-ColonMetLiver
3405	507349	1958.C13.gz43_250652	F	M00054609B:H11	UC2-ColonMetLiver
3406	549626	1958.E13.gz43_250654	F	M00054611B:F12	UC2-ColonMetLiver
3407	549388	1958.J13.gz43_250659	F	M00054617B:D06	UC2-ColonMetLiver
3408	478511	1958.E14.gz43_250670	F	M00054611B:G09	UC2-ColonMetLiver
3409	555371	1958.K14.gz43_250676	F	M00054618C:H02	UC2-ColonMetLiver
3410	553758	1958.I15.gz43_250690	F	M00054616A:H01	UC2-ColonMetLiver
3411	553204	1958.L15.gz43_250693	F	M00054620A:C09	UC2-ColonMetLiver
3412	497477	1958.H16.gz43_250705	F	M00054615B:E03	UC2-ColonMetLiver
3413	481360	1958.I16.gz43_250706	F	M00054616A:H03	UC2-ColonMetLiver
3414	552437	1958.K16.gz43_250708	F	M00054618D:D04	UC2-ColonMetLiver
3415	550164	1958.O16.gz43_250712	F	M00054624A:B11	UC2-ColonMetLiver
3416	555660	1958.E18.gz43_250734	F	M00054611C:E01	UC2-ColonMetLiver
3417	562932	1958.N18.gz43_250743	F	M00054622D:C02	UC2-ColonMetLiver
3418	490393	1958.B19.gz43_250747	F	M00054608B:D08	UC2-ColonMetLiver
3419	490890	1958.K19.gz43_250756	F	M00054618D:E06	UC2-ColonMetLiver
3420	451009	1958.K20.gz43_250772	F	M00054618D:E11	UC2-ColonMetLiver
3421	552194	1958.L20.gz43_250773	F	M00054620B:B10	UC2-ColonMetLiver
3422	451025	1958.M20.gz43_250774	F	M00054621C:G03	UC2-ColonMetLiver
3423	551463	1958.N20.gz43_250775	F	M00054622D:D10	UC2-ColonMetLiver
3424	553028	1958.G21.gz43_250784	F	M00054613D:H09	UC2-ColonMetLiver
3425	485504	1958.N21.gz43_250791	F	M00054622D:F05	UC2-ColonMetLiver
3426	562712	1958.P21.gz43_250793	F	M00054625D:F06	UC2-ColonMetLiver
3427	490152	1958.C22.gz43_250796	F	M00054609D:E12	UC2-ColonMetLiver
3428	552364	1958.F22.gz43_250799	F	M00054612D:B12	UC2-ColonMetLiver
3429	448276	1958.L22.gz43_250805	F	M00054620C:C08	UC2-ColonMetLiver
3430	556835	1958.N22.gz43_250807	F	M00054622D:G11	UC2-ColonMetLiver
3431	461734	1958.P22.gz43_250809	F	M00054625D:H07	UC2-ColonMetLiver
3432	557947	1958.H23.gz43_250817	F	M00054615C:D09	UC2-ColonMetLiver
3433	560491	1958.L23.gz43_250821	F	M00054620C:C12	UC2-ColonMetLiver
3434	554810	1958.O23.gz43_250824	F	M00054624D:B06	UC2-ColonMetLiver
3435	549829	1958.C24.gz43_250828	F	M00054609D:H06	UC2-ColonMetLiver
3436	518049	1958.M24.gz43_250838	F	M00054621D:A10	UC2-ColonMetLiver
3437	484669	1777.O01.gz43_251861	F	M00042831D:G06	UC2-PrimColon
3438	537506	1777.C03.gz43_251881	F	M00042811C:B06	UC2-PrimColon
3439	545162	1777.F03.gz43_251884	F	M00042816B:C08	UC2-PrimColon
3440	456793	1777.C11.gz43_252009	F	M00042812B:C01	UC2-PrimColon
3441	448340	1777.E11.gz43_252011	F	M00042815C:C02	UC2-PrimColon
3442	448793	1777.E13.gz43_252043	F	M00042815C:F10	UC2-PrimColon
3443	449718	1777.H14.gz43_252062	F	M00042819C:H02	UC2-PrimColon
3444	735534	1777.E17.gz43_252107	F	M00042816A:C09	UC2-PrimColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
3445	449258	1777.K17.gz43_252113	F	M00042825A:B05	UC2-PrimColon
3446	485020	1777.O18.gz43_252133	F	M00042833C:G05	UC2-PrimColon
3447	649735	1777.A23.gz43_252199	F	M00042809D:C12	UC2-PrimColon
3448	498504	1923.B01.gz43_252616	F	M00042352D:F11	UC2-ColonMetLiver
3449	424723	1923.C01.gz43_252617	F	M00042355A:H09	UC2-ColonMetLiver
3450	451124	1923.E01.gz43_252619	F	M00042444C:E02	UC2-ColonMetLiver
3451	553312	1923.O01.gz43_252629	F	M00042516D:H08	UC2-ColonMetLiver
3452	257547	1923.D02.gz43_252634	F	M00042442B:A07	UC2-ColonMetLiver
3453	492292	1923.J02.gz43_252640	F	M00042455B:G09	UC2-ColonMetLiver
3454	638444	1923.O02.gz43_252645	F	M00042516D:H09	UC2-ColonMetLiver
3455	451009	1923.C03.gz43_252649	F	M00042355B:B07	UC2-ColonMetLiver
3456	451518	1923.I03.gz43_252655	F	M00042453C:D12	UC2-ColonMetLiver
3457	450255	1923.J03.gz43_252656	F	M00042455C:D11	UC2-ColonMetLiver
3458	556804	1923.M03.gz43_252659	F	M00042460B:D10	UC2-ColonMetLiver
3459	497400	1923.C04.gz43_252665	F	M00042355B:E10	UC2-ColonMetLiver
3460	451618	1923.H04.gz43_252670	F	M00042451D:H10	UC2-ColonMetLiver
3461	490890	1923.J04.gz43_252672	F	M00042455C:E04	UC2-ColonMetLiver
3462	492982	1923.P04.gz43_252678	F	M00042519D:H07	UC2-ColonMetLiver
3463	498777	1923.A05.gz43_252679	F	M00042351C:G01	UC2-ColonMetLiver
3464	493575	1923.B05.gz43_252680	F	M00042353B:A11	UC2-ColonMetLiver
3465	556916	1923.L05.gz43_252690	F	M00042459B:F03	UC2-ColonMetLiver
3466	551755	1923.N05.gz43_252692	F	M00042460D:H06	UC2-ColonMetLiver
3467	495074	1923.O05.gz43_252693	F	M00042517C:B04	UC2-ColonMetLiver
3468	487745	1923.E06.gz43_252699	F	M00042445A:B04	UC2-ColonMetLiver
3469	448663	1923.F06.gz43_252700	F	M00042447C:H10	UC2-ColonMetLiver
3470	468729	1923.L06.gz43_252706	F	M00042459B:F12	UC2-ColonMetLiver
3471	451470	1923.C07.gz43_252713	F	M00042355C:G09	UC2-ColonMetLiver
3472	489426	1923.K07.gz43_252721	F	M00042457D:D02	UC2-ColonMetLiver
3473	450302	1923.F08.gz43_252732	F	M00042447D:E04	UC2-ColonMetLiver
3474	559575	1923.M08.gz43_252739	F	M00042460B:G12	UC2-ColonMetLiver
3475	496446	1923.A09.gz43_252743	F	M00042351D:D02	UC2-ColonMetLiver
3476	492110	1923.F09.gz43_252748	F	M00042447D:G10	UC2-ColonMetLiver
3477	495941	1923.G09.gz43_252749	F	M00042450A:D02	UC2-ColonMetLiver
3478	446621	1923.J09.gz43_252752	F	M00042455D:H08	UC2-ColonMetLiver
3479	562115	1923.N09.gz43_252756	F	M00042516A:A10	UC2-ColonMetLiver
3480	494300	1923.O09.gz43_252757	F	M00042517D:A12	UC2-ColonMetLiver
3481	451429	1923.A10.gz43_252759	F	M00042351D:F08	UC2-ColonMetLiver
3482	486912	1923.H10.gz43_252766	F	M00042452C:A09	UC2-ColonMetLiver
3483	456492	1923.J10.gz43_252768	F	M00042456A:C08	UC2-ColonMetLiver
3484	562060	1923.N10.gz43_252772	F	M00042516A:C08	UC2-ColonMetLiver
3485	4244	1923.P10.gz43_252774	F	M00042520A:F09	UC2-ColonMetLiver
3486	451429	1923.A11.gz43_252775	F	M00042351D:H05	UC2-ColonMetLiver

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SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
3487	449974	1923.H11.gz43_252782	F	M00042452C:C10	UC2-ColonMetLiver
3488	59512	1923.K11.gz43_252785	F	M00042458B:B08	UC2-ColonMetLiver
3489	550362	1923.M11.gz43_252787	F	M00042460C:A02	UC2-ColonMetLiver
3490	211273	1923.O11.gz43_252789	F	M00042517D:G04	UC2-ColonMetLiver
3491	450400	1923.I12.gz43_252799	F	M00042454A:F02	UC2-ColonMetLiver
3492	562627	1923.L12.gz43_252802	F	M00042459C:E06	UC2-ColonMetLiver
3493	494393	1923.B13.gz43_252808	F	M00042353D:B08	UC2-ColonMetLiver
3494	451049	1923.F13.gz43_252812	F	M00042448B:C04	UC2-ColonMetLiver
3495	558729	1923.K13.gz43_252817	F	M00042458B:G05	UC2-ColonMetLiver
3496	526733	1923.L13.gz43_252818	F	M00042459C:G02	UC2-ColonMetLiver
3497	558559	1923.N13.gz43_252820	F	M00042516B:E03	UC2-ColonMetLiver
3498	451518	1923.A14.gz43_252823	F	M00042352A:G05	UC2-ColonMetLiver
3499	349	1923.M14.gz43_252835	F	M00042460C:B02	UC2-ColonMetLiver
3500	456672	1923.A15.gz43_252839	F	M00042352A:G09	UC2-ColonMetLiver
3501	497101	1923.D15.gz43_252842	F	M00042443D:E01	UC2-ColonMetLiver
3502	488680	1923.H15.gz43_252846	F	M00042452D:C04	UC2-ColonMetLiver
3503	552236	1923.L15.gz43_252850	F	M00042459D:B07	UC2-ColonMetLiver
3504	450823	1923.B17.gz43_252872	F	M00042354B:A07	UC2-ColonMetLiver
3505	446263	1923.D17.gz43_252874	F	M00042444A:C10	UC2-ColonMetLiver
3506	492094	1923.H17.gz43_252878	F	M00042452D:G06	UC2-ColonMetLiver
3507	552581	1923.K17.gz43_252881	F	M00042458C:E06	UC2-ColonMetLiver
3508	494362	1923.G18.gz43_252893	F	M00042450C:B09	UC2-ColonMetLiver
3509	560420	1923.L18.gz43_252898	F	M00042459D:E03	UC2-ColonMetLiver
3510	562399	1923.N18.gz43_252900	F	M00042516C:C04	UC2-ColonMetLiver
3511	487522	1923.O18.gz43_252901	F	M00042518D:A08	UC2-ColonMetLiver
3512	498194	1923.A19.gz43_252903	F	M00042352B:F03	UC2-ColonMetLiver
3513	451126	1923.B19.gz43_252904	F	M00042354C:F04	UC2-ColonMetLiver
3514	450507	1923.E19.gz43_252907	F	M00042446B:G02	UC2-ColonMetLiver
3515	450723	1923.I19.gz43_252911	F	M00042454D:H10	UC2-ColonMetLiver
3516	492981	1923.J19.gz43_252912	F	M00042456C:H07	UC2-ColonMetLiver
3517	451054	1923.F20.gz43_252924	F	M00042448C:C09	UC2-ColonMetLiver
3518	453667	1923.J20.gz43_252928	F	M00042456D:B06	UC2-ColonMetLiver
3519	562588	1923.K20.gz43_252929	F	M00042458D:E06	UC2-ColonMetLiver
3520	527679	1923.L20.gz43_252930	F	M00042459D:G04	UC2-ColonMetLiver
3521	494133	1923.B22.gz43_252952	F	M00042355A:A12	UC2-ColonMetLiver
3522	492304	1923.I22.gz43_252959	F	M00042455A:G12	UC2-ColonMetLiver
3523	100821	1923.J22.gz43_252960	F	M00042456D:D07	UC2-ColonMetLiver
3524	562603	1923.M22.gz43_252963	F	M00042460C:G08	UC2-ColonMetLiver
3525	562275	1923.N22.gz43_252964	F	M00042516D:B11	UC2-ColonMetLiver
3526	451302	1923.A23.gz43_252967	F	M00042352C:G01	UC2-ColonMetLiver
3527	451126	1923.B23.gz43_252968	F	M00042355A:C03	UC2-ColonMetLiver
3528	494130	1923.C23.gz43_252969	F	M00042442A:A12	UC2-ColonMetLiver

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
3529	562587	1923.K23.gz43_252977	F	M00042459A:E04	UC2-ColonMetLiver
3530	562543	1923.M23.gz43_252979	F	M00042460C:H10	UC2-ColonMetLiver
3531	562398	1923.N23.gz43_252980	F	M00042516D:C01	UC2-ColonMetLiver
3532	497517	1923.P23.gz43_252982	F	M00043296A:E08	UC2-ColonMetLiver
3533	450902	1923.A24.gz43_252983	F	M00042352D:A11	UC2-ColonMetLiver
3534	499178	1923.C24.gz43_252985	F	M00042442A:G04	UC2-ColonMetLiver
3535	450507	1923.E24.gz43_252987	F	M00042446D:F04	UC2-ColonMetLiver
3536	448556	1923.F24.gz43_252988	F	M00042449A:H10	UC2-ColonMetLiver
3537	454575	1923.I24.gz43_252991	F	M00042455B:D05	UC2-ColonMetLiver
3538	275	1923.L24.gz43_252994	F	M00042460B:C06	UC2-ColonMetLiver
3539	452719	1934.C01.gz43_253001	F	M00043360C:E07	UC2-ColonMetLiver
3540	449842	1934.G02.gz43_253021	F	M00043369D:B01	UC2-ColonMetLiver
3541	489506	1934.N02.gz43_253028	F	M00043384D:D05	UC2-ColonMetLiver
3542	453893	1934.P02.gz43_253030	F	M00043388A:D05	UC2-ColonMetLiver
3543	452586	1934.A03.gz43_253031	F	M00043356B:E12	UC2-ColonMetLiver
3544	491177	1934.C03.gz43_253033	F	M00043360C:F11	UC2-ColonMetLiver
3545	496586	1934.M03.gz43_253043	F	M00043382C:D07	UC2-ColonMetLiver
3546	490393	1934.O03.gz43_253045	F	M00043387A:E02	UC2-ColonMetLiver
3547	450756	1934.D04.gz43_253050	F	M00043363B:A11	UC2-ColonMetLiver
3548	456492	1934.I04.gz43_253055	F	M00043373D:G04	UC2-ColonMetLiver
3549	490395	1934.O04.gz43_253061	F	M00043387A:E03	UC2-ColonMetLiver
3550	489275	1934.P04.gz43_253062	F	M00043388B:C02	UC2-ColonMetLiver
3551	489368	1934.C05.gz43_253065	F	M00043360D:D01	UC2-ColonMetLiver
3552	450756	1934.E05.gz43_253067	F	M00043364D:H11	UC2-ColonMetLiver
3553	496084	1934.K05.gz43_253073	F	M00043378D:D12	UC2-ColonMetLiver
3554	450193	1934.L05.gz43_253074	F	M00043380D:E10	UC2-ColonMetLiver
3555	499240	1934.M05.gz43_253075	F	M00043382C:G09	UC2-ColonMetLiver
3556	448230	1934.A06.gz43_253079	F	M00043356C:F03	UC2-ColonMetLiver
3557	455707	1934.H06.gz43_253086	F	M00043372B:B01	UC2-ColonMetLiver
3558	496760	1934.N06.gz43_253092	F	M00043385A:E01	UC2-ColonMetLiver
3559	447429	1934.A07.gz43_253095	F	M00043356C:H07	UC2-ColonMetLiver
3560	450551	1934.G07.gz43_253101	F	M00043369D:G10	UC2-ColonMetLiver
3561	451144	1934.J07.gz43_253104	F	M00043376B:C03	UC2-ColonMetLiver
3562	491402	1934.C08.gz43_253113	F	M00043361B:F02	UC2-ColonMetLiver
3563	449956	1934.E08.gz43_253115	F	M00043365A:C06	UC2-ColonMetLiver
3564	449959	1934.G08.gz43_253117	F	M00043370A:C08	UC2-ColonMetLiver
3565	560213	1934.I08.gz43_253119	F	M00043374A:E05	UC2-ColonMetLiver
3566	450482	1934.J08.gz43_253120	F	M00043376B:F06	UC2-ColonMetLiver
3567	449795	1934.B09.gz43_253128	F	M00043359B:A04	UC2-ColonMetLiver
3568	486856	1934.O09.gz43_253141	F	M00043387B:A03	UC2-ColonMetLiver
3569	450080	1934.C10.gz43_253145	F	M00043361D:A02	UC2-ColonMetLiver
3570	510272	1934.I10.gz43_253151	F	M00043374A:G04	UC2-ColonMetLiver

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
3571	450583	1934.A11.gz43_253159	F	M00043357A:G04	UC2-ColonMetLiver
3572	450193	1934.B11.gz43_253160	F	M00043359B:D06	UC2-ColonMetLiver
3573	134392	1934.M11.gz43_253171	F	M00043383B:F12	UC2-ColonMetLiver
3574	496234	1934.N11.gz43_253172	F	M00043385C:D06	UC2-ColonMetLiver
3575	487893	1934.A12.gz43_253175	F	M00043357B:B02	UC2-ColonMetLiver
3576	491507	1934.D12.gz43_253178	F	M00043363D:F07	UC2-ColonMetLiver
3577	233814	1934.J12.gz43_253184	F	M00043376D:A12	UC2-ColonMetLiver
3578	450189	1934.A13.gz43_253191	F	M00043357B:D01	UC2-ColonMetLiver
3579	488613	1934.E13.gz43_253195	F	M00043365B:C08	UC2-ColonMetLiver
3580	451011	1934.K13.gz43_253201	F	M00043379C:B09	UC2-ColonMetLiver
3581	450207	1934.G14.gz43_253213	F	M00043370B:D08	UC2-ColonMetLiver
3582	451185	1934.J14.gz43_253216	F	M00043376D:D12	UC2-ColonMetLiver
3583	551380	1934.L14.gz43_253218	F	M00043381B:E10	UC2-ColonMetLiver
3584	495143	1934.M14.gz43_253219	F	M00043383D:C07	UC2-ColonMetLiver
3585	487183	1934.O14.gz43_253221	F	M00043387C:A11	UC2-ColonMetLiver
3586	631526	1934.I15.gz43_253231	F	M00043374D:D07	UC2-ColonMetLiver
3587	449780	1934.E16.gz43_253243	F	M00043365C:A09	UC2-ColonMetLiver
3588	491492	1934.F16.gz43_253244	F	M00043368A:F03	UC2-ColonMetLiver
3589	494099	1934.K16.gz43_253249	F	M00043379D:A05	UC2-ColonMetLiver
3590	450819	1934.N16.gz43_253252	F	M00043386A:A11	UC2-ColonMetLiver
3591	488349	1934.P16.gz43_253254	F	M00043389D:B10	UC2-ColonMetLiver
3592	515423	1934.I17.gz43_253263	F	M00043374D:H09	UC2-ColonMetLiver
3593	490846	1934.C18.gz43_253273	F	M00043362C:E02	UC2-ColonMetLiver
3594	556511	1934.L18.gz43_253282	F	M00043381C:E10	UC2-ColonMetLiver
3595	487437	1934.M18.gz43_253283	F	M00043384B:A04	UC2-ColonMetLiver
3596	491240	1934.E19.gz43_253291	F	M00043365C:F06	UC2-ColonMetLiver
3597	452710	1934.H19.gz43_253294	F	M00043373A:G11	UC2-ColonMetLiver
3598	449959	1934.J20.gz43_253312	F	M00043377C:A11	UC2-ColonMetLiver
3599	449978	1934.P20.gz43_253318	F	M00043390B:C04	UC2-ColonMetLiver
3600	450242	1934.A21.gz43_253319	F	M00043358A:D02	UC2-ColonMetLiver
3601	451294	1934.I21.gz43_253327	F	M00043375A:E02	UC2-ColonMetLiver
3602	450080	1934.G22.gz43_253341	F	M00043371B:C10	UC2-ColonMetLiver
3603	451361	1934.J22.gz43_253344	F	M00043377D:E01	UC2-ColonMetLiver
3604	489207	1934.M22.gz43_253347	F	M00043384C:C02	UC2-ColonMetLiver
3605	488030	1934.O22.gz43_253349	F	M00043387D:B02	UC2-ColonMetLiver
3606	449908	1934.G23.gz43_253357	F	M00043371C:B02	UC2-ColonMetLiver
3607	450211	1934.O23.gz43_253365	F	M00043387D:D06	UC2-ColonMetLiver
3608	402916	1934.I24.gz43_253375	F	M00043375B:A04	UC2-ColonMetLiver
3609	494450	1934.J24.gz43_253376	F	M00043378B:B05	UC2-ColonMetLiver
3610	492627	1934.M24.gz43_253379	F	M00043384C:G01	UC2-ColonMetLiver
3611	550246	1947.J01.gz43_253404	F	M00054555D:C03	UC2-ColonMetLiver
3612	550952	1947.I06.gz43_253483	F	M00054555A:H09	UC2-ColonMetLiver

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SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
3613	555502	1947.A10.gz43_253539	F	M00054545C:B09	UC2-ColonMetLiver
3614	496586	1947.P21.gz43_253730	F	M00054566D:G08	UC2-ColonMetLiver
3615	515707	1947.G22.gz43_253737	F	M00054553D:E09	UC2-ColonMetLiver
3616	552092	1959.F03.gz43_253816	F	M00054631D:C02	UC2-ColonMetLiver
3617	549210	1959.M04.gz43_253839	F	M00054640B:C05	UC2-ColonMetLiver
3618	555923	1959.D08.gz43_253894	F	M00054629C:G06	UC2-ColonMetLiver
3619	461	1959.P08.gz43_253906	F	M00054644B:F02	UC2-ColonMetLiver
3620	551975	1959.D19.gz43_254070	F	M00054630B:A06	UC2-ColonMetLiver
3621	549516	1959.N22.gz43_254128	F	M00054642D:F11	UC2-ColonMetLiver
3622	555949	1959.K24.gz43_254157	F	M00054638D:F02	UC2-ColonMetLiver
3623	193991	1960.L03.gz43_254206	F	M00054661A:B03	UC2-ColonMetLiver
3624	561590	1960.I07.gz43_254267	F	M00054656C:E10	UC2-ColonMetLiver
3625	450867	1960.C12.gz43_254341	F	M00054648C:H10	UC2-ColonMetLiver
3626	264575	1960.N14.gz43_254384	F	M00054664D:A01	UC2-ColonMetLiver
3627	502683	1960.B23.gz43_254516	F	M00054647D:H02	UC2-ColonMetLiver
3628	452662	1960.E24.gz43_254535	F	M00054651D:D02	UC2-ColonMetLiver
3629	551269	1969.F03.gz43_254584	F	M00054674B:B03	UC2-ColonMetLiver
3630	579481	1969.C07.gz43_254645	F	M00054671A:H07	UC2-ColonMetLiver
3631	450624	1969.A10.gz43_254691	F	M00054668A:D01	UC2-ColonMetLiver
3632	415326	1969.N11.gz43_254720	F	M00054685D:D09	UC2-ColonMetLiver
3633	573733	1969.C24.gz43_254917	F	M00054671D:A12	UC2-ColonMetLiver
3634	551659	1983.D01.gz43_254934	F	M00054811D:F01	UC2-ColonMetLiver
3635	549816	1983.E06.gz43_255015	F	M00054812D:H05	UC2-ColonMetLiver
3636	557525	1983.F09.gz43_255064	F	M00054814A:F07	UC2-ColonMetLiver
3637	447405	1983.K11.gz43_255101	F	M00054823B:E07	UC2-ColonMetLiver
3638	494471	1983.C19.gz43_255221	F	M00054811B:H12	UC2-ColonMetLiver
3639	456520	1983.E19.gz43_255223	F	M00054813B:D11	UC2-ColonMetLiver
3640	533520	1984.N02.gz43_255344	F	M00054848B:E02	UC2-ColonMetLiver
3641	560984	1984.P06.gz43_255410	F	M00054851B:E03	UC2-ColonMetLiver
3642	562302	1984.G07.gz43_255417	F	M00054839D:F08	UC2-ColonMetLiver
3643	554196	1984.A12.gz43_255491	F	M00054831A:E11	UC2-ColonMetLiver
3644	557703	1984.G21.gz43_255641	F	M00054840D:B03	UC2-ColonMetLiver
3645	562243	1994.E15.gz43_255927	F	M00054877A:F01	UC2-ColonMetLiver
3646	559531	1994.A19.gz43_255987	F	M00054872A:H10	UC2-ColonMetLiver
3647	447483	1994.F22.gz43_256040	F	M00054878B:G03	UC2-ColonMetLiver
3648	549391	1994.K24.gz43_256077	F	M00054885C:G06	UC2-ColonMetLiver
3649	550204	1995.C02.gz43_256101	F	M00054893D:F07	UC2-ColonMetLiver
3650	554604	1995.K02.gz43_256109	F	M00054904A:F07	UC2-ColonMetLiver
3651	558326	1995.N02.gz43_256112	F	M00054908D:A07	UC2-ColonMetLiver
3652	557218	1995.A03.gz43_256115	F	M00054891D:H05	UC2-ColonMetLiver
3653	562152	1995.C03.gz43_256117	F	M00054893D:G09	UC2-ColonMetLiver
3654	562679	1995.F03.gz43_256120	F	M00054897C:F03	UC2-ColonMetLiver

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SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
3655	543855	1995.G03.gz43_256121	F	M00054898D:H12	UC2-ColonMetLiver
3656	555701	1995.J03.gz43_256124	F	M00054903A:G07	UC2-ColonMetLiver
3657	549376	1995.K03.gz43_256125	F	M00054904A:H10	UC2-ColonMetLiver
3658	522220	1995.M03.gz43_256127	F	M00054908A:F10	UC2-ColonMetLiver
3659	550710	1995.O03.gz43_256129	F	M00054922A:C11	UC2-ColonMetLiver
3660	562672	1995.E04.gz43_256135	F	M00054896B:E09	UC2-ColonMetLiver
3661	559088	1995.I04.gz43_256139	F	M00054901C:A04	UC2-ColonMetLiver
3662	447858	1995.D05.gz43_256150	F	M00054895B:D09	UC2-ColonMetLiver
3663	492256	1995.L05.gz43_256158	F	M00054906D:D06	UC2-ColonMetLiver
3664	550047	1995.B06.gz43_256164	F	M00054893A:F08	UC2-ColonMetLiver
3665	562579	1995.P06.gz43_256178	F	M00054923D:A08	UC2-ColonMetLiver
3666	556804	1995.F07.gz43_256184	F	M00054897D:E08	UC2-ColonMetLiver
3667	553102	1995.I07.gz43_256187	F	M00054901C:G01	UC2-ColonMetLiver
3668	559118	1995.P07.gz43_256194	F	M00054923D:D04	UC2-ColonMetLiver
3669	559554	1995.H08.gz43_256202	F	M00054900B:D12	UC2-ColonMetLiver
3670	510309	1995.K08.gz43_256205	F	M00054904C:B06	UC2-ColonMetLiver
3671	562492	1995.N08.gz43_256208	F	M00054910A:H12	UC2-ColonMetLiver
3672	553975	1995.O08.gz43_256209	F	M00054922B:A08	UC2-ColonMetLiver
3673	561525	1995.N09.gz43_256224	F	M00054910B:F07	UC2-ColonMetLiver
3674	150839	1995.O09.gz43_256225	F	M00054922B:A10	UC2-ColonMetLiver
3675	451049	1995.E10.gz43_256231	F	M00054896C:F01	UC2-ColonMetLiver
3676	560668	1995.H10.gz43_256234	F	M00054900B:G10	UC2-ColonMetLiver
3677	555260	1995.I10.gz43_256235	F	M00054901D:B01	UC2-ColonMetLiver
3678	555785	1995.J10.gz43_256236	F	M00054903C:F03	UC2-ColonMetLiver
3679	82864	1995.D11.gz43_256246	F	M00054895C:B07	UC2-ColonMetLiver
3680	559554	1995.H11.gz43_256250	F	M00054900C:B04	UC2-ColonMetLiver
3681	556404	1995.C12.gz43_256261	F	M00054894C:B11	UC2-ColonMetLiver
3682	516691	1995.H12.gz43_256266	F	M00054900C:C03	UC2-ColonMetLiver
3683	556499	1995.E13.gz43_256279	F	M00054896D:C01	UC2-ColonMetLiver
3684	453715	1995.F13.gz43_256280	F	M00054898A:G09	UC2-ColonMetLiver
3685	556753	1995.H13.gz43_256282	F	M00054900C:D08	UC2-ColonMetLiver
3686	549847	1995.J13.gz43_256284	F	M00054903C:G03	UC2-ColonMetLiver
3687	549822	1995.K13.gz43_256285	F	M00054904C:G09	UC2-ColonMetLiver
3688	489001	1995.L13.gz43_256286	F	M00054907B:E07	UC2-ColonMetLiver
3689	562989	1995.P13.gz43_256290	F	M00054924B:E10	UC2-ColonMetLiver
3690	555998	1995.A14.gz43_256291	F	M00054892C:G05	UC2-ColonMetLiver
3691	562106	1995.B14.gz43_256292	F	M00054893C:A06	UC2-ColonMetLiver
3692	557326	1995.E14.gz43_256295	F	M00054896D:C11	UC2-ColonMetLiver
3693	558935	1995.J14.gz43_256300	F	M00054903C:G04	UC2-ColonMetLiver
3694	399766	1995.L14.gz43_256302	F	M00054907B:F01	UC2-ColonMetLiver
3695	553976	1995.O14.gz43_256305	F	M00054922C:A11	UC2-ColonMetLiver
3696	554002	1995.B15.gz43_256308	F	M00054893C:A07	UC2-ColonMetLiver

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
3697	553691	1995.P15.gz43_256322	F	M00054924B:F07	UC2-ColonMetLiver
3698	556365	1995.B16.gz43_256324	F	M00054893C:B02	UC2-ColonMetLiver
3699	549228	1995.D16.gz43_256326	F	M00054895D:B02	UC2-ColonMetLiver
3700	553534	1995.G16.gz43_256329	F	M00054899C:D11	UC2-ColonMetLiver
3701	557004	1995.H16.gz43_256330	F	M00054900D:F11	UC2-ColonMetLiver
3702	555082	1995.M17.gz43_256351	F	M00054908C:A10	UC2-ColonMetLiver
3703	562714	1995.P17.gz43_256354	F	M00054924D:E01	UC2-ColonMetLiver
3704	552122	1995.D18.gz43_256358	F	M00054895D:C10	UC2-ColonMetLiver
3705	411272	1995.K18.gz43_256365	F	M00054904D:F07	UC2-ColonMetLiver
3706	454812	1995.A19.gz43_256371	F	M00054892D:D06	UC2-ColonMetLiver
3707	558177	1995.J19.gz43_256380	F	M00054903D:G01	UC2-ColonMetLiver
3708	556852	1995.P19.gz43_256386	F	M00054925A:B08	UC2-ColonMetLiver
3709	551463	1995.B20.gz43_256388	F	M00054893C:E04	UC2-ColonMetLiver
3710	558011	1995.G20.gz43_256393	F	M00054899D:C11	UC2-ColonMetLiver
3711	559088	1995.H20.gz43_256394	F	M00054901A:B04	UC2-ColonMetLiver
3712	595066	1995.I20.gz43_256395	F	M00054902B:G02	UC2-ColonMetLiver
3713	558868	1995.K20.gz43_256397	F	M00054904D:G04	UC2-ColonMetLiver
3714	458035	1995.F21.gz43_256408	F	M00054898B:D04	UC2-ColonMetLiver
3715	555837	1995.H21.gz43_256410	F	M00054901A:F01	UC2-ColonMetLiver
3716	452182	1995.I21.gz43_256411	F	M00054902C:A12	UC2-ColonMetLiver
3717	555967	1995.J21.gz43_256412	F	M00054903D:G10	UC2-ColonMetLiver
3718	474163	1995.B22.gz43_256420	F	M00054893C:G06	UC2-ColonMetLiver
3719	556169	1995.H22.gz43_256426	F	M00054901A:H11	UC2-ColonMetLiver
3720	558779	1995.C23.gz43_256437	F	M00054895B:A02	UC2-ColonMetLiver
3721	555830	1995.G23.gz43_256441	F	M00054899D:F07	UC2-ColonMetLiver
3722	974	1995.N23.gz43_256448	F	M00054921C:G01	UC2-ColonMetLiver
3723	556632	1995.B24.gz43_256452	F	M00054893D:D12	UC2-ColonMetLiver
3724	596809	1995.C24.gz43_256453	F	M00054895B:A08	UC2-ColonMetLiver
3725	495365	1995.N24.gz43_256464	F	M00054921C:G06	UC2-ColonMetLiver
3726	447639	1995.O24.gz43_256465	F	M00054923A:H02	UC2-ColonMetLiver
3727	418512	1996.K02.gz43_256517	F	M00054938A:B08	UC2-ColonMetLiver
3728	559728	1996.A04.gz43_256539	F	M00054925B:B01	UC2-ColonMetLiver
3729	67060	1996.P05.gz43_256570	F	M00054942C:B04	UC2-ColonMetLiver
3730	549171	1996.E06.gz43_256575	F	M00054931C:F10	UC2-ColonMetLiver
3731	562550	1996.O06.gz43_256585	F	M00054941C:G04	UC2-ColonMetLiver
3732	552566	1996.M08.gz43_256615	F	M00054939D:E03	UC2-ColonMetLiver
3733	473512	1996.B13.gz43_256684	F	M00054927C:C03	UC2-ColonMetLiver
3734	553535	1996.N16.gz43_256744	F	M00054940D:E06	UC2-ColonMetLiver
3735	555739	1996.I18.gz43_256771	F	M00054936B:G02	UC2-ColonMetLiver
3736	873	1996.N18.gz43_256776	F	M00054941A:A08	UC2-ColonMetLiver
3737	549805	1996.I19.gz43_256787	F	M00054936C:B08	UC2-ColonMetLiver
3738	550782	1996.B20.gz43_256796	F	M00054928A:C11	UC2-ColonMetLiver

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
3739	562106	1996.F20.gz43_256800	F	M00054933B:C02	UC2-ColonMetLiver
3740	481166	1996.P20.gz43_256810	F	M00054943A:H11	UC2-ColonMetLiver
3741	447585	1996.I21.gz43_256819	F	M00054936C:G03	UC2-ColonMetLiver
3742	561878	2005.K03.gz43_256919	F	M00054954A:F12	UC2-ColonMetLiver
3743	554833	2005.C07.gz43_256975	F	M00054945B:G09	UC2-ColonMetLiver
3744	126	2005.J08.gz43_256998	F	M00054952D:A11	UC2-ColonMetLiver
3745	496870	2005.I10.gz43_257029	F	M00054952A:B12	UC2-ColonMetLiver
3746	555526	2005.J12.gz43_257062	F	M00054953B:D07	UC2-ColonMetLiver
3747	562053	2005.A14.gz43_257085	F	M00054943D:F12	UC2-ColonMetLiver
3748	450524	2006.B02.gz43_257278	F	M00054961C:H07	UC2-ColonMetLiver
3749	557780	2006.P02.gz43_257292	F	M00054974C:A04	UC2-ColonMetLiver
3750	456795	2006.A03.gz43_257293	F	M00054960C:C03	UC2-ColonMetLiver
3751	556954	2006.E03.gz43_257297	F	M00054964A:F09	UC2-ColonMetLiver
3752	553021	2006.G03.gz43_257299	F	M00054966A:C11	UC2-ColonMetLiver
3753	494306	2006.H03.gz43_257300	F	M00054966D:H12	UC2-ColonMetLiver
3754	208278	2006.I03.gz43_257301	F	M00054967D:F08	UC2-ColonMetLiver
3755	504400	2006.L03.gz43_257304	F	M00054970C:C08	UC2-ColonMetLiver
3756	456203	2006.H05.gz43_257332	F	M00054967A:D11	UC2-ColonMetLiver
3757	599012	2006.C06.gz43_257343	F	M00054962C:D02	UC2-ColonMetLiver
3758	555394	2006.D06.gz43_257344	F	M00054963C:C08	UC2-ColonMetLiver
3759	593173	2006.G06.gz43_257347	F	M00054966A:D09	UC2-ColonMetLiver
3760	592941	2006.I06.gz43_257349	F	M00054968A:C11	UC2-ColonMetLiver
3761	554379	2006.K06.gz43_257351	F	M00054969D:D04	UC2-ColonMetLiver
3762	555103	2006.O06.gz43_257355	F	M00054973B:A10	UC2-ColonMetLiver
3763	556123	2006.J08.gz43_257382	F	M00054969A:E05	UC2-ColonMetLiver
3764	557421	2006.B09.gz43_257390	F	M00054961D:H08	UC2-ColonMetLiver
3765	450932	2006.K09.gz43_257399	F	M00054969D:G11	UC2-ColonMetLiver
3766	553204	2006.E10.gz43_257409	F	M00054964C:B07	UC2-ColonMetLiver
3767	556126	2006.G10.gz43_257411	F	M00054966A:G02	UC2-ColonMetLiver
3768	554204	2006.M11.gz43_257433	F	M00054971C:C11	UC2-ColonMetLiver
3769	556552	2006.P11.gz43_257436	F	M00054974D:C11	UC2-ColonMetLiver
3770	554524	2006.N12.gz43_257450	F	M00054972B:E06	UC2-ColonMetLiver
3771	559047	2006.P12.gz43_257452	F	M00054975A:C08	UC2-ColonMetLiver
3772	554365	2006.P15.gz43_257500	F	M00054975B:B06	UC2-ColonMetLiver
3773	556740	2006.A17.gz43_257517	F	M00054961B:D07	UC2-ColonMetLiver
3774	531145	2006.C17.gz43_257519	F	M00054963A:C12	UC2-ColonMetLiver
3775	557883	2006.F18.gz43_257538	F	M00054965C:C04	UC2-ColonMetLiver
3776	470386	2006.K18.gz43_257543	F	M00054970A:G03	UC2-ColonMetLiver
3777	596152	2006.M18.gz43_257545	F	M00054971C:H06	UC2-ColonMetLiver
3778	556552	2006.J19.gz43_257558	F	M00054969B:F12	UC2-ColonMetLiver
3779	560696	2006.C20.gz43_257567	F	M00054963A:E02	UC2-ColonMetLiver
3780	218113	2006.K20.gz43_257575	F	M00054970B:B02	UC2-ColonMetLiver

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SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
3781	557559	2006.L20.gz43_257576	F	M00054971A:D04	UC2-ColonMetLiver
3782	129715	2006.B22.gz43_257598	F	M00054962A:H07	UC2-ColonMetLiver
3783	553976	2006.C22.gz43_257599	F	M00054963A:G12	UC2-ColonMetLiver
3784	561984	2006.D22.gz43_257600	F	M00054964A:B09	UC2-ColonMetLiver
3785	497938	2006.G22.gz43_257603	F	M00054966D:C05	UC2-ColonMetLiver
3786	556951	2006.J22.gz43_257606	F	M00054969C:G09	UC2-ColonMetLiver
3787	553983	2006.N22.gz43_257610	F	M00054972D:A10	UC2-ColonMetLiver
3788	549579	2006.P22.gz43_257612	F	M00054975C:D08	UC2-ColonMetLiver
3789	555135	2006.B23.gz43_257614	F	M00054962B:A07	UC2-ColonMetLiver
3790	471257	2006.C23.gz43_257615	F	M00054963A:H04	UC2-ColonMetLiver
3791	557080	2006.J23.gz43_257622	F	M00054969C:H05	UC2-ColonMetLiver
3792	554643	2006.M23.gz43_257625	F	M00054971D:F04	UC2-ColonMetLiver
3793	558707	2007.A01.gz43_257645	F	M00054975C:E02	UC2-ColonMetLiver
3794	557420	2007.M02.gz43_257673	F	M00054993D:F04	UC2-ColonMetLiver
3795	482509	2007.A03.gz43_257677	F	M00054975C:G06	UC2-ColonMetLiver
3796	471827	2007.J03.gz43_257686	F	M00054989B:C11	UC2-ColonMetLiver
3797	556841	2007.K03.gz43_257687	F	M00054991B:E11	UC2-ColonMetLiver
3798	597957	2007.L03.gz43_257688	F	M00054992D:C12	UC2-ColonMetLiver
3799	556768	2007.C04.gz43_257695	F	M00054978C:E07	UC2-ColonMetLiver
3800	170450	2007.F04.gz43_257698	F	M00054983C:F05	UC2-ColonMetLiver
3801	555593	2007.I04.gz43_257701	F	M00054987B:D06	UC2-ColonMetLiver
3802	556839	2007.J04.gz43_257702	F	M00054989B:E04	UC2-ColonMetLiver
3803	551967	2007.A05.gz43_257709	F	M00054976A:A03	UC2-ColonMetLiver
3804	550814	2007.I05.gz43_257717	F	M00054987B:G05	UC2-ColonMetLiver
3805	557811	2007.L05.gz43_257720	F	M00054992D:F06	UC2-ColonMetLiver
3806	559580	2007.J06.gz43_257734	F	M00054989C:C12	UC2-ColonMetLiver
3807	554764	2007.N06.gz43_257738	F	M00054995B:G12	UC2-ColonMetLiver
3808	554395	2007.P06.gz43_257740	F	M00054997D:E01	UC2-ColonMetLiver
3809	555639	2007.H07.gz43_257748	F	M00054986B:D07	UC2-ColonMetLiver
3810	556561	2007.E08.gz43_257761	F	M00054981D:C06	UC2-ColonMetLiver
3811	454463	2007.I08.gz43_257765	F	M00054987C:A11	UC2-ColonMetLiver
3812	454463	2007.K08.gz43_257767	F	M00054991C:E01	UC2-ColonMetLiver
3813	562750	2007.C09.gz43_257775	F	M00054978D:H09	UC2-ColonMetLiver
3814	560652	2007.F09.gz43_257778	F	M00054983D:D05	UC2-ColonMetLiver
3815	553615	2007.I09.gz43_257781	F	M00054987C:B12	UC2-ColonMetLiver
3816	555512	2007.F10.gz43_257794	F	M00054984A:A05	UC2-ColonMetLiver
3817	556598	2007.I10.gz43_257797	F	M00054987C:G04	UC2-ColonMetLiver
3818	552188	2007.J10.gz43_257798	F	M00054990A:F10	UC2-ColonMetLiver
3819	558670	2007.A11.gz43_257805	F	M00054976C:A03	UC2-ColonMetLiver
3820	452682	2007.M11.gz43_257817	F	M00054994B:D11	UC2-ColonMetLiver
3821	553915	2007.P11.gz43_257820	F	M00055000A:H10	UC2-ColonMetLiver
3822	550886	2007.C12.gz43_257823	F	M00054979A:H10	UC2-ColonMetLiver

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SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
3823	553787	2007.H12.gz43_257828	F	M00054986C:D08	UC2-ColonMetLiver
3824	475624	2007.I12.gz43_257829	F	M00054987D:D01	UC2-ColonMetLiver
3825	554212	2007.O12.gz43_257835	F	M00054997A:C02	UC2-ColonMetLiver
3826	555883	2007.P12.gz43_257836	F	M00055000B:B04	UC2-ColonMetLiver
3827	458257	2007.B13.gz43_257838	F	M00054977C:A09	UC2-ColonMetLiver
3828	555197	2007.D13.gz43_257840	F	M00054980D:H07	UC2-ColonMetLiver
3829	553732	2007.P13.gz43_257852	F	M00055000B:F02	UC2-ColonMetLiver
3830	556416	2007.B14.gz43_257854	F	M00054977C:B08	UC2-ColonMetLiver
3831	501056	2007.B15.gz43_257870	F	M00054977C:D08	UC2-ColonMetLiver
3832	552437	2007.E15.gz43_257873	F	M00054982C:A02	UC2-ColonMetLiver
3833	555658	2007.L15.gz43_257880	F	M00054993B:H06	UC2-ColonMetLiver
3834	476732	2007.O15.gz43_257883	F	M00054997A:G11	UC2-ColonMetLiver
3835	556690	2007.B16.gz43_257886	F	M00054977C:D12	UC2-ColonMetLiver
3836	557615	2007.H16.gz43_257892	F	M00054986D:D11	UC2-ColonMetLiver
3837	543429	2007.G17.gz43_257907	F	M00054985C:B12	UC2-ColonMetLiver
3838	554793	2007.H17.gz43_257908	F	M00054986D:E03	UC2-ColonMetLiver
3839	556396	2007.I17.gz43_257909	F	M00054988C:B08	UC2-ColonMetLiver
3840	556288	2007.J17.gz43_257910	F	M00054990C:A08	UC2-ColonMetLiver
3841	552055	2007.L17.gz43_257912	F	M00054993C:C10	UC2-ColonMetLiver
3842	549516	2007.P17.gz43_257916	F	M00055000C:F08	UC2-ColonMetLiver
3843	561112	2007.B18.gz43_257918	F	M00054977C:F09	UC2-ColonMetLiver
3844	557054	2007.C18.gz43_257919	F	M00054979B:G12	UC2-ColonMetLiver
3845	483410	2007.D18.gz43_257920	F	M00054981B:B09	UC2-ColonMetLiver
3846	598589	2007.G18.gz43_257923	F	M00054985C:D04	UC2-ColonMetLiver
3847	559096	2007.O18.gz43_257931	F	M00054997B:F10	UC2-ColonMetLiver
3848	556759	2007.I19.gz43_257941	F	M00054988C:G02	UC2-ColonMetLiver
3849	555277	2007.K19.gz43_257943	F	M00054992A:C08	UC2-ColonMetLiver
3850	551694	2007.B20.gz43_257950	F	M00054977D:B06	UC2-ColonMetLiver
3851	562655	2007.E20.gz43_257953	F	M00054983A:F08	UC2-ColonMetLiver
3852	559053	2007.H20.gz43_257956	F	M00054987A:A09	UC2-ColonMetLiver
3853	556286	2007.J20.gz43_257958	F	M00054990D:A06	UC2-ColonMetLiver
3854	551798	2007.K20.gz43_257959	F	M00054992A:D11	UC2-ColonMetLiver
3855	549214	2007.N20.gz43_257962	F	M00054996A:D10	UC2-ColonMetLiver
3856	467293	2007.D21.gz43_257968	F	M00054981B:H12	UC2-ColonMetLiver
3857	503452	2007.J21.gz43_257974	F	M00054990D:F04	UC2-ColonMetLiver
3858	556019	2007.L22.gz43_257992	F	M00054993C:G12	UC2-ColonMetLiver
3859	560748	2007.G23.gz43_258003	F	M00054985D:E03	UC2-ColonMetLiver
3860	562323	2007.L23.gz43_258008	F	M00054993C:H05	UC2-ColonMetLiver
3861	2284	2007.A24.gz43_258013	F	M00054976D:F06	UC2-ColonMetLiver
3862	481243	2007.D24.gz43_258016	F	M00054981C:A11	UC2-ColonMetLiver
3863	555958	2007.N24.gz43_258026	F	M00054996B:C11	UC2-ColonMetLiver
3864	560984	2007.O24.gz43_258027	F	M00054997C:H03	UC2-ColonMetLiver

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SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
3865	555967	2008.N01.gz43_258044	F	M00055016D:C07	UC2-ColonMetLiver
3866	556488	2008.P01.gz43_258046	F	M00055019B:B11	UC2-ColonMetLiver
3867	553064	2008.A02.gz43_258047	F	M00055001A:B10	UC2-ColonMetLiver
3868	552006	2008.D02.gz43_258050	F	M00055005A:C07	UC2-ColonMetLiver
3869	559676	2008.E02.gz43_258051	F	M00055006A:D01	UC2-ColonMetLiver
3870	557308	2008.J02.gz43_258056	F	M00055011B:F09	UC2-ColonMetLiver
3871	549723	2008.N02.gz43_258060	F	M00055016D:C11	UC2-ColonMetLiver
3872	549912	2008.B03.gz43_258064	F	M00055002B:E07	UC2-ColonMetLiver
3873	551444	2008.G03.gz43_258069	F	M00055008C:F09	UC2-ColonMetLiver
3874	557240	2008.P03.gz43_258078	F	M00055019B:H10	UC2-ColonMetLiver
3875	559011	2008.C04.gz43_258081	F	M00055003C:E08	UC2-ColonMetLiver
3876	555701	2008.D04.gz43_258082	F	M00055005A:E02	UC2-ColonMetLiver
3877	556115	2008.P04.gz43_258094	F	M00055019C:C01	UC2-ColonMetLiver
3878	556042	2008.B05.gz43_258096	F	M00055002B:G03	UC2-ColonMetLiver
3879	558212	2008.E05.gz43_258099	F	M00055006B:A09	UC2-ColonMetLiver
3880	554932	2008.G05.gz43_258101	F	M00055008C:H10	UC2-ColonMetLiver
3881	548858	2008.J05.gz43_258104	F	M00055011C:E04	UC2-ColonMetLiver
3882	605117	2008.L05.gz43_258106	F	M00055014B:E08	UC2-ColonMetLiver
3883	560525	2008.M05.gz43_258107	F	M00055015D:C09	UC2-ColonMetLiver
3884	597780	2008.I06.gz43_258119	F	M00055010C:C10	UC2-ColonMetLiver
3885	411113	2008.N06.gz43_258124	F	M00055017A:A11	UC2-ColonMetLiver
3886	552674	2008.E07.gz43_258131	F	M00055006B:C08	UC2-ColonMetLiver
3887	495942	2008.O07.gz43_258141	F	M00055018C:C06	UC2-ColonMetLiver
3888	34381	2008.F08.gz43_258148	F	M00055007C:D01	UC2-ColonMetLiver
3889	549195	2008.H08.gz43_258150	F	M00055009C:F06	UC2-ColonMetLiver
3890	554084	2008.L08.gz43_258154	F	M00055014C:F05	UC2-ColonMetLiver
3891	557121	2008.P08.gz43_258158	F	M00055019C:G06	UC2-ColonMetLiver
3892	554693	2008.A09.gz43_258159	F	M00055001A:G05	UC2-ColonMetLiver
3893	134237	2008.C09.gz43_258161	F	M00055003D:F09	UC2-ColonMetLiver
3894	594994	2008.H09.gz43_258166	F	M00055009C:F07	UC2-ColonMetLiver
3895	555371	2008.I09.gz43_258167	F	M00055010D:A02	UC2-ColonMetLiver
3896	347057	2008.E10.gz43_258179	F	M00055006B:E05	UC2-ColonMetLiver
3897	558378	2008.H10.gz43_258182	F	M00055009D:D12	UC2-ColonMetLiver
3898	497086	2008.K10.gz43_258185	F	M00055013B:B07	UC2-ColonMetLiver
3899	554379	2008.B11.gz43_258192	F	M00055002D:A07	UC2-ColonMetLiver
3900	451118	2008.L11.gz43_258202	F	M00055014D:A11	UC2-ColonMetLiver
3901	557059	2008.M11.gz43_258203	F	M00055015D:G05	UC2-ColonMetLiver
3902	604179	2008.O11.gz43_258205	F	M00055018D:D01	UC2-ColonMetLiver
3903	556487	2008.P11.gz43_258206	F	M00055019D:B02	UC2-ColonMetLiver
3904	562550	2008.B12.gz43_258208	F	M00055002D:E04	UC2-ColonMetLiver
3905	556530	2008.L12.gz43_258218	F	M00055015A:C08	UC2-ColonMetLiver
3906	524897	2008.O12.gz43_258221	F	M00055018D:E05	UC2-ColonMetLiver

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SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
3907	480960	2008.F13.gz43_258228	F	M00055007D:D11	UC2-ColonMetLiver
3908	560563	2008.G13.gz43_258229	F	M00055008D:F05	UC2-ColonMetLiver
3909	555512	2008.I13.gz43_258231	F	M00055010D:D08	UC2-ColonMetLiver
3910	143218	2008.L13.gz43_258234	F	M00055015A:E04	UC2-ColonMetLiver
3911	556616	2008.N13.gz43_258236	F	M00055017C:C12	UC2-ColonMetLiver
3912	552613	2008.A14.gz43_258239	F	M00055001B:H05	UC2-ColonMetLiver
3913	555658	2008.I14.gz43_258247	F	M00055010D:E08	UC2-ColonMetLiver
3914	516018	2008.K14.gz43_258249	F	M00055013B:H01	UC2-ColonMetLiver
3915	604859	2008.M14.gz43_258251	F	M00055016A:E04	UC2-ColonMetLiver
3916	553967	2008.A15.gz43_258255	F	M00055001C:A11	UC2-ColonMetLiver
3917	600021	2008.I15.gz43_258263	F	M00055010D:F11	UC2-ColonMetLiver
3918	437580	2008.B16.gz43_258272	F	M00055003A:D11	UC2-ColonMetLiver
3919	556616	2008.D16.gz43_258274	F	M00055005C:G04	UC2-ColonMetLiver
3920	551268	2008.O16.gz43_258285	F	M00055018D:H03	UC2-ColonMetLiver
3921	335714	2008.A17.gz43_258287	F	M00055001C:C10	UC2-ColonMetLiver
3922	460445	2008.D17.gz43_258290	F	M00055005D:B08	UC2-ColonMetLiver
3923	362109	2008.I17.gz43_258295	F	M00055011A:B11	UC2-ColonMetLiver
3924	556320	2008.J17.gz43_258296	F	M00055012B:A10	UC2-ColonMetLiver
3925	931	2008.L17.gz43_258298	F	M00055015B:A04	UC2-ColonMetLiver
3926	494300	2008.M17.gz43_258299	F	M00055016B:E02	UC2-ColonMetLiver
3927	453908	2008.N17.gz43_258300	F	M00055017D:D05	UC2-ColonMetLiver
3928	549690	2008.A18.gz43_258303	F	M00055001C:G07	UC2-ColonMetLiver
3929	555949	2008.B18.gz43_258304	F	M00055003A:G04	UC2-ColonMetLiver
3930	555289	2008.D18.gz43_258306	F	M00055005D:C11	UC2-ColonMetLiver
3931	550497	2008.F18.gz43_258308	F	M00055008B:E08	UC2-ColonMetLiver
3932	559464	2008.I18.gz43_258311	F	M00055011A:C06	UC2-ColonMetLiver
3933	601219	2008.B19.gz43_258320	F	M00055003A:H01	UC2-ColonMetLiver
3934	522762	2008.F19.gz43_258324	F	M00055008B:F03	UC2-ColonMetLiver
3935	558530	2008.F20.gz43_258340	F	M00055008B:F04	UC2-ColonMetLiver
3936	551656	2008.H20.gz43_258342	F	M00055010A:H05	UC2-ColonMetLiver
3937	554245	2008.N20.gz43_258348	F	M00055017D:E08	UC2-ColonMetLiver
3938	562142	2008.P20.gz43_258350	F	M00055020A:G11	UC2-ColonMetLiver
3939	555639	2008.B21.gz43_258352	F	M00055003B:E07	UC2-ColonMetLiver
3940	388688	2008.I21.gz43_258359	F	M00055011A:F06	UC2-ColonMetLiver
3941	476438	2008.J21.gz43_258360	F	M00055012B:H12	UC2-ColonMetLiver
3942	560097	2008.L21.gz43_258362	F	M00055015B:E09	UC2-ColonMetLiver
3943	557308	2008.M21.gz43_258363	F	M00055016C:G04	UC2-ColonMetLiver
3944	553523	2008.D22.gz43_258370	F	M00055005D:G04	UC2-ColonMetLiver
3945	460169	2008.H22.gz43_258374	F	M00055010B:A06	UC2-ColonMetLiver
3946	558744	2008.B23.gz43_258384	F	M00055003B:G11	UC2-ColonMetLiver
3947	495984	2008.I23.gz43_258391	F	M00055011A:G12	UC2-ColonMetLiver
3948	497513	2008.H24.gz43_258406	F	M00055010B:C11	UC2-ColonMetLiver

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
3949	557910	2017.B02.gz43_258434	F	M00055020D:G06	UC2-ColonMetLiver
3950	557603	2017.I02.gz43_258441	F	M00055029C:D05	UC2-ColonMetLiver
3951	523495	2017.M03.gz43_258461	F	M00055034B:G04	UC2-ColonMetLiver
3952	390017	2017.H04.gz43_258472	F	M00055028C:D05	UC2-ColonMetLiver
3953	610986	2017.B05.gz43_258482	F	M00055021A:F08	UC2-ColonMetLiver
3954	551884	2017.E05.gz43_258485	F	M00055024D:E09	UC2-ColonMetLiver
3955	559447	2017.E06.gz43_258501	F	M00055024D:F07	UC2-ColonMetLiver
3956	322123	2017.F06.gz43_258502	F	M00055026A:G08	UC2-ColonMetLiver
3957	556258	2017.H06.gz43_258504	F	M00055028D:A08	UC2-ColonMetLiver
3958	561279	2017.K06.gz43_258507	F	M00055032B:D08	UC2-ColonMetLiver
3959	550815	2017.E07.gz43_258517	F	M00055024D:G09	UC2-ColonMetLiver
3960	561935	2017.D08.gz43_258532	F	M00055023C:G11	UC2-ColonMetLiver
3961	557733	2017.J08.gz43_258538	F	M00055031B:E05	UC2-ColonMetLiver
3962	556852	2017.N09.gz43_258558	F	M00055035D:E07	UC2-ColonMetLiver
3963	557049	2017.D10.gz43_258564	F	M00055023D:G02	UC2-ColonMetLiver
3964	560250	2017.E10.gz43_258565	F	M00055025A:D11	UC2-ColonMetLiver
3965	560294	2017.H10.gz43_258568	F	M00055028D:E10	UC2-ColonMetLiver
3966	481930	2017.D11.gz43_258580	F	M00055024A:B04	UC2-ColonMetLiver
3967	550986	2017.E11.gz43_258581	F	M00055025B:A03	UC2-ColonMetLiver
3968	560621	2017.H11.gz43_258584	F	M00055029A:A02	UC2-ColonMetLiver
3969	549599	2017.I11.gz43_258585	F	M00055030B:E03	UC2-ColonMetLiver
3970	558004	2017.J11.gz43_258586	F	M00055031B:H08	UC2-ColonMetLiver
3971	562590	2017.L12.gz43_258604	F	M00055033B:H01	UC2-ColonMetLiver
3972	558755	2017.N12.gz43_258606	F	M00055035D:F09	UC2-ColonMetLiver
3973	556458	2017.M13.gz43_258621	F	M00055034D:A10	UC2-ColonMetLiver
3974	450059	2017.B14.gz43_258626	F	M00055021B:G09	UC2-ColonMetLiver
3975	557353	2017.C14.gz43_258627	F	M00055022C:B12	UC2-ColonMetLiver
3976	560898	2017.D14.gz43_258628	F	M00055024A:C07	UC2-ColonMetLiver
3977	461850	2017.I14.gz43_258633	F	M00055030B:H07	UC2-ColonMetLiver
3978	552848	2017.J14.gz43_258634	F	M00055031C:B11	UC2-ColonMetLiver
3979	552891	2017.F16.gz43_258662	F	M00055026C:E07	UC2-ColonMetLiver
3980	454483	2017.G16.gz43_258663	F	M00055027D:E08	UC2-ColonMetLiver
3981	508671	2017.D18.gz43_258692	F	M00055024B:E02	UC2-ColonMetLiver
3982	456183	2017.N18.gz43_258702	F	M00055036A:H10	UC2-ColonMetLiver
3983	557578	2017.O18.gz43_258703	F	M00055037C:D01	UC2-ColonMetLiver
3984	561868	2017.D19.gz43_258708	F	M00055024B:E03	UC2-ColonMetLiver
3985	556856	2017.F19.gz43_258710	F	M00055026D:E12	UC2-ColonMetLiver
3986	557010	2017.L19.gz43_258716	F	M00055033D:D03	UC2-ColonMetLiver
3987	529356	2017.D21.gz43_258740	F	M00055024B:E06	UC2-ColonMetLiver
3988	557883	2017.L21.gz43_258748	F	M00055033D:G01	UC2-ColonMetLiver
3989	549114	2017.B22.gz43_258754	F	M00055021D:F06	UC2-ColonMetLiver
3990	556933	2017.D22.gz43_258756	F	M00055024B:F02	UC2-ColonMetLiver

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
3991	494314	2017.F22.gz43_258758	F	M00055027A:E04	UC2-ColonMetLiver
3992	408586	2017.M22.gz43_258765	F	M00055035B:D11	UC2-ColonMetLiver
3993	460078	2017.L23.gz43_258780	F	M00055034A:G01	UC2-ColonMetLiver
3994	561836	2017.N23.gz43_258782	F	M00055036B:H02	UC2-ColonMetLiver
3995	558185	2043.D03.gz43_259228	F	M00055222D:B11	UC2-ColonMetLiver
3996	550632	2043.F03.gz43_259230	F	M00055225C:E08	UC2-ColonMetLiver
3997	551677	2043.J03.gz43_259234	F	M00055230A:H01	UC2-ColonMetLiver
3998	451720	2043.N03.gz43_259238	F	M00055236C:E05	UC2-ColonMetLiver
3999	559447	2043.L05.gz43_259268	F	M00055233C:F09	UC2-ColonMetLiver
4000	558230	2043.P05.gz43_259272	F	M00055239B:C05	UC2-ColonMetLiver
4001	554627	2043.A06.gz43_259273	F	M00055219B:B04	UC2-ColonMetLiver
4002	558422	2043.N06.gz43_259286	F	M00055236D:E04	UC2-ColonMetLiver
4003	558679	2043.G08.gz43_259311	F	M00055226C:H05	UC2-ColonMetLiver
4004	491240	2043.F09.gz43_259326	F	M00055225D:G11	UC2-ColonMetLiver
4005	550815	2043.H09.gz43_259328	F	M00055227C:D02	UC2-ColonMetLiver
4006	481362	2043.P10.gz43_259352	F	M00055239C:F08	UC2-ColonMetLiver
4007	467710	2043.C11.gz43_259355	F	M00055221D:H08	UC2-ColonMetLiver
4008	557965	2043.B12.gz43_259370	F	M00055220D:G07	UC2-ColonMetLiver
4009	380127	2043.C12.gz43_259371	F	M00055222A:A06	UC2-ColonMetLiver
4010	374281	2043.M12.gz43_259381	F	M00055235B:C01	UC2-ColonMetLiver
4011	464067	2043.C13.gz43_259387	F	M00055222A:C08	UC2-ColonMetLiver
4012	552521	2043.D13.gz43_259388	F	M00055223B:C04	UC2-ColonMetLiver
4013	552019	2043.P13.gz43_259400	F	M00055239D:C01	UC2-ColonMetLiver
4014	556790	2043.A14.gz43_259401	F	M00055219C:C10	UC2-ColonMetLiver
4015	557411	2043.K14.gz43_259411	F	M00055232C:D04	UC2-ColonMetLiver
4016	378459	2043.L15.gz43_259428	F	M00055233D:G11	UC2-ColonMetLiver
4017	550571	2043.H16.gz43_259440	F	M00055227D:E07	UC2-ColonMetLiver
4018	557676	2043.P16.gz43_259448	F	M00055239D:G04	UC2-ColonMetLiver
4019	558652	2043.A17.gz43_259449	F	M00055219C:H06	UC2-ColonMetLiver
4020	559053	2043.I17.gz43_259457	F	M00055229C:D01	UC2-ColonMetLiver
4021	552086	2043.C18.gz43_259467	F	M00055222B:A01	UC2-ColonMetLiver
4022	552430	2043.L18.gz43_259476	F	M00055234A:G12	UC2-ColonMetLiver
4023	562317	2043.P19.gz43_259496	F	M00055240A:B07	UC2-ColonMetLiver
4024	543540	2043.I22.gz43_259537	F	M00055229D:D07	UC2-ColonMetLiver
4025	489275	2043.F23.gz43_259550	F	M00055226C:A11	UC2-ColonMetLiver
4026	450193	2043.M23.gz43_259557	F	M00055236B:C07	UC2-ColonMetLiver
4027	557656	2043.O23.gz43_259559	F	M00055238D:D10	UC2-ColonMetLiver
4028	559764	2043.D24.gz43_259564	F	M00055223D:H03	UC2-ColonMetLiver
4029	560717	2043.E24.gz43_259565	F	M00055225B:H01	UC2-ColonMetLiver
4030	552249	2043.P24.gz43_259576	F	M00055240B:E12	UC2-ColonMetLiver
4031	556829	2044.G02.gz43_259603	F	M00055248D:B12	UC2-ColonMetLiver
4032	558093	2044.A03.gz43_259613	F	M00055240C:A03	UC2-ColonMetLiver

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SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
4033	616134	2044.B03.gz43_259614	F	M00055241D:F10	UC2-ColonMetLiver
4034	558355	2044.E03.gz43_259617	F	M00055245D:A04	UC2-ColonMetLiver
4035	558785	2044.J03.gz43_259622	F	M00055252B:D07	UC2-ColonMetLiver
4036	607430	2044.F04.gz43_259634	F	M00055247B:A11	UC2-ColonMetLiver
4037	558512	2044.L04.gz43_259640	F	M00055255B:F05	UC2-ColonMetLiver
4038	488574	2044.N04.gz43_259642	F	M00055257D:A11	UC2-ColonMetLiver
4039	558098	2044.P04.gz43_259644	F	M00055260B:A05	UC2-ColonMetLiver
4040	557389	2044.F05.gz43_259650	F	M00055247C:B01	UC2-ColonMetLiver
4041	557928	2044.K05.gz43_259655	F	M00055254A:E02	UC2-ColonMetLiver
4042	551305	2044.E06.gz43_259665	F	M00055245D:D01	UC2-ColonMetLiver
4043	504415	2044.H06.gz43_259668	F	M00055250B:A05	UC2-ColonMetLiver
4044	549052	2044.I06.gz43_259669	F	M00055251C:D01	UC2-ColonMetLiver
4045	138927	2044.O06.gz43_259675	F	M00055259A:G06	UC2-ColonMetLiver
4046	554246	2044.N07.gz43_259690	F	M00055257D:E02	UC2-ColonMetLiver
4047	159419	2044.J08.gz43_259702	F	M00055252C:E02	UC2-ColonMetLiver
4048	460049	2044.P08.gz43_259708	F	M00055260B:H06	UC2-ColonMetLiver
4049	560317	2044.D09.gz43_259712	F	M00055244D:C07	UC2-ColonMetLiver
4050	560317	2044.E09.gz43_259713	F	M00055246A:C01	UC2-ColonMetLiver
4051	552357	2044.H09.gz43_259716	F	M00055250B:G09	UC2-ColonMetLiver
4052	560144	2044.P09.gz43_259724	F	M00055260C:A11	UC2-ColonMetLiver
4053	560669	2044.E10.gz43_259729	F	M00055246A:E10	UC2-ColonMetLiver
4054	423884	2044.N10.gz43_259738	F	M00055258A:C07	UC2-ColonMetLiver
4055	523732	2044.I11.gz43_259749	F	M00055251C:H07	UC2-ColonMetLiver
4056	493359	2044.K11.gz43_259751	F	M00055254C:A06	UC2-ColonMetLiver
4057	560204	2044.E14.gz43_259793	F	M00055246B:C04	UC2-ColonMetLiver
4058	558461	2044.F14.gz43_259794	F	M00055248A:F10	UC2-ColonMetLiver
4059	447380	2044.J14.gz43_259798	F	M00055252D:C10	UC2-ColonMetLiver
4060	558559	2044.O14.gz43_259803	F	M00055259B:G11	UC2-ColonMetLiver
4061	450025	2044.A15.gz43_259805	F	M00055241A:C06	UC2-ColonMetLiver
4062	484086	2044.E15.gz43_259809	F	M00055246B:D10	UC2-ColonMetLiver
4063	558861	2044.K15.gz43_259815	F	M00055254D:B10	UC2-ColonMetLiver
4064	486787	2044.C16.gz43_259823	F	M00055243D:C06	UC2-ColonMetLiver
4065	562256	2044.L16.gz43_259832	F	M00055256A:D12	UC2-ColonMetLiver
4066	561579	2044.E17.gz43_259841	F	M00055246C:F08	UC2-ColonMetLiver
4067	560205	2044.J17.gz43_259846	F	M00055253A:C07	UC2-ColonMetLiver
4068	558134	2044.M17.gz43_259849	F	M00055257B:B10	UC2-ColonMetLiver
4069	488143	2044.H18.gz43_259860	F	M00055251A:B09	UC2-ColonMetLiver
4070	500737	2044.I18.gz43_259861	F	M00055251D:H11	UC2-ColonMetLiver
4071	238121	2044.C20.gz43_259887	F	M00055244A:C06	UC2-ColonMetLiver
4072	629002	2044.D20.gz43_259888	F	M00055245B:H01	UC2-ColonMetLiver
4073	562256	2044.L21.gz43_259912	F	M00055256B:C07	UC2-ColonMetLiver
4074	541784	2044.B22.gz43_259918	F	M00055242D:E02	UC2-ColonMetLiver

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
4075	560507	2044.D22.gz43_259920	F	M00055245C:D04	UC2-ColonMetLiver
4076	555340	2044.F22.gz43_259922	F	M00055248C:B11	UC2-ColonMetLiver
4077	560059	2044.G22.gz43_259923	F	M00055249C:B12	UC2-ColonMetLiver
4078	494130	2044.K24.gz43_259959	F	M00055255A:F11	UC2-ColonMetLiver
4079	557928	2044.L24.gz43_259960	F	M00055256B:G05	UC2-ColonMetLiver
4080	559321	2053.K01.gz43_259984	F	M00055272D:E04	UC2-ColonMetLiver
4081	34381	2053.E02.gz43_259994	F	M00055265A:G01	UC2-ColonMetLiver
4082	556447	2053.H02.gz43_259997	F	M00055268B:D12	UC2-ColonMetLiver
4083	555564	2053.E03.gz43_260010	F	M00055265A:G07	UC2-ColonMetLiver
4084	558360	2053.M03.gz43_260018	F	M00055275B:H06	UC2-ColonMetLiver
4085	558120	2053.B05.gz43_260039	F	M00055262B:A11	UC2-ColonMetLiver
4086	511276	2053.D05.gz43_260041	F	M00055264A:F03	UC2-ColonMetLiver
4087	550074	2053.F05.gz43_260043	F	M00055266B:C12	UC2-ColonMetLiver
4088	558867	2053.L05.gz43_260049	F	M00055274C:C06	UC2-ColonMetLiver
4089	555564	2053.N05.gz43_260051	F	M00055277D:A02	UC2-ColonMetLiver
4090	551798	2053.O05.gz43_260052	F	M00055279A:E03	UC2-ColonMetLiver
4091	556019	2053.D08.gz43_260089	F	M00055264B:E06	UC2-ColonMetLiver
4092	480960	2053.O09.gz43_260116	F	M00055279B:D02	UC2-ColonMetLiver
4093	478087	2053.C10.gz43_260120	F	M00055263C:D02	UC2-ColonMetLiver
4094	450507	2053.D10.gz43_260121	F	M00055264B:H12	UC2-ColonMetLiver
4095	512721	2053.E10.gz43_260122	F	M00055265C:A04	UC2-ColonMetLiver
4096	558052	2053.B11.gz43_260135	F	M00055262C:B08	UC2-ColonMetLiver
4097	550863	2053.A12.gz43_260150	F	M00055261B:G12	UC2-ColonMetLiver
4098	560957	2053.L12.gz43_260161	F	M00055274D:A11	UC2-ColonMetLiver
4099	560621	2053.M12.gz43_260162	F	M00055275D:E12	UC2-ColonMetLiver
4100	450242	2053.C13.gz43_260168	F	M00055263C:F10	UC2-ColonMetLiver
4101	446557	2053.B14.gz43_260183	F	M00055262C:F05	UC2-ColonMetLiver
4102	560678	2053.E14.gz43_260186	F	M00055265C:E01	UC2-ColonMetLiver
4103	557561	2053.F14.gz43_260187	F	M00055266D:C09	UC2-ColonMetLiver
4104	505858	2053.C15.gz43_260200	F	M00055263C:G09	UC2-ColonMetLiver
4105	557561	2053.E15.gz43_260202	F	M00055265C:F01	UC2-ColonMetLiver
4106	448450	2053.H15.gz43_260205	F	M00055268D:G09	UC2-ColonMetLiver
4107	475578	2053.I15.gz43_260206	F	M00055270D:B05	UC2-ColonMetLiver
4108	549052	2053.L15.gz43_260209	F	M00055274D:B10	UC2-ColonMetLiver
4109	562871	2053.M15.gz43_260210	F	M00055275D:H08	UC2-ColonMetLiver
4110	558263	2053.L18.gz43_260257	F	M00055274D:C10	UC2-ColonMetLiver
4111	560538	2053.O18.gz43_260260	F	M00055280A:C09	UC2-ColonMetLiver
4112	554000	2053.C19.gz43_260264	F	M00055263D:C03	UC2-ColonMetLiver
4113	128962	2053.A20.gz43_260278	F	M00055261D:D09	UC2-ColonMetLiver
4114	560278	2053.M20.gz43_260290	F	M00055276B:C09	UC2-ColonMetLiver
4115	420892	2053.F21.gz43_260299	F	M00055267A:D01	UC2-ColonMetLiver
4116	558513	2053.P21.gz43_260309	F	M00055281A:F08	UC2-ColonMetLiver

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SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
4117	511847	2053.F22.gz43_260315	F	M00055267A:G11	UC2-ColonMetLiver
4118	481958	2053.P22.gz43_260325	F	M00055281B:D04	UC2-ColonMetLiver
4119	561666	2053.F24.gz43_260347	F	M00055267B:B06	UC2-ColonMetLiver
4120	553665	2053.I24.gz43_260350	F	M00055271B:C01	UC2-ColonMetLiver
4121	643513	1669.A01.gz43_260687	F	M00055651C:F07	UC2-NormColon
4122	641658	1669.J01.gz43_260696	F	M00055663A:H10	UC2-NormColon
4123	639752	1669.M01.gz43_260699	F	M00055667B:C08	UC2-NormColon
4124	518569	1669.P01.gz43_260702	F	M00055671A:H03	UC2-NormColon
4125	642068	1669.N02.gz43_260716	F	M00055668C:A04	UC2-NormColon
4126	639743	1669.O02.gz43_260717	F	M00055669D:B08	UC2-NormColon
4127	642230	1669.P03.gz43_260734	F	M00055671B:B02	UC2-NormColon
4128	447585	1669.I04.gz43_260743	F	M00055662B:F11	UC2-NormColon
4129	640078	1669.J04.gz43_260744	F	M00055663B:E02	UC2-NormColon
4130	647333	1669.B06.gz43_260768	F	M00055653B:C03	UC2-NormColon
4131	472226	1669.C06.gz43_260769	F	M00055654B:G09	UC2-NormColon
4132	455778	1669.H06.gz43_260774	F	M00055661B:E07	UC2-NormColon
4133	523875	1669.I07.gz43_260791	F	M00055662C:C11	UC2-NormColon
4134	658271	1669.J07.gz43_260792	F	M00055663C:D05	UC2-NormColon
4135	465104	1669.K07.gz43_260793	F	M00055665B:B10	UC2-NormColon
4136	648352	1669.O07.gz43_260797	F	M00055670A:B04	UC2-NormColon
4137	641469	1669.C08.gz43_260801	F	M00055654C:A05	UC2-NormColon
4138	450883	1669.E08.gz43_260803	F	M00055657A:B04	UC2-NormColon
4139	638971	1669.C09.gz43_260817	F	M00055654C:C10	UC2-NormColon
4140	641379	1669.I09.gz43_260823	F	M00055662C:D12	UC2-NormColon
4141	618998	1669.A10.gz43_260831	F	M00055652B:B11	UC2-NormColon
4142	644971	1669.B10.gz43_260832	F	M00055653B:G01	UC2-NormColon
4143	556488	1669.C10.gz43_260833	F	M00055654C:D03	UC2-NormColon
4144	452687	1669.G10.gz43_260837	F	M00055660A:A06	UC2-NormColon
4145	643909	1669.J10.gz43_260840	F	M00055663D:B05	UC2-NormColon
4146	646894	1669.M10.gz43_260843	F	M00055667C:F07	UC2-NormColon
4147	556750	1669.N10.gz43_260844	F	M00055668D:E11	UC2-NormColon
4148	640259	1669.B11.gz43_260848	F	M00055653B:G11	UC2-NormColon
4149	643804	1669.D11.gz43_260850	F	M00055656A:E09	UC2-NormColon
4150	97909	1669.F11.gz43_260852	F	M00055659A:A08	UC2-NormColon
4151	503275	1669.G11.gz43_260853	F	M00055660A:C05	UC2-NormColon
4152	640678	1669.L11.gz43_260858	F	M00055666B:E06	UC2-NormColon
4153	406734	1669.A12.gz43_260863	F	M00055652B:F12	UC2-NormColon
4154	643563	1669.G12.gz43_260869	F	M00055660A:C08	UC2-NormColon
4155	658447	1669.H12.gz43_260870	F	M00055661C:E11	UC2-NormColon
4156	446188	1669.I12.gz43_260871	F	M00055662C:H06	UC2-NormColon
4157	603857	1669.L12.gz43_260874	F	M00055666C:C11	UC2-NormColon
4158	561894	1669.M12.gz43_260875	F	M00055667D:B01	UC2-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
4159	639596	1669.I15.gz43_260919	F	M00055662D:A09	UC2-NormColon
4160	589483	1669.G17.gz43_260949	F	M00055660B:H02	UC2-NormColon
4161	639665	1669.I17.gz43_260951	F	M00055662D:B07	UC2-NormColon
4162	641683	1669.O17.gz43_260957	F	M00055670D:F02	UC2-NormColon
4163	642111	1669.C18.gz43_260961	F	M00055655A:A09	UC2-NormColon
4164	640179	1669.K18.gz43_260969	F	M00055665D:F11	UC2-NormColon
4165	648352	1669.N18.gz43_260972	F	M00055669B:G02	UC2-NormColon
4166	640018	1669.I20.gz43_260999	F	M00055662D:E05	UC2-NormColon
4167	642332	1669.L20.gz43_261002	F	M00055667A:B12	UC2-NormColon
4168	639706	1669.F21.gz43_261012	F	M00055659C:B10	UC2-NormColon
4169	642411	1669.C22.gz43_261025	F	M00055655B:B08	UC2-NormColon
4170	641091	1669.I22.gz43_261031	F	M00055663A:B02	UC2-NormColon
4171	463312	1669.B23.gz43_261040	F	M00055653D:H02	UC2-NormColon
4172	456561	1669.L23.gz43_261050	F	M00055667A:H10	UC2-NormColon
4173	649631	1669.A24.gz43_261055	F	M00055653A:G08	UC2-NormColon
4174	639674	1669.F24.gz43_261060	F	M00055659C:D06	UC2-NormColon
4175	640261	1669.I24.gz43_261063	F	M00055663A:G04	UC2-NormColon
4176	640889	1670.N03.gz43_261116	F	M00055691B:E07	UC2-NormColon
4177	426366	1670.D05.gz43_261138	F	M00055676D:H07	UC2-NormColon
4178	643594	1670.L05.gz43_261146	F	M00055687C:F01	UC2-NormColon
4179	446675	1670.M05.gz43_261147	F	M00055689B:F04	UC2-NormColon
4180	640645	1670.H06.gz43_261158	F	M00055683B:D10	UC2-NormColon
4181	645909	1670.J06.gz43_261160	F	M00055685B:E12	UC2-NormColon
4182	551287	1670.K06.gz43_261161	F	M00055686B:D03	UC2-NormColon
4183	646638	1670.N06.gz43_261164	F	M00055691C:E02	UC2-NormColon
4184	639805	1670.B07.gz43_261168	F	M00055673D:C01	UC2-NormColon
4185	640092	1670.A08.gz43_261183	F	M00055672D:F06	UC2-NormColon
4186	634122	1670.M08.gz43_261195	F	M00055689C:B03	UC2-NormColon
4187	641618	1670.G09.gz43_261205	F	M00055682C:D06	UC2-NormColon
4188	641287	1670.L09.gz43_261210	F	M00055688A:A02	UC2-NormColon
4189	557625	1670.H10.gz43_261222	F	M00055683C:A03	UC2-NormColon
4190	599838	1670.I10.gz43_261223	F	M00055684B:D06	UC2-NormColon
4191	634122	1670.M10.gz43_261227	F	M00055689C:C03	UC2-NormColon
4192	641726	1670.K12.gz43_261257	F	M00055686D:E04	UC2-NormColon
4193	649921	1670.L12.gz43_261258	F	M00055688A:E04	UC2-NormColon
4194	645431	1670.P12.gz43_261262	F	M00055695D:E01	UC2-NormColon
4195	641728	1670.K13.gz43_261273	F	M00055686D:E10	UC2-NormColon
4196	502609	1670.N13.gz43_261276	F	M00055691D:E04	UC2-NormColon
4197	650673	1670.C14.gz43_261281	F	M00055675D:E04	UC2-NormColon
4198	644699	1670.H14.gz43_261286	F	M00055683C:D11	UC2-NormColon
4199	645146	1670.A16.gz43_261311	F	M00055673B:A04	UC2-NormColon
4200	647427	1670.E17.gz43_261331	F	M00055680B:H04	UC2-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
4201	553921	1670.H17.gz43_261334	F	M00055683C:H11	UC2-NormColon
4202	639469	1670.A18.gz43_261343	F	M00055673B:B08	UC2-NormColon
4203	359500	1670.F18.gz43_261348	F	M00055681D:F11	UC2-NormColon
4204	649558	1670.J18.gz43_261352	F	M00055685D:B06	UC2-NormColon
4205	561920	1670.N18.gz43_261356	F	M00055692A:E05	UC2-NormColon
4206	446242	1670.C20.gz43_261377	F	M00055676B:D05	UC2-NormColon
4207	645968	1670.B21.gz43_261392	F	M00055674C:E05	UC2-NormColon
4208	637966	1670.F22.gz43_261412	F	M00055682A:B07	UC2-NormColon
4209	640826	1670.M22.gz43_261419	F	M00055691A:D08	UC2-NormColon
4210	642321	1670.D23.gz43_261426	F	M00055679B:E03	UC2-NormColon
4211	601137	1670.I23.gz43_261431	F	M00055685A:E10	UC2-NormColon
4212	416808	1670.E24.gz43_261443	F	M00055681A:F02	UC2-NormColon
4213	647856	1670.I24.gz43_261447	F	M00055685A:F02	UC2-NormColon
4214	554564	1670.K24.gz43_261449	F	M00055687C:B04	UC2-NormColon
4215	561422	1671.I07.gz43_261559	F	M00055711B:B08	UC2-NormColon
4216	642288	1671.P07.gz43_261566	F	M00055721B:D08	UC2-NormColon
4217	642062	1671.E08.gz43_261571	F	M00055704A:D09	UC2-NormColon
4218	463368	1671.K08.gz43_261577	F	M00055715A:D10	UC2-NormColon
4219	646028	1671.D09.gz43_261586	F	M00055702C:D01	UC2-NormColon
4220	478192	1671.M09.gz43_261595	F	M00055718A:F01	UC2-NormColon
4221	640947	1671.D10.gz43_261602	F	M00055702C:F11	UC2-NormColon
4222	463548	1671.G10.gz43_261605	F	M00055706B:H12	UC2-NormColon
4223	640282	1671.M10.gz43_261611	F	M00055718A:H05	UC2-NormColon
4224	41141	1671.B11.gz43_261616	F	M00055699C:D02	UC2-NormColon
4225	463368	1671.I11.gz43_261623	F	M00055711C:A07	UC2-NormColon
4226	558086	1671.J11.gz43_261624	F	M00055713C:F12	UC2-NormColon
4227	560546	1671.C12.gz43_261633	F	M00055701A:B04	UC2-NormColon
4228	551415	1671.E12.gz43_261635	F	M00055704B:C04	UC2-NormColon
4229	557710	1671.N12.gz43_261644	F	M00055719A:D11	UC2-NormColon
4230	649429	1671.G14.gz43_261669	F	M00055707A:B07	UC2-NormColon
4231	451401	1671.L14.gz43_261674	F	M00055717B:A03	UC2-NormColon
4232	642039	1671.C17.gz43_261713	F	M00055701B:C03	UC2-NormColon
4233	471268	1671.F17.gz43_261716	F	M00055705C:F12	UC2-NormColon
4234	417259	1671.H17.gz43_261718	F	M00055709D:G10	UC2-NormColon
4235	421826	1671.L17.gz43_261722	F	M00055717B:E04	UC2-NormColon
4236	465589	1671.M17.gz43_261723	F	M00055718B:H11	UC2-NormColon
4237	645505	1671.N17.gz43_261724	F	M00055719A:G04	UC2-NormColon
4238	510195	1671.N18.gz43_261740	F	M00055719A:G12	UC2-NormColon
4239	492094	1671.P18.gz43_261742	F	M00055722A:B05	UC2-NormColon
4240	453006	1671.G20.gz43_261765	F	M00055707A:F11	UC2-NormColon
4241	600115	1671.P21.gz43_261790	F	M00055722A:C04	UC2-NormColon
4242	641700	1671.H22.gz43_261798	F	M00055710B:E04	UC2-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
4243	466265	1671.O22.gz43_261805	F	M00055721A:A07	UC2-NormColon
4244	553985	1671.B23.gz43_261808	F	M00055700B:E10	UC2-NormColon
4245	536415	1671.L23.gz43_261818	F	M00055717C:B07	UC2-NormColon
4246	640282	1671.N23.gz43_261820	F	M00055719C:A09	UC2-NormColon
4247	498194	1672.A01.gz43_261841	F	M00055722B:A01	UC2-NormColon
4248	641305	1672.E02.gz43_261861	F	M00055725A:F12	UC2-NormColon
4249	641070	1672.H02.gz43_261864	F	M00055727D:G01	UC2-NormColon
4250	556326	1672.B03.gz43_261874	F	M00055723A:B08	UC2-NormColon
4251	522497	1672.C03.gz43_261875	F	M00055723D:C04	UC2-NormColon
4252	557833	1672.E03.gz43_261877	F	M00055725A:G07	UC2-NormColon
4253	647688	1672.B04.gz43_261890	F	M00055723A:C04	UC2-NormColon
4254	416377	1672.M04.gz43_261901	F	M00055733D:H01	UC2-NormColon
4255	643897	1672.O04.gz43_261903	F	M00055736B:C08	UC2-NormColon
4256	645171	1672.A06.gz43_261921	F	M00055722B:G12	UC2-NormColon
4257	649106	1672.C06.gz43_261923	F	M00055723D:E05	UC2-NormColon
4258	454383	1672.K06.gz43_261931	F	M00055731C:F09	UC2-NormColon
4259	649360	1672.B07.gz43_261938	F	M00055723A:F04	UC2-NormColon
4260	639458	1672.K08.gz43_261963	F	M00055731C:H07	UC2-NormColon
4261	642078	1672.B11.gz43_262002	F	M00055723B:A09	UC2-NormColon
4262	642631	1672.L11.gz43_262012	F	M00055733A:G04	UC2-NormColon
4263	650303	1672.A12.gz43_262017	F	M00055722C:E11	UC2-NormColon
4264	284586	1672.C12.gz43_262019	F	M00055724A:C12	UC2-NormColon
4265	642535	1672.G12.gz43_262023	F	M00055727B:F10	UC2-NormColon
4266	642491	1672.A13.gz43_262033	F	M00055722C:F11	UC2-NormColon
4267	100821	1672.P13.gz43_262048	F	M00055738B:H11	UC2-NormColon
4268	641056	1672.A14.gz43_262049	F	M00055722D:A07	UC2-NormColon
4269	642197	1672.B14.gz43_262050	F	M00055723B:C03	UC2-NormColon
4270	801	1672.E14.gz43_262053	F	M00055725D:B02	UC2-NormColon
4271	449956	1672.N14.gz43_262062	F	M00055735C:G08	UC2-NormColon
4272	645018	1672.C15.gz43_262067	F	M00055724A:E03	UC2-NormColon
4273	640879	1672.K15.gz43_262075	F	M00055731D:F09	UC2-NormColon
4274	642263	1672.O15.gz43_262079	F	M00055736D:D11	UC2-NormColon
4275	647906	1672.P15.gz43_262080	F	M00055738C:C02	UC2-NormColon
4276	559776	1672.G16.gz43_262087	F	M00055727C:B02	UC2-NormColon
4277	647060	1672.H16.gz43_262088	F	M00055728B:G11	UC2-NormColon
4278	642315	1672.I16.gz43_262089	F	M00055729C:D11	UC2-NormColon
4279	504501	1672.L16.gz43_262092	F	M00055733B:F11	UC2-NormColon
4280	460967	1672.A17.gz43_262097	F	M00055722D:B10	UC2-NormColon
4281	504568	1672.C17.gz43_262099	F	M00055724A:G08	UC2-NormColon
4282	559828	1672.D17.gz43_262100	F	M00055724D:A02	UC2-NormColon
4283	455113	1672.H17.gz43_262104	F	M00055728C:B08	UC2-NormColon
4284	477064	1672.I17.gz43_262105	F	M00055729C:E02	UC2-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
4285	1558	1672.J17.gz43_262106	F	M00055731A:G05	UC2-NormColon
4286	419443	1672.L17.gz43_262108	F	M00055733B:H05	UC2-NormColon
4287	546705	1672.I18.gz43_262121	F	M00055729D:A06	UC2-NormColon
4288	235397	1672.J18.gz43_262122	F	M00055731A:H07	UC2-NormColon
4289	651085	1672.K18.gz43_262123	F	M00055732A:B04	UC2-NormColon
4290	502826	1672.N18.gz43_262126	F	M00055735D:C01	UC2-NormColon
4291	544797	1672.A19.gz43_262129	F	M00055722D:E05	UC2-NormColon
4292	489426	1672.B19.gz43_262130	F	M00055723C:B02	UC2-NormColon
4293	452212	1672.E19.gz43_262133	F	M00055725D:F05	UC2-NormColon
4294	646609	1672.M19.gz43_262141	F	M00055734D:D01	UC2-NormColon
4295	556336	1672.N19.gz43_262142	F	M00055735D:E10	UC2-NormColon
4296	467822	1672.C20.gz43_262147	F	M00055724B:D04	UC2-NormColon
4297	650397	1672.L20.gz43_262156	F	M00055733C:H12	UC2-NormColon
4298	37862	1672.P20.gz43_262160	F	M00055738D:G08	UC2-NormColon
4299	644609	1672.I21.gz43_262169	F	M00055729D:F05	UC2-NormColon
4300	561968	1672.L21.gz43_262172	F	M00055733D:B11	UC2-NormColon
4301	550049	1672.P21.gz43_262176	F	M00055739A:B02	UC2-NormColon
4302	554708	1672.H22.gz43_262184	F	M00055728D:F02	UC2-NormColon
4303	608540	1672.P22.gz43_262192	F	M00055739A:B04	UC2-NormColon
4304	470769	1672.A23.gz43_262193	F	M00055722D:G12	UC2-NormColon
4305	642722	1672.C23.gz43_262195	F	M00055724B:G03	UC2-NormColon
4306	645151	1672.L23.gz43_262204	F	M00055733D:D04	UC2-NormColon
4307	648265	1672.N23.gz43_262206	F	M00055736A:B11	UC2-NormColon
4308	489249	1672.F24.gz43_262214	F	M00055726D:H12	UC2-NormColon
4309	644173	1682.H02.gz43_262248	F	M00055770A:G08	UC2-NormColon
4310	642417	1682.L02.gz43_262252	F	M00055774D:A05	UC2-NormColon
4311	553877	1682.M02.gz43_262253	F	M00055775C:B10	UC2-NormColon
4312	530238	1682.H03.gz43_262264	F	M00055770A:H11	UC2-NormColon
4313	553380	1682.L03.gz43_262268	F	M00055774D:B07	UC2-NormColon
4314	637387	1682.E04.gz43_262277	F	M00055766B:E11	UC2-NormColon
4315	634660	1682.F04.gz43_262278	F	M00055767A:D10	UC2-NormColon
4316	642791	1682.J04.gz43_262282	F	M00055772A:H08	UC2-NormColon
4317	446163	1682.K04.gz43_262283	F	M00055773C:C09	UC2-NormColon
4318	641056	1682.M04.gz43_262285	F	M00055775C:E10	UC2-NormColon
4319	550562	1682.B05.gz43_262290	F	M00055763B:D07	UC2-NormColon
4320	648320	1682.A06.gz43_262305	F	M00055761D:C03	UC2-NormColon
4321	446757	1682.H06.gz43_262312	F	M00055770B:D06	UC2-NormColon
4322	454540	1682.K06.gz43_262315	F	M00055773C:H12	UC2-NormColon
4323	458979	1682.L06.gz43_262316	F	M00055774D:E02	UC2-NormColon
4324	641174	1682.P06.gz43_262320	F	M00055780C:E02	UC2-NormColon
4325	642852	1682.E08.gz43_262341	F	M00055766B:H10	UC2-NormColon
4326	488680	1682.A09.gz43_262353	F	M00055761D:H08	UC2-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
4327	27083	1682.K09.gz43_262363	F	M00055773D:G11	UC2-NormColon
4328	524470	1682.C10.gz43_262371	F	M00055765A:A04	UC2-NormColon
4329	463951	1682.J10.gz43_262378	F	M00055772C:E11	UC2-NormColon
4330	584179	1682.C11.gz43_262387	F	M00055765A:B02	UC2-NormColon
4331	642460	1682.D11.gz43_262388	F	M00055765D:E06	UC2-NormColon
4332	448944	1682.E11.gz43_262389	F	M00055766C:C11	UC2-NormColon
4333	642082	1682.F11.gz43_262390	F	M00055767B:D02	UC2-NormColon
4334	642095	1682.N11.gz43_262398	F	M00055778D:A03	UC2-NormColon
4335	562876	1682.H12.gz43_262408	F	M00055770C:H11	UC2-NormColon
4336	453079	1682.I12.gz43_262409	F	M00055771C:A11	UC2-NormColon
4337	101499	1682.L12.gz43_262412	F	M00055775A:G09	UC2-NormColon
4338	639829	1682.N12.gz43_262414	F	M00055778D:C03	UC2-NormColon
4339	642332	1682.P12.gz43_262416	F	M00055780D:D09	UC2-NormColon
4340	541499	1682.G13.gz43_262423	F	M00055768B:H12	UC2-NormColon
4341	509410	1682.I13.gz43_262425	F	M00055771C:D09	UC2-NormColon
4342	89082	1682.O13.gz43_262431	F	M00055780A:C04	UC2-NormColon
4343	453091	1682.P13.gz43_262432	F	M00055780D:F08	UC2-NormColon
4344	639981	1682.A14.gz43_262433	F	M00055762B:B11	UC2-NormColon
4345	642564	1682.B14.gz43_262434	F	M00055763C:G08	UC2-NormColon
4346	561558	1682.O14.gz43_262447	F	M00055780A:C06	UC2-NormColon
4347	562870	1682.B15.gz43_262450	F	M00055763D:B11	UC2-NormColon
4348	462742	1682.D15.gz43_262452	F	M00055766A:A01	UC2-NormColon
4349	451037	1682.E15.gz43_262453	F	M00055766C:G12	UC2-NormColon
4350	641563	1682.J15.gz43_262458	F	M00055772D:C10	UC2-NormColon
4351	643940	1682.A16.gz43_262465	F	M00055762C:B04	UC2-NormColon
4352	642204	1682.C16.gz43_262467	F	M00055765A:C11	UC2-NormColon
4353	517912	1682.J16.gz43_262474	F	M00055772D:D03	UC2-NormColon
4354	641576	1682.D17.gz43_262484	F	M00055766A:D08	UC2-NormColon
4355	642082	1682.F17.gz43_262486	F	M00055767D:A12	UC2-NormColon
4356	450211	1682.O17.gz43_262495	F	M00055780A:E11	UC2-NormColon
4357	621636	1682.B18.gz43_262498	F	M00055764A:F02	UC2-NormColon
4358	639232	1682.D18.gz43_262500	F	M00055766A:E08	UC2-NormColon
4359	450553	1682.J18.gz43_262506	F	M00055772D:F10	UC2-NormColon
4360	647940	1682.K18.gz43_262507	F	M00055774B:F07	UC2-NormColon
4361	461835	1682.M18.gz43_262509	F	M00055778A:F09	UC2-NormColon
4362	641496	1682.O18.gz43_262511	F	M00055780A:F07	UC2-NormColon
4363	464510	1682.H19.gz43_262520	F	M00055770D:E10	UC2-NormColon
4364	642564	1682.M19.gz43_262525	F	M00055778A:F12	UC2-NormColon
4365	629002	1682.C20.gz43_262531	F	M00055765A:G02	UC2-NormColon
4366	1093	1682.D20.gz43_262532	F	M00055766A:H03	UC2-NormColon
4367	50351	1682.E20.gz43_262533	F	M00055766D:D05	UC2-NormColon
4368	642417	1682.F20.gz43_262534	F	M00055767D:E07	UC2-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
4369	466971	1682.J20.gz43_262538	F	M00055772D:H04	UC2-NormColon
4370	641185	1682.K20.gz43_262539	F	M00055774B:H01	UC2-NormColon
4371	644240	1682.L20.gz43_262540	F	M00055775B:G02	UC2-NormColon
4372	509027	1682.M20.gz43_262541	F	M00055778A:G02	UC2-NormColon
4373	546740	1682.F21.gz43_262550	F	M00055767D:F04	UC2-NormColon
4374	559662	1682.L21.gz43_262556	F	M00055775B:G04	UC2-NormColon
4375	388688	1682.B22.gz43_262562	F	M00055764B:F05	UC2-NormColon
4376	555140	1682.G22.gz43_262567	F	M00055768D:G02	UC2-NormColon
4377	640617	1682.K22.gz43_262571	F	M00055774C:D09	UC2-NormColon
4378	447224	1682.D23.gz43_262580	F	M00055766B:B01	UC2-NormColon
4379	644765	1682.B24.gz43_262594	F	M00055764C:C07	UC2-NormColon
4380	648996	1682.F24.gz43_262598	F	M00055768A:B05	UC2-NormColon
4381	642036	1682.I24.gz43_262601	F	M00055772A:C10	UC2-NormColon
4382	644914	1682.J24.gz43_262602	F	M00055773B:A07	UC2-NormColon
4383	458425	1682.M24.gz43_262605	F	M00055778B:E01	UC2-NormColon
4384	556476	1682.N24.gz43_262606	F	M00055779B:F06	UC2-NormColon
4385	672601	1683.E01.gz43_262613	F	M00055785D:C06	UC2-NormColon
4386	463290	1683.H01.gz43_262616	F	M00055789C:F10	UC2-NormColon
4387	675768	1683.D03.gz43_262644	F	M00055784C:H02	UC2-NormColon
4388	642146	1683.H03.gz43_262648	F	M00055789D:B04	UC2-NormColon
4389	648905	1683.F04.gz43_262662	F	M00055787B:F10	UC2-NormColon
4390	467306	1683.I04.gz43_262665	F	M00055790D:G10	UC2-NormColon
4391	497971	1683.C05.gz43_262675	F	M00055783D:B02	UC2-NormColon
4392	645508	1683.N05.gz43_262686	F	M00055795D:E09	UC2-NormColon
4393	644047	1683.O05.gz43_262687	F	M00055796B:G05	UC2-NormColon
4394	554117	1683.K06.gz43_262699	F	M00055793A:H09	UC2-NormColon
4395	641919	1683.K08.gz43_262731	F	M00055793B:B06	UC2-NormColon
4396	605761	1683.L08.gz43_262732	F	M00055794A:D08	UC2-NormColon
4397	549434	1683.D09.gz43_262740	F	M00055785A:H08	UC2-NormColon
4398	446595	1683.M09.gz43_262749	F	M00055795A:F09	UC2-NormColon
4399	643350	1683.F10.gz43_262758	F	M00055787C:D09	UC2-NormColon
4400	454485	1683.M10.gz43_262765	F	M00055795A:F12	UC2-NormColon
4401	647639	1683.O10.gz43_262767	F	M00055796C:E11	UC2-NormColon
4402	510545	1683.I11.gz43_262777	F	M00055791B:E02	UC2-NormColon
4403	77144	1683.N11.gz43_262782	F	M00055795D:H08	UC2-NormColon
4404	140909	1683.C12.gz43_262787	F	M00055784A:B07	UC2-NormColon
4405	650076	1683.D12.gz43_262788	F	M00055785B:B06	UC2-NormColon
4406	449836	1683.F12.gz43_262790	F	M00055787C:E12	UC2-NormColon
4407	642184	1683.B14.gz43_262818	F	M00055783A:C06	UC2-NormColon
4408	638962	1683.H14.gz43_262824	F	M00055790B:A08	UC2-NormColon
4409	641700	1683.M15.gz43_262845	F	M00055795B:F09	UC2-NormColon
4410	437580	1683.N15.gz43_262846	F	M00055796A:A08	UC2-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
4411	456626	1683.C16.gz43_262851	F	M00055784A:D05	UC2-NormColon
4412	553979	1683.O16.gz43_262863	F	M00055796D:E06	UC2-NormColon
4413	640525	1683.O17.gz43_262879	F	M00055796D:E10	UC2-NormColon
4414	553546	1683.H18.gz43_262888	F	M00055790B:D05	UC2-NormColon
4415	643230	1683.A19.gz43_262897	F	M00055782B:C08	UC2-NormColon
4416	523590	1683.B20.gz43_262914	F	M00055783B:A04	UC2-NormColon
4417	388085	1683.M20.gz43_262925	F	M00055795C:B10	UC2-NormColon
4418	457396	1683.L21.gz43_262940	F	M00055794C:D10	UC2-NormColon
4419	417617	1683.O23.gz43_262975	F	M00055797B:A11	UC2-NormColon
4420	463821	1684.G01.gz43_262999	F	M00055804D:F02	UC2-NormColon
4421	448787	1684.M01.gz43_263005	F	M00055811C:A01	UC2-NormColon
4422	32812	1684.I03.gz43_263033	F	M00055807A:B10	UC2-NormColon
4423	418340	1684.A04.gz43_263041	F	M00055798B:D12	UC2-NormColon
4424	462249	1684.C04.gz43_263043	F	M00055800D:B03	UC2-NormColon
4425	642099	1684.P04.gz43_263056	F	M00055815C:B03	UC2-NormColon
4426	644915	1684.A05.gz43_263057	F	M00055798B:F02	UC2-NormColon
4427	640222	1684.G05.gz43_263063	F	M00055805A:A02	UC2-NormColon
4428	550370	1684.K05.gz43_263067	F	M00055809A:B10	UC2-NormColon
4429	645560	1684.A06.gz43_263073	F	M00055798B:G04	UC2-NormColon
4430	513238	1684.E06.gz43_263077	F	M00055803A:C06	UC2-NormColon
4431	650231	1684.M07.gz43_263101	F	M00055811D:C02	UC2-NormColon
4432	644314	1684.H08.gz43_263112	F	M00055806B:B10	UC2-NormColon
4433	650782	1684.J08.gz43_263114	F	M00055808B:A04	UC2-NormColon
4434	648221	1684.P08.gz43_263120	F	M00055815C:G05	UC2-NormColon
4435	554742	1684.M09.gz43_263133	F	M00055811D:C12	UC2-NormColon
4436	642962	1684.P09.gz43_263136	F	M00055815D:A11	UC2-NormColon
4437	455028	1684.A10.gz43_263137	F	M00055798D:A10	UC2-NormColon
4438	447015	1684.P10.gz43_263152	F	M00055815D:B02	UC2-NormColon
4439	642653	1684.E11.gz43_263157	F	M00055803A:G08	UC2-NormColon
4440	647336	1684.O11.gz43_263167	F	M00055814C:C07	UC2-NormColon
4441	549640	1684.P11.gz43_263168	F	M00055815D:B03	UC2-NormColon
4442	642198	1684.G12.gz43_263175	F	M00055805B:C08	UC2-NormColon
4443	520320	1684.I12.gz43_263177	F	M00055807B:F05	UC2-NormColon
4444	644147	1684.N12.gz43_263182	F	M00055813A:D10	UC2-NormColon
4445	530774	1684.E13.gz43_263189	F	M00055803B:A11	UC2-NormColon
4446	375814	1684.H14.gz43_263208	F	M00055806C:E09	UC2-NormColon
4447	446789	1684.I14.gz43_263209	F	M00055807B:G10	UC2-NormColon
4448	210839	1684.J14.gz43_263210	F	M00055808B:H07	UC2-NormColon
4449	490414	1684.B15.gz43_263218	F	M00055800A:F02	UC2-NormColon
4450	503491	1684.M15.gz43_263229	F	M00055812A:E01	UC2-NormColon
4451	486134	1684.D17.gz43_263252	F	M00055802B:H03	UC2-NormColon
4452	639441	1684.I17.gz43_263257	F	M00055807C:F05	UC2-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
4453	551683	1684.N17.gz43_263262	F	M00055813C:E03	UC2-NormColon
4454	649035	1684.P17.gz43_263264	F	M00055816A:C04	UC2-NormColon
4455	639194	1684.F18.gz43_263270	F	M00055804B:C02	UC2-NormColon
4456	454772	1684.K19.gz43_263291	F	M00055809C:E11	UC2-NormColon
4457	649995	1684.L19.gz43_263292	F	M00055810D:G04	UC2-NormColon
4458	466016	1684.M19.gz43_263293	F	M00055812B:F03	UC2-NormColon
4459	494271	1684.N19.gz43_263294	F	M00055813D:B12	UC2-NormColon
4460	460517	1684.J20.gz43_263306	F	M00055808D:C12	UC2-NormColon
4461	470602	1684.I21.gz43_263321	F	M00055807D:C04	UC2-NormColon
4462	640537	1684.B22.gz43_263330	F	M00055800C:E11	UC2-NormColon
4463	643991	1684.D22.gz43_263332	F	M00055802C:E12	UC2-NormColon
4464	564382	1684.C23.gz43_263347	F	M00055801D:E06	UC2-NormColon
4465	529325	1684.G23.gz43_263351	F	M00055805D:H01	UC2-NormColon
4466	455665	1684.L23.gz43_263356	F	M00055811B:A03	UC2-NormColon
4467	645700	1684.A24.gz43_263361	F	M00055799C:D09	UC2-NormColon
4468	520320	1684.J24.gz43_263370	F	M00055808D:F09	UC2-NormColon
4469	648752	1684.M24.gz43_263373	F	M00055812C:B07	UC2-NormColon
4470	642850	1684.O24.gz43_263375	F	M00055815A:H12	UC2-NormColon
4471	556896	1970.H01.gz43_263397	F	M00054702A:C06	UC2-ColonMetLiver
4472	549238	1970.I01.gz43_263398	F	M00054703D:E07	UC2-ColonMetLiver
4473	551941	1970.M01.gz43_263402	F	M00054710D:A02	UC2-ColonMetLiver
4474	552055	1970.G02.gz43_263412	F	M00054699D:A12	UC2-ColonMetLiver
4475	483141	1970.H02.gz43_263413	F	M00054702A:F03	UC2-ColonMetLiver
4476	561434	1970.I02.gz43_263414	F	M00054703D:F04	UC2-ColonMetLiver
4477	453708	1970.K02.gz43_263416	F	M00054707B:B08	UC2-ColonMetLiver
4478	557935	1970.A03.gz43_263422	F	M00054689C:B11	UC2-ColonMetLiver
4479	509202	1970.H03.gz43_263429	F	M00054702A:H03	UC2-ColonMetLiver
4480	549388	1970.B04.gz43_263439	F	M00054690D:G03	UC2-ColonMetLiver
4481	551243	1970.C05.gz43_263456	F	M00054693A:C09	UC2-ColonMetLiver
4482	549557	1970.N05.gz43_263467	F	M00054712C:C07	UC2-ColonMetLiver
4483	551527	1970.A06.gz43_263470	F	M00054689D:E12	UC2-ColonMetLiver
4484	553128	1970.E06.gz43_263474	F	M00054696B:H11	UC2-ColonMetLiver
4485	549151	1970.K06.gz43_263480	F	M00054707C:D02	UC2-ColonMetLiver
4486	32021	1970.O06.gz43_263484	F	M00054714B:F05	UC2-ColonMetLiver
4487	552598	1970.P07.gz43_263501	F	M00054715D:E11	UC2-ColonMetLiver
4488	552051	1970.D08.gz43_263505	F	M00054695A:A12	UC2-ColonMetLiver
4489	491827	1970.J09.gz43_263527	F	M00054706A:G10	UC2-ColonMetLiver
4490	552625	1970.O09.gz43_263532	F	M00054714C:E01	UC2-ColonMetLiver
4491	552073	1970.M11.gz43_263562	F	M00054711C:A08	UC2-ColonMetLiver
4492	552649	1970.E12.gz43_263570	F	M00054697A:E03	UC2-ColonMetLiver
4493	389201	1970.H12.gz43_263573	F	M00054702D:E07	UC2-ColonMetLiver
4494	552682	1970.I12.gz43_263574	F	M00054704D:F02	UC2-ColonMetLiver

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
4495	552686	1970.K12.gz43_263576	F	M00054708A:F11	UC2-ColonMetLiver
4496	559389	1970.A14.gz43_263598	F	M00054690B:B02	UC2-ColonMetLiver
4497	562216	1970.E14.gz43_263602	F	M00054697A:G06	UC2-ColonMetLiver
4498	452392	1970.H14.gz43_263605	F	M00054702D:F05	UC2-ColonMetLiver
4499	552314	1970.I14.gz43_263606	F	M00054705B:C08	UC2-ColonMetLiver
4500	584499	1970.F15.gz43_263619	F	M00054699A:G01	UC2-ColonMetLiver
4501	552418	1970.A16.gz43_263630	F	M00054690B:D10	UC2-ColonMetLiver
4502	551996	1970.F16.gz43_263635	F	M00054699B:A05	UC2-ColonMetLiver
4503	549945	1970.H16.gz43_263637	F	M00054702D:H10	UC2-ColonMetLiver
4504	527679	1970.I16.gz43_263638	F	M00054705B:D02	UC2-ColonMetLiver
4505	391511	1970.K16.gz43_263640	F	M00054708B:F04	UC2-ColonMetLiver
4506	490393	1970.P16.gz43_263645	F	M00054716B:D06	UC2-ColonMetLiver
4507	552197	1970.L17.gz43_263657	F	M00054710B:B10	UC2-ColonMetLiver
4508	550975	1970.O17.gz43_263660	F	M00054715A:G02	UC2-ColonMetLiver
4509	498454	1970.I18.gz43_263670	F	M00054705B:E04	UC2-ColonMetLiver
4510	553938	1970.N18.gz43_263675	F	M00054713C:D07	UC2-ColonMetLiver
4511	448332	1970.C19.gz43_263680	F	M00054693D:A08	UC2-ColonMetLiver
4512	550053	1970.J19.gz43_263687	F	M00054706C:B12	UC2-ColonMetLiver
4513	550330	1970.B20.gz43_263695	F	M00054692B:C06	UC2-ColonMetLiver
4514	450755	1970.C20.gz43_263696	F	M00054693D:C04	UC2-ColonMetLiver
4515	420686	1970.B21.gz43_263711	F	M00054692B:D01	UC2-ColonMetLiver
4516	552581	1970.E21.gz43_263714	F	M00054697C:E11	UC2-ColonMetLiver
4517	551995	1970.F21.gz43_263715	F	M00054699C:A04	UC2-ColonMetLiver
4518	521552	1970.H22.gz43_263733	F	M00054703C:F01	UC2-ColonMetLiver
4519	553358	1970.J22.gz43_263735	F	M00054706D:B03	UC2-ColonMetLiver
4520	558768	1970.L22.gz43_263737	F	M00054710C:A12	UC2-ColonMetLiver
4521	42994	1970.B23.gz43_263743	F	M00054692C:B02	UC2-ColonMetLiver
4522	555255	1970.G23.gz43_263748	F	M00054701D:H05	UC2-ColonMetLiver
4523	451032	1970.O23.gz43_263756	F	M00054715C:D05	UC2-ColonMetLiver
4524	554477	1970.I24.gz43_263766	F	M00054705C:D11	UC2-ColonMetLiver
4525	560317	1970.K24.gz43_263768	F	M00054709A:A10	UC2-ColonMetLiver
4526	554900	1993.J01.gz43_263783	F	M00054863D:H05	UC2-ColonMetLiver
4527	560254	1993.L01.gz43_263785	F	M00054866B:C01	UC2-ColonMetLiver
4528	555740	1993.E02.gz43_263794	F	M00054857C:G09	UC2-ColonMetLiver
4529	551212	1993.F02.gz43_263795	F	M00054858D:C04	UC2-ColonMetLiver
4530	554456	1993.G03.gz43_263812	F	M00054859D:E09	UC2-ColonMetLiver
4531	493303	1993.M03.gz43_263818	F	M00054867B:D02	UC2-ColonMetLiver
4532	522648	1993.P03.gz43_263821	F	M00054870C:C05	UC2-ColonMetLiver
4533	559885	1993.A04.gz43_263822	F	M00054852C:G03	UC2-ColonMetLiver
4534	554257	1993.H04.gz43_263829	F	M00054860D:D01	UC2-ColonMetLiver
4535	554524	1993.B05.gz43_263839	F	M00054854A:H06	UC2-ColonMetLiver
4536	554672	1993.C05.gz43_263840	F	M00054855B:E04	UC2-ColonMetLiver

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
4537	560714	1993.D05.gz43_263841	F	M00054856D:E11	UC2-ColonMetLiver
4538	557852	1993.G05.gz43_263844	F	M00054859D:G04	UC2-ColonMetLiver
4539	553295	1993.J05.gz43_263847	F	M00054864B:B02	UC2-ColonMetLiver
4540	559027	1993.N06.gz43_263867	F	M00054868C:G11	UC2-ColonMetLiver
4541	548861	1993.B07.gz43_263871	F	M00054854B:C04	UC2-ColonMetLiver
4542	554500	1993.E07.gz43_263874	F	M00054857D:E12	UC2-ColonMetLiver
4543	522507	1993.I07.gz43_263878	F	M00054862C:D05	UC2-ColonMetLiver
4544	501534	1993.J08.gz43_263895	F	M00054864B:D08	UC2-ColonMetLiver
4545	556715	1993.A09.gz43_263902	F	M00054852D:D09	UC2-ColonMetLiver
4546	496897	1993.C09.gz43_263904	F	M00054855C:B06	UC2-ColonMetLiver
4547	554084	1993.D09.gz43_263905	F	M00054857A:B11	UC2-ColonMetLiver
4548	554497	1993.E10.gz43_263922	F	M00054858A:B05	UC2-ColonMetLiver
4549	555968	1993.F10.gz43_263923	F	M00054859A:D10	UC2-ColonMetLiver
4550	43642	1993.K10.gz43_263928	F	M00054865B:H04	UC2-ColonMetLiver
4551	595506	1993.L10.gz43_263929	F	M00054866C:G07	UC2-ColonMetLiver
4552	594434	1993.O10.gz43_263932	F	M00054869D:F02	UC2-ColonMetLiver
4553	555702	1993.P10.gz43_263933	F	M00054870D:G08	UC2-ColonMetLiver
4554	556132	1993.A11.gz43_263934	F	M00054853A:A10	UC2-ColonMetLiver
4555	555667	1993.F11.gz43_263939	F	M00054859A:E02	UC2-ColonMetLiver
4556	519109	1993.J11.gz43_263943	F	M00054864C:A01	UC2-ColonMetLiver
4557	450829	1993.B12.gz43_263951	F	M00054854C:H02	UC2-ColonMetLiver
4558	463513	1993.M13.gz43_263978	F	M00054867D:H03	UC2-ColonMetLiver
4559	552396	1993.N13.gz43_263979	F	M00054869A:A09	UC2-ColonMetLiver
4560	557077	1993.C14.gz43_263984	F	M00054855D:G12	UC2-ColonMetLiver
4561	554756	1993.D14.gz43_263985	F	M00054857A:G09	UC2-ColonMetLiver
4562	482306	1993.E14.gz43_263986	F	M00054858A:D06	UC2-ColonMetLiver
4563	560259	1993.H14.gz43_263989	F	M00054861B:H08	UC2-ColonMetLiver
4564	402742	1993.L14.gz43_263993	F	M00054866D:C03	UC2-ColonMetLiver
4565	390017	1993.P14.gz43_263997	F	M00054871A:C04	UC2-ColonMetLiver
4566	554989	1993.D15.gz43_264001	F	M00054857A:G12	UC2-ColonMetLiver
4567	550714	1993.E15.gz43_264002	F	M00054858A:D08	UC2-ColonMetLiver
4568	562962	1993.I15.gz43_264006	F	M00054863A:A11	UC2-ColonMetLiver
4569	394567	1993.K16.gz43_264024	F	M00054865D:F05	UC2-ColonMetLiver
4570	457825	1993.N17.gz43_264043	F	M00054869A:D03	UC2-ColonMetLiver
4571	553072	1993.O17.gz43_264044	F	M00054870B:A12	UC2-ColonMetLiver
4572	522703	1993.A18.gz43_264046	F	M00054853B:E07	UC2-ColonMetLiver
4573	451491	1993.E18.gz43_264050	F	M00054858B:A10	UC2-ColonMetLiver
4574	551811	1993.H18.gz43_264053	F	M00054861C:E10	UC2-ColonMetLiver
4575	599433	1993.A19.gz43_264062	F	M00054853B:E10	UC2-ColonMetLiver
4576	593343	1993.D19.gz43_264065	F	M00054857B:D08	UC2-ColonMetLiver
4577	554613	1993.C20.gz43_264080	F	M00054856A:F08	UC2-ColonMetLiver
4578	497365	1993.G21.gz43_264100	F	M00054860C:E04	UC2-ColonMetLiver

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SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
4579	555553	1993.O21.gz43_264108	F	M00054870B:G12	UC2-ColonMetLiver
4580	481641	1993.P21.gz43_264109	F	M00054871A:H07	UC2-ColonMetLiver
4581	557974	1993.M23.gz43_264138	F	M00054868B:A05	UC2-ColonMetLiver
4582	557719	1993.F24.gz43_264147	F	M00054859D:D02	UC2-ColonMetLiver
4583	551591	1993.L24.gz43_264153	F	M00054867A:G01	UC2-ColonMetLiver
4584	553586	1993.P24.gz43_264157	F	M00054871B:E10	UC2-ColonMetLiver
4585	553983	2018.J01.gz43_264167	F	M00055049B:F05	UC2-ColonMetLiver
4586	557939	2018.N01.gz43_264171	F	M00055053D:G04	UC2-ColonMetLiver
4587	549858	2018.P01.gz43_264173	F	M00055056C:A05	UC2-ColonMetLiver
4588	561838	2018.F02.gz43_264179	F	M00055045D:F10	UC2-ColonMetLiver
4589	561438	2018.A03.gz43_264190	F	M00055039A:G06	UC2-ColonMetLiver
4590	447555	2018.N03.gz43_264203	F	M00055054A:A10	UC2-ColonMetLiver
4591	556490	2018.I04.gz43_264214	F	M00055048C:C06	UC2-ColonMetLiver
4592	554372	2018.L04.gz43_264217	F	M00055051C:F10	UC2-ColonMetLiver
4593	557504	2018.P04.gz43_264221	F	M00055056C:C05	UC2-ColonMetLiver
4594	555340	2018.B05.gz43_264223	F	M00055041A:C02	UC2-ColonMetLiver
4595	540000	2018.L05.gz43_264233	F	M00055051D:D12	UC2-ColonMetLiver
4596	528775	2018.O05.gz43_264236	F	M00055055B:H11	UC2-ColonMetLiver
4597	553012	2018.P05.gz43_264237	F	M00055056C:D07	UC2-ColonMetLiver
4598	386940	2018.H06.gz43_264245	F	M00055047C:D11	UC2-ColonMetLiver
4599	559775	2018.K06.gz43_264248	F	M00055050D:C01	UC2-ColonMetLiver
4600	493261	2018.M06.gz43_264250	F	M00055052D:G12	UC2-ColonMetLiver
4601	555660	2018.A07.gz43_264254	F	M00055039B:E02	UC2-ColonMetLiver
4602	561901	2018.C07.gz43_264256	F	M00055042A:D09	UC2-ColonMetLiver
4603	554936	2018.H07.gz43_264261	F	M00055047C:F07	UC2-ColonMetLiver
4604	555010	2018.J07.gz43_264263	F	M00055049C:H12	UC2-ColonMetLiver
4605	560801	2018.L07.gz43_264265	F	M00055051D:F01	UC2-ColonMetLiver
4606	555993	2018.A08.gz43_264270	F	M00055039B:G11	UC2-ColonMetLiver
4607	465207	2018.H08.gz43_264277	F	M00055047C:F08	UC2-ColonMetLiver
4608	419153	2018.I08.gz43_264278	F	M00055048D:D08	UC2-ColonMetLiver
4609	562808	2018.P08.gz43_264285	F	M00055056C:F04	UC2-ColonMetLiver
4610	601365	2018.A09.gz43_264286	F	M00055039B:H10	UC2-ColonMetLiver
4611	375380	2018.F09.gz43_264291	F	M00055046B:C07	UC2-ColonMetLiver
4612	561216	2018.J09.gz43_264295	F	M00055049D:D09	UC2-ColonMetLiver
4613	498629	2018.O09.gz43_264300	F	M00055055C:C09	UC2-ColonMetLiver
4614	555524	2018.B10.gz43_264303	F	M00055041B:D11	UC2-ColonMetLiver
4615	549008	2018.C10.gz43_264304	F	M00055042B:B09	UC2-ColonMetLiver
4616	555771	2018.E10.gz43_264306	F	M00055045A:F03	UC2-ColonMetLiver
4617	515115	2018.O10.gz43_264316	F	M00055055C:D02	UC2-ColonMetLiver
4618	529733	2018.A11.gz43_264318	F	M00055039C:B05	UC2-ColonMetLiver
4619	553850	2018.E11.gz43_264322	F	M00055045A:F12	UC2-ColonMetLiver
4620	557735	2018.G11.gz43_264324	F	M00055047A:E07	UC2-ColonMetLiver

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SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
4621	555798	2018.H11.gz43_264325	F	M00055047D:C12	UC2-ColonMetLiver
4622	553108	2018.M11.gz43_264330	F	M00055053B:A02	UC2-ColonMetLiver
4623	555708	2018.C12.gz43_264336	F	M00055042B:E02	UC2-ColonMetLiver
4624	559699	2018.E12.gz43_264338	F	M00055045B:A04	UC2-ColonMetLiver
4625	551068	2018.K12.gz43_264344	F	M00055051A:C09	UC2-ColonMetLiver
4626	559246	2018.L12.gz43_264345	F	M00055052A:F07	UC2-ColonMetLiver
4627	557401	2018.P12.gz43_264349	F	M00055056D:B06	UC2-ColonMetLiver
4628	557525	2018.M13.gz43_264362	F	M00055053B:C02	UC2-ColonMetLiver
4629	8997	2018.N13.gz43_264363	F	M00055054B:E10	UC2-ColonMetLiver
4630	560720	2018.E14.gz43_264370	F	M00055045B:C08	UC2-ColonMetLiver
4631	558120	2018.G14.gz43_264372	F	M00055047A:H05	UC2-ColonMetLiver
4632	349744	2018.I14.gz43_264374	F	M00055048D:H04	UC2-ColonMetLiver
4633	561259	2018.A15.gz43_264382	F	M00055039D:D07	UC2-ColonMetLiver
4634	557326	2018.G15.gz43_264388	F	M00055047B:A10	UC2-ColonMetLiver
4635	449437	2018.J15.gz43_264391	F	M00055050A:D11	UC2-ColonMetLiver
4636	555340	2018.K15.gz43_264392	F	M00055051A:G09	UC2-ColonMetLiver
4637	555172	2018.C16.gz43_264400	F	M00055042C:B05	UC2-ColonMetLiver
4638	289316	2018.G16.gz43_264404	F	M00055047B:B03	UC2-ColonMetLiver
4639	557279	2018.H16.gz43_264405	F	M00055048A:A04	UC2-ColonMetLiver
4640	556169	2018.J16.gz43_264407	F	M00055050A:H08	UC2-ColonMetLiver
4641	551897	2018.K16.gz43_264408	F	M00055051A:H10	UC2-ColonMetLiver
4642	556391	2018.P16.gz43_264413	F	M00055056D:H12	UC2-ColonMetLiver
4643	562949	2018.D17.gz43_264417	F	M00055044A:A08	UC2-ColonMetLiver
4644	551371	2018.L17.gz43_264425	F	M00055052B:E03	UC2-ColonMetLiver
4645	562292	2018.M17.gz43_264426	F	M00055053C:B03	UC2-ColonMetLiver
4646	555082	2018.N17.gz43_264427	F	M00055054B:G12	UC2-ColonMetLiver
4647	562272	2018.P17.gz43_264429	F	M00055057A:A04	UC2-ColonMetLiver
4648	555883	2018.A18.gz43_264430	F	M00055040A:F01	UC2-ColonMetLiver
4649	558389	2018.F18.gz43_264435	F	M00055046C:C05	UC2-ColonMetLiver
4650	463341	2018.O18.gz43_264444	F	M00055056A:H12	UC2-ColonMetLiver
4651	553002	2018.P18.gz43_264445	F	M00055057A:A05	UC2-ColonMetLiver
4652	224812	2018.E19.gz43_264450	F	M00055045C:H05	UC2-ColonMetLiver
4653	206098	2018.J19.gz43_264455	F	M00055050B:E11	UC2-ColonMetLiver
4654	453893	2018.H20.gz43_264469	F	M00055048A:F04	UC2-ColonMetLiver
4655	557308	2018.N21.gz43_264491	F	M00055054D:A02	UC2-ColonMetLiver
4656	470617	2018.B22.gz43_264495	F	M00055041C:H12	UC2-ColonMetLiver
4657	555057	2018.N22.gz43_264507	F	M00055054D:E12	UC2-ColonMetLiver
4658	447815	2018.A23.gz43_264510	F	M00055040C:G08	UC2-ColonMetLiver
4659	561963	2018.N24.gz43_264539	F	M00055055A:B03	UC2-ColonMetLiver
4660	551544	2018.P24.gz43_264541	F	M00055057B:B01	UC2-ColonMetLiver
4661	555213	2018.D07.gz43_264641	F	M00055043B:B01	UC2-ColonMetLiver
4662	555010	2018.J07.gz43_264647	F	M00055049C:H12	UC2-ColonMetLiver

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SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
4663	505451	2018.P07.gz43_264653	F	M00055056C:E10	UC2-ColonMetLiver
4664	555993	2018.A08.gz43_264654	F	M00055039B:G11	UC2-ColonMetLiver
4665	465207	2018.H08.gz43_264661	F	M00055047C:F08	UC2-ColonMetLiver
4666	557834	2018.K08.gz43_264664	F	M00055050D:F04	UC2-ColonMetLiver
4667	557882	2018.L08.gz43_264665	F	M00055051D:G01	UC2-ColonMetLiver
4668	551711	2018.B09.gz43_264671	F	M00055041B:C10	UC2-ColonMetLiver
4669	555524	2018.B10.gz43_264687	F	M00055041B:D11	UC2-ColonMetLiver
4670	446739	2018.J10.gz43_264695	F	M00055049D:D10	UC2-ColonMetLiver
4671	385531	2018.P10.gz43_264701	F	M00055056C:H07	UC2-ColonMetLiver
4672	559052	2018.F11.gz43_264707	F	M00055046B:D02	UC2-ColonMetLiver
4673	553108	2018.M11.gz43_264714	F	M00055053B:A02	UC2-ColonMetLiver
4674	397338	2018.A12.gz43_264718	F	M00055039C:D11	UC2-ColonMetLiver
4675	559699	2018.E12.gz43_264722	F	M00055045B:A04	UC2-ColonMetLiver
4676	553975	2018.O12.gz43_264732	F	M00055055C:E08	UC2-ColonMetLiver
4677	561994	2018.B13.gz43_264735	F	M00055041B:F04	UC2-ColonMetLiver
4678	448098	2018.C13.gz43_264736	F	M00055042B:E05	UC2-ColonMetLiver
4679	558254	2018.D13.gz43_264737	F	M00055043D:D10	UC2-ColonMetLiver
4680	557420	2018.F13.gz43_264739	F	M00055046B:E08	UC2-ColonMetLiver
4681	558007	2018.G13.gz43_264740	F	M00055047A:H04	UC2-ColonMetLiver
4682	557525	2018.M13.gz43_264746	F	M00055053B:C02	UC2-ColonMetLiver
4683	450765	2018.C14.gz43_264752	F	M00055042B:E08	UC2-ColonMetLiver
4684	247	2018.D14.gz43_264753	F	M00055043D:F07	UC2-ColonMetLiver
4685	560720	2018.E14.gz43_264754	F	M00055045B:C08	UC2-ColonMetLiver
4686	491799	2018.F14.gz43_264755	F	M00055046B:F06	UC2-ColonMetLiver
4687	558120	2018.G14.gz43_264756	F	M00055047A:H05	UC2-ColonMetLiver
4688	432970	2018.K14.gz43_264760	F	M00055051A:E11	UC2-ColonMetLiver
4689	561259	2018.A15.gz43_264766	F	M00055039D:D07	UC2-ColonMetLiver
4690	551630	2018.O15.gz43_264780	F	M00055055D:D11	UC2-ColonMetLiver
4691	461	2018.M16.gz43_264794	F	M00055053C:A12	UC2-ColonMetLiver
4692	555399	2018.A17.gz43_264798	F	M00055040A:C02	UC2-ColonMetLiver
4693	554149	2018.B17.gz43_264799	F	M00055041C:C10	UC2-ColonMetLiver
4694	553603	2018.G17.gz43_264804	F	M00055047B:B10	UC2-ColonMetLiver
4695	552641	2018.K17.gz43_264808	F	M00055051B:B08	UC2-ColonMetLiver
4696	562292	2018.M17.gz43_264810	F	M00055053C:B03	UC2-ColonMetLiver
4697	562272	2018.P17.gz43_264813	F	M00055057A:A04	UC2-ColonMetLiver
4698	450755	2018.D18.gz43_264817	F	M00055044A:C02	UC2-ColonMetLiver
4699	555892	2018.E18.gz43_264818	F	M00055045C:F09	UC2-ColonMetLiver
4700	551793	2018.G18.gz43_264820	F	M00055047B:C03	UC2-ColonMetLiver
4701	553002	2018.P18.gz43_264829	F	M00055057A:A05	UC2-ColonMetLiver
4702	487182	2018.I19.gz43_264838	F	M00055049A:F10	UC2-ColonMetLiver
4703	206098	2018.J19.gz43_264839	F	M00055050B:E11	UC2-ColonMetLiver
4704	557572	2018.K19.gz43_264840	F	M00055051B:D07	UC2-ColonMetLiver

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SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
4705	551334	2018.M19.gz43_264842	F	M00055053C:F06	UC2-ColonMetLiver
4706	561046	2018.I20.gz43_264854	F	M00055049A:G03	UC2-ColonMetLiver
4707	454664	2018.L20.gz43_264857	F	M00055052C:B12	UC2-ColonMetLiver
4708	551616	2018.N20.gz43_264859	F	M00055054C:G10	UC2-ColonMetLiver
4709	559294	2018.P20.gz43_264861	F	M00055057A:D10	UC2-ColonMetLiver
4710	548935	2018.C21.gz43_264864	F	M00055042D:G03	UC2-ColonMetLiver
4711	488970	2018.F21.gz43_264867	F	M00055046C:E07	UC2-ColonMetLiver
4712	555751	2018.A22.gz43_264878	F	M00055040B:F02	UC2-ColonMetLiver
4713	423588	2018.C22.gz43_264880	F	M00055042D:H02	UC2-ColonMetLiver
4714	551578	2018.E22.gz43_264882	F	M00055045D:A07	UC2-ColonMetLiver
4715	556171	2018.G22.gz43_264884	F	M00055047B:G06	UC2-ColonMetLiver
4716	451172	2018.P22.gz43_264893	F	M00055057A:F10	UC2-ColonMetLiver
4717	555250	2018.B23.gz43_264895	F	M00055041D:B07	UC2-ColonMetLiver
4718	476268	2018.G23.gz43_264900	F	M00055047B:G10	UC2-ColonMetLiver
4719	553349	2018.K23.gz43_264904	F	M00055051C:B05	UC2-ColonMetLiver
4720	551561	2018.O23.gz43_264908	F	M00055056B:G01	UC2-ColonMetLiver
4721	555173	2018.C24.gz43_264912	F	M00055043A:B06	UC2-ColonMetLiver
4722	557382	2018.L24.gz43_264921	F	M00055052D:B05	UC2-ColonMetLiver
4723	555616	2020.H01.gz43_264933	F	M00055081A:E08	UC2-ColonMetLiver
4724	549607	2020.J01.gz43_264935	F	M00055083B:E05	UC2-ColonMetLiver
4725	492893	2020.L01.gz43_264937	F	M00055086A:B10	UC2-ColonMetLiver
4726	556471	2020.E02.gz43_264946	F	M00055077D:B01	UC2-ColonMetLiver
4727	556542	2020.L02.gz43_264953	F	M00055086A:C09	UC2-ColonMetLiver
4728	551283	2020.N02.gz43_264955	F	M00055088D:A01	UC2-ColonMetLiver
4729	558720	2020.C03.gz43_264960	F	M00055076A:C06	UC2-ColonMetLiver
4730	555512	2020.A04.gz43_264974	F	M00055073D:F06	UC2-ColonMetLiver
4731	549129	2020.D04.gz43_264977	F	M00055077A:B07	UC2-ColonMetLiver
4732	556497	2020.J04.gz43_264983	F	M00055083C:C05	UC2-ColonMetLiver
4733	561422	2020.N04.gz43_264987	F	M00055088D:B08	UC2-ColonMetLiver
4734	556408	2020.O04.gz43_264988	F	M00055090C:B03	UC2-ColonMetLiver
4735	556635	2020.B05.gz43_264991	F	M00055075A:C09	UC2-ColonMetLiver
4736	555368	2020.C05.gz43_264992	F	M00055076A:D11	UC2-ColonMetLiver
4737	495408	2020.F06.gz43_265011	F	M00055078D:G04	UC2-ColonMetLiver
4738	552361	2020.H06.gz43_265013	F	M00055081B:E10	UC2-ColonMetLiver
4739	556446	2020.K06.gz43_265016	F	M00055084D:B01	UC2-ColonMetLiver
4740	557476	2020.L06.gz43_265017	F	M00055086B:D10	UC2-ColonMetLiver
4741	556559	2020.O06.gz43_265020	F	M00055090C:C12	UC2-ColonMetLiver
4742	548943	2020.K07.gz43_265032	F	M00055084D:C09	UC2-ColonMetLiver
4743	555126	2020.P07.gz43_265037	F	M00055091B:A07	UC2-ColonMetLiver
4744	142614	2020.E08.gz43_265042	F	M00055078A:C05	UC2-ColonMetLiver
4745	453756	2020.M08.gz43_265050	F	M00055087D:D08	UC2-ColonMetLiver
4746	556040	2020.G09.gz43_265060	F	M00055080B:G10	UC2-ColonMetLiver

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
4747	557454	2020.N09.gz43_265067	F	M00055089A:H06	UC2-ColonMetLiver
4748	452822	2020.C11.gz43_265088	F	M00055076B:E08	UC2-ColonMetLiver
4749	464905	2020.E11.gz43_265090	F	M00055078A:E10	UC2-ColonMetLiver
4750	509505	2020.F11.gz43_265091	F	M00055079A:H05	UC2-ColonMetLiver
4751	555061	2020.H11.gz43_265093	F	M00055081C:A12	UC2-ColonMetLiver
4752	556668	2020.J11.gz43_265095	F	M00055083D:D08	UC2-ColonMetLiver
4753	549810	2020.C12.gz43_265104	F	M00055076B:F04	UC2-ColonMetLiver
4754	557760	2020.E12.gz43_265106	F	M00055078A:F01	UC2-ColonMetLiver
4755	554084	2020.N12.gz43_265115	F	M00055089B:C01	UC2-ColonMetLiver
4756	16092	2020.P12.gz43_265117	F	M00055091C:B04	UC2-ColonMetLiver
4757	551342	2020.L13.gz43_265129	F	M00055086D:C07	UC2-ColonMetLiver
4758	455820	2020.A14.gz43_265134	F	M00055074B:E05	UC2-ColonMetLiver
4759	555710	2020.I14.gz43_265142	F	M00055082D:E08	UC2-ColonMetLiver
4760	497086	2020.O14.gz43_265148	F	M00055090D:E03	UC2-ColonMetLiver
4761	561489	2020.E15.gz43_265154	F	M00055078B:F05	UC2-ColonMetLiver
4762	558616	2020.F15.gz43_265155	F	M00055079C:G06	UC2-ColonMetLiver
4763	559071	2020.P15.gz43_265165	F	M00055091C:D11	UC2-ColonMetLiver
4764	550701	2020.C16.gz43_265168	F	M00055076B:H06	UC2-ColonMetLiver
4765	551976	2020.G16.gz43_265172	F	M00055080D:A01	UC2-ColonMetLiver
4766	460244	2020.I16.gz43_265174	F	M00055082D:G01	UC2-ColonMetLiver
4767	556802	2020.J16.gz43_265175	F	M00055084A:E10	UC2-ColonMetLiver
4768	454910	2020.K16.gz43_265176	F	M00055085B:D02	UC2-ColonMetLiver
4769	557214	2020.L16.gz43_265177	F	M00055086D:H07	UC2-ColonMetLiver
4770	612961	2020.F17.gz43_265187	F	M00055079D:A03	UC2-ColonMetLiver
4771	465446	2020.I17.gz43_265190	F	M00055082D:H02	UC2-ColonMetLiver
4772	556925	2020.J17.gz43_265191	F	M00055084A:F10	UC2-ColonMetLiver
4773	98869	2020.O17.gz43_265196	F	M00055090D:F03	UC2-ColonMetLiver
4774	553372	2020.H18.gz43_265205	F	M00055081C:G01	UC2-ColonMetLiver
4775	558231	2020.J18.gz43_265207	F	M00055084B:A04	UC2-ColonMetLiver
4776	553318	2020.G19.gz43_265220	F	M00055080D:E07	UC2-ColonMetLiver
4777	449613	2020.H19.gz43_265221	F	M00055081C:H04	UC2-ColonMetLiver
4778	560507	2020.N19.gz43_265227	F	M00055089C:D06	UC2-ColonMetLiver
4779	560069	2020.B20.gz43_265231	F	M00055075D:D05	UC2-ColonMetLiver
4780	557954	2020.C20.gz43_265232	F	M00055076C:H07	UC2-ColonMetLiver
4781	555996	2020.E21.gz43_265250	F	M00055078D:A07	UC2-ColonMetLiver
4782	494625	2020.G21.gz43_265252	F	M00055080D:F01	UC2-ColonMetLiver
4783	554828	2020.P21.gz43_265261	F	M00055091D:A03	UC2-ColonMetLiver
4784	562229	2020.A22.gz43_265262	F	M00055074D:B04	UC2-ColonMetLiver
4785	561975	2020.M22.gz43_265274	F	M00055088C:D01	UC2-ColonMetLiver
4786	560080	2020.N22.gz43_265275	F	M00055090A:F02	UC2-ColonMetLiver
4787	557783	2020.C23.gz43_265280	F	M00055076D:F11	UC2-ColonMetLiver
4788	556881	2020.K23.gz43_265288	F	M00055085D:F03	UC2-ColonMetLiver

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SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
4789	557747	2020.M23.gz43_265290	F	M00055088C:D02	UC2-ColonMetLiver
4790	598101	2020.O23.gz43_265292	F	M00055091A:C09	UC2-ColonMetLiver
4791	451185	2020.F24.gz43_265299	F	M00055080A:F05	UC2-ColonMetLiver
4792	552019	2020.H24.gz43_265301	F	M00055082A:A12	UC2-ColonMetLiver
4793	555725	2020.K24.gz43_265304	F	M00055085D:G09	UC2-ColonMetLiver
4794	562748	2029.P01.gz43_265325	F	M00055111A:F10	UC2-ColonMetLiver
4795	562989	2029.I02.gz43_265334	F	M00055100C:H06	UC2-ColonMetLiver
4796	562243	2029.I03.gz43_265350	F	M00055100D:B02	UC2-ColonMetLiver
4797	562768	2029.B06.gz43_265391	F	M00055093A:F07	UC2-ColonMetLiver
4798	491127	2029.D06.gz43_265393	F	M00055094D:F09	UC2-ColonMetLiver
4799	555330	2029.H07.gz43_265413	F	M00055100A:C05	UC2-ColonMetLiver
4800	552704	2029.L07.gz43_265417	F	M00055105D:B06	UC2-ColonMetLiver
4801	561426	2029.O08.gz43_265436	F	M00055110A:C03	UC2-ColonMetLiver
4802	551967	2029.E09.gz43_265442	F	M00055096A:G08	UC2-ColonMetLiver
4803	453533	2029.F09.gz43_265443	F	M00055097B:B12	UC2-ColonMetLiver
4804	394189	2029.O09.gz43_265452	F	M00055110A:C05	UC2-ColonMetLiver
4805	562719	2029.F10.gz43_265459	F	M00055097B:F08	UC2-ColonMetLiver
4806	562307	2029.C11.gz43_265472	F	M00055094B:B11	UC2-ColonMetLiver
4807	98484	2029.D11.gz43_265473	F	M00055095A:D08	UC2-ColonMetLiver
4808	558118	2029.G11.gz43_265476	F	M00055099A:G05	UC2-ColonMetLiver
4809	562881	2029.B14.gz43_265519	F	M00055093B:G08	UC2-ColonMetLiver
4810	553548	2029.K14.gz43_265528	F	M00055104B:F09	UC2-ColonMetLiver
4811	637966	2029.A15.gz43_265534	F	M00055092B:G09	UC2-ColonMetLiver
4812	560575	2029.L15.gz43_265545	F	M00055106A:E04	UC2-ColonMetLiver
4813	554496	2029.E16.gz43_265554	F	M00055096C:C03	UC2-ColonMetLiver
4814	561144	2029.J16.gz43_265559	F	M00055103A:H11	UC2-ColonMetLiver
4815	560628	2029.I20.gz43_265622	F	M00055102A:E11	UC2-ColonMetLiver
4816	558511	2029.J20.gz43_265623	F	M00055103C:B07	UC2-ColonMetLiver
4817	402488	2029.C21.gz43_265632	F	M00055094C:C10	UC2-ColonMetLiver
4818	556613	2029.J21.gz43_265639	F	M00055103C:D05	UC2-ColonMetLiver
4819	560898	2029.J22.gz43_265655	F	M00055103C:G03	UC2-ColonMetLiver
4820	454499	2029.L22.gz43_265657	F	M00055106C:B06	UC2-ColonMetLiver
4821	559955	2029.K23.gz43_265672	F	M00055105A:A05	UC2-ColonMetLiver
4822	554233	2030.J01.gz43_265703	F	M00055128A:C10	UC2-ColonMetLiver
4823	557615	2030.K01.gz43_265704	F	M00055128D:D04	UC2-ColonMetLiver
4824	449035	2030.C02.gz43_265712	F	M00055115C:G09	UC2-ColonMetLiver
4825	452525	2030.E03.gz43_265730	F	M00055118C:B03	UC2-ColonMetLiver
4826	452775	2030.L03.gz43_265737	F	M00055129D:C02	UC2-ColonMetLiver
4827	560868	2030.E05.gz43_265762	F	M00055118D:B04	UC2-ColonMetLiver
4828	538830	2030.H05.gz43_265765	F	M00055125A:A02	UC2-ColonMetLiver
4829	486683	2030.K05.gz43_265768	F	M00055129A:B03	UC2-ColonMetLiver
4830	488030	2030.L06.gz43_265785	F	M00055129D:F11	UC2-ColonMetLiver

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SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
4831	66678	2030.M06.gz43_265786	F	M00055130D:F08	UC2-ColonMetLiver
4832	528369	2030.J07.gz43_265799	F	M00055128B:B12	UC2-ColonMetLiver
4833	479732	2030.G08.gz43_265812	F	M00055124A:F01	UC2-ColonMetLiver
4834	557747	2030.O08.gz43_265820	F	M00055133B:E08	UC2-ColonMetLiver
4835	558534	2030.H09.gz43_265829	F	M00055125B:F01	UC2-ColonMetLiver
4836	312036	2030.D10.gz43_265841	F	M00055117A:G08	UC2-ColonMetLiver
4837	461653	2030.J10.gz43_265847	F	M00055128B:E12	UC2-ColonMetLiver
4838	558060	2030.G11.gz43_265860	F	M00055124B:A11	UC2-ColonMetLiver
4839	557610	2030.L11.gz43_265865	F	M00055130A:D10	UC2-ColonMetLiver
4840	557284	2030.P11.gz43_265869	F	M00055134C:A01	UC2-ColonMetLiver
4841	562714	2030.A12.gz43_265870	F	M00055113B:F02	UC2-ColonMetLiver
4842	453274	2030.C12.gz43_265872	F	M00055116A:C07	UC2-ColonMetLiver
4843	551068	2030.P12.gz43_265885	F	M00055134C:B01	UC2-ColonMetLiver
4844	125543	2030.J13.gz43_265895	F	M00055128B:G01	UC2-ColonMetLiver
4845	449454	2030.M13.gz43_265898	F	M00055131A:D07	UC2-ColonMetLiver
4846	562760	2030.O13.gz43_265900	F	M00055133C:C06	UC2-ColonMetLiver
4847	557710	2030.P13.gz43_265901	F	M00055134C:E09	UC2-ColonMetLiver
4848	526334	2030.E14.gz43_265906	F	M00055119D:F08	UC2-ColonMetLiver
4849	451392	2030.O15.gz43_265932	F	M00055133C:G07	UC2-ColonMetLiver
4850	549591	2030.D16.gz43_265937	F	M00055117C:C03	UC2-ColonMetLiver
4851	557895	2030.H16.gz43_265941	F	M00055125C:H03	UC2-ColonMetLiver
4852	554989	2030.J16.gz43_265943	F	M00055128C:E03	UC2-ColonMetLiver
4853	561265	2030.D17.gz43_265953	F	M00055117C:F02	UC2-ColonMetLiver
4854	558015	2030.O17.gz43_265964	F	M00055133C:H11	UC2-ColonMetLiver
4855	561741	2030.A18.gz43_265966	F	M00055114A:E02	UC2-ColonMetLiver
4856	477295	2030.O18.gz43_265980	F	M00055133D:A02	UC2-ColonMetLiver
4857	556310	2030.E19.gz43_265986	F	M00055120B:F12	UC2-ColonMetLiver
4858	558452	2030.H20.gz43_266005	F	M00055125D:E02	UC2-ColonMetLiver
4859	610269	2030.N21.gz43_266027	F	M00055132D:E07	UC2-ColonMetLiver
4860	561279	2030.J22.gz43_266039	F	M00055128D:C11	UC2-ColonMetLiver
4861	557719	2030.N22.gz43_266043	F	M00055132D:E10	UC2-ColonMetLiver
4862	451391	2030.O22.gz43_266044	F	M00055133D:F02	UC2-ColonMetLiver
4863	554737	2030.D24.gz43_266065	F	M00055118B:A09	UC2-ColonMetLiver
4864	452759	2030.K24.gz43_266072	F	M00055129C:H08	UC2-ColonMetLiver
4865	562683	2031.A01.gz43_266078	F	M00055135A:E07	UC2-ColonMetLiver
4866	558463	2031.C04.gz43_266128	F	M00055138A:E08	UC2-ColonMetLiver
4867	211273	2031.I04.gz43_266134	F	M00055146A:B12	UC2-ColonMetLiver
4868	468257	2031.N04.gz43_266139	F	M00055152D:C03	UC2-ColonMetLiver
4869	558768	2031.B05.gz43_266143	F	M00055136D:D09	UC2-ColonMetLiver
4870	561245	2031.G05.gz43_266148	F	M00055144A:A11	UC2-ColonMetLiver
4871	557783	2031.K05.gz43_266152	F	M00055149B:F09	UC2-ColonMetLiver
4872	549930	2031.O05.gz43_266156	F	M00055154D:F06	UC2-ColonMetLiver

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SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
4873	558619	2031.C06.gz43_266160	F	M00055138A:G08	UC2-ColonMetLiver
4874	450630	2031.G06.gz43_266164	F	M00055144A:E09	UC2-ColonMetLiver
4875	524721	2031.O06.gz43_266172	F	M00055154D:G12	UC2-ColonMetLiver
4876	561624	2031.P06.gz43_266173	F	M00055156A:D02	UC2-ColonMetLiver
4877	497493	2031.N07.gz43_266187	F	M00055152D:H09	UC2-ColonMetLiver
4878	490846	2031.M08.gz43_266202	F	M00055152A:B05	UC2-ColonMetLiver
4879	558645	2031.P08.gz43_266205	F	M00055156B:C11	UC2-ColonMetLiver
4880	553969	2031.D09.gz43_266209	F	M00055139B:E10	UC2-ColonMetLiver
4881	558007	2031.P09.gz43_266221	F	M00055156C:A08	UC2-ColonMetLiver
4882	550047	2031.B10.gz43_266223	F	M00055137A:E05	UC2-ColonMetLiver
4883	562000	2031.I10.gz43_266230	F	M00055146B:E09	UC2-ColonMetLiver
4884	160289	2031.L10.gz43_266233	F	M00055150D:C06	UC2-ColonMetLiver
4885	27586	2031.C11.gz43_266240	F	M00055138B:H12	UC2-ColonMetLiver
4886	558230	2031.D11.gz43_266241	F	M00055139B:G03	UC2-ColonMetLiver
4887	549739	2031.M12.gz43_266266	F	M00055152A:E09	UC2-ColonMetLiver
4888	561558	2031.P12.gz43_266269	F	M00055156C:D06	UC2-ColonMetLiver
4889	556630	2031.B14.gz43_266287	F	M00055137B:B11	UC2-ColonMetLiver
4890	561178	2031.P15.gz43_266317	F	M00055156D:A02	UC2-ColonMetLiver
4891	558477	2031.B16.gz43_266319	F	M00055137B:F12	UC2-ColonMetLiver
4892	557250	2031.M16.gz43_266330	F	M00055152B:A03	UC2-ColonMetLiver
4893	556288	2031.P17.gz43_266349	F	M00055157A:B04	UC2-ColonMetLiver
4894	610893	2031.L18.gz43_266361	F	M00055151A:F10	UC2-ColonMetLiver
4895	557708	2031.O24.gz43_266460	F	M00055155D:B02	UC2-ColonMetLiver
4896	562881	2032.E01.gz43_266466	F	M00055162A:B03	UC2-ColonMetLiver
4897	494198	2032.L01.gz43_266473	F	M00055170D:B09	UC2-ColonMetLiver
4898	551475	2032.O01.gz43_266476	F	M00055177A:F05	UC2-ColonMetLiver
4899	558720	2032.K02.gz43_266488	F	M00055169D:A11	UC2-ColonMetLiver
4900	2435	2032.E03.gz43_266498	F	M00055162A:C12	UC2-ColonMetLiver
4901	559464	2032.I04.gz43_266518	F	M00055166D:F02	UC2-ColonMetLiver
4902	559389	2032.A05.gz43_266526	F	M00055157C:C11	UC2-ColonMetLiver
4903	559562	2032.H05.gz43_266533	F	M00055165B:G09	UC2-ColonMetLiver
4904	402799	2032.M05.gz43_266538	F	M00055172A:C09	UC2-ColonMetLiver
4905	557316	2032.J06.gz43_266551	F	M00055168B:F11	UC2-ColonMetLiver
4906	557209	2032.K06.gz43_266552	F	M00055170A:A09	UC2-ColonMetLiver
4907	554604	2032.M06.gz43_266554	F	M00055172A:F03	UC2-ColonMetLiver
4908	558917	2032.H07.gz43_266565	F	M00055165C:H08	UC2-ColonMetLiver
4909	493261	2032.I07.gz43_266566	F	M00055167A:A02	UC2-ColonMetLiver
4910	558755	2032.K07.gz43_266568	F	M00055170A:A11	UC2-ColonMetLiver
4911	558900	2032.M09.gz43_266602	F	M00055172B:B04	UC2-ColonMetLiver
4912	553537	2032.C10.gz43_266608	F	M00055160C:D02	UC2-ColonMetLiver
4913	561413	2032.E10.gz43_266610	F	M00055162B:B04	UC2-ColonMetLiver
4914	561876	2032.F10.gz43_266611	F	M00055163B:F07	UC2-ColonMetLiver

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SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
4915	553797	2032.H10.gz43_266613	F	M00055165D:C03	UC2-ColonMetLiver
4916	558965	2032.G11.gz43_266628	F	M00055164C:C10	UC2-ColonMetLiver
4917	561911	2032.B12.gz43_266639	F	M00055159B:G09	UC2-ColonMetLiver
4918	557961	2032.I12.gz43_266646	F	M00055167B:A08	UC2-ColonMetLiver
4919	558022	2032.K12.gz43_266648	F	M00055170B:B06	UC2-ColonMetLiver
4920	409262	2032.M12.gz43_266650	F	M00055172B:H07	UC2-ColonMetLiver
4921	415538	2032.I15.gz43_266694	F	M00055167B:H07	UC2-ColonMetLiver
4922	559057	2032.M15.gz43_266698	F	M00055172D:D04	UC2-ColonMetLiver
4923	215005	2032.B16.gz43_266703	F	M00055159C:B02	UC2-ColonMetLiver
4924	556542	2032.M16.gz43_266714	F	M00055172D:D07	UC2-ColonMetLiver
4925	562989	2032.O17.gz43_266732	F	M00055177D:F07	UC2-ColonMetLiver
4926	394772	2032.A19.gz43_266750	F	M00055158D:C01	UC2-ColonMetLiver
4927	553877	2032.E19.gz43_266754	F	M00055162C:E12	UC2-ColonMetLiver
4928	558858	2032.I19.gz43_266758	F	M00055167D:B05	UC2-ColonMetLiver
4929	559355	2032.J19.gz43_266759	F	M00055169B:F04	UC2-ColonMetLiver
4930	551693	2032.M19.gz43_266762	F	M00055172D:F12	UC2-ColonMetLiver
4931	323165	2032.E20.gz43_266770	F	M00055162C:G03	UC2-ColonMetLiver
4932	558981	2032.O20.gz43_266780	F	M00055178A:C07	UC2-ColonMetLiver
4933	561507	2032.C21.gz43_266784	F	M00055161A:C02	UC2-ColonMetLiver
4934	555883	2032.E22.gz43_266802	F	M00055162D:B01	UC2-ColonMetLiver
4935	559088	2032.O22.gz43_266812	F	M00055178A:D03	UC2-ColonMetLiver
4936	558395	2032.C23.gz43_266816	F	M00055161A:E05	UC2-ColonMetLiver
4937	447386	2032.D23.gz43_266817	F	M00055161D:H03	UC2-ColonMetLiver
4938	450566	2032.L23.gz43_266825	F	M00055171C:C01	UC2-ColonMetLiver
4939	561918	2032.E24.gz43_266834	F	M00055162D:G04	UC2-ColonMetLiver
4940	559389	2032.G24.gz43_266836	F	M00055165A:F05	UC2-ColonMetLiver
4941	555202	2032.M24.gz43_266842	F	M00055174A:H12	UC2-ColonMetLiver
4942	559752	2032.N24.gz43_266843	F	M00055176D:H01	UC2-ColonMetLiver
4943	478511	2041.B01.gz43_266847	F	M00055181B:A10	UC2-ColonMetLiver
4944	456517	2041.D01.gz43_266849	F	M00055183A:C06	UC2-ColonMetLiver
4945	557895	2041.H01.gz43_266853	F	M00055187D:G11	UC2-ColonMetLiver
4946	561975	2041.A02.gz43_266862	F	M00055179A:G08	UC2-ColonMetLiver
4947	557714	2041.D02.gz43_266865	F	M00055183A:E10	UC2-ColonMetLiver
4948	550874	2041.K02.gz43_266872	F	M00055192C:E04	UC2-ColonMetLiver
4949	539142	2041.L02.gz43_266873	F	M00055193C:C11	UC2-ColonMetLiver
4950	549911	2041.M02.gz43_266874	F	M00055194D:C05	UC2-ColonMetLiver
4951	561830	2041.N02.gz43_266875	F	M00055195C:H05	UC2-ColonMetLiver
4952	479851	2041.A03.gz43_266878	F	M00055179A:H11	UC2-ColonMetLiver
4953	549472	2041.B03.gz43_266879	F	M00055181B:E06	UC2-ColonMetLiver
4954	561687	2041.F03.gz43_266883	F	M00055185D:A02	UC2-ColonMetLiver
4955	504880	2041.L03.gz43_266889	F	M00055193C:E10	UC2-ColonMetLiver
4956	558212	2041.E04.gz43_266898	F	M00055184C:C07	UC2-ColonMetLiver

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
4957	559050	2041.A05.gz43_266910	F	M00055179B:D05	UC2-ColonMetLiver
4958	554520	2041.C05.gz43_266912	F	M00055182A:D07	UC2-ColonMetLiver
4959	409612	2041.E05.gz43_266914	F	M00055184C:D02	UC2-ColonMetLiver
4960	488613	2041.J05.gz43_266919	F	M00055191B:A10	UC2-ColonMetLiver
4961	558326	2041.K05.gz43_266920	F	M00055192C:H06	UC2-ColonMetLiver
4962	555394	2041.F06.gz43_266931	F	M00055185D:D11	UC2-ColonMetLiver
4963	559610	2041.H06.gz43_266933	F	M00055188A:G11	UC2-ColonMetLiver
4964	560080	2041.I06.gz43_266934	F	M00055189B:B12	UC2-ColonMetLiver
4965	555742	2041.N06.gz43_266939	F	M00055195D:B10	UC2-ColonMetLiver
4966	460727	2041.P06.gz43_266941	F	M00055198A:E05	UC2-ColonMetLiver
4967	476199	2041.B07.gz43_266943	F	M00055181C:B07	UC2-ColonMetLiver
4968	516484	2041.G07.gz43_266948	F	M00055187A:F02	UC2-ColonMetLiver
4969	187704	2041.H07.gz43_266949	F	M00055188A:H10	UC2-ColonMetLiver
4970	559000	2041.A08.gz43_266958	F	M00055179B:G07	UC2-ColonMetLiver
4971	553002	2041.B08.gz43_266959	F	M00055181C:B12	UC2-ColonMetLiver
4972	226324	2041.C08.gz43_266960	F	M00055182B:C07	UC2-ColonMetLiver
4973	562840	2041.D08.gz43_266961	F	M00055183C:A02	UC2-ColonMetLiver
4974	561513	2041.E08.gz43_266962	F	M00055184C:F01	UC2-ColonMetLiver
4975	477046	2041.F08.gz43_266963	F	M00055185D:F07	UC2-ColonMetLiver
4976	492627	2041.G08.gz43_266964	F	M00055187A:F06	UC2-ColonMetLiver
4977	559262	2041.H08.gz43_266965	F	M00055188B:E06	UC2-ColonMetLiver
4978	561513	2041.B09.gz43_266975	F	M00055181C:C09	UC2-ColonMetLiver
4979	556632	2041.C09.gz43_266976	F	M00055182B:F05	UC2-ColonMetLiver
4980	552629	2041.G09.gz43_266980	F	M00055187A:G02	UC2-ColonMetLiver
4981	549304	2041.M09.gz43_266986	F	M00055195A:B08	UC2-ColonMetLiver
4982	550652	2041.N09.gz43_266987	F	M00055195D:E11	UC2-ColonMetLiver
4983	490154	2041.P09.gz43_266989	F	M00055198B:H08	UC2-ColonMetLiver
4984	559383	2041.A10.gz43_266990	F	M00055179C:F11	UC2-ColonMetLiver
4985	502343	2041.F10.gz43_266995	F	M00055185D:H01	UC2-ColonMetLiver
4986	413915	2041.I10.gz43_266998	F	M00055189C:C01	UC2-ColonMetLiver
4987	495591	2041.L10.gz43_267001	F	M00055194A:A01	UC2-ColonMetLiver
4988	481231	2041.O10.gz43_267004	F	M00055196D:F07	UC2-ColonMetLiver
4989	559710	2041.A11.gz43_267006	F	M00055179C:H02	UC2-ColonMetLiver
4990	562569	2041.B11.gz43_267007	F	M00055181C:D06	UC2-ColonMetLiver
4991	552629	2041.F11.gz43_267011	F	M00055186A:D04	UC2-ColonMetLiver
4992	560003	2041.K11.gz43_267016	F	M00055193A:A08	UC2-ColonMetLiver
4993	550704	2041.M11.gz43_267018	F	M00055195A:C10	UC2-ColonMetLiver
4994	562569	2041.O11.gz43_267020	F	M00055196D:H02	UC2-ColonMetLiver
4995	561963	2041.D12.gz43_267025	F	M00055183C:D07	UC2-ColonMetLiver
4996	557867	2041.F12.gz43_267027	F	M00055186A:E08	UC2-ColonMetLiver
4997	143218	2041.M12.gz43_267034	F	M00055195A:E07	UC2-ColonMetLiver
4998	495074	2041.N12.gz43_267035	F	M00055196A:C04	UC2-ColonMetLiver

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
4999	560213	2041.J13.gz43_267047	F	M00055191D:C05	UC2-ColonMetLiver
5000	558413	2041.L13.gz43_267049	F	M00055194A:E07	UC2-ColonMetLiver
5001	551977	2041.N13.gz43_267051	F	M00055196A:E01	UC2-ColonMetLiver
5002	558582	2041.E14.gz43_267058	F	M00055185A:G11	UC2-ColonMetLiver
5003	549665	2041.H14.gz43_267061	F	M00055188C:F08	UC2-ColonMetLiver
5004	451544	2041.K14.gz43_267064	F	M00055193A:C06	UC2-ColonMetLiver
5005	450623	2041.M14.gz43_267066	F	M00055195B:B09	UC2-ColonMetLiver
5006	551855	2041.G15.gz43_267076	F	M00055187C:C02	UC2-ColonMetLiver
5007	2284	2041.I15.gz43_267078	F	M00055190A:A05	UC2-ColonMetLiver
5008	559883	2041.J15.gz43_267079	F	M00055192A:A09	UC2-ColonMetLiver
5009	614369	2041.M15.gz43_267082	F	M00055195B:C04	UC2-ColonMetLiver
5010	553237	2041.N15.gz43_267083	F	M00055196A:H07	UC2-ColonMetLiver
5011	559883	2041.E16.gz43_267090	F	M00055185B:B01	UC2-ColonMetLiver
5012	481136	2041.F16.gz43_267091	F	M00055186C:A02	UC2-ColonMetLiver
5013	559885	2041.O16.gz43_267100	F	M00055197B:A10	UC2-ColonMetLiver
5014	551415	2041.P16.gz43_267101	F	M00055198D:A12	UC2-ColonMetLiver
5015	561351	2041.B17.gz43_267103	F	M00055181C:H01	UC2-ColonMetLiver
5016	556881	2041.C17.gz43_267104	F	M00055182C:E09	UC2-ColonMetLiver
5017	549588	2041.G17.gz43_267108	F	M00055187C:E07	UC2-ColonMetLiver
5018	365634	2041.N17.gz43_267115	F	M00055196B:A09	UC2-ColonMetLiver
5019	556343	2041.P17.gz43_267117	F	M00055198D:B08	UC2-ColonMetLiver
5020	624044	2041.K18.gz43_267128	F	M00055193B:A08	UC2-ColonMetLiver
5021	562336	2041.N18.gz43_267131	F	M00055196B:C06	UC2-ColonMetLiver
5022	557935	2041.D19.gz43_267137	F	M00055184A:G02	UC2-ColonMetLiver
5023	557298	2041.G19.gz43_267140	F	M00055187D:A08	UC2-ColonMetLiver
5024	559146	2041.H19.gz43_267141	F	M00055188D:D05	UC2-ColonMetLiver
5025	455814	2041.I19.gz43_267142	F	M00055190A:F11	UC2-ColonMetLiver
5026	549829	2041.A20.gz43_267150	F	M00055181A:E01	UC2-ColonMetLiver
5027	473742	2041.B21.gz43_267167	F	M00055181D:D05	UC2-ColonMetLiver
5028	559333	2041.C21.gz43_267168	F	M00055182D:E06	UC2-ColonMetLiver
5029	559825	2041.H21.gz43_267173	F	M00055188D:H03	UC2-ColonMetLiver
5030	625988	2041.O21.gz43_267180	F	M00055197C:D10	UC2-ColonMetLiver
5031	491260	2041.P21.gz43_267181	F	M00055198D:G03	UC2-ColonMetLiver
5032	557644	2041.A22.gz43_267182	F	M00055181A:G02	UC2-ColonMetLiver
5033	411113	2041.E22.gz43_267186	F	M00055185C:B01	UC2-ColonMetLiver
5034	557961	2041.C23.gz43_267200	F	M00055182D:H08	UC2-ColonMetLiver
5035	559194	2041.A24.gz43_267214	F	M00055181A:H01	UC2-ColonMetLiver
5036	558463	2041.H24.gz43_267221	F	M00055189A:C11	UC2-ColonMetLiver
5037	560859	2041.I24.gz43_267222	F	M00055190C:G08	UC2-ColonMetLiver
5038	456697	2041.N24.gz43_267227	F	M00055196C:B07	UC2-ColonMetLiver
5039	559127	2054.E01.gz43_267234	F	M00055288B:D01	UC2-ColonMetLiver
5040	559460	2054.L01.gz43_267241	F	M00055300C:F11	UC2-ColonMetLiver

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
5041	624133	2054.M03.gz43_267274	F	M00055302B:B10	UC2-ColonMetLiver
5042	1079	2054.M05.gz43_267306	F	M00055302B:F07	UC2-ColonMetLiver
5043	559113	2054.A07.gz43_267326	F	M00055282A:A01	UC2-ColonMetLiver
5044	500337	2054.J13.gz43_267431	F	M00055297D:C02	UC2-ColonMetLiver
5045	558730	2054.E14.gz43_267442	F	M00055288D:A03	UC2-ColonMetLiver
5046	561779	2054.I14.gz43_267446	F	M00055296A:C05	UC2-ColonMetLiver
5047	397581	2054.H17.gz43_267493	F	M00055294B:C03	UC2-ColonMetLiver
5048	560420	2054.O18.gz43_267516	F	M00055305C:D08	UC2-ColonMetLiver
5049	559728	2054.C19.gz43_267520	F	M00055286A:H08	UC2-ColonMetLiver
5050	559531	2054.H20.gz43_267541	F	M00055294B:G01	UC2-ColonMetLiver
5051	23961	2054.K20.gz43_267544	F	M00055300A:B06	UC2-ColonMetLiver
5052	558446	2054.I21.gz43_267558	F	M00055296C:E08	UC2-ColonMetLiver
5053	562236	2055.K01.gz43_267624	F	M00055323D:A12	UC2-ColonMetLiver
5054	559776	2055.N01.gz43_267627	F	M00055330D:H12	UC2-ColonMetLiver
5055	559574	2055.J04.gz43_267671	F	M00055322C:G11	UC2-ColonMetLiver
5056	558890	2055.I05.gz43_267686	F	M00055321B:B10	UC2-ColonMetLiver
5057	552673	2055.J05.gz43_267687	F	M00055322D:A01	UC2-ColonMetLiver
5058	446900	2055.J07.gz43_267719	F	M00055322D:C12	UC2-ColonMetLiver
5059	559112	2055.C08.gz43_267728	F	M00055312A:D11	UC2-ColonMetLiver
5060	440707	2055.C09.gz43_267744	F	M00055312A:E10	UC2-ColonMetLiver
5061	555359	2055.F12.gz43_267795	F	M00055317C:D04	UC2-ColonMetLiver
5062	472188	2055.P12.gz43_267805	F	M00055335D:A03	UC2-ColonMetLiver
5063	617813	2055.E13.gz43_267810	F	M00055315C:A09	UC2-ColonMetLiver
5064	559027	2055.I13.gz43_267814	F	M00055321D:C12	UC2-ColonMetLiver
5065	448677	2055.K13.gz43_267816	F	M00055324C:H10	UC2-ColonMetLiver
5066	555277	2055.K15.gz43_267848	F	M00055324D:B02	UC2-ColonMetLiver
5067	560538	2055.O16.gz43_267868	F	M00055334C:E11	UC2-ColonMetLiver
5068	560369	2055.D17.gz43_267873	F	M00055313D:E10	UC2-ColonMetLiver
5069	559794	2055.G19.gz43_267908	F	M00055319B:H06	UC2-ColonMetLiver
5070	138470	2055.B20.gz43_267919	F	M00055310B:E02	UC2-ColonMetLiver
5071	558105	2055.H20.gz43_267925	F	M00055320D:E09	UC2-ColonMetLiver
5072	473343	2055.K21.gz43_267944	F	M00055325A:E12	UC2-ColonMetLiver
5073	554176	2055.O21.gz43_267948	F	M00055334D:G07	UC2-ColonMetLiver
5074	477757	2055.E22.gz43_267954	F	M00055316B:B10	UC2-ColonMetLiver
5075	553709	2055.G22.gz43_267956	F	M00055319C:C03	UC2-ColonMetLiver
5076	554585	2055.K22.gz43_267960	F	M00055325A:H02	UC2-ColonMetLiver
5077	451429	2055.N22.gz43_267963	F	M00055333C:F12	UC2-ColonMetLiver
5078	551811	2055.A23.gz43_267966	F	M00055308D:C09	UC2-ColonMetLiver
5079	62458	2055.C23.gz43_267968	F	M00055312D:A09	UC2-ColonMetLiver
5080	551912	2055.D23.gz43_267969	F	M00055314B:G07	UC2-ColonMetLiver
5081	552857	2055.G23.gz43_267972	F	M00055319C:C07	UC2-ColonMetLiver
5082	555349	2055.N23.gz43_267979	F	M00055333C:H07	UC2-ColonMetLiver

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
5083	560259	2056.F01.gz43_268003	F	M00055343D:C12	UC2-ColonMetLiver
5084	550063	2056.G01.gz43_268004	F	M00055344D:A09	UC2-ColonMetLiver
5085	560544	2056.M01.gz43_268010	F	M00055352B:E06	UC2-ColonMetLiver
5086	561108	2056.P01.gz43_268013	F	M00055356C:H02	UC2-ColonMetLiver
5087	512014	2056.L02.gz43_268025	F	M00055351B:H12	UC2-ColonMetLiver
5088	627386	2056.D03.gz43_268033	F	M00055341C:F04	UC2-ColonMetLiver
5089	561124	2056.E03.gz43_268034	F	M00055342C:H06	UC2-ColonMetLiver
5090	418482	2056.H03.gz43_268037	F	M00055346A:E12	UC2-ColonMetLiver
5091	558562	2056.A04.gz43_268046	F	M00055336D:B03	UC2-ColonMetLiver
5092	551912	2056.B04.gz43_268047	F	M00055338C:F03	UC2-ColonMetLiver
5093	552669	2056.D04.gz43_268049	F	M00055341C:G12	UC2-ColonMetLiver
5094	559857	2056.J04.gz43_268055	F	M00055348D:A01	UC2-ColonMetLiver
5095	557372	2056.M04.gz43_268058	F	M00055352B:H05	UC2-ColonMetLiver
5096	558182	2056.N04.gz43_268059	F	M00055354A:A01	UC2-ColonMetLiver
5097	552430	2056.B05.gz43_268063	F	M00055338C:G04	UC2-ColonMetLiver
5098	560932	2056.F05.gz43_268067	F	M00055343D:G03	UC2-ColonMetLiver
5099	559049	2056.G05.gz43_268068	F	M00055345A:D05	UC2-ColonMetLiver
5100	449405	2056.C06.gz43_268080	F	M00055340B:C03	UC2-ColonMetLiver
5101	558769	2056.G06.gz43_268084	F	M00055345B:B03	UC2-ColonMetLiver
5102	556216	2056.K06.gz43_268088	F	M00055350A:F01	UC2-ColonMetLiver
5103	553591	2056.M06.gz43_268090	F	M00055352C:A07	UC2-ColonMetLiver
5104	561024	2056.B07.gz43_268095	F	M00055338C:H06	UC2-ColonMetLiver
5105	560652	2056.C07.gz43_268096	F	M00055340B:E06	UC2-ColonMetLiver
5106	559296	2056.F07.gz43_268099	F	M00055343D:H04	UC2-ColonMetLiver
5107	560174	2056.P07.gz43_268109	F	M00055356D:C11	UC2-ColonMetLiver
5108	552357	2056.D08.gz43_268113	F	M00055341D:H07	UC2-ColonMetLiver
5109	627139	2056.E08.gz43_268114	F	M00055342D:F07	UC2-ColonMetLiver
5110	509505	2056.H08.gz43_268117	F	M00055346B:G03	UC2-ColonMetLiver
5111	560369	2056.C09.gz43_268128	F	M00055340C:D01	UC2-ColonMetLiver
5112	559375	2056.G09.gz43_268132	F	M00055345B:F03	UC2-ColonMetLiver
5113	449927	2056.K09.gz43_268136	F	M00055350B:B12	UC2-ColonMetLiver
5114	449751	2056.P10.gz43_268157	F	M00055357A:A09	UC2-ColonMetLiver
5115	560370	2056.C11.gz43_268160	F	M00055340D:D01	UC2-ColonMetLiver
5116	561124	2056.E11.gz43_268162	F	M00055342D:H05	UC2-ColonMetLiver
5117	549041	2056.J11.gz43_268167	F	M00055349A:F07	UC2-ColonMetLiver
5118	560695	2056.K11.gz43_268168	F	M00055350B:D09	UC2-ColonMetLiver
5119	471712	2056.N11.gz43_268171	F	M00055354A:G11	UC2-ColonMetLiver
5120	448285	2056.F12.gz43_268179	F	M00055344A:G11	UC2-ColonMetLiver
5121	561068	2056.N12.gz43_268187	F	M00055354A:H08	UC2-ColonMetLiver
5122	562883	2056.B13.gz43_268191	F	M00055339B:D10	UC2-ColonMetLiver
5123	560717	2056.C13.gz43_268192	F	M00055340D:F08	UC2-ColonMetLiver
5124	560199	2056.E13.gz43_268194	F	M00055343A:C09	UC2-ColonMetLiver

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
5125	618311	2056.F13.gz43_268195	F	M00055344B:A12	UC2-ColonMetLiver
5126	455379	2056.M13.gz43_268202	F	M00055353B:B09	UC2-ColonMetLiver
5127	471272	2056.O13.gz43_268204	F	M00055356A:B06	UC2-ColonMetLiver
5128	562576	2056.D14.gz43_268209	F	M00055342A:E08	UC2-ColonMetLiver
5129	626061	2056.O14.gz43_268220	F	M00055356A:D04	UC2-ColonMetLiver
5130	558867	2056.A15.gz43_268222	F	M00055337D:B10	UC2-ColonMetLiver
5131	553875	2056.K15.gz43_268232	F	M00055350C:G11	UC2-ColonMetLiver
5132	556365	2056.O15.gz43_268236	F	M00055356A:D09	UC2-ColonMetLiver
5133	453004	2056.A16.gz43_268238	F	M00055338A:A02	UC2-ColonMetLiver
5134	558653	2056.C16.gz43_268240	F	M00055341B:A01	UC2-ColonMetLiver
5135	560868	2056.E16.gz43_268242	F	M00055343A:G03	UC2-ColonMetLiver
5136	551305	2056.G16.gz43_268244	F	M00055345D:A04	UC2-ColonMetLiver
5137	559004	2056.H16.gz43_268245	F	M00055347A:C03	UC2-ColonMetLiver
5138	238146	2056.N16.gz43_268251	F	M00055354C:C12	UC2-ColonMetLiver
5139	559971	2056.A17.gz43_268254	F	M00055338A:A03	UC2-ColonMetLiver
5140	559963	2056.I17.gz43_268262	F	M00055348B:A02	UC2-ColonMetLiver
5141	549781	2056.O17.gz43_268268	F	M00055356B:B04	UC2-ColonMetLiver
5142	491240	2056.F18.gz43_268275	F	M00055344C:C08	UC2-ColonMetLiver
5143	559087	2056.G18.gz43_268276	F	M00055345D:D01	UC2-ColonMetLiver
5144	103123	2056.I18.gz43_268278	F	M00055348B:B05	UC2-ColonMetLiver
5145	426698	2056.M18.gz43_268282	F	M00055353C:A05	UC2-ColonMetLiver
5146	560254	2056.C19.gz43_268288	F	M00055341B:C07	UC2-ColonMetLiver
5147	403419	2056.D19.gz43_268289	F	M00055342B:C08	UC2-ColonMetLiver
5148	400047	2056.E19.gz43_268290	F	M00055343C:B11	UC2-ColonMetLiver
5149	559093	2056.G19.gz43_268292	F	M00055345D:D12	UC2-ColonMetLiver
5150	458618	2056.J19.gz43_268295	F	M00055349C:G07	UC2-ColonMetLiver
5151	558890	2056.F20.gz43_268307	F	M00055344C:F09	UC2-ColonMetLiver
5152	559246	2056.G20.gz43_268308	F	M00055345D:E02	UC2-ColonMetLiver
5153	562849	2056.J20.gz43_268311	F	M00055349C:H12	UC2-ColonMetLiver
5154	561116	2056.A21.gz43_268318	F	M00055338A:H10	UC2-ColonMetLiver
5155	558334	2056.G21.gz43_268324	F	M00055345D:E05	UC2-ColonMetLiver
5156	552258	2056.I22.gz43_268342	F	M00055348B:F05	UC2-ColonMetLiver
5157	560311	2056.K22.gz43_268344	F	M00055351A:C09	UC2-ColonMetLiver
5158	560714	2056.A23.gz43_268350	F	M00055338B:F06	UC2-ColonMetLiver
5159	496460	2056.D23.gz43_268353	F	M00055342C:E03	UC2-ColonMetLiver
5160	487623	2056.N23.gz43_268363	F	M00055355A:A10	UC2-ColonMetLiver
5161	559806	2056.F24.gz43_268371	F	M00055344C:H09	UC2-ColonMetLiver
5162	560088	2056.G24.gz43_268372	F	M00055346A:B01	UC2-ColonMetLiver
5163	556011	2056.J24.gz43_268375	F	M00055349D:F02	UC2-ColonMetLiver
5164	555095	2056.L24.gz43_268377	F	M00055352B:E01	UC2-ColonMetLiver
5165	558959	2056.M24.gz43_268378	F	M00055353D:C05	UC2-ColonMetLiver
5166	466887	2065.M01.gz43_268394	F	M00055373C:F05	UC2-ColonMetLiver

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
5167	495799	2065.C02.gz43_268400	F	M00055360C:C05	UC2-ColonMetLiver
5168	550562	2065.E02.gz43_268402	F	M00055363A:F07	UC2-ColonMetLiver
5169	523606	2065.H02.gz43_268405	F	M00055367D:A05	UC2-ColonMetLiver
5170	549163	2065.J02.gz43_268407	F	M00055370B:F07	UC2-ColonMetLiver
5171	562844	2065.P02.gz43_268413	F	M00055377B:E10	UC2-ColonMetLiver
5172	636651	2065.F03.gz43_268419	F	M00055364D:E09	UC2-ColonMetLiver
5173	543323	2065.M03.gz43_268426	F	M00055373C:H10	UC2-ColonMetLiver
5174	556416	2065.L04.gz43_268441	F	M00055372D:C11	UC2-ColonMetLiver
5175	498509	2065.M04.gz43_268442	F	M00055373D:B08	UC2-ColonMetLiver
5176	376726	2065.N04.gz43_268443	F	M00055374C:F01	UC2-ColonMetLiver
5177	559696	2065.D05.gz43_268449	F	M00055361D:H12	UC2-ColonMetLiver
5178	484748	2065.K05.gz43_268456	F	M00055371D:B08	UC2-ColonMetLiver
5179	561229	2065.O05.gz43_268460	F	M00055376A:A08	UC2-ColonMetLiver
5180	627297	2065.A06.gz43_268462	F	M00055358A:F09	UC2-ColonMetLiver
5181	456469	2065.C06.gz43_268464	F	M00055360C:G11	UC2-ColonMetLiver
5182	552031	2065.J06.gz43_268471	F	M00055370C:D02	UC2-ColonMetLiver
5183	527410	2065.G07.gz43_268484	F	M00055366D:G10	UC2-ColonMetLiver
5184	556959	2065.I07.gz43_268486	F	M00055369A:H08	UC2-ColonMetLiver
5185	501534	2065.B08.gz43_268495	F	M00055359C:H09	UC2-ColonMetLiver
5186	91178	2065.E08.gz43_268498	F	M00055363C:E02	UC2-ColonMetLiver
5187	461325	2065.P08.gz43_268509	F	M00055377C:G01	UC2-ColonMetLiver
5188	561485	2065.A09.gz43_268510	F	M00055358B:C01	UC2-ColonMetLiver
5189	557783	2065.I09.gz43_268518	F	M00055369C:D04	UC2-ColonMetLiver
5190	474580	2065.O09.gz43_268524	F	M00055376B:A03	UC2-ColonMetLiver
5191	450637	2065.P09.gz43_268525	F	M00055377C:H08	UC2-ColonMetLiver
5192	504167	2065.N10.gz43_268539	F	M00055374D:C09	UC2-ColonMetLiver
5193	561279	2065.O10.gz43_268540	F	M00055376B:A11	UC2-ColonMetLiver
5194	451124	2065.B11.gz43_268543	F	M00055359D:C12	UC2-ColonMetLiver
5195	558412	2065.D11.gz43_268545	F	M00055362C:B06	UC2-ColonMetLiver
5196	558334	2065.F11.gz43_268547	F	M00055365C:D12	UC2-ColonMetLiver
5197	552265	2065.K11.gz43_268552	F	M00055372A:H02	UC2-ColonMetLiver
5198	555796	2065.M11.gz43_268554	F	M00055374A:B11	UC2-ColonMetLiver
5199	558507	2065.N11.gz43_268555	F	M00055374D:F10	UC2-ColonMetLiver
5200	453846	2065.O11.gz43_268556	F	M00055376B:B01	UC2-ColonMetLiver
5201	556430	2065.G12.gz43_268564	F	M00055367A:B11	UC2-ColonMetLiver
5202	549984	2065.J12.gz43_268567	F	M00055370D:F06	UC2-ColonMetLiver
5203	561825	2065.F13.gz43_268579	F	M00055365C:F11	UC2-ColonMetLiver
5204	560959	2065.J13.gz43_268583	F	M00055370D:H07	UC2-ColonMetLiver
5205	636876	2065.M13.gz43_268586	F	M00055374A:E01	UC2-ColonMetLiver
5206	562801	2065.P13.gz43_268589	F	M00055377D:F12	UC2-ColonMetLiver
5207	559675	2065.D14.gz43_268593	F	M00055362C:G08	UC2-ColonMetLiver
5208	632260	2065.K14.gz43_268600	F	M00055372B:E01	UC2-ColonMetLiver

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
5209	490308	2065.L14.gz43_268601	F	M00055373B:A09	UC2-ColonMetLiver
5210	559828	2065.B15.gz43_268607	F	M00055359D:H02	UC2-ColonMetLiver
5211	559022	2065.C15.gz43_268608	F	M00055361A:C01	UC2-ColonMetLiver
5212	556850	2065.F15.gz43_268611	F	M00055366A:B04	UC2-ColonMetLiver
5213	508515	2065.J15.gz43_268615	F	M00055371A:B05	UC2-ColonMetLiver
5214	465610	2065.A17.gz43_268638	F	M00055358D:G04	UC2-ColonMetLiver
5215	463304	2065.E17.gz43_268642	F	M00055364B:D01	UC2-ColonMetLiver
5216	551551	2065.F17.gz43_268643	F	M00055366A:H08	UC2-ColonMetLiver
5217	559963	2065.E18.gz43_268658	F	M00055364B:E10	UC2-ColonMetLiver
5218	562027	2065.J18.gz43_268663	F	M00055371A:H10	UC2-ColonMetLiver
5219	561868	2065.K18.gz43_268664	F	M00055372B:F11	UC2-ColonMetLiver
5220	561610	2065.J19.gz43_268679	F	M00055371B:D01	UC2-ColonMetLiver
5221	562565	2065.M19.gz43_268682	F	M00055374B:D05	UC2-ColonMetLiver
5222	235456	2065.P19.gz43_268685	F	M00055378A:B12	UC2-ColonMetLiver
5223	553615	2065.C20.gz43_268688	F	M00055361B:F12	UC2-ColonMetLiver
5224	534054	2065.E20.gz43_268690	F	M00055364C:B08	UC2-ColonMetLiver
5225	511746	2065.F20.gz43_268691	F	M00055366B:C04	UC2-ColonMetLiver
5226	559495	2065.A21.gz43_268702	F	M00055359B:F03	UC2-ColonMetLiver
5227	559675	2065.C21.gz43_268704	F	M00055361B:G08	UC2-ColonMetLiver
5228	553705	2065.J21.gz43_268711	F	M00055371B:F01	UC2-ColonMetLiver
5229	559764	2065.M21.gz43_268714	F	M00055374B:F06	UC2-ColonMetLiver
5230	482090	2065.N21.gz43_268715	F	M00055375B:H02	UC2-ColonMetLiver
5231	562459	2065.C22.gz43_268720	F	M00055361C:E05	UC2-ColonMetLiver
5232	553904	2065.K22.gz43_268728	F	M00055372C:E03	UC2-ColonMetLiver
5233	555878	2065.N22.gz43_268731	F	M00055375B:H07	UC2-ColonMetLiver
5234	559676	2065.A23.gz43_268734	F	M00055359B:G09	UC2-ColonMetLiver
5235	505971	2065.F23.gz43_268739	F	M00055366C:B11	UC2-ColonMetLiver
5236	62458	2065.H23.gz43_268741	F	M00055368D:E03	UC2-ColonMetLiver
5237	207099	2065.O23.gz43_268748	F	M00055377A:B11	UC2-ColonMetLiver
5238	491635	2065.A24.gz43_268750	F	M00055359B:H07	UC2-ColonMetLiver
5239	32021	2065.D24.gz43_268753	F	M00055363A:D02	UC2-ColonMetLiver
5240	448741	2065.N24.gz43_268763	F	M00055375C:C08	UC2-ColonMetLiver
5241	504560	2078.H01.gz43_269031	F	M00042953B:D02	UC3-NormColon
5242	516415	2078.M01.gz43_269036	F	M00042965A:G02	UC3-NormColon
5243	452981	2078.J02.gz43_269049	F	M00042958B:H04	UC3-NormColon
5244	514594	2078.L02.gz43_269051	F	M00042963B:E12	UC3-NormColon
5245	451923	2078.B03.gz43_269057	F	M00042586C:E01	UC3-NormColon
5246	512721	2078.J03.gz43_269065	F	M00042958C:D04	UC3-NormColon
5247	512051	2078.K03.gz43_269066	F	M00042960D:C11	UC3-NormColon
5248	506920	2078.P03.gz43_269071	F	M00042976B:F05	UC3-NormColon
5249	451401	2078.F04.gz43_269077	F	M00042628B:G11	UC3-NormColon
5250	448594	2078.I04.gz43_269080	F	M00042955D:H03	UC3-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
5251	452898	2078.M04.gz43_269084	F	M00042965B:G08	UC3-NormColon
5252	505679	2078.N04.gz43_269085	F	M00042969B:E01	UC3-NormColon
5253	451618	2078.O04.gz43_269086	F	M00042972C:F07	UC3-NormColon
5254	451841	2078.G05.gz43_269094	F	M00042951D:C05	UC3-NormColon
5255	448090	2078.I05.gz43_269096	F	M00042956A:H02	UC3-NormColon
5256	449000	2078.N05.gz43_269101	F	M00042969B:G10	UC3-NormColon
5257	373239	2078.O05.gz43_269102	F	M00042972C:F09	UC3-NormColon
5258	451802	2078.D06.gz43_269107	F	M00042623B:B09	UC3-NormColon
5259	511746	2078.E06.gz43_269108	F	M00042625D:C07	UC3-NormColon
5260	516522	2078.F06.gz43_269109	F	M00042628C:G10	UC3-NormColon
5261	423578	2078.J06.gz43_269113	F	M00042959A:B07	UC3-NormColon
5262	513888	2078.E07.gz43_269124	F	M00042625D:E08	UC3-NormColon
5263	452801	2078.L07.gz43_269131	F	M00042963D:F11	UC3-NormColon
5264	452775	2078.M07.gz43_269132	F	M00042965C:E06	UC3-NormColon
5265	415825	2078.C08.gz43_269138	F	M00042589D:D08	UC3-NormColon
5266	447904	2078.F08.gz43_269141	F	M00042628D:F12	UC3-NormColon
5267	514142	2078.J08.gz43_269145	F	M00042959A:E08	UC3-NormColon
5268	92639	2078.B09.gz43_269153	F	M00042587B:G07	UC3-NormColon
5269	452182	2078.C09.gz43_269154	F	M00042589D:F02	UC3-NormColon
5270	447210	2078.D09.gz43_269155	F	M00042623D:C02	UC3-NormColon
5271	452500	2078.O09.gz43_269166	F	M00042973B:B10	UC3-NormColon
5272	452204	2078.A10.gz43_269168	F	M00042583D:F03	UC3-NormColon
5273	447025	2078.E10.gz43_269172	F	M00042626B:A12	UC3-NormColon
5274	452324	2078.G10.gz43_269174	F	M00042952A:H12	UC3-NormColon
5275	506901	2078.A11.gz43_269184	F	M00042583D:F11	UC3-NormColon
5276	507349	2078.C11.gz43_269186	F	M00042590B:G02	UC3-NormColon
5277	452052	2078.F11.gz43_269189	F	M00042629A:E11	UC3-NormColon
5278	500853	2078.G11.gz43_269190	F	M00042952B:A08	UC3-NormColon
5279	514160	2078.J11.gz43_269193	F	M00042959B:E11	UC3-NormColon
5280	418340	2078.C12.gz43_269202	F	M00042590C:C09	UC3-NormColon
5281	452142	2078.H12.gz43_269207	F	M00042954A:F04	UC3-NormColon
5282	451994	2078.I12.gz43_269208	F	M00042957A:D06	UC3-NormColon
5283	452615	2078.J12.gz43_269209	F	M00042959C:C06	UC3-NormColon
5284	452899	2078.K12.gz43_269210	F	M00042962A:G04	UC3-NormColon
5285	446438	2078.K13.gz43_269226	F	M00042962B:A03	UC3-NormColon
5286	452462	2078.D14.gz43_269235	F	M00042624D:B05	UC3-NormColon
5287	510169	2078.J14.gz43_269241	F	M00042959D:A05	UC3-NormColon
5288	508088	2078.B16.gz43_269265	F	M00042588A:G10	UC3-NormColon
5289	452031	2078.E16.gz43_269268	F	M00042626D:D12	UC3-NormColon
5290	513155	2078.K16.gz43_269274	F	M00042962C:D05	UC3-NormColon
5291	513156	2078.L16.gz43_269275	F	M00042964C:D06	UC3-NormColon
5292	452695	2078.N16.gz43_269277	F	M00042970D:D02	UC3-NormColon

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SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
5293	448332	2078.J17.gz43_269289	F	M00042960A:B10	UC3-NormColon
5294	513168	2078.L17.gz43_269291	F	M00042964C:D10	UC3-NormColon
5295	510717	2078.N17.gz43_269293	F	M00042971A:B09	UC3-NormColon
5296	456545	2078.O17.gz43_269294	F	M00042974D:B07	UC3-NormColon
5297	4244	2078.P17.gz43_269295	F	M00042978B:F03	UC3-NormColon
5298	452376	2078.E18.gz43_269300	F	M00042627B:A10	UC3-NormColon
5299	451993	2078.H18.gz43_269303	F	M00042954D:D04	UC3-NormColon
5300	451929	2078.I18.gz43_269304	F	M00042957D:C09	UC3-NormColon
5301	511351	2078.K18.gz43_269306	F	M00042962D:B09	UC3-NormColon
5302	505858	2078.B19.gz43_269313	F	M00042588C:E07	UC3-NormColon
5303	501401	2078.C19.gz43_269314	F	M00042621D:A03	UC3-NormColon
5304	452662	2078.N19.gz43_269325	F	M00042971A:D12	UC3-NormColon
5305	512059	2078.L21.gz43_269355	F	M00042964D:C02	UC3-NormColon
5306	450805	2078.O21.gz43_269358	F	M00042975C:A08	UC3-NormColon
5307	504007	2078.B22.gz43_269361	F	M00042589B:D04	UC3-NormColon
5308	450262	2078.A23.gz43_269376	F	M00042586B:A09	UC3-NormColon
5309	452066	2078.B23.gz43_269377	F	M00042589B:E03	UC3-NormColon
5310	452459	2078.K23.gz43_269386	F	M00042963B:A02	UC3-NormColon
5311	452506	2078.L23.gz43_269387	F	M00042965A:B03	UC3-NormColon
5312	448453	2078.A24.gz43_269392	F	M00042586B:A10	UC3-NormColon
5313	7022	2089.A01.gz43_269708	F	M00042611A:A01	UC3-PrimColon
5314	523182	2089.E01.gz43_269712	F	M00043079D:G10	UC3-PrimColon
5315	2930	2089.L01.gz43_269719	F	M00043108B:D12	UC3-PrimColon
5316	454701	2089.H02.gz43_269731	F	M00043093D:F12	UC3-PrimColon
5317	454226	2089.I02.gz43_269732	F	M00043097D:B12	UC3-PrimColon
5318	524624	2089.O02.gz43_269738	F	M00043139D:A06	UC3-PrimColon
5319	453220	2089.B03.gz43_269741	F	M00042614D:A12	UC3-PrimColon
5320	453893	2089.C03.gz43_269742	F	M00042618B:G04	UC3-PrimColon
5321	453470	2089.F03.gz43_269745	F	M00043086A:C02	UC3-PrimColon
5322	524478	2089.G03.gz43_269746	F	M00043090D:H07	UC3-PrimColon
5323	529219	2089.H03.gz43_269747	F	M00043094A:F01	UC3-PrimColon
5324	454050	2089.P03.gz43_269755	F	M00043144D:H01	UC3-PrimColon
5325	519988	2089.E04.gz43_269760	F	M00043080B:C11	UC3-PrimColon
5326	523590	2089.J04.gz43_269765	F	M00043102A:G12	UC3-PrimColon
5327	452936	2089.N04.gz43_269769	F	M00043137C:D02	UC3-PrimColon
5328	453761	2089.J05.gz43_269781	F	M00043102B:F05	UC3-PrimColon
5329	405102	2089.A06.gz43_269788	F	M00042612A:B06	UC3-PrimColon
5330	454720	2089.L06.gz43_269799	F	M00043109C:F04	UC3-PrimColon
5331	454438	2089.N06.gz43_269801	F	M00043137D:D10	UC3-PrimColon
5332	448985	2089.D07.gz43_269807	F	M00043077B:H01	UC3-PrimColon
5333	530656	2089.G07.gz43_269810	F	M00043091C:H05	UC3-PrimColon
5334	454134	2089.L07.gz43_269815	F	M00043131B:A11	UC3-PrimColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
5335	454910	2089.G08.gz43_269826	F	M00043091C:H08	UC3-PrimColon
5336	417549	2089.D09.gz43_269839	F	M00043077D:E12	UC3-PrimColon
5337	454374	2089.G09.gz43_269842	F	M00043091D:C01	UC3-PrimColon
5338	454518	2089.M09.gz43_269848	F	M00043134C:D06	UC3-PrimColon
5339	523753	2089.N09.gz43_269849	F	M00043138A:H03	UC3-PrimColon
5340	522648	2089.D10.gz43_269855	F	M00043077D:F04	UC3-PrimColon
5341	407275	2089.N10.gz43_269865	F	M00043138B:B08	UC3-PrimColon
5342	415326	2089.O10.gz43_269866	F	M00043141C:C12	UC3-PrimColon
5343	453756	2089.P10.gz43_269867	F	M00043146C:F10	UC3-PrimColon
5344	453766	2089.J11.gz43_269877	F	M00043102D:F11	UC3-PrimColon
5345	450287	2089.K11.gz43_269878	F	M00043106B:F07	UC3-PrimColon
5346	454825	2089.L11.gz43_269879	F	M00043131B:G10	UC3-PrimColon
5347	449335	2089.J12.gz43_269893	F	M00043103A:G05	UC3-PrimColon
5348	453572	2089.K12.gz43_269894	F	M00043106C:D05	UC3-PrimColon
5349	454550	2089.M12.gz43_269896	F	M00043135C:E07	UC3-PrimColon
5350	23649	2089.N12.gz43_269897	F	M00043138B:F02	UC3-PrimColon
5351	449430	2089.F13.gz43_269905	F	M00043087B:D10	UC3-PrimColon
5352	528134	2089.H13.gz43_269907	F	M00043096A:E01	UC3-PrimColon
5353	451391	2089.L13.gz43_269911	F	M00043131C:A11	UC3-PrimColon
5354	454126	2089.M13.gz43_269912	F	M00043135D:A11	UC3-PrimColon
5355	437064	2089.N13.gz43_269913	F	M00043138B:G11	UC3-PrimColon
5356	454129	2089.O13.gz43_269914	F	M00043141D:A12	UC3-PrimColon
5357	519109	2089.C14.gz43_269918	F	M00043075A:B12	UC3-PrimColon
5358	519641	2089.D14.gz43_269919	F	M00043078C:C04	UC3-PrimColon
5359	526575	2089.M14.gz43_269928	F	M00043135D:C07	UC3-PrimColon
5360	453783	2089.A15.gz43_269932	F	M00042613A:H01	UC3-PrimColon
5361	453533	2089.I15.gz43_269940	F	M00043100C:D08	UC3-PrimColon
5362	449394	2089.N15.gz43_269945	F	M00043138C:D09	UC3-PrimColon
5363	523732	2089.D16.gz43_269951	F	M00043078C:H05	UC3-PrimColon
5364	395536	2089.F16.gz43_269953	F	M00043088B:D07	UC3-PrimColon
5365	454509	2089.H16.gz43_269955	F	M00043096C:D02	UC3-PrimColon
5366	454562	2089.E17.gz43_269968	F	M00043082D:B05	UC3-PrimColon
5367	451972	2089.H17.gz43_269971	F	M00043096C:H04	UC3-PrimColon
5368	453726	2089.K17.gz43_269974	F	M00043107A:E07	UC3-PrimColon
5369	527361	2089.M17.gz43_269976	F	M00043136A:D03	UC3-PrimColon
5370	453783	2089.A18.gz43_269980	F	M00042613C:F06	UC3-PrimColon
5371	453385	2089.B20.gz43_270013	F	M00042617C:B07	UC3-PrimColon
5372	454177	2089.G20.gz43_270018	F	M00043093A:A06	UC3-PrimColon
5373	801	2089.I20.gz43_270020	F	M00043101A:F12	UC3-PrimColon
5374	453494	2089.J20.gz43_270021	F	M00043104B:C09	UC3-PrimColon
5375	453202	2089.P20.gz43_270027	F	M00043149B:A01	UC3-PrimColon
5376	520616	2089.F21.gz43_270033	F	M00043089A:D06	UC3-PrimColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
5377	527873	2089.H21.gz43_270035	F	M00043097A:D11	UC3-PrimColon
5378	450566	2089.K21.gz43_270038	F	M00043107D:H04	UC3-PrimColon
5379	520074	2089.A22.gz43_270044	F	M00042614A:C04	UC3-PrimColon
5380	518566	2089.C22.gz43_270046	F	M00043076A:A09	UC3-PrimColon
5381	387530	2089.H22.gz43_270051	F	M00043097A:F06	UC3-PrimColon
5382	453846	2089.I22.gz43_270052	F	M00043101C:F12	UC3-PrimColon
5383	454483	2089.L22.gz43_270055	F	M00043132C:D02	UC3-PrimColon
5384	524157	2089.A23.gz43_270060	F	M00042614A:H02	UC3-PrimColon
5385	453132	2089.K23.gz43_270070	F	M00043108B:A01	UC3-PrimColon
5386	524622	2089.N23.gz43_270073	F	M00043139C:A05	UC3-PrimColon
5387	447446	2089.A24.gz43_270076	F	M00042614C:B09	UC3-PrimColon
5388	524470	2089.F24.gz43_270081	F	M00043090B:H06	UC3-PrimColon
5389	446242	2066.N03.gz43_270439	F	M00055392A:H06	UC2-ColonMetLiver
5390	554908	2066.P07.gz43_270505	F	M00055394D:F03	UC2-ColonMetLiver
5391	551995	2066.F08.gz43_270511	F	M00055383B:H09	UC2-ColonMetLiver
5392	561325	2066.H08.gz43_270513	F	M00055385C:F06	UC2-ColonMetLiver
5393	553244	2066.J08.gz43_270515	F	M00055388A:A09	UC2-ColonMetLiver
5394	562876	2066.D09.gz43_270525	F	M00055381C:G03	UC2-ColonMetLiver
5395	562216	2066.F09.gz43_270527	F	M00055383C:A08	UC2-ColonMetLiver
5396	560948	2066.J09.gz43_270531	F	M00055388A:B06	UC2-ColonMetLiver
5397	446531	2066.P09.gz43_270537	F	M00055395A:C02	UC2-ColonMetLiver
5398	556793	2066.K10.gz43_270548	F	M00055388D:F11	UC2-ColonMetLiver
5399	499690	2066.M10.gz43_270550	F	M00055391B:D05	UC2-ColonMetLiver
5400	558297	2066.I11.gz43_270562	F	M00055386D:G02	UC2-ColonMetLiver
5401	453508	2066.M11.gz43_270566	F	M00055391B:D07	UC2-ColonMetLiver
5402	551640	2066.N11.gz43_270567	F	M00055392C:G07	UC2-ColonMetLiver
5403	562085	2066.C12.gz43_270572	F	M00055380D:H02	UC2-ColonMetLiver
5404	446399	2066.E12.gz43_270574	F	M00055382C:H06	UC2-ColonMetLiver
5405	562498	2066.G12.gz43_270576	F	M00055384B:D10	UC2-ColonMetLiver
5406	562524	2066.A13.gz43_270586	F	M00055378D:D04	UC2-ColonMetLiver
5407	465836	2066.J13.gz43_270595	F	M00055388B:B02	UC2-ColonMetLiver
5408	562701	2066.N13.gz43_270599	F	M00055392D:A06	UC2-ColonMetLiver
5409	561457	2066.O13.gz43_270600	F	M00055394B:C06	UC2-ColonMetLiver
5410	549082	2066.C14.gz43_270604	F	M00055381A:F02	UC2-ColonMetLiver
5411	418622	2066.H14.gz43_270609	F	M00055385D:D03	UC2-ColonMetLiver
5412	238196	2066.K14.gz43_270612	F	M00055389A:D08	UC2-ColonMetLiver
5413	560868	2066.D15.gz43_270621	F	M00055381D:D08	UC2-ColonMetLiver
5414	459764	2066.E15.gz43_270622	F	M00055382D:D04	UC2-ColonMetLiver
5415	555639	2066.M15.gz43_270630	F	M00055391B:H08	UC2-ColonMetLiver
5416	556011	2066.O15.gz43_270632	F	M00055394B:D08	UC2-ColonMetLiver
5417	468565	2066.A17.gz43_270650	F	M00055379A:D07	UC2-ColonMetLiver
5418	448949	2066.B17.gz43_270651	F	M00055380A:C06	UC2-ColonMetLiver

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
5419	636532	2066.J17.gz43_270659	F	M00055388B:E01	UC2-ColonMetLiver
5420	561487	2066.P17.gz43_270665	F	M00055395B:C04	UC2-ColonMetLiver
5421	50604	2066.L18.gz43_270677	F	M00055390C:E06	UC2-ColonMetLiver
5422	557249	2066.J20.gz43_270707	F	M00055388B:H04	UC2-ColonMetLiver
5423	562849	2066.H21.gz43_270721	F	M00055386A:G05	UC2-ColonMetLiver
5424	562386	2066.C22.gz43_270732	F	M00055381B:C10	UC2-ColonMetLiver
5425	635965	2066.J22.gz43_270739	F	M00055388C:D01	UC2-ColonMetLiver
5426	493487	2066.D23.gz43_270749	F	M00055382B:E02	UC2-ColonMetLiver
5427	44015	2066.N23.gz43_270759	F	M00055393B:F04	UC2-ColonMetLiver
5428	559854	2066.F24.gz43_270767	F	M00055383D:H11	UC2-ColonMetLiver
5429	282015	2066.K24.gz43_270772	F	M00055389C:F12	UC2-ColonMetLiver
5430	561206	2067.F02.gz43_270799	F	M00055402A:A05	UC2-ColonMetLiver
5431	486834	2067.G02.gz43_270800	F	M00055402D:A11	UC2-ColonMetLiver
5432	550730	2067.K02.gz43_270804	F	M00055407B:G07	UC2-ColonMetLiver
5433	560838	2067.P03.gz43_270825	F	M00055412D:A12	UC2-ColonMetLiver
5434	556382	2067.E04.gz43_270830	F	M00055400D:G01	UC2-ColonMetLiver
5435	561236	2067.I05.gz43_270850	F	M00055405A:A02	UC2-ColonMetLiver
5436	562584	2067.J05.gz43_270851	F	M00055406B:E07	UC2-ColonMetLiver
5437	550135	2067.N05.gz43_270855	F	M00055410C:G08	UC2-ColonMetLiver
5438	556380	2067.B06.gz43_270859	F	M00055397A:H07	UC2-ColonMetLiver
5439	511792	2067.C06.gz43_270860	F	M00055398C:F07	UC2-ColonMetLiver
5440	452761	2067.I06.gz43_270866	F	M00055405A:C01	UC2-ColonMetLiver
5441	465284	2067.K06.gz43_270868	F	M00055407C:E04	UC2-ColonMetLiver
5442	419489	2067.I07.gz43_270882	F	M00055405A:G11	UC2-ColonMetLiver
5443	540000	2067.P07.gz43_270889	F	M00055413A:A02	UC2-ColonMetLiver
5444	556105	2067.K08.gz43_270900	F	M00055407C:G04	UC2-ColonMetLiver
5445	562001	2067.N08.gz43_270903	F	M00055410C:H11	UC2-ColonMetLiver
5446	288626	2067.N09.gz43_270919	F	M00055410D:B02	UC2-ColonMetLiver
5447	561325	2067.H10.gz43_270929	F	M00055404A:B10	UC2-ColonMetLiver
5448	554742	2067.I10.gz43_270930	F	M00055405B:H05	UC2-ColonMetLiver
5449	560003	2067.A11.gz43_270938	F	M00055396B:C06	UC2-ColonMetLiver
5450	555856	2067.G11.gz43_270944	F	M00055403A:C07	UC2-ColonMetLiver
5451	633189	2067.N11.gz43_270951	F	M00055410D:G01	UC2-ColonMetLiver
5452	562147	2067.B12.gz43_270955	F	M00055397D:A01	UC2-ColonMetLiver
5453	553766	2067.H12.gz43_270961	F	M00055404A:D08	UC2-ColonMetLiver
5454	63669	2067.I13.gz43_270978	F	M00055405C:C04	UC2-ColonMetLiver
5455	491260	2067.J13.gz43_270979	F	M00055406D:A03	UC2-ColonMetLiver
5456	559776	2067.L13.gz43_270981	F	M00055408C:E04	UC2-ColonMetLiver
5457	561922	2067.A14.gz43_270986	F	M00055396B:G02	UC2-ColonMetLiver
5458	559102	2067.I14.gz43_270994	F	M00055405C:H07	UC2-ColonMetLiver
5459	440833	2067.O14.gz43_271000	F	M00055412A:C05	UC2-ColonMetLiver
5460	561212	2067.K15.gz43_271012	F	M00055408A:A05	UC2-ColonMetLiver

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
5461	556734	2067.O15.gz43_271016	F	M00055412A:F09	UC2-ColonMetLiver
5462	487893	2067.J16.gz43_271027	F	M00055406D:C10	UC2-ColonMetLiver
5463	558180	2067.G18.gz43_271056	F	M00055403B:A10	UC2-ColonMetLiver
5464	557853	2067.J18.gz43_271059	F	M00055406D:G12	UC2-ColonMetLiver
5465	446171	2067.P19.gz43_271081	F	M00055413C:B09	UC2-ColonMetLiver
5466	561438	2067.B20.gz43_271083	F	M00055398A:C11	UC2-ColonMetLiver
5467	551617	2067.I20.gz43_271090	F	M00055405D:G05	UC2-ColonMetLiver
5468	469852	2067.B21.gz43_271099	F	M00055398B:A05	UC2-ColonMetLiver
5469	556126	2067.P21.gz43_271113	F	M00055413C:G09	UC2-ColonMetLiver
5470	551928	2067.F22.gz43_271119	F	M00055402C:C12	UC2-ColonMetLiver
5471	562236	2067.A23.gz43_271130	F	M00055397A:B10	UC2-ColonMetLiver
5472	456687	2067.B23.gz43_271131	F	M00055398B:C05	UC2-ColonMetLiver
5473	530715	2067.H23.gz43_271137	F	M00055404C:C11	UC2-ColonMetLiver
5474	66014	2067.K23.gz43_271140	F	M00055408A:F12	UC2-ColonMetLiver
5475	100821	2067.L23.gz43_271141	F	M00055409A:E06	UC2-ColonMetLiver
5476	154980	2067.A24.gz43_271146	F	M00055397A:C06	UC2-ColonMetLiver
5477	561236	2067.G24.gz43_271152	F	M00055403B:G12	UC2-ColonMetLiver
5478	516043	2067.L24.gz43_271157	F	M00055409A:E10	UC2-ColonMetLiver
5479	559380	2068.K01.gz43_271172	F	M00055424B:D04	UC2-ColonMetLiver
5480	449795	2068.O03.gz43_271208	F	M00055474A:G06	UC2-ColonMetLiver
5481	550166	2068.D04.gz43_271213	F	M00055417C:A05	UC2-ColonMetLiver
5482	561646	2068.F04.gz43_271215	F	M00055419D:D04	UC2-ColonMetLiver
5483	561112	2068.D05.gz43_271229	F	M00055417C:G03	UC2-ColonMetLiver
5484	418562	2068.E05.gz43_271230	F	M00055418C:D08	UC2-ColonMetLiver
5485	559385	2068.J05.gz43_271235	F	M00055423C:D05	UC2-ColonMetLiver
5486	561411	2068.M05.gz43_271238	F	M00055472A:B12	UC2-ColonMetLiver
5487	561770	2068.C07.gz43_271260	F	M00055416B:F11	UC2-ColonMetLiver
5488	557760	2068.D08.gz43_271277	F	M00055417D:D08	UC2-ColonMetLiver
5489	468672	2068.M08.gz43_271286	F	M00055472A:F02	UC2-ColonMetLiver
5490	556490	2068.N08.gz43_271287	F	M00055473B:D01	UC2-ColonMetLiver
5491	550018	2068.F09.gz43_271295	F	M00055419D:H07	UC2-ColonMetLiver
5492	561837	2068.H09.gz43_271297	F	M00055421C:F06	UC2-ColonMetLiver
5493	554028	2068.I09.gz43_271298	F	M00055422C:E10	UC2-ColonMetLiver
5494	470667	2068.D10.gz43_271309	F	M00055417D:H08	UC2-ColonMetLiver
5495	552561	2068.E10.gz43_271310	F	M00055418D:A03	UC2-ColonMetLiver
5496	556793	2068.G10.gz43_271312	F	M00055421A:A09	UC2-ColonMetLiver
5497	561718	2068.N10.gz43_271319	F	M00055473B:E10	UC2-ColonMetLiver
5498	630348	2068.E11.gz43_271326	F	M00055418D:B05	UC2-ColonMetLiver
5499	491728	2068.H11.gz43_271329	F	M00055421C:G07	UC2-ColonMetLiver
5500	562477	2068.C12.gz43_271340	F	M00055416D:B03	UC2-ColonMetLiver
5501	402836	2068.D12.gz43_271341	F	M00055418A:C12	UC2-ColonMetLiver
5502	556511	2068.J12.gz43_271347	F	M00055424A:A08	UC2-ColonMetLiver

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
5503	559076	2068.N12.gz43_271351	F	M00055473C:A05	UC2-ColonMetLiver
5504	417426	2068.P12.gz43_271353	F	M00055475D:A05	UC2-ColonMetLiver
5505	456520	2068.A13.gz43_271354	F	M00055414C:C02	UC2-ColonMetLiver
5506	492982	2068.J13.gz43_271363	F	M00055424A:C10	UC2-ColonMetLiver
5507	558679	2068.C14.gz43_271372	F	M00055416D:D11	UC2-ColonMetLiver
5508	561707	2068.F14.gz43_271375	F	M00055420A:E12	UC2-ColonMetLiver
5509	561180	2068.I14.gz43_271378	F	M00055423A:A10	UC2-ColonMetLiver
5510	554953	2068.K14.gz43_271380	F	M00055425A:H03	UC2-ColonMetLiver
5511	492876	2068.L14.gz43_271381	F	M00055471C:B01	UC2-ColonMetLiver
5512	555933	2068.O14.gz43_271384	F	M00055474C:H12	UC2-ColonMetLiver
5513	562137	2068.P14.gz43_271385	F	M00055475D:A10	UC2-ColonMetLiver
5514	561500	2068.B15.gz43_271387	F	M00055415D:C12	UC2-ColonMetLiver
5515	561682	2068.D15.gz43_271389	F	M00055418A:E07	UC2-ColonMetLiver
5516	560118	2068.I15.gz43_271394	F	M00055423A:D02	UC2-ColonMetLiver
5517	512392	2068.J15.gz43_271395	F	M00055424A:F04	UC2-ColonMetLiver
5518	449356	2068.I16.gz43_271410	F	M00055423A:G08	UC2-ColonMetLiver
5519	447098	2068.L16.gz43_271413	F	M00055471C:D04	UC2-ColonMetLiver
5520	522220	2068.N16.gz43_271415	F	M00055473C:H05	UC2-ColonMetLiver
5521	453715	2068.P16.gz43_271417	F	M00055475D:B07	UC2-ColonMetLiver
5522	554774	2068.D17.gz43_271421	F	M00055418A:H04	UC2-ColonMetLiver
5523	553987	2068.I17.gz43_271426	F	M00055423B:A06	UC2-ColonMetLiver
5524	561645	2068.K17.gz43_271428	F	M00055425B:D12	UC2-ColonMetLiver
5525	549511	2068.M18.gz43_271446	F	M00055472C:G11	UC2-ColonMetLiver
5526	560700	2068.P18.gz43_271449	F	M00055475D:G08	UC2-ColonMetLiver
5527	493410	2068.K20.gz43_271476	F	M00055425B:F06	UC2-ColonMetLiver
5528	482425	2068.A21.gz43_271482	F	M00055414D:G10	UC2-ColonMetLiver
5529	561497	2068.B21.gz43_271483	F	M00055416A:C04	UC2-ColonMetLiver
5530	131130	2068.C21.gz43_271484	F	M00055417A:G11	UC2-ColonMetLiver
5531	524736	2068.F22.gz43_271503	F	M00055420C:E08	UC2-ColonMetLiver
5532	58680	2068.G22.gz43_271504	F	M00055421B:E05	UC2-ColonMetLiver
5533	562302	2068.N22.gz43_271511	F	M00055474A:B05	UC2-ColonMetLiver
5534	514824	2079.M01.gz43_271558	F	M00043021D:F10	UC3-NormColon
5535	452523	2079.P02.gz43_271577	F	M00043031A:B01	UC3-NormColon
5536	453572	2079.K04.gz43_271604	F	M00043012A:F06	UC3-NormColon
5537	406092	2079.I05.gz43_271618	F	M00043007D:F07	UC3-NormColon
5538	452759	2079.O05.gz43_271624	F	M00043029A:E11	UC3-NormColon
5539	456756	2079.B06.gz43_271627	F	M00042983D:A03	UC3-NormColon
5540	505226	2079.C06.gz43_271628	F	M00042987C:E04	UC3-NormColon
5541	238196	2079.D06.gz43_271629	F	M00042991C:C02	UC3-NormColon
5542	235874	2079.H06.gz43_271633	F	M00043005A:B06	UC3-NormColon
5543	512432	2079.O07.gz43_271656	F	M00043029B:C09	UC3-NormColon
5544	269927	2079.O09.gz43_271688	F	M00043029B:F09	UC3-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
5545	449510	2079.K10.gz43_271700	F	M00043012D:A06	UC3-NormColon
5546	516799	2079.O10.gz43_271704	F	M00043029B:G10	UC3-NormColon
5547	455716	2079.E11.gz43_271710	F	M00042995C:E04	UC3-NormColon
5548	452976	2079.G11.gz43_271712	F	M00043003A:H07	UC3-NormColon
5549	452031	2079.N11.gz43_271719	F	M00043026D:D06	UC3-NormColon
5550	452957	2079.P11.gz43_271721	F	M00043032B:H01	UC3-NormColon
5551	452830	2079.D12.gz43_271725	F	M00042991D:F06	UC3-NormColon
5552	452220	2079.C13.gz43_271740	F	M00042988D:G10	UC3-NormColon
5553	500896	2079.K13.gz43_271748	F	M00043013B:A06	UC3-NormColon
5554	455855	2079.L13.gz43_271749	F	M00043017D:B06	UC3-NormColon
5555	513381	2079.M13.gz43_271750	F	M00043023D:D06	UC3-NormColon
5556	448200	2079.B14.gz43_271755	F	M00042985B:C05	UC3-NormColon
5557	509027	2079.F14.gz43_271759	F	M00043000C:H06	UC3-NormColon
5558	452618	2079.N14.gz43_271767	F	M00043027B:C04	UC3-NormColon
5559	510254	2079.C15.gz43_271772	F	M00042989C:A06	UC3-NormColon
5560	451812	2079.D15.gz43_271773	F	M00042992B:B03	UC3-NormColon
5561	452392	2079.G15.gz43_271776	F	M00043003C:A02	UC3-NormColon
5562	504812	2079.I15.gz43_271778	F	M00043008D:E12	UC3-NormColon
5563	504431	2079.J15.gz43_271779	F	M00043011B:D03	UC3-NormColon
5564	452440	2079.L15.gz43_271781	F	M00043020A:A03	UC3-NormColon
5565	450225	2079.B16.gz43_271787	F	M00042985C:B03	UC3-NormColon
5566	511348	2079.C16.gz43_271788	F	M00042989C:B07	UC3-NormColon
5567	502343	2079.D16.gz43_271789	F	M00042992B:B11	UC3-NormColon
5568	451850	2079.F16.gz43_271791	F	M00043001A:C10	UC3-NormColon
5569	455117	2079.K16.gz43_271796	F	M00043013C:A01	UC3-NormColon
5570	452922	2079.L16.gz43_271797	F	M00043020A:G12	UC3-NormColon
5571	504501	2079.B17.gz43_271803	F	M00042985C:D02	UC3-NormColon
5572	503122	2079.F17.gz43_271807	F	M00043001B:C01	UC3-NormColon
5573	508126	2079.I17.gz43_271810	F	M00043008D:H09	UC3-NormColon
5574	448687	2079.A18.gz43_271818	F	M00042982C:G02	UC3-NormColon
5575	451491	2079.B18.gz43_271819	F	M00042985C:D04	UC3-NormColon
5576	452969	2079.F18.gz43_271823	F	M00043001B:E02	UC3-NormColon
5577	452866	2079.G18.gz43_271824	F	M00043003C:G10	UC3-NormColon
5578	446936	2079.K18.gz43_271828	F	M00043013D:F03	UC3-NormColon
5579	452445	2079.L18.gz43_271829	F	M00043021A:A09	UC3-NormColon
5580	451092	2079.N18.gz43_271831	F	M00043027D:G12	UC3-NormColon
5581	75212	2079.D19.gz43_271837	F	M00042992D:H02	UC3-NormColon
5582	452325	2079.F19.gz43_271839	F	M00043001B:H01	UC3-NormColon
5583	502984	2079.I19.gz43_271842	F	M00043009B:C09	UC3-NormColon
5584	508125	2079.J19.gz43_271843	F	M00043011C:H09	UC3-NormColon
5585	452528	2079.L19.gz43_271845	F	M00043021A:B06	UC3-NormColon
5586	509505	2079.C20.gz43_271852	F	M00042989D:A07	UC3-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
5587	455132	2079.G20.gz43_271856	F	M00043003D:D10	UC3-NormColon
5588	452160	2079.I20.gz43_271858	F	M00043009B:F11	UC3-NormColon
5589	453079	2079.M20.gz43_271862	F	M00043024B:H11	UC3-NormColon
5590	448813	2079.C21.gz43_271868	F	M00042990A:E05	UC3-NormColon
5591	513178	2079.D21.gz43_271869	F	M00042993A:D12	UC3-NormColon
5592	453804	2079.E21.gz43_271870	F	M00042996D:D12	UC3-NormColon
5593	453078	2079.L21.gz43_271877	F	M00043021A:H06	UC3-NormColon
5594	452611	2079.P21.gz43_271881	F	M00043033C:C05	UC3-NormColon
5595	504880	2079.A22.gz43_271882	F	M00042983A:E09	UC3-NormColon
5596	447445	2079.B22.gz43_271883	F	M00042986B:E06	UC3-NormColon
5597	503625	2079.G22.gz43_271888	F	M00043004A:C08	UC3-NormColon
5598	502614	2079.J22.gz43_271891	F	M00043011D:C12	UC3-NormColon
5599	454226	2079.K22.gz43_271892	F	M00043014B:G12	UC3-NormColon
5600	452973	2079.L22.gz43_271893	F	M00043021B:H03	UC3-NormColon
5601	456755	2079.M22.gz43_271894	F	M00043025A:C01	UC3-NormColon
5602	515127	2079.O22.gz43_271896	F	M00043030C:F03	UC3-NormColon
5603	507450	2079.F23.gz43_271903	F	M00043002A:G09	UC3-NormColon
5604	448381	2079.G23.gz43_271904	F	M00043004A:C10	UC3-NormColon
5605	505933	2079.K23.gz43_271908	F	M00043014C:F07	UC3-NormColon
5606	452648	2079.M23.gz43_271910	F	M00043025A:D09	UC3-NormColon
5607	453038	2079.N23.gz43_271911	F	M00043028C:H09	UC3-NormColon
5608	452611	2079.P23.gz43_271913	F	M00043033C:D05	UC3-NormColon
5609	501534	2079.B24.gz43_271915	F	M00042986C:B07	UC3-NormColon
5610	454849	2079.F24.gz43_271919	F	M00043002B:E06	UC3-NormColon
5611	366607	2079.H24.gz43_271921	F	M00043007B:D12	UC3-NormColon
5612	507066	2079.K24.gz43_271924	F	M00043014C:G06	UC3-NormColon
5613	519378	2090.B01.gz43_273908	F	M00043153B:B09	UC3-PrimColon
5614	453946	2090.H01.gz43_273914	F	M00043172C:G06	UC3-PrimColon
5615	527679	2090.L01.gz43_273918	F	M00043185B:D02	UC3-PrimColon
5616	454463	2090.P01.gz43_273922	F	M00043201D:D03	UC3-PrimColon
5617	521840	2090.D02.gz43_273926	F	M00043160B:E05	UC3-PrimColon
5618	528981	2090.M02.gz43_273935	F	M00043189C:F08	UC3-PrimColon
5619	528404	2090.C03.gz43_273941	F	M00043156C:E05	UC3-PrimColon
5620	523674	2090.N04.gz43_273968	F	M00043193C:G11	UC3-PrimColon
5621	446768	2090.F05.gz43_273976	F	M00043168C:F03	UC3-PrimColon
5622	128749	2090.H06.gz43_273994	F	M00043172D:H03	UC3-PrimColon
5623	525781	2090.K06.gz43_273997	F	M00043183C:B08	UC3-PrimColon
5624	452775	2090.N06.gz43_274000	F	M00043193C:H09	UC3-PrimColon
5625	524721	2090.L07.gz43_274014	F	M00043186C:A11	UC3-PrimColon
5626	454202	2090.M07.gz43_274015	F	M00043190A:B10	UC3-PrimColon
5627	452325	2090.J08.gz43_274028	F	M00043180C:B02	UC3-PrimColon
5628	453804	2090.F09.gz43_274040	F	M00043169A:F05	UC3-PrimColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
5629	454007	2090.O09.gz43_274049	F	M00043197D:H12	UC3-PrimColon
5630	425455	2090.L10.gz43_274062	F	M00043186D:B09	UC3-PrimColon
5631	453354	2090.H11.gz43_274074	F	M00043173B:F03	UC3-PrimColon
5632	525315	2090.I11.gz43_274075	F	M00043176C:A01	UC3-PrimColon
5633	453890	2090.N11.gz43_274080	F	M00043194A:G06	UC3-PrimColon
5634	454460	2090.A12.gz43_274083	F	M00043151B:D02	UC3-PrimColon
5635	522869	2090.C12.gz43_274085	F	M00043158A:F03	UC3-PrimColon
5636	454664	2090.I13.gz43_274107	F	M00043176C:E12	UC3-PrimColon
5637	528369	2090.L13.gz43_274110	F	M00043187C:E06	UC3-PrimColon
5638	526539	2090.J14.gz43_274124	F	M00043181C:C10	UC3-PrimColon
5639	452182	2090.O14.gz43_274129	F	M00043199A:F03	UC3-PrimColon
5640	520599	2090.H15.gz43_274138	F	M00043173C:D12	UC3-PrimColon
5641	530971	2090.L16.gz43_274158	F	M00043187D:H04	UC3-PrimColon
5642	289316	2090.N16.gz43_274160	F	M00043194D:E10	UC3-PrimColon
5643	454731	2090.A17.gz43_274163	F	M00043152A:F10	UC3-PrimColon
5644	453730	2090.D17.gz43_274166	F	M00043162D:E06	UC3-PrimColon
5645	450784	2090.G17.gz43_274169	F	M00043171D:G08	UC3-PrimColon
5646	404081	2090.M17.gz43_274175	F	M00043191C:G05	UC3-PrimColon
5647	456723	2090.A18.gz43_274179	F	M00043152A:G08	UC3-PrimColon
5648	526449	2090.C18.gz43_274181	F	M00043159A:C01	UC3-PrimColon
5649	413693	2090.H18.gz43_274186	F	M00043174B:B06	UC3-PrimColon
5650	454311	2090.J18.gz43_274188	F	M00043182B:C02	UC3-PrimColon
5651	526733	2090.H20.gz43_274218	F	M00043174C:C06	UC3-PrimColon
5652	432159	2090.K20.gz43_274221	F	M00043184D:G06	UC3-PrimColon
5653	453983	2090.M20.gz43_274223	F	M00043192B:H06	UC3-PrimColon
5654	518172	2090.N20.gz43_274224	F	M00043195D:A05	UC3-PrimColon
5655	454629	2090.P22.gz43_274258	F	M00043210C:E08	UC3-PrimColon
5656	530939	2090.A23.gz43_274259	F	M00043152B:H04	UC3-PrimColon
5657	234270	2090.G23.gz43_274265	F	M00043172C:B05	UC3-PrimColon
5658	529742	2090.I24.gz43_274283	F	M00043178C:G06	UC3-PrimColon
5659	404461	2092.G04.gz43_274444	F	M00043438B:E10	UC3-ColonMetLiver
5660	451023	2092.I04.gz43_274446	F	M00043448D:H09	UC3-ColonMetLiver
5661	535436	2092.G05.gz43_274460	F	M00043438C:D12	UC3-ColonMetLiver
5662	456001	2092.N05.gz43_274467	F	M00043470C:A01	UC3-ColonMetLiver
5663	450724	2092.O06.gz43_274484	F	M00043478B:D01	UC3-ColonMetLiver
5664	539142	2092.A07.gz43_274486	F	M00042592A:H02	UC3-ColonMetLiver
5665	450914	2092.K07.gz43_274496	F	M00043455C:G07	UC3-ColonMetLiver
5666	455855	2092.P07.gz43_274501	F	M00043484D:H08	UC3-ColonMetLiver
5667	537451	2092.F08.gz43_274507	F	M00043433A:F02	UC3-ColonMetLiver
5668	535123	2092.G08.gz43_274508	F	M00043439C:D05	UC3-ColonMetLiver
5669	452830	2092.J08.gz43_274511	F	M00043452D:D05	UC3-ColonMetLiver
5670	534054	2092.L08.gz43_274513	F	M00043460D:C03	UC3-ColonMetLiver

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
5671	162851	2092.M08.gz43_274514	F	M00043465B:G08	UC3-ColonMetLiver
5672	455289	2092.D09.gz43_274521	F	M00043420C:C02	UC3-ColonMetLiver
5673	456020	2092.H09.gz43_274525	F	M00043446B:H01	UC3-ColonMetLiver
5674	448946	2092.I09.gz43_274526	F	M00043449C:H09	UC3-ColonMetLiver
5675	539353	2092.L09.gz43_274529	F	M00043460D:H01	UC3-ColonMetLiver
5676	450658	2092.P09.gz43_274533	F	M00043485A:C04	UC3-ColonMetLiver
5677	544355	2092.E10.gz43_274538	F	M00043427C:E11	UC3-ColonMetLiver
5678	452128	2092.F10.gz43_274539	F	M00043434A:H02	UC3-ColonMetLiver
5679	447534	2092.I10.gz43_274542	F	M00043449D:A06	UC3-ColonMetLiver
5680	455256	2092.P10.gz43_274549	F	M00043485B:C09	UC3-ColonMetLiver
5681	455201	2092.C11.gz43_274552	F	M00042640C:C10	UC3-ColonMetLiver
5682	535129	2092.F11.gz43_274555	F	M00043434B:D06	UC3-ColonMetLiver
5683	455808	2092.H11.gz43_274557	F	M00043446C:E04	UC3-ColonMetLiver
5684	215366	2092.I11.gz43_274558	F	M00043449D:E09	UC3-ColonMetLiver
5685	456254	2092.J11.gz43_274559	F	M00043453B:C06	UC3-ColonMetLiver
5686	536415	2092.N11.gz43_274563	F	M00043472A:E06	UC3-ColonMetLiver
5687	452801	2092.F12.gz43_274571	F	M00043434B:E04	UC3-ColonMetLiver
5688	400258	2092.H12.gz43_274573	F	M00043446C:E08	UC3-ColonMetLiver
5689	546121	2092.J12.gz43_274575	F	M00043453B:F02	UC3-ColonMetLiver
5690	454621	2092.K12.gz43_274576	F	M00043457C:B12	UC3-ColonMetLiver
5691	455162	2092.D13.gz43_274585	F	M00043422B:C03	UC3-ColonMetLiver
5692	543429	2092.P13.gz43_274597	F	M00043486B:D02	UC3-ColonMetLiver
5693	456249	2092.I14.gz43_274606	F	M00043450B:C11	UC3-ColonMetLiver
5694	531461	2092.E15.gz43_274618	F	M00043428C:A08	UC3-ColonMetLiver
5695	455572	2092.H15.gz43_274621	F	M00043447A:F02	UC3-ColonMetLiver
5696	456783	2092.I15.gz43_274622	F	M00043450B:H05	UC3-ColonMetLiver
5697	2544	2092.N15.gz43_274627	F	M00043473C:B11	UC3-ColonMetLiver
5698	543431	2092.P15.gz43_274629	F	M00043486C:D02	UC3-ColonMetLiver
5699	402534	2092.O16.gz43_274644	F	M00043481A:G02	UC3-ColonMetLiver
5700	454563	2092.I17.gz43_274654	F	M00043450C:F11	UC3-ColonMetLiver
5701	541901	2092.K17.gz43_274656	F	M00043459A:B08	UC3-ColonMetLiver
5702	536225	2092.L17.gz43_274657	F	M00043462C:E12	UC3-ColonMetLiver
5703	455379	2092.M17.gz43_274658	F	M00043468C:D08	UC3-ColonMetLiver
5704	456567	2092.P17.gz43_274661	F	M00043486C:F07	UC3-ColonMetLiver
5705	539804	2092.C18.gz43_274664	F	M00043417A:H12	UC3-ColonMetLiver
5706	452618	2092.N18.gz43_274675	F	M00043473D:D11	UC3-ColonMetLiver
5707	543855	2092.J19.gz43_274687	F	M00043453D:D02	UC3-ColonMetLiver
5708	415326	2092.L19.gz43_274689	F	M00043462D:C09	UC3-ColonMetLiver
5709	455117	2092.B20.gz43_274695	F	M00042600D:B08	UC3-ColonMetLiver
5710	455601	2092.C20.gz43_274696	F	M00043417B:F12	UC3-ColonMetLiver
5711	455254	2092.E20.gz43_274698	F	M00043430D:C01	UC3-ColonMetLiver
5712	402916	2092.I20.gz43_274702	F	M00043451A:B02	UC3-ColonMetLiver

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SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
5713	455864	2092.N20.gz43_274707	F	M00043474C:H05	UC3-ColonMetLiver
5714	27586	2092.P20.gz43_274709	F	M00043489C:H06	UC3-ColonMetLiver
5715	452392	2092.B21.gz43_274711	F	M00042600D:E11	UC3-ColonMetLiver
5716	447380	2092.C21.gz43_274712	F	M00043417C:F12	UC3-ColonMetLiver
5717	448250	2092.I21.gz43_274718	F	M00043451B:D08	UC3-ColonMetLiver
5718	536171	2092.B22.gz43_274727	F	M00042637C:E12	UC3-ColonMetLiver
5719	455501	2092.H22.gz43_274733	F	M00043448B:E08	UC3-ColonMetLiver
5720	455808	2092.O22.gz43_274740	F	M00043483B:G01	UC3-ColonMetLiver
5721	422223	2092.C23.gz43_274744	F	M00043418A:A06	UC3-ColonMetLiver
5722	455814	2092.O23.gz43_274756	F	M00043483B:G11	UC3-ColonMetLiver
5723	538582	2092.H24.gz43_274765	F	M00043448C:G07	UC3-ColonMetLiver
5724	447238	2092.I24.gz43_274766	F	M00043451C:H03	UC3-ColonMetLiver
5725	456577	2092.P24.gz43_274773	F	M00043490A:F03	UC3-ColonMetLiver
5726	11576	2176.F01.gz43_281685	F	M00039503B:G05	HMEC-Unt
5727	401426	2176.P01.gz43_281695	F	M00039605D:E02	HMEC-Unt
5728	409330	2176.B02.gz43_281697	F	M00039363B:H10	HMEC-Unt
5729	407195	2176.C02.gz43_281698	F	M00039369D:D11	HMEC-Unt
5730	411985	2176.D02.gz43_281699	F	M00039379A:D03	HMEC-Unt
5731	412621	2176.F02.gz43_281701	F	M00039503D:E08	HMEC-Unt
5732	407711	2176.H02.gz43_281703	F	M00039514B:E07	HMEC-Unt
5733	411113	2176.G03.gz43_281718	F	M00039508D:C03	HMEC-Unt
5734	402411	2176.I04.gz43_281736	F	M00039523A:D09	HMEC-Unt
5735	147279	2176.F06.gz43_281765	F	M00039504B:F05	HMEC-Unt
5736	400628	2176.L06.gz43_281771	F	M00039566D:E08	HMEC-Unt
5737	407443	2176.C07.gz43_281778	F	M00039371A:E01	HMEC-Unt
5738	413346	2176.N07.gz43_281789	F	M00039592C:F09	HMEC-Unt
5739	125543	2176.O07.gz43_281790	F	M00039599A:E08	HMEC-Unt
5740	202308	2176.P07.gz43_281791	F	M00039606C:B07	HMEC-Unt
5741	400428	2176.K08.gz43_281802	F	M00039562A:D10	HMEC-Unt
5742	400426	2176.H09.gz43_281815	F	M00039516C:H06	HMEC-Unt
5743	402147	2176.P09.gz43_281823	F	M00039607A:F05	HMEC-Unt
5744	400233	2176.K10.gz43_281834	F	M00039562D:B02	HMEC-Unt
5745	408986	2176.K11.gz43_281850	F	M00039562D:G01	HMEC-Unt
5746	400171	2176.B12.gz43_281857	F	M00039366C:B10	HMEC-Unt
5747	403671	2176.C12.gz43_281858	F	M00039373B:B09	HMEC-Unt
5748	400047	2176.A13.gz43_281872	F	M00039184A:A08	HMEC-Unt
5749	404736	2176.B13.gz43_281873	F	M00039366D:A02	HMEC-Unt
5750	413627	2176.F13.gz43_281877	F	M00039505B:G07	HMEC-Unt
5751	407260	2176.K13.gz43_281882	F	M00039563C:D01	HMEC-Unt
5752	155374	2176.M13.gz43_281884	F	M00039586A:C03	HMEC-Unt
5753	409612	2176.I14.gz43_281896	F	M00039525B:H03	HMEC-Unt
5754	402411	2176.A16.gz43_281920	F	M00039184C:C05	HMEC-Unt

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
5755	411124	2176.C17.gz43_281938	F	M00039375A:C09	HMEC-Unt
5756	412416	2176.J17.gz43_281945	F	M00039534D:E07	HMEC-Unt
5757	406734	2176.M17.gz43_281948	F	M00039586D:D05	HMEC-Unt
5758	408306	2176.K18.gz43_281962	F	M00039564B:F08	HMEC-Unt
5759	1054	2176.E19.gz43_281972	F	M00039502D:H03	HMEC-Unt
5760	406855	2176.I19.gz43_281976	F	M00039527B:D06	HMEC-Unt
5761	400454	2176.H20.gz43_281991	F	M00039521A:D02	HMEC-Unt
5762	402147	2176.J20.gz43_281993	F	M00039536B:E10	HMEC-Unt
5763	202308	2176.M20.gz43_281996	F	M00039588A:H12	HMEC-Unt
5764	413997	2176.J21.gz43_282009	F	M00039536B:H03	HMEC-Unt
5765	409589	2176.K21.gz43_282010	F	M00039564C:H05	HMEC-Unt
5766	409262	2176.M21.gz43_282012	F	M00039588B:H02	HMEC-Unt
5767	405932	2176.H22.gz43_282023	F	M00039521C:B01	HMEC-Unt
5768	20517	2176.M22.gz43_282028	F	M00039588D:F10	HMEC-Unt
5769	413915	2176.P23.gz43_282047	F	M00039610A:G11	HMEC-Unt
5770	412483	2176.F24.gz43_282053	F	M00039507D:E03	HMEC-Unt
5771	402392	2176.G24.gz43_282054	F	M00039514A:G03	HMEC-Unt
5772	401510	2176.J24.gz43_282057	F	M00039537B:F06	HMEC-Unt
5773	408649	2176.L24.gz43_282059	F	M00039583A:G09	HMEC-Unt
5774	418682	2178.K02.gz43_282160	F	M00040183B:C06	HMEC-bFGF
5775	417259	2178.E04.gz43_282186	F	M00040141A:G10	HMEC-bFGF
5776	20517	2178.P04.gz43_282197	F	M00040235C:D02	HMEC-bFGF
5777	414821	2178.G05.gz43_282204	F	M00040160C:A04	HMEC-bFGF
5778	402534	2178.K05.gz43_282208	F	M00040183D:C08	HMEC-bFGF
5779	402411	2178.D07.gz43_282233	F	M00040134A:A07	HMEC-bFGF
5780	419255	2178.L07.gz43_282241	F	M00040188B:E05	HMEC-bFGF
5781	417426	2178.G11.gz43_282300	F	M00040161C:H06	HMEC-bFGF
5782	415527	2178.G12.gz43_282316	F	M00040161D:C03	HMEC-bFGF
5783	418340	2178.J12.gz43_282319	F	M00040181B:B06	HMEC-bFGF
5784	403154	2178.L12.gz43_282321	F	M00040189D:A06	HMEC-bFGF
5785	403837	2178.J13.gz43_282335	F	M00040181B:C05	HMEC-bFGF
5786	418482	2178.L14.gz43_282353	F	M00040190B:C02	HMEC-bFGF
5787	419751	2178.C15.gz43_282360	F	M00039760B:F12	HMEC-bFGF
5788	402070	2178.B16.gz43_282375	F	M00039752D:D07	HMEC-bFGF
5789	402070	2178.N16.gz43_282387	F	M00040227A:E07	HMEC-bFGF
5790	420504	2178.C18.gz43_282408	F	M00039760C:H07	HMEC-bFGF
5791	147279	2178.P19.gz43_282437	F	M00040248A:G09	HMEC-bFGF
5792	402353	2178.H20.gz43_282445	F	M00040171B:H03	HMEC-bFGF
5793	416914	2178.L20.gz43_282449	F	M00040196B:F10	HMEC-bFGF
5794	163970	2178.E21.gz43_282458	F	M00040145B:C12	HMEC-bFGF
5795	416762	2178.O21.gz43_282468	F	M00040233C:F09	HMEC-bFGF
5796	57183	2178.M22.gz43_282482	F	M00040222A:E06	HMEC-bFGF

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
5797	403306	2184.D01.gz43_282670	F	M00039950C:C05	HMEC-VEGF
5798	402298	2184.L01.gz43_282678	F	M00040328D:A03	HMEC-VEGF
5799	420958	2184.K02.gz43_282693	F	M00040322B:A08	HMEC-VEGF
5800	423884	2184.A03.gz43_282699	F	M00039747A:H06	HMEC-VEGF
5801	268336	2184.J04.gz43_282724	F	M00040318C:B09	HMEC-VEGF
5802	422590	2184.O07.gz43_282777	F	M00040364B:E11	HMEC-VEGF
5803	402298	2184.A08.gz43_282779	F	M00039749B:G05	HMEC-VEGF
5804	423534	2184.J11.gz43_282836	F	M00040319D:G10	HMEC-VEGF
5805	423008	2184.K13.gz43_282869	F	M00040323D:F04	HMEC-VEGF
5806	424723	2184.N13.gz43_282872	F	M00040347B:B11	HMEC-VEGF
5807	20517	2184.D16.gz43_282910	F	M00039958D:D05	HMEC-VEGF
5808	403306	2184.A17.gz43_282923	F	M00039750C:F08	HMEC-VEGF
5809	140224	2184.A22.gz43_283003	F	M00039762C:D11	HMEC-VEGF
5810	402298	2184.G24.gz43_283041	F	M00040294B:E09	HMEC-VEGF
5811	468930	1564.A01.gz43_296552	F	M00042709B:G05	UC2-NormColon
5812	463143	1564.B01.gz43_296553	F	M00042711B:H04	UC2-NormColon
5813	465785	1564.C01.gz43_296554	F	M00042713B:C08	UC2-NormColon
5814	453766	1564.I01.gz43_296560	F	M00042724A:G02	UC2-NormColon
5815	462398	1564.J01.gz43_296561	F	M00042726D:G11	UC2-NormColon
5816	390563	1564.O01.gz43_296566	F	M00042737B:C07	UC2-NormColon
5817	447189	1564.C03.gz43_296586	F	M00042713B:F03	UC2-NormColon
5818	462348	1564.H03.gz43_296591	F	M00042722A:G08	UC2-NormColon
5819	446740	1564.O04.gz43_296614	F	M00042737C:C07	UC2-NormColon
5820	447268	1564.C05.gz43_296618	F	M00042713C:B08	UC2-NormColon
5821	461316	1564.K05.gz43_296626	F	M00042729A:F11	UC2-NormColon
5822	420686	1564.N05.gz43_296629	F	M00042735C:G02	UC2-NormColon
5823	447579	1564.O05.gz43_296630	F	M00042737C:E03	UC2-NormColon
5824	447006	1564.B06.gz43_296633	F	M00042711C:H10	UC2-NormColon
5825	463824	1564.N06.gz43_296645	F	M00042735D:A07	UC2-NormColon
5826	461135	1564.G07.gz43_296654	F	M00042720C:E03	UC2-NormColon
5827	388688	1564.A08.gz43_296664	F	M00042710A:G10	UC2-NormColon
5828	462986	1564.K08.gz43_296674	F	M00042729A:H08	UC2-NormColon
5829	454825	1564.M08.gz43_296676	F	M00042733C:C05	UC2-NormColon
5830	466614	1564.O08.gz43_296678	F	M00042737D:D03	UC2-NormColon
5831	457975	1564.A09.gz43_296680	F	M00042710B:B09	UC2-NormColon
5832	446345	1564.I09.gz43_296688	F	M00042724D:B04	UC2-NormColon
5833	456530	1564.C11.gz43_296714	F	M00042714A:G04	UC2-NormColon
5834	462337	1564.E11.gz43_296716	F	M00042716D:G04	UC2-NormColon
5835	447387	1564.N11.gz43_296725	F	M00042736A:F03	UC2-NormColon
5836	467780	1564.B12.gz43_296729	F	M00042712A:E08	UC2-NormColon
5837	447561	1564.C12.gz43_296730	F	M00042714A:H05	UC2-NormColon
5838	461313	1564.K12.gz43_296738	F	M00042729B:F10	UC2-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
5839	453679	1564.L12.gz43_296739	F	M00042732A:A11	UC2-NormColon
5840	446964	1564.G13.gz43_296750	F	M00042721A:G07	UC2-NormColon
5841	459158	1564.H13.gz43_296751	F	M00042722D:C12	UC2-NormColon
5842	450723	1564.M13.gz43_296756	F	M00042733D:G08	UC2-NormColon
5843	447826	1564.C15.gz43_296778	F	M00042714B:E01	UC2-NormColon
5844	446741	1564.D15.gz43_296779	F	M00042715D:E02	UC2-NormColon
5845	452687	1564.F15.gz43_296781	F	M00042719A:H06	UC2-NormColon
5846	446601	1564.H15.gz43_296783	F	M00042723A:D09	UC2-NormColon
5847	447649	1564.B19.gz43_296841	F	M00042712C:E06	UC2-NormColon
5848	465528	1564.C19.gz43_296842	F	M00042714C:C10	UC2-NormColon
5849	462865	1564.E19.gz43_296844	F	M00042717B:G11	UC2-NormColon
5850	405932	1564.F19.gz43_296845	F	M00042719C:H05	UC2-NormColon
5851	457922	1564.G19.gz43_296846	F	M00042721D:B03	UC2-NormColon
5852	463821	1564.N19.gz43_296853	F	M00042737A:A07	UC2-NormColon
5853	463217	1564.O19.gz43_296854	F	M00042738D:H12	UC2-NormColon
5854	389425	1564.A20.gz43_296856	F	M00042711A:F01	UC2-NormColon
5855	446242	1564.O20.gz43_296870	F	M00042739A:C06	UC2-NormColon
5856	449171	1564.C21.gz43_296874	F	M00042714C:F12	UC2-NormColon
5857	450723	1564.G21.gz43_296878	F	M00042721D:D01	UC2-NormColon
5858	469766	1564.M21.gz43_296884	F	M00042735A:G12	UC2-NormColon
5859	446866	1564.D22.gz43_296891	F	M00042716A:F09	UC2-NormColon
5860	403949	1564.M23.gz43_296916	F	M00042735B:A06	UC2-NormColon
5861	446922	1564.O23.gz43_296918	F	M00042739A:G07	UC2-NormColon
5862	235874	1564.C24.gz43_296922	F	M00042714D:E11	UC2-NormColon
5863	558301	1681.A01.gz43_296936	F	M00055739A:C09	UC2-NormColon
5864	426366	1681.I01.gz43_296944	F	M00055749D:B07	UC2-NormColon
5865	638943	1681.J01.gz43_296945	F	M00055750C:H10	UC2-NormColon
5866	645603	1681.O01.gz43_296950	F	M00055758C:H10	UC2-NormColon
5867	642644	1681.E02.gz43_296956	F	M00055744C:D02	UC2-NormColon
5868	644105	1681.I02.gz43_296960	F	M00055749D:C01	UC2-NormColon
5869	468613	1681.A03.gz43_296968	F	M00055739B:B06	UC2-NormColon
5870	648905	1681.B03.gz43_296969	F	M00055740C:A07	UC2-NormColon
5871	446925	1681.H03.gz43_296975	F	M00055748C:C07	UC2-NormColon
5872	649356	1681.I03.gz43_296976	F	M00055749D:D06	UC2-NormColon
5873	510724	1681.K03.gz43_296978	F	M00055752C:C06	UC2-NormColon
5874	446676	1681.L03.gz43_296979	F	M00055753D:C06	UC2-NormColon
5875	644937	1681.B04.gz43_296985	F	M00055740C:E06	UC2-NormColon
5876	644342	1681.I04.gz43_296992	F	M00055749D:F12	UC2-NormColon
5877	640264	1681.O04.gz43_296998	F	M00055758D:E02	UC2-NormColon
5878	463951	1681.D05.gz43_297003	F	M00055743C:D12	UC2-NormColon
5879	644345	1681.K05.gz43_297010	F	M00055752C:F06	UC2-NormColon
5880	646552	1681.N06.gz43_297029	F	M00055757B:B07	UC2-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
5881	611927	1681.K07.gz43_297042	F	M00055752C:H07	UC2-NormColon
5882	639420	1681.N07.gz43_297045	F	M00055757B:C04	UC2-NormColon
5883	568467	1681.A08.gz43_297048	F	M00055739B:H08	UC2-NormColon
5884	645147	1681.C08.gz43_297050	F	M00055742B:H06	UC2-NormColon
5885	447936	1681.E08.gz43_297052	F	M00055744D:A11	UC2-NormColon
5886	492917	1681.O08.gz43_297062	F	M00055759A:B02	UC2-NormColon
5887	649427	1681.D09.gz43_297067	F	M00055743D:D04	UC2-NormColon
5888	556654	1681.F09.gz43_297069	F	M00055745D:F11	UC2-NormColon
5889	594040	1681.H09.gz43_297071	F	M00055748D:C03	UC2-NormColon
5890	488432	1681.J09.gz43_297073	F	M00055751A:F06	UC2-NormColon
5891	641144	1681.K09.gz43_297074	F	M00055752D:C01	UC2-NormColon
5892	550223	1681.L09.gz43_297075	F	M00055754A:E07	UC2-NormColon
5893	491544	1681.M09.gz43_297076	F	M00055755D:C09	UC2-NormColon
5894	648481	1681.A10.gz43_297080	F	M00055739C:D11	UC2-NormColon
5895	150839	1681.B10.gz43_297081	F	M00055740D:G12	UC2-NormColon
5896	644053	1681.F10.gz43_297085	F	M00055746A:C09	UC2-NormColon
5897	644342	1681.K10.gz43_297090	F	M00055752D:F01	UC2-NormColon
5898	419479	1681.C11.gz43_297098	F	M00055742C:C01	UC2-NormColon
5899	645000	1681.E11.gz43_297100	F	M00055744D:F03	UC2-NormColon
5900	478833	1681.L11.gz43_297107	F	M00055754A:H06	UC2-NormColon
5901	644684	1681.A13.gz43_297128	F	M00055739D:B12	UC2-NormColon
5902	640504	1681.B13.gz43_297129	F	M00055741A:D09	UC2-NormColon
5903	463815	1681.A14.gz43_297144	F	M00055739D:C03	UC2-NormColon
5904	640997	1681.B15.gz43_297161	F	M00055741B:B12	UC2-NormColon
5905	642263	1681.D15.gz43_297163	F	M00055744A:B04	UC2-NormColon
5906	451508	1681.P15.gz43_297175	F	M00055761A:E06	UC2-NormColon
5907	644919	1681.A16.gz43_297176	F	M00055739D:E04	UC2-NormColon
5908	639703	1681.K16.gz43_297186	F	M00055753A:D04	UC2-NormColon
5909	639750	1681.M16.gz43_297188	F	M00055756C:C03	UC2-NormColon
5910	587696	1681.F17.gz43_297197	F	M00055746C:F06	UC2-NormColon
5911	461917	1681.H17.gz43_297199	F	M00055749B:C10	UC2-NormColon
5912	644510	1681.I17.gz43_297200	F	M00055750B:H01	UC2-NormColon
5913	526459	1681.B18.gz43_297209	F	M00055741C:A09	UC2-NormColon
5914	471277	1681.F18.gz43_297213	F	M00055746C:F10	UC2-NormColon
5915	483042	1681.K18.gz43_297218	F	M00055753B:A02	UC2-NormColon
5916	514838	1681.L18.gz43_297219	F	M00055755A:B11	UC2-NormColon
5917	643984	1681.N18.gz43_297221	F	M00055757D:B05	UC2-NormColon
5918	462245	1681.A19.gz43_297224	F	M00055740A:B03	UC2-NormColon
5919	640017	1681.D19.gz43_297227	F	M00055744B:B02	UC2-NormColon
5920	453726	1681.E19.gz43_297228	F	M00055745A:H02	UC2-NormColon
5921	644468	1681.F19.gz43_297229	F	M00055746C:G06	UC2-NormColon
5922	644105	1681.H19.gz43_297231	F	M00055749C:B03	UC2-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
5923	447485	1681.K19.gz43_297234	F	M00055753B:A06	UC2-NormColon
5924	218416	1681.D20.gz43_297243	F	M00055744B:C08	UC2-NormColon
5925	489040	1681.H20.gz43_297247	F	M00055749C:C04	UC2-NormColon
5926	649702	1681.J20.gz43_297249	F	M00055752A:E10	UC2-NormColon
5927	643142	1681.A21.gz43_297256	F	M00055740B:C06	UC2-NormColon
5928	448251	1681.G21.gz43_297262	F	M00055748A:D07	UC2-NormColon
5929	644461	1681.N21.gz43_297269	F	M00055758A:G02	UC2-NormColon
5930	641968	1681.P22.gz43_297287	F	M00055761B:F09	UC2-NormColon
5931	470667	1681.E23.gz43_297292	F	M00055745B:H02	UC2-NormColon
5932	644479	1681.J23.gz43_297297	F	M00055752A:G10	UC2-NormColon
5933	463824	1681.A24.gz43_297304	F	M00055740B:F09	UC2-NormColon
5934	389377	1681.C24.gz43_297306	F	M00055743B:E01	UC2-NormColon
5935	468959	1681.E24.gz43_297308	F	M00055745C:A06	UC2-NormColon
5936	553675	1681.M24.gz43_297316	F	M00055757A:A07	UC2-NormColon
5937	449978	1561.C01.gz43_314395	F	M00042344D:F03	UC2-NormColon
5938	463920	1561.G01.gz43_314399	F	M00042526D:A05	UC2-NormColon
5939	456267	1561.J01.gz43_314402	F	M00042531B:G12	UC2-NormColon
5940	459997	1561.M01.gz43_314405	F	M00042537A:D12	UC2-NormColon
5941	447386	1561.I02.gz43_314417	F	M00042529D:D07	UC2-NormColon
5942	468257	1561.K02.gz43_314419	F	M00042533B:F11	UC2-NormColon
5943	18786	1561.E03.gz43_314429	F	M00042523C:H06	UC2-NormColon
5944	447494	1561.A04.gz43_314441	F	M00042341A:D08	UC2-NormColon
5945	459893	1561.B04.gz43_314442	F	M00042343B:D05	UC2-NormColon
5946	462558	1561.M04.gz43_314453	F	M00042537A:G09	UC2-NormColon
5947	458425	1561.O04.gz43_314455	F	M00042541A:B07	UC2-NormColon
5948	249178	1561.C05.gz43_314459	F	M00042345B:A05	UC2-NormColon
5949	462815	1561.J05.gz43_314466	F	M00042531D:G08	UC2-NormColon
5950	417291	1561.K05.gz43_314467	F	M00042533C:F04	UC2-NormColon
5951	463341	1561.M05.gz43_314469	F	M00042537A:H04	UC2-NormColon
5952	447868	1561.A06.gz43_314473	F	M00042341A:H04	UC2-NormColon
5953	461653	1561.B06.gz43_314474	F	M00042343B:F12	UC2-NormColon
5954	465127	1561.K06.gz43_314483	F	M00042533D:B05	UC2-NormColon
5955	460246	1561.N06.gz43_314486	F	M00042539B:D09	UC2-NormColon
5956	33139	1561.O06.gz43_314487	F	M00042541A:E06	UC2-NormColon
5957	457508	1561.N07.gz43_314502	F	M00042539C:A04	UC2-NormColon
5958	461917	1561.B09.gz43_314522	F	M00042343D:F08	UC2-NormColon
5959	447568	1561.H09.gz43_314528	F	M00042528D:D09	UC2-NormColon
5960	467094	1561.J09.gz43_314530	F	M00042532A:D08	UC2-NormColon
5961	447087	1561.N09.gz43_314534	F	M00042539C:H08	UC2-NormColon
5962	458419	1561.O09.gz43_314535	F	M00042541B:B05	UC2-NormColon
5963	446952	1561.D10.gz43_314540	F	M00042522C:H10	UC2-NormColon
5964	470513	1561.H10.gz43_314544	F	M00042528D:H03	UC2-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
5965	459974	1561.M10.gz43_314549	F	M00042537C:D04	UC2-NormColon
5966	1454	1561.N10.gz43_314550	F	M00042539D:A04	UC2-NormColon
5967	464510	1561.D11.gz43_314556	F	M00042522D:A08	UC2-NormColon
5968	457846	1561.G11.gz43_314559	F	M00042527B:B01	UC2-NormColon
5969	15296	1561.I11.gz43_314561	F	M00042530C:H02	UC2-NormColon
5970	446578	1561.C12.gz43_314571	F	M00042345D:D04	UC2-NormColon
5971	463086	1561.F12.gz43_314574	F	M00042525C:H07	UC2-NormColon
5972	464287	1561.I12.gz43_314577	F	M00042530D:A02	UC2-NormColon
5973	447805	1561.A14.gz43_314601	F	M00042341D:G11	UC2-NormColon
5974	446188	1561.G14.gz43_314607	F	M00042527C:A10	UC2-NormColon
5975	468565	1561.I14.gz43_314609	F	M00042530D:F09	UC2-NormColon
5976	470600	1561.J14.gz43_314610	F	M00042532A:H03	UC2-NormColon
5977	457772	1561.A15.gz43_314617	F	M00042342A:B04	UC2-NormColon
5978	446383	1561.E15.gz43_314621	F	M00042524C:C12	UC2-NormColon
5979	446673	1561.F15.gz43_314622	F	M00042525D:E01	UC2-NormColon
5980	462779	1561.L15.gz43_314628	F	M00042536B:G08	UC2-NormColon
5981	446289	1561.C16.gz43_314635	F	M00042521A:E10	UC2-NormColon
5982	458146	1561.K16.gz43_314643	F	M00042534B:B08	UC2-NormColon
5983	447690	1561.L16.gz43_314644	F	M00042536C:A06	UC2-NormColon
5984	452888	1561.N16.gz43_314646	F	M00042540B:B03	UC2-NormColon
5985	461327	1561.B17.gz43_314650	F	M00042344B:F02	UC2-NormColon
5986	456958	1561.E17.gz43_314653	F	M00042524D:A10	UC2-NormColon
5987	467901	1561.F17.gz43_314654	F	M00042526A:E10	UC2-NormColon
5988	459981	1561.K17.gz43_314659	F	M00042534B:D06	UC2-NormColon
5989	457218	1561.N17.gz43_314662	F	M00042540C:A12	UC2-NormColon
5990	463008	1561.A18.gz43_314665	F	M00042342C:H03	UC2-NormColon
5991	446341	1561.L18.gz43_314676	F	M00042536C:B03	UC2-NormColon
5992	446389	1561.O18.gz43_314679	F	M00042542A:C11	UC2-NormColon
5993	447096	1561.P18.gz43_314680	F	M00042543B:H12	UC2-NormColon
5994	446984	1561.B19.gz43_314682	F	M00042344B:H12	UC2-NormColon
5995	468767	1561.F19.gz43_314686	F	M00042526A:F11	UC2-NormColon
5996	467884	1561.H19.gz43_314688	F	M00042529B:E03	UC2-NormColon
5997	459881	1561.A20.gz43_314697	F	M00042342D:D03	UC2-NormColon
5998	447027	1561.D20.gz43_314700	F	M00042523B:H01	UC2-NormColon
5999	447380	1561.F20.gz43_314702	F	M00042526B:C12	UC2-NormColon
6000	446304	1561.O21.gz43_314727	F	M00042542B:B01	UC2-NormColon
6001	447072	1561.C22.gz43_314731	F	M00042521D:G09	UC2-NormColon
6002	379335	1561.I22.gz43_314737	F	M00042531B:D12	UC2-NormColon
6003	228873	1561.L22.gz43_314740	F	M00042537A:A07	UC2-NormColon
6004	446663	1561.D23.gz43_314748	F	M00042523C:E08	UC2-NormColon
6005	464791	1561.F23.gz43_314750	F	M00042526C:B12	UC2-NormColon
6006	446595	1561.K23.gz43_314755	F	M00042534D:D10	UC2-NormColon

Table 2

SEQ ID NO	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
6007	446439	1561.O23.gz43_314759	F	M00042542B:C11	UC2-NormColon
6008	458979	1561.A24.gz43_314761	F	M00042343A:C05	UC2-NormColon
6009	446620	1561.C24.gz43_314763	F	M00042522A:A05	UC2-NormColon
6010	452507	1561.F24.gz43_314766	F	M00042526D:A02	UC2-NormColon

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
1	AJ251957	Ciona intestinalis mRNA for nuclear lamin (lamin L2 gene)	2.2
2	AF133812	Strongylocentrotus pallidus isolate pR31 bindin gene, partial cds	0.88
3	AF051651	Homo sapiens squalene synthase gene, intron 3, 5' end	0.0001
4	NM_016701	Mus musculus nestin (Nes), mRNA	0.24
5	Y09000	R.norvegicus mRNA for dendrin	0.11
6	U67519	Methanococcus jannaschii section 61 of 150 of the complete genome	6.1
7	AK005889	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:1700012B08, full insert sequence	e-139
8	AB029343	Homo sapiens HCR (a-helix coiled-coil rod homologue) gene, complete cds	0.023
9	AB017505	Homo sapiens mRNA for Nori-2p, complete cds	0
10	AY024246	Oryza sativa microsatellite MRG6571 containing (TCTA)X6, genomic sequence	6.3
11	U32309	Acipenser fulvescens Af14 cytochrome b gene, partial cds, tRNA-Thr, tRNA-Pro and partial D-loop, mitochondrial genes encoding mitochondrial products	6.3
12	XM_046070	Homo sapiens KIAA0853 protein (KIAA0853), mRNA	3E-48
13	AK001945	Homo sapiens cDNA FLJ11083 fis, clone PLACE1005232	2.2
14	AF111457	Meleagris gallopavo clone TUCA1141 microsatellite sequence	0.076
15	AK018499	Mus musculus adult male colon cDNA, RIKEN full-length enriched library, clone:9030409O13, full insert sequence	0
16	AE002648	Drosophila melanogaster genomic scaffold 142000013385436, complete sequence	2.2
17	AC001011	Homo sapiens (subclone 1_e5 from P1 H43) DNA sequence, complete sequence	0.003
18	XM_039942	Homo sapiens Meis (mouse) homolog 3 (MEIS3), mRNA	0.75
19	AF099003	Caenorhabditis elegans cosmid Y59C2A	0.75
20	U92972	Mus musculus protease-activated receptor 3 (PAR3) mRNA, complete cds	0.08
21	AE003935	Xylella fastidiosa 9a5c, section 81 of 229 of the complete genome	0.067
22	AB031009	Homo sapiens DNA, MHC class I CL region, 7.1 ancestral haplotype	0.019
23	X94207	H.sapiens TPR gene (1365bp)	4.8
24	AK025678	Homo sapiens cDNA: FLJ22025 fis, clone HEP08518	2.2
25	AK014552	Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched library, clone:4632404O06, full insert sequence	e-176
26	XM_044013	Homo sapiens kinesin-like protein 2 (hklp2), mRNA	0
27	NM_032993	Homo sapiens nucleolar protein family A, member 1 (H/ACA small nucleolar RNPs) (NOLA1), transcript variant 2, mRNA	4E-50
28	NM_032315	Homo sapiens hypothetical protein MGC4399 (MGC4399), mRNA	0
29	AK020701	Mus musculus 6 days neonate skin cDNA, RIKEN full-length enriched library, clone:A030009B12, full insert sequence	0.0000002
30	AK021717	Homo sapiens cDNA FLJ11655 fis, clone HEMBA1004554	0

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
31	AL512453	Human DNA sequence from clone CTC-1516K22 on chromosome 6, complete sequence [Homo sapiens]	0.00004
32	XM_005034	Homo sapiens hypothetical protein FLJ10511 (FLJ10511), mRNA	2E-22
33	AF318896	Cricetulus griseus beta-1,4-galactosyltransferase 1 (beta4GalT-1) mRNA, complete cds	0.78
34	D29757	Human gene for cytochrome P-450 aromatase, exon 1 (brain specific)	3E-24
35	AJ311520	Ostreopsis ovata 5.8S rRNA gene, internal transcribed spacer 1 (ITS1) and internal transcribed spacer 2 (ITS2), strain A1	0.79
36	XM_038521	Homo sapiens phosphatidylserine decarboxylase (PISD), mRNA	0
37	AK023043	Homo sapiens cDNA FLJ12981 fis, clone NT2RP2006454	3E-96
38	XM_045520	Homo sapiens KIAA1595 protein (KIAA1595), mRNA	4E-16
39	AB017505	Homo sapiens mRNA for Nori-2p, complete cds	0
40	AK002682	Mus musculus adult male kidney cDNA, RIKEN full-length enriched library, clone:0610027B03, full insert sequence	e-138
41	NC_001712	Locusta migratoria mitochondrion, complete genome	0.009
42	AL512453	Human DNA sequence from clone CTC-1516K22 on chromosome 6, complete sequence [Homo sapiens]	0.00001
43	AK002682	Mus musculus adult male kidney cDNA, RIKEN full-length enriched library, clone:0610027B03, full insert sequence	e-125
44	XM_039088	Homo sapiens KIAA0914 gene product (KIAA0914), mRNA	0.76
45	U30291	Schistosoma mansoni synaptobrevin-like protein gene, exon 2 and partial cds	0.69
46	XM_052543	Homo sapiens mitochondrial ribosomal protein L42 (MRPL42), mRNA	1E-26
47	AK026225	Homo sapiens cDNA: FLJ22572 fis, clone HSI02313	0.0008
48	XM_043007	Homo sapiens hypothetical gene supported by AK021969 (LOC92132), mRNA	1E-99
49	M18824	P.faciparum S antigen gene, complete cds	0.003
50	XM_009311	Homo sapiens zinc finger protein 304 (ZNF304), mRNA	0.003
51	AK026697	Homo sapiens cDNA: FLJ23044 fis, clone LNG02454	0
52	XM_035597	Homo sapiens hypothetical protein AF140225 (AF140225), mRNA	1E-98
53	U81366	Plasmid Rts1 killer protein and antidote protein genes, complete cds	0.26
54	U28921	Phaseolus vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds	0.27
55	AF305083	Homo sapiens alpha(1,3)-fucosyltransferase IV (FUTIV) gene, 3' UTR	0.031
56	D29757	Human gene for cytochrome P-450 aromatase, exon 1 (brain specific)	7E-20
57	XM_038048	Homo sapiens similar to APICAL ENDOSOMAL GLYCOPROTEIN PRECURSOR (R. norvegicus) (LOC91372), mRNA	0.0004
58	AK026860	Homo sapiens cDNA: FLJ23207 fis, clone ADSE00968	8E-12

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
59	BC010849	Homo sapiens, Similar to hypothetical protein FLJ20561, clone MGC:8851 IMAGE:3878776, mRNA, complete cds	0
60	XM_036092	Homo sapiens signal recognition particle 68kD (SRP68), mRNA	0
61	XM_003184	Homo sapiens zinc finger protein ANC_2H01 (LOC51193), mRNA	0
63	Z49806	B.taurus mRNA for adenylyl cyclase type VII	6.8
64	XM_048858	Homo sapiens hypothetical protein FLJ23384 (FLJ23384), mRNA	0
65	NM_032315	Homo sapiens hypothetical protein MGC4399 (MGC4399), mRNA	0
66	AB057594	Homo sapiens GSTT1 gene for glutathione S-transferase TT1, complete cds	3E-69
67	XM_035597	Homo sapiens hypothetical protein AF140225 (AF140225), mRNA	2E-75
68	XM_035597	Homo sapiens hypothetical protein AF140225 (AF140225), mRNA	1E-71
69	AB017505	Homo sapiens mRNA for Nori-2p, complete cds	0
70	AK010143	Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310074B19, full insert sequence	1.7
71	AK008666	Mus musculus adult male stomach cDNA, RIKEN full-length enriched library, clone:2210008A03, full insert sequence	e-173
72	L18785	Plasmodium falciparum DNA polymerase alpha gene, complete cds	0.007
73	XM_003327	Homo sapiens hypothetical protein FLJ10858 (FLJ10858), mRNA	0
74	AK004786	Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200015F23, full insert sequence	2E-11
75	Z29969	E.histolytica plasmid genes for ribosomal RNA and hemolysins HLY1, HLY5mc1 HLY5mc2 HLY4	0.028
76	AK024945	Homo sapiens cDNA: FLJ21292 fis, clone COL01969	0
77	Y15931	Homo sapiens CTNS gene, exon 10 and flanking intronic regions	0.78
78	BC000610	Homo sapiens, hypothetical protein FLJ10986, clone MGC:908 IMAGE:3347108, mRNA, complete cds	0
79	XM_050424	Homo sapiens KIAA1244 protein (KIAA1244), mRNA	0.75
80	NC_001807	Human mitochondrion, complete genome	1E-36
81	AF360266	Arabidopsis thaliana unknown protein (F28C11.8) mRNA, complete cds	6.8
82	BC000225	Homo sapiens, Similar to hypothetical protein FLJ10656, clone IMAGE:3350951, mRNA	0
83	XM_034107	Homo sapiens hypothetical protein FLJ20758 (FLJ20758), mRNA	7E-32
84	AF305816	Homo sapiens PRO0633 mRNA, complete cds	0.67
85	AF196678	HIV-1 isolate 96RW34 from Rwanda, gag protein (gag) gene, partial cds	2.1
86	AK024927	Homo sapiens cDNA: FLJ21274 fis, clone COL01781	6E-75
87	X77394	P.philodendra mitochondrial DNA repeat unit	0.23

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
88	U41203	Human short tandem repeat polymorphism UM32, D17S1333	0.0001
89	AC015937	Homo sapiens chromosome 17, clone CTD-2542F12, complete sequence	0.65
90	AF245117	Mus musculus leukocyte cell-surface molecule (Ly9) gene, exon 1	0.74
91	XM_001412	Homo sapiens metal-regulatory transcription factor 1 (MTF1), mRNA	2E-50
92	AE006690	Sulfolobus solfataricus section 49 of 272 of the complete genome	0.26
93	AJ292466	Homo sapiens mRNA for WDR9 protein (WDR9 gene), form B	9E-44
94	NM_013983	Homo sapiens neuregulin 2 (NRG2), transcript variant 4, mRNA	0.27
95	J01390	Emericella nidulans mtDNA between h2/h5 and bh2/b2 junctions. genes for ATPase subunit 6, cytochrome oxidase subunit 3, seven. unidentified proteins, twentyfour tRNA's and L-rRNA	2.2
96	AP000384	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:MCE21	0.22
97	AE001397	Plasmodium falciparum chromosome 2, section 34 of 73 of the complete sequence	2.4
98	AE000192	Escherichia coli K12 MG1655 section 82 of 400 of the complete genome	0.003
99	AF316828	Schistosoma mansoni zinc finger protein SmZF1 gene, complete cds	1.7
100	BC007942	Homo sapiens, nucleolar autoantigen (55kD) similar to rat synaptonemal complex protein, clone MGC:14267 IMAGE:4130726, mRNA, complete cds	2E-59
101	L35301	Homo sapiens nucleoside diphsophate kinase A (nm23-H1) gene fragment	0.003
102	AF114927	Saccharomyces pastorianus CBS1538 small subunit ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, complete sequence	0.27
103	AF299248	Drosophila melanogaster talin mRNA, complete cds	1.8
104	BC003191	Homo sapiens, GL004 protein, clone MGC:895 IMAGE:3502929, mRNA, complete cds	2E-10
105	U29926	Human AMP deaminase (AMPD3) gene, exon 14 and 15, and complete cds	0.06
106	BC003191	Homo sapiens, GL004 protein, clone MGC:895 IMAGE:3502929, mRNA, complete cds	0
107	AK022127	Homo sapiens cDNA FLJ12065 fis, clone HEMBB1002249	0.0008
108	D16360	Human DNA for plasma glutathione peroxidase, exon 1	0.091
109	AK014138	Mus musculus 13 days embryo head cDNA, RIKEN full-length enriched library, clone:3110038A11, full insert sequence	6
110	XM_006914	Homo sapiens cold shock domain protein A (CSDA), mRNA	0.079
111	U31283	Mesotaenium caldariorum clone mesphy1a phytochrome gene, partial cds, exons 4 through 10	0.56
112	XM_049935	Homo sapiens hypothetical protein FLJ14950 (FLJ14950), mRNA	0

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
113	AE001329	Chlamydia trachomatis section 56 of 87 of the complete genome	0.75
114	XM_037830	Homo sapiens OLF-1/EBF associated zinc finger gene (KIAA0760), mRNA	0.25
115	AE006368	Lactococcus lactis subsp. lactis IL1403 section 130 of 218 of the complete genome	0.0003
116	XM_049935	Homo sapiens hypothetical protein FLJ14950 (FLJ14950), mRNA	0
117	XM_032533	Homo sapiens hypothetical protein FLJ12787 (FLJ12787), mRNA	0
118	AJ309861	Homo sapiens partial mRNA for putative protein kinase WNK4 (PRKWNK4 gene)	9E-76
119	BC005173	Homo sapiens, KIAA0255 gene product, clone IMAGE:3507918, mRNA	2E-38
120	AF068758	Drosophila melanogaster SIR2 (Sir2) mRNA, complete cds	0.083
121	AK017307	Mus musculus 6 days neonate head cDNA, RIKEN full-length enriched library, clone:5430414B19, full insert sequence	0.003
122	XM_036208	Homo sapiens sphingosine kinase 1 (SPHK1), mRNA	2.1
123	XM_039960	Homo sapiens PC3-96 protein (PC3-96), mRNA	0
124	XM_039306	Homo sapiens hypothetical protein FLJ20400 (FLJ20400), mRNA	0.08
125	XM_049935	Homo sapiens hypothetical protein FLJ14950 (FLJ14950), mRNA	0
126	AE006080	Pasteurella multocida PM70 section 47 of 204 of the complete genome	2.1
127	XM_009518	Homo sapiens WNT1 inducible signaling pathway protein 2 (WISP2), mRNA	0.16
128	U36263	Homo sapiens beta-prime-adaptin (AP1B1) gene, exon 15	0.022
129	AF267996	Homo sapiens muscle-specific protein (C4orf5) gene, intron 3	0.34
130	AF131859	Homo sapiens clone 24923 mRNA sequence	1.8
131	L48479	Homo sapiens (subclone 6_h1 from P1 H21) DNA sequence	0.01
132	XM_018317	Homo sapiens ubiquitination factor E4B (homologous to yeast UFD2) (UBE4B), mRNA	1.6
133	XM_008267	Homo sapiens solute carrier family 16 (monocarboxylic acid transporters), member 6 (SLC16A6), mRNA	0.23
134	AF162923	Beet soil-borne virus RNA3 isolate 6b 22K protein gene, partial cds	6.6
135	NM_010053	Mus musculus distal-less homeobox 1 (Dlx1), mRNA	2.5
136	AF257303	Mus musculus synaptotagmin II (Syt2) gene, complete cds	0.85
137	Z92837	Caenorhabditis elegans cosmid R03E1, complete sequence	0.027
138	AF258528	Loligo pealei phospholipase C mRNA, complete cds	0.74
139	M65252	Bacillus thuringiensis alesti delta endotoxin gene, complete cds	0.075
140	M14954	D.melanogaster (W-IR1 mutation) I factor DNA, complete cds	0.053
141	Z48636	C.novyi gene for alpha-toxin	0.026
142	XM_036491	Homo sapiens hypothetical protein MGC3771 (MGC3771), mRNA	0.002

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
143	AK020198	Mus musculus 15 days embryo male testis cDNA, RIKEN full-length enriched library, clone:8030442B05, full insert sequence	0.53
144	AJ404228	Saccharomyces douglasii mitochondrial tRNA gene cluster	0.022
145	AJ297708	Rattus norvegicus RT6 gene for T cell differentiation marker RT6.2, exons 1-8	0.024
146	AK026697	Homo sapiens cDNA: FLJ23044 fis, clone LNG02454	1.9
147	AE001370	Plasmodium falciparum chromosome 2, section 7 of 73 of the complete sequence	0.017
148	AF325208	Acetabularia acetabulum nicotinamide nucleotide transhydrogenase (Nnt) gene, exons 6, 7, 8, and complete cds	5.2
149	L78770	Homo sapiens (subclone 1_f7 from P1 H43) DNA sequence	0.068
150	AF182214	Glycine max glutamine synthetase gamma 2 subunit gene, 5'-flanking region and partial cds	0.2
151	AF359513	Lolium rigidum clone LR1 acetyl-CoA carboxylase mRNA, partial cds; nuclear gene for plastid product	0.2
152	AE004798	Pseudomonas aeruginosa PA01, section 359 of 529 of the complete genome	2.6
153	NM_021699	Rattus norvegicus serine/threonine kinase (LOC60328), mRNA	1.8
154	XM_040539	Homo sapiens interphotoreceptor matrix proteoglycan 200 (SPACRCAN), mRNA	2.3
155	AE006894	Sulfolobus solfataricus section 253 of 272 of the complete genome	0.027
156	Y14603	Erwinia amylovora srlA, srlE, srlB, srlD, srlM and srlR genes	0.8
157	AF181720	Homo sapiens RU2AS (RU2) gene, complete cds; and RU2S (RU2) gene, partial cds	0.051
158	XM_043815	Homo sapiens hypothetical protein FLJ21736 (FLJ21736), mRNA	1.1
159	AE006059	Pasteurella multocida PM70 section 26 of 204 of the complete genome	1.6
160	AF151097	Homo sapiens voltage-dependent anion channel (VDAC1) gene, exons 8 and 9 and complete cds	0.074
161	AF165136	Mycoplasma mycoides mycoides LC hypothetical surface located membrane protein and lipoprotein B precursor (lppB) genes, partial cds	0.23
162	XM_016392	Homo sapiens hypothetical protein FLJ12768 (FLJ12768), mRNA	2.1
163	AF170544	Magnaporthe grisea vacuolar-ATPase (VATP) mRNA, complete cds	0.15
164	AY045680	Arabidopsis thaliana At1g08350/T27G7_4 mRNA, complete cds	0.009
165	AF285100	Bos taurus lysophosphatidic acid acyltransfesrase gene, complete cds	1.6
166	AF194170	Dictyostelium discoideum cudA protein gene, promotor sequence and partial cds	0.039
167	AF242446	Homo sapiens LINE-1 insertion dimorphism LID-3 empty site sequence	0.043

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
168	AF084196	Pan troglodytes gamma-aminobutyric acid receptor A5 subunit duplicated gene, 5'UTR region	0.88
169	AK021754	Homo sapiens cDNA FLJ11692 fis, clone HEMBA1004983	0
170	AE006002	Caulobacter crescentus section 328 of 359 of the complete genome	1.6
171	AL096734	Homo sapiens mRNA; cDNA DKFZp434M011 (from clone DKFZp434M011)	0.015
172	AF251351	Homo sapiens 2'-5'oligoadenylate synthetase 3 (OAS3) gene, promoter region	2.7
173	AF061244	Agrocybe aegerita B type DNA polymerase (Mtpol) gene, complete cds; tRNA-Asn gene, complete sequence; and unknown genes, mitochondrial genes for mitochondrial products	0.0006
174	X95275	P.falciparum complete gene map of plastid-like DNA (IR-A)	0.1
176	M88599	Entamoeba histolytica P-glycoprotein-1 (pgp1) gene, complete cds	0.12
177	AY019624	Oryza sativa microsatellite MRG1949 containing (AT)X40, closest to marker R1167, genomic sequence	0.017
178	NM_026040	Mus musculus RIKEN cDNA 2810036K01 gene (2810036K01Rik), mRNA	e-101
179	AL162040	Homo sapiens mRNA; cDNA DKFZp434N199 (from clone DKFZp434N199)	e-152
180	AJ295190	Human coxsackievirus A11 genomic RNA for partial polyprotein gene, isolate VR-169, ATCC	1.5
181	AJ298684	Phylloxera sp. MBLM2 mitochondrial ATP6 gene for ATP synthase A chain subunit 6	0.51
183	AF268064	Candidatus Carsonella ruddii natural-host Calophya schini RNA polymerase beta subunit (rpoB) and RNA polymerase beta-prime subunit (rpoC) genes, partial cds	0.012
184	U27374	Human Menkes disease gene (ATP7A), exon 16	0.51
185	D10767	Epizootic haemorrhagic disease virus serotype 1 (EHDV-1) gene encoding VP2 protein	0.049
186	AJ002256	Mus musculus minisatellite tandem repeat (MMS73)	0.058
187	AB007546	Homo sapiens gene for LECT2, complete cds	2E-11
188	AF254573	Cricetulus griseus origin recognition complex subunit 2 mRNA, complete cds	0.57
189	AK024903	Homo sapiens cDNA: FLJ21250 fis, clone COL01253, highly similar to AB020527 Homo sapiens mRNA for Na/PO4 cotransporter homolog	e-135
190	AF359513	Lolium rigidum clone LR1 acetyl-CoA carboxylase mRNA, partial cds; nuclear gene for plastid product	0.15
191	AJ237585	Mus musculus mRNA for hypothetical protein expressed in thymocytes (clone MFT.M05.13/MTA.B10.066), partial	4.4
192	AF233591	Mus musculus son-of-sevenless 1 (Sos1) gene, partial cds	0.52
193	X81190	M.musculus DNA flanking site of transgene insertion	4.8
194	AF232246	Tetrahymena thermophila clone Tlr1 Int integrase-like protein gene, complete cds	0.53

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
195	AB034969	Thermococcus sp. B1001 cgtB, cgtA, cgtC, cgtD, cgtE genes for cyclomaltodextrinase, cyclomaltodextrin glucanotransferase, cyclomaltodextrin binding protein, cyclomaltodextrin transport membrane protein, complete cds	1.8
196	U95885	Ixodes granulatus 16S ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence	0.048
198	XM_016002	Homo sapiens LOC88174 (LOC88174), mRNA	4
199	AC091698	Homo sapiens clone RP11-596J6, complete sequence	0.000003
200	Z99763	Flaveria pringlei gdcsH gene	0.02
201	AB048873	Macaca fascicularis brain cDNA, clone:QnpA-10763	0.053
202	AF286367	Homo sapiens HMGIY gene, promoter	0.007
203	AB029073	Mus musculus Kkm gene for Ser/Thr kinase KKIAMRE, exon 13, 14, and complete cds	3.9
204	AF262582	Dolichorhinotermes sp. 'Manaus' 16S mitochondrial ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	0.045
205	AL360005	Human DNA sequence from clone RP11-436H17 on chromosome Xq26.1-27.1, complete sequence [Homo sapiens]	0.16
206	NM_019054	Homo sapiens hypothetical protein MGC5560 (MGC5560), mRNA	9E-35
207	AK014626	Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched library, clone:4731413G05, full insert sequence	0.82
208	AK027128	Homo sapiens cDNA: FLJ23475 fis, clone HSI13659	0.021
209	J00778	Rat pancreatic trypsin I gene, complete cds	0.016
210	D49412	Human gene for interleukin 3 receptor alpha subunit, exon 11	0.067
211	AY045578	Arabidopsis thaliana AT4g37000/C7A10_360 mRNA, complete cds	2
213	AJ011013	Cicer arietinum epicotyl EST, clone Can133	4.7
214	XM_008731	Homo sapiens meprin A, beta (MEP1B), mRNA	5.6
215	AL023830	Caenorhabditis elegans cosmid Y26E6A, complete sequence	0.084
216	AK027136	Homo sapiens cDNA: FLJ23483 fis, clone KAIA04052	6.6
217	U03554	Bacillus thuringiensis morrisoni EG2158 transposon Tn5401 site-specific recombinase (tnpI) and transposase (tpnA) genes, complete cds	0.46
218	XM_043584	Homo sapiens ankyrin repeat and SOCS box-containing 1 (ASB1), mRNA	2.2
219	AE001177	Borrelia burgdorferi (section 63 of 70) of the complete genome	0.094
220	AK018148	Mus musculus adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:6330408P11, full insert sequence	1.6
221	AF271148	Botryosphaeria ribis isolate 96-131 small subunit ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	0.65
222	XM_008090	Homo sapiens KIAA0419 gene product (KIAA0419), mRNA	0.25
223	Z54541	H.sapiens CpG island DNA genomic Mse1 fragment, clone 132c11, forward read cpg132c11.ft1b	6.4

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
225	XM_042689	Homo sapiens fasciculation and elongation protein zeta 2 (zygin II) (FEZ2), mRNA	0.69
226	AF317083	Anoplostoma viviparum isolate Brh10 large subunit ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	0.22
227	AE006436	Lactococcus lactis subsp. lactis IL1403 section 198 of 218 of the complete genome	0.029
228	AK027535	Homo sapiens cDNA FLJ14629 fis, clone NT2RP2000448, weakly similar to KES1 PROTEIN	7E-76
229	BC004209	Homo sapiens, NIMA (never in mitosis gene a)-related kinase 6, clone MGC:4434 IMAGE:2958695, mRNA, complete cds	3E-36
230	AC002183	Homo sapiens (subclone 2_h8 from BAC H111) DNA sequence, complete sequence	0.0000004
231	AF242489	Prochlorococcus marinus UreC (ureC), UreB (ureB), UreA (ureA), UreD (ureD), UreE (ureE), UreF (ureF), and UreG (ureG) genes, complete cds	0.0003
232	AF385396	Homo sapiens psoriasis susceptibility gene, partial sequence	0.027
233	AE006749	Sulfolobus solfataricus section 108 of 272 of the complete genome	2.1
234	X73501	H.sapiens gene for cytokeratin 20	0.25
235	AJ296801	Glyptotendipes pallens 18S rRNA gene (partial), 2S rRNA gene, 28S rRNA gene (partial), internal transcribed spacer 1 (ITS1) and internal transcribed spacer 2 (ITS2), clone Gpaits9	0.49
236	X17627	C. thummi DNA transposable element TECth1	0.59
237	AF157924	Eutamias dorsalis cytochrome b (cytb) gene, complete cds; mitochondrial gene for mitochondrial product	0.19
238	XM_040836	Homo sapiens similar to calcium channel, voltage-dependent, alpha 1H subunit (H. sapiens) (LOC91809), mRNA	0.38
239	AF097103	Oreina melanocephala 16S large subunit ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	0.23
240	AK013974	Mus musculus 13 days embryo head cDNA, RIKEN full-length enriched library, clone:3110002D09, full insert sequence	0.73
241	AK022073	Homo sapiens cDNA FLJ12011 fis, clone HEMBB1001653	0.26
242	XM_012392	Homo sapiens ubiquitin specific protease 8 (USP8), mRNA	2
243	AB048604	Mus musculus Neu-2 mRNA for sialidase, complete cds	0.54
244	AF275235	Drepanaphis utahensis 12S small subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and 16S large subunit ribosomal RNA gene, partial sequence; mitochondrial genes for mitochondrial products	0.076
245	XM_032956	Homo sapiens cat eye syndrome chromosome region, candidate 2 (CECR2), mRNA	2.2
246	XM_050246	Homo sapiens secretory protein SEC8; KIAA1699 protein (SEC8), mRNA	0
247	X69200	D.tigrina Dth-1 gene, exon 2	0.49
248	M33582	O.cuniculus beta-casein gene, complete cds	0.006
250	AB048604	Mus musculus Neu-2 mRNA for sialidase, complete cds	0.46

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
251	U48594	Heliothis virescens insect storage protein (SP4) mRNA, partial cds	0.022
252	AL162583	Human DNA sequence from clone RP1-250J21 on chromosome Xp11.22-11.4, complete sequence [Homo sapiens]	0.2
253	AF284038	Cucurbita maxima phloem serpin-1 mRNA, complete cds	0.19
254	AK026699	Homo sapiens cDNA: FLJ23046 fis, clone LNG02491	0.6
255	AF069199	Trioxys betulae NADH dehydrogenase 1 gene, mitochondrial gene encoding mitochondrial protein, partial cds	0.19
256	Z12028	L.pimpinellifolium gene encoding vacuolar invertase	0.7
257	AB041256	Panonychus mori mitochondrial CO1 gene for cytochrome oxidase subunit 1, partial cds, strain:TtDe	0.21
258	AK022820	Homo sapiens cDNA FLJ12758 fis, clone NT2RP2001328	0.25
259	AE006782	Sulfolobus solfataricus section 141 of 272 of the complete genome	1.4
260	AF027656	Homo sapiens cholesteryl ester transfer protein gene, promoter region	0.00004
261	Z57957	H.sapiens CpG island DNA genomic Mse1 fragment, clone 22b3, reverse read cpg22b3.rt1a	0.00003
262	AF266097	Orthetrum cancellatum large subunit ribosomal RNA gene, partial sequence; tRNA-Valine gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence; mitochondrial genes for mitochondrial products	0.077
263	XM_003119	Homo sapiens dynein light chain-A (LOC51143), mRNA	5.6
264	AF099990	Rattus norvegicus Ste-20 related kinase SPAK mRNA, complete cds	0.54
265	AE007394	Streptococcus pneumoniae section 77 of 194 of the complete genome	2.2
266	L07545	Leishmania tarentolae kinetoplast mitochondrial MURF2 edited mRNA, complete cds	0.002
267	L09706	Homo sapiens complement component 2 (C2) gene allele b, exons 1 through 8	0.073
268	AF174326	Pauesia unilachni 16S ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	0.063
269	Z79794	M.musculus dystrobrevin gene, exon 8	1.8
270	AB029325	Oryza sativa gene for water channel protein RWC3, promoter region and complete cds	1.7
271	U42461	Xenopus laevis neural specific DNA binding protein (Xgli3) mRNA, complete cds	1.6
272	XM_029784	Homo sapiens CGI-53 protein (LOC51098), mRNA	6E-23
273	D14011	Mouse reg II gene for regenerating protein II, complete cds	0.071
274	AF179235	Homo sapiens short-chain dehydrogenase/reductase 1 (SDR1) gene, exons 2, 3, and 4	2.1

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
275	AF264911	Campylobacter jejuni putative UDP-N-acetylmuramate-alanine ligase (murC) gene, partial cds; putative integral membrane protein, putative MutS (mutS), restriction and modification enzyme CjeI (cjeI), putative transferase, and putative integral membrane >	0.22
276	AF266074	Gomphus exilis large subunit ribosomal RNA gene, partial sequence; tRNA-Valine gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence; mitochondrial genes for mitochondrial products	0.021
277	AF229988	Cryptosporidium parvum P-type ATPase3 gene, complete cds	1.9
278	AF250346	Xenopus laevis early growth response protein 1 (egr1) gene, partial cds	0.25
279	AL157448	Homo sapiens mRNA; cDNA DKFZp761E0311 (from clone DKFZp761E0311)	0.00001
280	AF386078	Homo sapiens serine-cysteine proteinase inhibitor clade C member 1 (SERPINC1) gene, complete cds	2.1
281	S80932	MVAT5-RX2 VSG=variant surface glycoprotein {promoter} [Trypanosoma brucei=African trypanosomes, Genomic, 6583 nt]	0.003
282	U09478	Dictyostelium discoideum KAx-3 LagC protein (lagC) mRNA, complete cds	0.008
283	U63580	Oxytricha fallax micronuclear actin I gene, partial sequence	0.022
284	AF348411	Macaca mulatta Per4 pseudogene sequence	0.0008
285	AF053645	Homo sapiens cellular apoptosis susceptibility protein (CSE1) gene, exons 3 through 10	0.0002
287	U90928	Arabidopsis thaliana glyoxalase II mitochondrial isozyme (Glx2-1) mRNA, nuclear gene encoding mitochondrial protein, complete cds	2.2
288	AB050751	Carabus pseudopusio mitochondrial ND5 gene for NADH dehydrogenase subunit 5, partial cds	1.6
289	AF275220	Prociphilus fraxinifolii 12S small subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and 16S large subunit ribosomal RNA gene, partial sequence; mitochondrial genes for mitochondrial products	0.003
290	NM_014358	Homo sapiens C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 9 (CLECSF9), mRNA	0.009
291	D25274	Homo sapiens mRNA, clone:PO2ST9	1E-38
292	AF111936	Callithrix jacchus isolate MJ50037 alpha (1,2) fucosyltransferase (FUT1) gene, partial cds	1.8
293	AL592159	Human DNA sequence from clone RP13-237P14 on chromosome X, complete sequence [Homo sapiens]	0.18
294	AK013928	Mus musculus 13 days embryo head cDNA, RIKEN full-length enriched library, clone:3100003M19, full insert sequence	1.9
295	AF289199	Mus musculus junctin and aspartyl beta-hydroxylase (Asph) genes, partial cds	0.079

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
296	AE001425	Plasmodium falciparum chromosome 2, section 62 of 73 of the complete sequence	0.008
297	XM_011029	Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP), mRNA	0.23
298	AF105034	Arabidopsis thaliana delta7 sterol C-5 desaturase (STE1) gene, complete cds	0.009
299	L77040	Homo sapiens (subclone 8_c11 from P1 H22) DNA sequence	9E-14
300	AF278536	Parastrongyloides trichosuri heat shock 70 protein gene, complete cds	0.61
302	Z28216	S.cerevisiae chromosome XI reading frame ORF YKL216w	1.7
303	AJ008049	Chrysolina colasi 16S rRNA gene	0.0007
304	AF280812	Glycine max putative Hs1pro-1-like receptor mRNA, complete cds	0.67
305	AK007831	Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810048N21, full insert sequence	0.047
306	AL163543	Human DNA sequence from clone RP11-424E21 on chromosome 13, complete sequence [Homo sapiens]	0.64
307	AF045022	Bos taurus phosphatidic acid-preferring phospholipase A1 mRNA, complete cds	5
308	AB052731	Oikopleura longicauda OilBra mRNA for brachyury protein, complete cds	1.8
309	AF194275	Holbrookia maculata clone HMFL 12S ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	6.3
310	AJ400814	Dictyostelium discoideum srfA gene, alternative promoters	0.024
311	AK002854	Mus musculus adult male kidney cDNA, RIKEN full-length enriched library, clone:0610039P13, full insert sequence	0.68
312	U25177	Helobdella robusta cyclin A mRNA, partial cds	0.023
313	AK011102	Mus musculus 13 days embryo liver cDNA, RIKEN full-length enriched library, clone:2510044F14, full insert sequence	0.51
314	AK002181	Homo sapiens cDNA FLJ11319 fis, clone PLACE1010293	0.0006
315	U67282	Human mis5 homolog (MCM6) gene, exon x	0.014
316	XM_040357	Homo sapiens chromosome 6 open reading frame 5 (C6orf5), mRNA	1.5
317	AK006073	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:1700017M07, full insert sequence	6.7
318	AE001381	Plasmodium falciparum chromosome 2, section 18 of 73 of the complete sequence	0.18
319	NM_017678	Homo sapiens hypothetical protein FLJ20127 (FLJ20127), mRNA	3E-57
320	BC004680	Mus musculus, Similar to coxsackievirus and adenovirus receptor, clone MGC:5878 IMAGE:3500491, mRNA, complete cds	0.24
321	AK002181	Homo sapiens cDNA FLJ11319 fis, clone PLACE1010293	0.007
322	U90946	Dictyostelium discoideum myosin heavy chain kinase B (MHCK-B) mRNA, complete cds	0.003
323	Y14277	Drosophila melanogaster mRNA for nuclear protein SA	0.062

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
324	Z17272	H. sapiens DNA segment containing (CA) repeat; clone AFM248wc1; single read	0.25
325	M37526	E.gracilis chloroplast P-700 chlorophyll alpha apoprotein (psaA and psaB) genes, complete cds	0.025
326	Y14952	Mus musculus gene encoding immunoglobulin J chain precursor	0.24
327	AE006596	Streptococcus pyogenes M1 GAS strain SF370, section 125 of 167 of the complete genome	6.8
328	AF079804	Candida albicans N-acetyl-glucosamine-6-phosphate deacetylase (DAC1) and glucosamine-6-phosphate deaminase (NAG1) genes, complete cds; and hexokinase (HXK1) pseudogene, complete sequence	2
329	XM_029315	Homo sapiens Machado-Joseph disease (spinocerebellar ataxia 3, olivopontocerebellar ataxia 3, autosomal dominant, ataxin 3) (MJD), mRNA	7.8
330	AK022820	Homo sapiens cDNA FLJ12758 fis, clone NT2RP2001328	0.24
331	AF059275	Mus musculus heat shock transcription factor 1 (Hsf1) gene, partial cds	0.085
332	AL049263	Homo sapiens mRNA; cDNA DKFZp564F133 (from clone DKFZp564F133)	0.059
333	AP001233	Homo sapiens genomic DNA, chromosome 2p11.2, clone:cos607/2	0.003
334	AC017021	Homo sapiens BAC clone RP11-208M4 from 7, complete sequence	0.0000005
335	U03248	Human chromosome 21 clone pVC1.23c	3E-56
336	XM_046758	Homo sapiens tensin (TNS), mRNA	2
337	AJ279150	Homo sapiens partial TFNR gene for transcription factor-like nuclear regulator, exon 31	0
338	AF282896	Rattus norvegicus chemokine RANTES gene, promoter sequence	0.001
339	AK000939	Homo sapiens cDNA FLJ10077 fis, clone HEMBA1001864	0.21
340	AF188517	Staphylococcus aureus Blt-like protein SbtA (sbtA) gene, complete cds	0.008
341	AF202562	Homo sapiens DNA methyltransferase (DNMT1) gene, exon 13	0.22
342	XM_017967	Homo sapiens hypothetical protein FLJ13732 similar to tensin (FLJ13732), mRNA	2.7
343	AF051685	Homo sapiens clone SBS-12 SATB1 binding sequence in vivo	0.21
344	M77188	Campylobacter jejuni argininosuccinate lyase (argH) gene, complete cds	0.22
345	U95137	Rattus norvegicus Na+-Ca+ exchanger (NCX1) gene, exon 1-Ht	0.24
346	AK019943	Mus musculus 6 days neonate head cDNA, RIKEN full-length enriched library, clone:5430403G16, full insert sequence	0.74
347	BC005571	Mus musculus, ubiquitin specific protease 14, clone MGC:7106 IMAGE:3157723, mRNA, complete cds	0.41
348	XM_026968	Homo sapiens hypothetical protein MGC2668 (MGC2668), mRNA	4E-16

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
349	AK024903	Homo sapiens cDNA: FLJ21250 fis, clone COL01253, highly similar to AB020527 Homo sapiens mRNA for Na/PO4 cotransporter homolog	7E-28
350	U85645	Oryctolagus cuniculus fructose 1,6, bisphosphate aldolase (AldB) gene, complete cds	0.075
351	AF388026	Homo sapiens fibrinogen, B beta polypeptide (FGB) gene, complete cds	5.8
352	AY028321	Homo sapiens pro-melanin-concentrating hormone-like 2 protein (PMCHL2) gene, exons 4, 5a, and 5b, alternatively spliced	0.0003
353	AL513491	Human DNA sequence from clone RP11-79A21 on chromosome X, complete sequence [Homo sapiens]	1.9
354	M92068	Chimpanzee retrovirus-like sequence-isoleucine b (RTVL-Ib) gene, 5' and 3' LTR	1.5
355	XM_002120	Homo sapiens zinc finger protein 262 (ZNF262), mRNA	0.007
356	X02435	Tetrahymena mitochondrial gene for tRNA-Phe (GAA)	0.028
357	XM_033459	Homo sapiens syntaxin binding protein 1 (STXBP1), mRNA	2.1
358	NM_015770	Mus musculus non-agouti (a), mRNA	0.64
359	AJ296103	Staphylococcus aureus repNVH99 gene for replication protein and smr gene	0.15
360	Z12840	O.cuniculus mRNA for protein of unknown function	e-131
361	XM_038370	Homo sapiens hypothetical gene supported by AK001938; AK001941 (LOC91424), mRNA	0.0002
362	AF108684	Rhipidomys mastacalis cytochrome B (cytB) gene, mitochondrial gene encoding mitochondrial protein, partial cds	0.009
363	NM_020045	Mus musculus HIRA-interacting protein 5 (HIRIP5), mRNA	1.8
364	AK024439	Homo sapiens mRNA for FLJ00029 protein, partial cds	0.73
365	AK025445	Homo sapiens cDNA: FLJ21792 fis, clone HEP00441	2.1
366	AP000307	Homo sapiens genomic DNA, chromosome 21q22.1, D21S226-AML region, clone:f6C7, complete sequence	0.00004
367	AE000818	Methanobacterium thermoautotrophicum from bases 264585 to 276866 (section 24 of 148) of the complete genome	2.3
368	AK001164	Homo sapiens cDNA FLJ10302 fis, clone NT2RM2000042	0.13
369	XM_029101	Homo sapiens KIAA0947 protein (KIAA0947), mRNA	0.95
370	AK022191	Homo sapiens cDNA FLJ12129 fis, clone MAMMA1000198	0.029
371	Z54280	S.scrofa gene for skeletal muscle ryanodine receptor	1.9
372	AY037259	Arabidopsis thaliana AT3g52120/F4F15_230 mRNA, complete cds	9.6
373	XM_034599	Homo sapiens acid sphingomyelinase-like phosphodiesterase (ASM3A), mRNA	0
374	XM_046914	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily f, member 1 (SMARCF1), mRNA	3E-16
375	M86340	Mycoplasma-like sp. 23S and 16S ribosomal RNAs, Tyr-transfer RNA and Ile-transfer RNA, complete cds	0.24
376	AB019507	Drosophila kanekoi gene for glycerol-3-phosphate dehydrogenase, complete cds	1.3

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
377	AF106915	Phodopus sungorus luteinizing hormone beta subunit mRNA, partial cds	0.61
378	AL354800	Human DNA sequence from clone RP1-316I5 on chromosome 20 Contains the 3' end of the KIF3B gene encoding a kinesin family member 3B (KIAA0359) and ESTs, complete sequence [Homo sapiens]	0.0001
379	AL133430	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 233360	0.66
380	AF085894	Homo sapiens full length insert cDNA clone YP97D11	0.0002
381	AJ286750	Sesbania rostrata mRNA for phosphoenolpyruvate carboxylase (pepc gene)	0.068
382	XM_040415	Homo sapiens region containing hypothetical protein; mutL (E. coli) homolog 3 (LOC82389), mRNA	e-128
383	Y09794	A.rabiei microsatellite DNA	1.2
384	AB047905	Macaca fascicularis brain cDNA, clone:QnpA-15911	1.8
385	AK001451	Homo sapiens cDNA FLJ10589 fis, clone NT2RP2004389, weakly similar to PROBABLE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S9 PRECURSOR	1.5
386	AF010473	Schizosaccharomyces pombe myosin-like protein Sp8 (sp8) mRNA, partial cds	0.19
388	AL133604	Homo sapiens mRNA; cDNA DKFZp434G1615 (from clone DKFZp434G1615)	0.00006
389	XM_009252	Homo sapiens methyl-CpG binding domain protein 3 (MBD3), mRNA	0.055
390	AB053116	Polyandrocarpa misakiensis mRNA for putative eukaryotic petide chain release factor subunit 1, complete cds	1.5
391	AL138666	S.pombe chromosome I cosmid c694	1.3
392	AF091933	Pleurotus ostreatus small subunit ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	0.078
393	Z37964	Staphylococcus sp. genes encoding QacC and replication protein (rep827)	0.073
394	AB020712	Homo sapiens mRNA for KIAA0905 protein, complete cds	2E-64
395	BC009023	Mus musculus, Similar to prostaglandin E receptor 4 (subtype EP4), clone MGC:7183 IMAGE:3481696, mRNA, complete cds	1.5
396	XM_010128	Homo sapiens odz (odd Oz/ten-m, Drosophila) homolog 1 (ODZ1), mRNA	0.55
397	XM_011386	Homo sapiens hypothetical protein PRO0813 (PRO0813), mRNA	5.3
398	XM_040694	Homo sapiens AD031 protein (AD031), mRNA	1.3
399	AE006177	Pasteurella multocida PM70 section 144 of 204 of the complete genome	5
400	AL113079	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation	1.2
401	U39694	Mycoplasma genitalium section 16 of 51 of the complete genome	0.84
402	XM_016314	Homo sapiens ankyrin 2, neuronal (ANK2), mRNA	4.6

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
403	XM_045362	Homo sapiens likely homolog of rat kinase D-interacting substance of 220 kDa; KIAA1250 protein (KIAA1250), mRNA	7E-77
404	NM_028513	Mus musculus RIKEN cDNA 1700052K15 gene (1700052K15Rik), mRNA	9
405	U47416	Solanum allophyllum NADH dehydrogenase subunit (ndhF) gene, chloroplast gene encoding chloroplast protein, partial cds	0.2
406	NC_002502	Lactococcus lactis subsp. lactis plasmid pCI305, complete sequence	5.3
407	AF269561	Staphylococcus epidermidis strain SR1 clone step.1010e06 genomic sequence	0.19
409	AF336128	Lumpy skin disease virus strain Neethling, 5' partial sequence	1.5
410	AB058397	Oryza sativa CHS gene for chalcone synthase, complete cds	0.16
411	AE006830	Sulfolobus solfataricus section 189 of 272 of the complete genome	0.21
412	AY035064	Arabidopsis thaliana unknown protein (T20O10_100/AT3g63000) mRNA, complete cds	0.22
413	AF158049	Platybrachys decemmacula 16S ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	0.063
414	NM_026444	Mus musculus citrate synthase (Cs), mRNA	1.7
415	BC007820	Homo sapiens, clone IMAGE:4303165, mRNA	0
416	AJ295228	Caenorhabditis elegans mRNA for MAGUK protein DLG-1 (dlg-1 gene)	0.2
417	AB028633	Flammulina velutipes mitochondrial gene for DNA polymerase, RNA polymerase, complete and partial cds	0.6
418	Y09794	A.rabiei microsatellite DNA	1.2
419	AB054063	Pagrus major lpl gene for lipoprotein lipase, complete cds	5.9
420	AF323928	Plasmodium falciparum GcpE (gcpE) gene, complete cds	0.14
421	M31012	Chicken MHC class I B-FIV-B12 alpha-chain gene, complete cds	1.2
422	Z49806	B.taurus mRNA for adenylyl cyclase type VII	6.1
423	AB009907	Luciola kuroiwae mitochondrial DNA for 16S rRNA, partial sequence	0.003
424	X76693	C.coli (UA585) sodB gene for superoxide dismutase	0.45
425	AF284942	Carex capitata tRNA-Thr, partial sequence; trnT-trnL intergenic spacer, tRNA-Leu, and trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe, partial sequence; chloroplast genes for chloroplast products	0.29
426	AK017986	Mus musculus adult male thymus cDNA, RIKEN full-length enriched library, clone:5830443G21, full insert sequence	5.1
427	AL512549	S.pombe chromosome I BAC pB2B4	1.6
428	AF283669	Homo sapiens kallikrein 14 (KLK14) gene, complete cds	2.3
429	Z12842	O.cuniculus mRNA for protein of unknown function	5E-73
430	XM_016894	Homo sapiens LOC86241 (LOC86241), mRNA	3E-65
431	X96616	P.primaurelia gene encoding 156D surface antigen	0.23
432	X02175	Schizosaccharomyces pombe cdc10 start gene	0.027
433	AK021807	Homo sapiens cDNA FLJ11745 fis, clone HEMBA1005526	0.001

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
434	XM_005233	Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform (PPP2R2A), mRNA	5E-09
435	X52623	Rice 4-CL gene for 4-coumarate-CoA ligase (EC 6.2.1.12)	0.63
436	AK005294	Mus musculus adult male cerebellum cDNA, RIKEN full-length enriched library, clone:1500019O16, full insert sequence	1E-16
437	AE002337	Chlamydia muridarum, section 65 of 85 of the complete genome	0.049
438	AF106574	Caenorhabditis elegans cosmid E02D9, complete sequence	0.7
439	X56866	S.alba 5S rRNA gene	0.74
440	AF127158	Drosophila mauritiana Cu-Zn superoxide dismutase (Sod) gene, exons 1 and 2 and complete cds	1.7
441	U08466	Nephila clavipes alanine tRNA gene, complete sequence	2.1
442	AY021236	Oryza sativa microsatellite MRG3561 containing (TA)X22, genomic sequence	1.5
443	L09262	Arabidopsis thaliana phytochrome b gene, exons 2 and 3	0.079
444	AC007095	Homo sapiens BAC clone RP11-303A22 from 7, complete sequence	0.23
445	AK012607	Mus musculus 11 days embryo cDNA, RIKEN full-length enriched library, clone:2700094F01, full insert sequence	0.19
446	AF309415	Cyprinus carpio ovarian fibroin-like substance-2 mRNA, partial cds	0.008
447	X03956	Potato (tetraploid variety Maris piper) patatin gene	0.003
448	BC008617	Mus musculus, clone IMAGE:3588380, mRNA, partial cds	0.07
449	AJ242146	Mauritiella armata 18S rRNa gene (partial), 5.8S rRNA gene, 26S rRNA gene (partial) and internal transcribed spacers 1 and 2 (ITS1, ITS2), clone 1	0.07
450	M67489	Bovine desmocollin mRNA, complete cds	0.066
451	AB048954	Macaca fascicularis brain cDNA, clone:QnpA-10509	0.48
452	AE001136	Borrelia burgdorferi (section 22 of 70) of the complete genome	0.18
453	AE001398	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence	0.025
454	AF218904	Homo sapiens attractin precursor (ATRN) gene, exon 19	1.6
455	AK025078	Homo sapiens cDNA: FLJ21425 fis, clone COL04162	1E-71
456	M11449	Yeast mitochondrial ori2-ori7 region DNA with putative peptide	0.34
457	XM_031156	Homo sapiens hypothetical gene supported by AB007970 (LOC90360), mRNA	0.006
458	AK015180	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930422I22, full insert sequence	0.007
459	AC090422	Homo sapiens clone RP11-691A12, complete sequence	0.013
460	U06154	Human clone 2004V-I-1 from chromosome 1q terminal region	1E-19
461	AE001123	Borrelia burgdorferi (section 9 of 70) of the complete genome	0.83
462	Y17797	Enterococcus faecalis gph, ydjH, ydjG, ydjI, pbp4 and ydiC, ORF2 and ORF3 genes, partial	0.22
463	AB026906	Homo sapiens SDHD gene for small subunit of cytochrome b of succinate dehydrogenase, complete cds	0.042
464	L13942	Human (clone Cos35) glycerol kinase (GK) gene, exons 1-3	0.042
465	U81510	Spodoptera frugiperda caspase-1 mRNA, complete cds	0.041

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
466	AJ003222	Borrelia burgdorferi flgK, flbF, thdF, gidA, gidB, moxR, orf1, orf2, orf3, orf4 and orf5 genes	0.58
467	AY034379	Capsicum annuum branched-chain amino acid aminotransferase mRNA, complete cds	1.8
468	AF120317	Mus musculus mahogany (mg) gene, exons	0.56
469	AE007451	Streptococcus pneumoniae section 134 of 194 of the complete genome	0.005
470	AF305819	Homo sapiens PRO0777 mRNA, complete cds	0.055
471	AF045950	Mus musculus D16Jhu5 YAC 183G11 acentric end, partial sequence	0.22
473	XM_010416	Homo sapiens GTP-binding protein ragB (RAGB), mRNA	0.14
474	XM_028004	Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 3 (ALS2CR3), mRNA	0.00005
475	AK021820	Homo sapiens cDNA FLJ11758 fis, clone HEMBA1005609, highly similar to Homo sapiens mRNA; cDNA DKFZp564K133 (from clone DKFZp564K133)	0.004
476	AE002579	Drosophila melanogaster genomic scaffold 142000013385638, complete sequence	6.7
477	AF047677	Homo sapiens dystrophin (DMD) gene, deletion breakpoints 1-3 in intron 5	0.64
478	AL589203	Human DNA sequence from clone RP11-391F23 on chromosome 6, complete sequence [Homo sapiens]	0.00009
479	AF265343	Danio rerio protein kinase Npk mRNA, complete cds	0.14
480	XM_031879	Homo sapiens CREB/ATF family transcription factor (CREB-H), mRNA	0.44
481	XM_050760	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 2 (ABCC2), mRNA	0.077
482	AF069508	Homo sapiens human endogenous retrovirus HML6.28 gag and pol pseudogenes, complete sequence	0.23
483	AK022914	Homo sapiens cDNA FLJ12852 fis, clone NT2RP2003445	2
484	XM_032753	Homo sapiens hypothetical gene supported by AK022412 (LOC90584), mRNA	1.9
485	XM_018436	Homo sapiens hypothetical protein FLJ14327 (FLJ14327), mRNA	0.66
486	AF130764	Equus caballus FN1 gene, partial sequence	4
487	AK024286	Homo sapiens cDNA FLJ14224 fis, clone NT2RP3004028	2E-18
488	AF348342	Plasmodium malariae caseinolytic protease C (clpC) gene, partial cds; apicoplast gene for apicoplast product	0.23
489	XM_029336	Homo sapiens similar to potassium voltage-gated channel, subfamily H (eag-related), member 2; ether a go-go related (M. musculus) (LOC90134), mRNA	6.2
490	BC005951	Homo sapiens, clone MGC:14588 IMAGE:4249174, mRNA, complete cds	5E-35
491	AJ391749	Vicia melanops genomic repetitive element, clone M29	0.13
492	AF154170	Sceloporus dugesii 12S ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	0.21

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
493	X84060	H.sapiens TCF11 gene, exon 3-6	0.21
494	AP000418	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:MPK17	0.003
495	AJ277428	Scenedesmus obliquus mitochondrial tRNA-Ser, tRNA-Asp, 16S rRNA, 23S rRNA genes, strain KS3-2	0.65
496	L11447	Mycoplasma hyorhinis repeat regions in potential metal binding protein gene region	0.046
497	AY029764	Mus musculus TRAM1 mRNA, complete cds	0.23
498	XM_031173	Homo sapiens parathyroid hormone (PTH), mRNA	0.22
499	AF270168	Staphylococcus epidermidis strain SR1 clone step.1051f02 genomic sequence	0.24
500	AF336131	Lumpy skin disease virus strain Neethling, 3' partial sequence	3.5
501	AF195272	Mus musculus serine/threonine kinase AIE1 gene, complete cds	6.7
502	NC_002322	Laqueus rubellus mitochondrion, complete genome	0.26
503	AK007179	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:1700112J16, full insert sequence	0.24
504	U32706	Haemophilus influenzae Rd section 21 of 163 of the complete genome	0.68
505	AF247555	Drosophila mauritiana heat shock protein 68 gene, partial cds	1.9
506	NM_011146	Mus musculus peroxisome proliferator activated receptor gamma (Pparg), mRNA	0.024
507	M26940	Mouse beta-casein gene, complete cds	0.002
508	AB003043	Phycomyces blakesleeanus classII chitin synthase (PbCHS1) gene, complete cds	0.68
509	U89348	Human papillomavirus type 16 variant, complete sequence	0.62
511	AF270160	Staphylococcus epidermidis strain SR1 clone step.1051e03 genomic sequence	0.077
512	AF119554	Plasmodium falciparum para-aminobenzoic acid synthetase gene, complete cds	0.078
513	AY014991	Waterstoniella sp. CAM-2000 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial gene for mitochondrial product	0.68
514	NM_013037	Rattus norvegicus Fos-responsive gene 1 (St2), mRNA	0.085
515	AF169003	Hepatitis C virus isolate G2aK1 polyprotein gene, complete cds	0.028
516	U23442	Tetrahymena thermophila RR internal deletion sequence	0.25
517	AF381638	Homo sapiens SNP EC11 psoriasis susceptibility gene candidate interval, partial sequence	0.0003
518	NM_023755	Mus musculus Tcfcp2-related transcriptional repressor 1 (Crtr1-pending), mRNA	0.009
519	NM_004706	Homo sapiens Rho guanine nucleotide exchange factor (GEF) 1 (ARHGEF1), mRNA	3.4
520	X67164	P.hybrida T-DNA integration region	0.063
521	AB042275	Canine herpesvirus CICP0 gene for infected cell protein 0, complete cds	0.66
522	AB019942	Arabidopsis thaliana gene for sigma factor SigA, complete cds	1.4

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
523	AF270382	Staphylococcus epidermidis strain SR1 clone step.4041f02 genomic sequence	0.23
524	AF284897	Carex supina tRNA-Thr, partial sequence; trnT-trnL intergenic spacer, tRNA-Leu, and trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe, partial sequence; chloroplast genes for chloroplast products	0.23
525	AK000493	Homo sapiens cDNA FLJ20486 fis, clone KAT08039	0.17
526	U67535	Methanococcus jannaschii section 77 of 150 of the complete genome	0.6
527	AE002754	Drosophila melanogaster genomic scaffold 142000013385431, complete sequence	1.8
528	AF241656	Caenorhabditis elegans SR protein specfic kinase SPK-1 mRNA, complete cds	1.7
529	AF173828	Caenorhabditis elegans putative potassium channel Slo-2 mRNA, complete cds	0.21
530	AE005382	Escherichia coli O157:H7 EDL933 genome, contig 3 of 3, section 1 of 290	2.3
531	Z36154	S.cerevisiae chromosome II reading frame ORF YBR285w	0.68
532	AF054126	Rattus norvegicus polymorphic marker D6UIA6 sequence	0.061
533	AK004780	Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200015C19, full insert sequence	0.7
534	AF352555	Staphylococcus aureus subsp. aureus strain ATCC31889 leukocidin LukS component gene, partial cds	0.2
535	AF352555	Staphylococcus aureus subsp. aureus strain ATCC31889 leukocidin LukS component gene, partial cds	0.1
536	J05246	Mouse alpha-fetoprotein (AFP) gene, 5' flank	0.024
537	AF021935	Rattus norvegicus mytonic dystrophy kinase-related Cdc42-binding kinase (MRCK) mRNA, complete cds	e-141
538	Y12573	D.melanogaster Jun and 14-3-3 zeta gene	0.5
539	AF248584	Moraxella catarrhalis UDP-glucose dehydrogenase gene, partial cds; and UDP-glucose 4-epimerase (galE) and L-glutamine:D-fructose-6-phosphate aminotransferase (glmS) genes, complete cds	0.026
540	AL136554	Homo sapiens mRNA; cDNA DKFZp761D0712 (from clone DKFZp761D0712)	0.089
541	AF158049	Platybrachys decemmacula 16S ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	0.082
542	AY023618	Oryza sativa microsatellite MRG5943 containing (TTA)X55, closest to marker RG908, genomic sequence	0.00009
543	AL591498	Human DNA sequence from clone RP11-113L12 on chromosome 13, complete sequence [Homo sapiens]	3E-14
544	AF183908	Danio rerio P450 aromatase (cyp19b) mRNA, complete cds	0.069
545	AK016658	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4933405A14, full insert sequence	0.53
546	AB014084	Homo sapiens genomic DNA, chromosome 6p21.3, HLA class I region, Cosmid clone:TY7A5, complete sequence	0.011

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
547	AF285076	Scleria reticularis tRNA-Leu, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe, partial sequence; chloroplast genes for chloroplast products	0.19
548	XM_047604	Homo sapiens coproporphyrinogen oxidase (coproporphyria, harderoporphyria) (CPO), mRNA	0.17
549	Z81538	Caenorhabditis elegans cosmid F45H10, complete sequence	0.24
550	AF026800	Fundulus heteroclitus cytochrome P4501A (CYP1A) mRNA, complete cds	1.9
551	XM_051897	Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA	9E-08
552	XM_015200	Homo sapiens hypothetical protein FLJ22724 (FLJ22724), mRNA	2.1
553	AF266244	Gillichthys mirabilis adenylate cyclase type v-like protein mRNA, complete cds	6
554	Z21818	H.sapiens carcinoembryonic antigen gene	0.23
555	AE002100	Ureaplasma urealyticum section 1 of 59 of the complete genome	0.023
556	XM_045179	Homo sapiens hypothetical gene supported by AL137724 (LOC92454), mRNA	0.19
557	X16509	Rice alpha-amylase gene	1.8
558	M33753	D.melanogaster crumbs protein mRNA, complete cds	5.4
559	D32022	Human mRNA for T cell receptor V beta 8 CDR3, parcial sequence	1.5
560	AF188893	Homo sapiens guanidinoacetate N-methyltransferase (GAMT) gene, complete cds	0.18
561	AF367310	Arabidopsis thaliana At2g36880/T1J8.6 gene, complete cds	0.11
562	AF207699	Elaeis guineensis agamous-like MADS box protein OPMADS1 mRNA, complete cds	0.45
564	AB014586	Homo sapiens mRNA for KIAA0686 protein, partial cds	0.17
565	L77040	Homo sapiens (subclone 8_c11 from P1 H22) DNA sequence	8E-14
566	NM_024942	Homo sapiens hypothetical protein FLJ13490 (FLJ13490), mRNA	0.013
567	U88158	Tetrahymena thermophila micronuclear developmentally eliminated sequence region	0.18
568	AF210744	Nannochloropsis oculata large subunit ribosomal RNA gene, partial sequence	0.057
569	AL590384	Human DNA sequence from clone RP11-349A16 on chromosome Xq22.3-24, complete sequence [Homo sapiens]	2E-15
570	AY034379	Capsicum annuum branched-chain amino acid aminotransferase mRNA, complete cds	1.2
571	AF038283	Campylobacter jejuni cytolethal distending toxin A (cdtA), cytolethal distending toxin B (cdtB), and cytolethal distending toxin C (cdtC) genes, complete cds	0.4
572	X98807	A.thaliana mRNA for peroxidase ATP21a	1.8
573	AF111941	Dictyostelium discoideum AX4 development protein DG1148 (DG1148) gene, complete cds	0.0009

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
574	AE002247	Chlamydophila pneumoniae AR39, section 74 of 94 of the complete genome	1.7
575	AF247555	Drosophila mauritiana heat shock protein 68 gene, partial cds	1.4
576	AJ237599	Gallus gallus mRNA for iroquois homologue-2	0.056
577	NM_030995	Rattus norvegicus Microtubule-associated protein 1a (Map1a), mRNA	0.21
578	XM_027638	Homo sapiens KIAA0240 protein (KIAA0240), mRNA	1.5
579	AF310886	Dictyostelium discoideum RacA (racA) gene, complete cds	0.065
580	AB001090	Homo sapiens gene for H-cadherin, exon 1	0.2
581	BC009101	Mus musculus, Similar to hypothetical protein DKFZp761C121, clone MGC:12146 IMAGE:3710846, mRNA, complete cds	0.0008
582	XM_011473	Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 9 (SERPINB9), mRNA	1.8
583	AF004051	Galium hypocarpium rps16 gene, chloroplast gene, partial intron sequence	0.068
584	AE007440	Streptococcus pneumoniae section 123 of 194 of the complete genome	0.066
585	L25647	Homo sapiens fibroblast growth factor receptor gene (located in the central MHC) signal peptide and consecutive exon	0.069
586	AF191079	Stealth virus 1 clone 3B632, genomic sequence	0.009
587	L20465	Onchocerca volvulus nicotinic acetylcholine receptor mRNA, partial cds	0.72
588	NM_008713	Mus musculus nitric oxide synthase 3, endothelial cell (Nos3), mRNA	2
589	NM_004052	Homo sapiens BCL2/adenovirus E1B 19kD-interacting protein 3 (BNIP3), nuclear gene encoding mitochondrial protein, mRNA	4E-26
590	U40228	Plasmodium falciparum ADP-ribosylation factor 1 (pARF1) mRNA, complete cds	0.009
591	AL049435	Homo sapiens mRNA; cDNA DKFZp586B0220 (from clone DKFZp586B0220)	0.008
592	AC000981	Homo sapiens (subclone 2_c6 from P1 H31) DNA sequence, complete sequence	0.68
593	AF304319	Neospora caninum small subunit ribosomal RNA and large subunit ribosomal RNA genes, partial sequences and intergenic region, plastid genes for plastid products	0.009
594	BC006517	Homo sapiens, Similar to PPAR binding protein, clone IMAGE:3546031, mRNA	7E-43
595	AJ249162	Homo sapiens promotor enhancer from ISG20 gene	2.1
596	AJ297708	Rattus norvegicus RT6 gene for T cell differentiation marker RT6.2, exons 1-8	0.024
597	Y11779	R.prowazekii ygjT-like gene and 4 open reading frames	0.078
598	AE005660	Escherichia coli O157:H7 EDL933 genome, contig 3 of 3, section 279 of 290	0.53
599	XM_041617	Homo sapiens RAB11B, member RAS oncogene family (RAB11B), mRNA	4.8
600	AK023165	Homo sapiens cDNA FLJ13103 fis, clone NT2RP3002304	0.25

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
601	Z69388	Human DNA sequence from cosmid L60G9A, Huntington's Disease Region, chromosome 4p16.3 contains ESTs and a CpG island	0.084
602	U84760	Chromatium vinosum dsr locus, complete sequence	0.022
603	AF122050	Hordeum vulgare limit dextrinase gene, complete cds	1.8
604	AJ308471	Mus musculus partial gene for acetyl-CoA carboxylase-alpha, promoter I	0.022
605	AF158032	Cixius inflatus 16S ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	0.008
607	XM_012733	Homo sapiens KIAA1012 protein (KIAA1012), mRNA	0.005
608	D37781	Human mRNA for protein-tyrosine phosphatase HPTPeta, complete cds	0.059
609	AC002252	Homo sapiens (subclone 1_g7 from BAC H76) DNA sequence, complete sequence	7E-11
610	AF160964	Peanut witches'-broom phytoplasma RNA polymerase sigma factor (rpoD) gene, complete cds	0.63
611	U67528	Methanococcus jannaschii section 70 of 150 of the complete genome	0.67
612	AF063134	Justicia caudata tRNA-Leu (trnL) gene, chloroplast gene for chloroplast RNA, partial sequence	1.2
613	U67527	Methanococcus jannaschii section 69 of 150 of the complete genome	1.5
614	AK022455	Homo sapiens cDNA FLJ12393 fis, clone MAMMA1002711	0.000001
615	AF272082	Poiretia punctata trnK gene, intron, 3' partial sequence; and maturase (matK) gene, partial cds; chloroplast genes for chloroplast products	0.075
616	AF112461	Homo sapiens G protein-coupled receptor 57 (GPR57) gene, complete cds	0.025
617	AF310884	Dictyostelium discoideum Rac1B (rac1B) gene, complete cds; racK pseudogene, complete sequence; and unknown genes	5.6
618	AF348342	Plasmodium malariae caseinolytic protease C (clpC) gene, partial cds; apicoplast gene for apicoplast product	0.22
619	AB043965	Danio rerio gene for dharma, promoter and partial cds	0.054
620	NC_001839	Petunia vein clearing virus, complete genome	0.61
621	AK023959	Homo sapiens cDNA FLJ13897 fis, clone THYRO1001706	0.67
622	AF028835	Drosophila pallidosa vermilion (v) gene, complete cds	0.13
623	U67598	Methanococcus jannaschii section 140 of 150 of the complete genome	0.072
624	AF283103	Pineapple mealybug wilt associated virus-2 polyprotein (ORF1a) and RNA-dependent RNA polymerase genes, partial cds; and hydrophobic protein p5, heat shock protein 70, p46, coat protein, diverged coat protein, p20, p22, and p6 genes, complete cds	1.5
625	XM_008161	Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA	1E-15
626	XM_035599	Homo sapiens adaptor-related protein complex 4, epsilon 1 subunit (AP4E1), mRNA	6E-22

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
627	AF143066	Lepidopilum scabrisetum ribosomal protein system 4 (rps4) gene, partial cds	0.61
628	U89283	Biomphalaria glabrata myoglobin gene, complete cds	0.46
629	U44949	Xenopus laevis zona pellucida A glycoprotein homolog (xlZPA) mRNA, complete cds	1.6
630	AE007395	Streptococcus pneumoniae section 78 of 194 of the complete genome	0.15
631	BC006963	Mus musculus, clone IMAGE:3708410, mRNA, partial cds	1.6
632	XM_031120	Homo sapiens peptidylglycine alpha-amidating monooxygenase (PAM), mRNA	4E-40
633	AF316122	Kinosternon arizonense isolate KariAZ2 mitochondrial control region, complete sequence	0.69
634	U67561	Methanococcus jannaschii section 103 of 150 of the complete genome	0.22
635	D88010	Human DNA for ribosomal protein S13, complete cds, U14 small nucleolar RNA, complete sequence	0.24
636	AE006321	Lactococcus lactis subsp. lactis IL1403 section 83 of 218 of the complete genome	2.2
637	AF045595	Carassius auratus clone gf-40 glutamic acid decarboxylase isoform 67 (GAD67) mRNA, complete cds	0.74
638	D38378	Human DNA, novel tandem repeat sequence	0.21
639	AF260819	Plasmodium falciparum CG1 protein gene, complete cds	0.003
640	NC_000857	Ceratitis capitata complete mitochondrial genome	0.23
641	AK015383	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930444M15, full insert sequence	2.1
642	AF286367	Homo sapiens HMGIY gene, promoter	1.6
643	AK019143	Mus musculus 10 days embryo cDNA, RIKEN full-length enriched library, clone:2600001P13, full insert sequence	0.69
644	AE001421	Plasmodium falciparum chromosome 2, section 58 of 73 of the complete sequence	2
645	D16904	Human HepG2 3' region cDNA, clone hmd3a02	0.21
646	XM_003799	Homo sapiens protocadherin beta 10 (PCDHB10), mRNA	0.69
647	NC_001438	Bean golden mosaic virus A component DNA, complete sequence	0.66
648	AK013971	Mus musculus 13 days embryo head cDNA, RIKEN full-length enriched library, clone:3110001P07, full insert sequence	2
649	AF078880	Prosimulium formosum dopa decarboxylase (DDC) gene, partial cds	0.076
650	AJ009600	Begonia taipeiensis rbcL promoter, clone 16320	0.22
651	AF042834	Homo sapiens phosphodiesterase delta subunit gene, exons 2, 3 and 4	5.8
652	AF244214	Dysdera ratonensis 16S ribosomal RNA gene, partial sequence	0.075
653	XM_043252	Homo sapiens PCAF associated factor 65 alpha (PAF65A), mRNA	2E-33

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
654	AF105116	Streptococcus pneumoniae type 19C Cps19CR (cps19CR) gene, partial cds; putative oligosaccharide repeat unit transporter (cps19CJ), UDP-N-acetyl glucosamine-2-epimerase (cps19CK), and putative glucosyl transferase (cps19CS) genes, complete cds; and gluc>	1.9
655	AF181720	Homo sapiens RU2AS (RU2) gene, complete cds; and RU2S (RU2) gene, partial cds	0.23
656	AL392164	Human DNA sequence from clone RP11-269L6 on chromosome X, complete sequence [Homo sapiens]	0.0003
657	AF189720	Oryctolagus cuniculus chloride channel (CFTR) mRNA, complete cds	0.18
658	AF077821	Canis familiaris inducible nitric oxide synthase mRNA, complete cds	0.077
659	NC_001327	Ascaris suum mitochondrion, complete genome	0.074
660	XM_003164	Homo sapiens KIAA0218 gene product (KIAA0218), mRNA	5.8
661	M22207	T.gratilla 217g gene encoding 217g protein, complete cds	0.071
662	BC004062	Mus musculus, Similar to cofactor required for Sp1 transcriptional activation, subunit 6 (77kD), clone IMAGE:3590309, mRNA, partial cds	0.22
663	AF007132	Homo sapiens clone 23551 mRNA sequence	0.023
666	XM_007847	Homo sapiens hypothetical protein from clone 24796 (LOC57146), mRNA	5E-32
667	AE002755	Drosophila melanogaster genomic scaffold 142000013385531, complete sequence	5.8
668	U70780	Clostridium botulinum unidentified protein P-48 gene, complete cds and neurotoxin binding protein gene, partial cds	0.075
669	XM_029131	Homo sapiens similar to KIAA0773 gene product (H. sapiens) (LOC90115), mRNA	2
670	XM_003091	Homo sapiens KIAA0001 gene product; putative G-protein-coupled receptor; G protein coupled receptor for UDP-glucose (KIAA0001), mRNA	1.7
671	AF284881	Carex pauciflora tRNA-Thr, partial sequence; trnT-trnL intergenic spacer, tRNA-Leu, and trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe, partial sequence; chloroplast genes for chloroplast products	1.6
672	NC_001381	Plasmid pAL5000, complete sequence	6.1
673	AF081201	Arabidopsis thaliana villin 1 (VLN1) mRNA, complete cds	0.21
674	AK023674	Homo sapiens cDNA FLJ13612 fis, clone PLACE1010833, weakly similar to CALTRACTIN	0.54
675	X60097	Streptococcus sp. (group C) emm gene for M protein	0.063
676	AF026087	Schizosaccharomyces pombe Sat1 gene, partial cds	0.22
677	X00117	Galago Alu repeat type I, GAL9	0.0001
678	AJ276629	Rattus norvegicus Sacm21/RT1-A intergenic region, haplotype RT1n and partial RT1-A gene for MHC Class I antigen	1.9
679	AK021058	Mus musculus adult male corpus striatum cDNA, RIKEN full-length enriched library, clone:C030009O12, full insert sequence	0.23

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
680	BC003727	Mus musculus, Similar to Interleukin 1 alpha, clone MGC:5780 IMAGE:3599550, mRNA, complete cds	1.9
681	XM_048261	Homo sapiens similar to ring finger protein 23; RING-B box-coiled coil-B30.2 (M. musculus) (LOC92947), mRNA	5E-18
682	XM_038154	Homo sapiens KIAA1016 protein (KIAA1016), mRNA	0.23
683	XM_049918	Homo sapiens similar to hypothetical protein MGC10940 (H. sapiens) (LOC93230), mRNA	0
684	X14727	Sheep beta-B globin gene	0.68
685	AB052187	Macaca fascicularis brain cDNA, clone:QnpA-12170	0.024
686	AK004783	Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200015E14, full insert sequence	5.8
687	AE002799	Drosophila melanogaster genomic scaffold 142000013385566, complete sequence	0.003
688	AF190395	Corymbia calophylla tRNA-Leu and tRNA-Phe genes, partial sequence; chloroplast genes for chloroplast products	1.9
689	U57896	Candida albicans cytochrome C gene (CYC1) gene, complete cds	0.22
690	AE006710	Sulfolobus solfataricus section 69 of 272 of the complete genome	2
691	AL392164	Human DNA sequence from clone RP11-269L6 on chromosome X, complete sequence [Homo sapiens]	0.0003
692	D87001	Homo sapiens immunoglobulin lambda gene locus DNA, clone:47H9 downstream contig	0.008
693	Y13853	Drosophila erecta clone Er1 inactive Bari-1 family transposon	0.16
694	AB022927	Oryctolagus cuniculus HAC4 mRNA for hyperpolarization activated cation channel, complete cds	0.66
695	AF307327	Araraquara virus medium RNA segment, G1/G2 glycoprotein precursor gene, partial cds	2
696	AF269369	Staphylococcus epidermidis strain SR1 clone step.1002g02 genomic sequence	0.57
697	XM_043252	Homo sapiens PCAF associated factor 65 alpha (PAF65A), mRNA	2E-33
698	XM_008640	Homo sapiens lethal giant larvae (Drosophila) homolog 1 (LLGL1), mRNA	0.22
699	AC024829	Caenorhabditis elegans cosmid Y55F3BM, complete sequence	0.023
700	M83660	Dictyostelium discoideum clathrin heavy chain (chcA) mRNA, complete cds	1.9
701	X95481	S.cerevisiae ARC1 gene	1.9
702	AJ408897	Homo sapiens chromosomal breakpoint fragment derivative 4, AF4/MLL fusion, patient UPN006	4.9
703	AF110007	Molgula oculata p68 RNA helicase (bobcat) and transcription factor (manx) genes, complete cds	0.68
704	AL133339	Human DNA sequence from clone RP4-807J1 on chromosome 20. Contains a GSS and a CpG island, complete sequence [Homo sapiens]	2
705	U10116	Human superoxide dismutase (SOD3) gene, complete cds	0.23
706	AB037771	Homo sapiens mRNA for KIAA1350 protein, partial cds	0

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
707	AF023840	Homo sapiens natural killer group protein 2-A (NKG2-A) gene, complete cds	0.68
708	U49023	Tegeticula maculata extranea cytochrome oxidase subunit I, cytochrome oxidase subunit II genes, mitochondrial genes encoding mitochondrial proteins, partial cds, and tRNA-Leu gene, mitochondrial gene	0.001
709	XM_044768	Homo sapiens similar to death receptor 6 (H. sapiens) (LOC92385), mRNA	e-126
710	D50006	Human DNA for alpha-platelet-derived growth factor receptor, exon 6-10	2.1
711	Y14524	Tetrahymena thermophila tRNA-Tyr gene, exons 1 and 2, clone pTetY2	0.057
712	AL592159	Human DNA sequence from clone RP13-237P14 on chromosome X, complete sequence [Homo sapiens]	0.52
713	U88825	HIV-1 isolate 92NG003 from Nigeria complete genome	3.1
714	U05813	Blastocrithidia culicis ATCC 30268 kinetoplast (MURF1) and apocytochrome B (cytB) genes, partial cds, and ATPase subunit 6 (MURF4) gene, complete pre-RNA-edited DNA sequence	0.23
715	AF048990	Homo sapiens MutS homolog 5 (MSH5) gene, exons 11 and 12	0.0009
716	AF317082	Adoncholaimus thalassophygas isolate Sou39 large subunit ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	0.0008
717	AK013269	Mus musculus 10, 11 days embryo cDNA, RIKEN full-length enriched library, clone:2810439K08, full insert sequence	0.024
718	L14769	Physarum polycephalum cytochrome oxidase subunit 1 mRNA, complete cds; mitochondrial gene for mitochondrial product	1.6
720	U45453	Xenopus laevis transcription factor xGATA-4 mRNA, complete cds	0.61
721	AF090432	Danio rerio serrateB mRNA, complete cds	0.075
722	M62504	Spiroplasma citri fibril protein gene, complete cds	0.024
723	AK000939	Homo sapiens cDNA FLJ10077 fis, clone HEMBA1001864	0
724	XM_032587	Homo sapiens 2127 (KIAA1754), mRNA	0.22
726	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.000001
727	S82175	RAR-gamma 2.2=retinoic acid receptor gamma isoform 2.2 {alternatively spliced} [Xenopus laevis, embryos, stage 24, mRNA, 2154 nt]	0.008
728	AK002856	Mus musculus adult male kidney cDNA, RIKEN full-length enriched library, clone:0610040A09, full insert sequence	0.44
729	AF077828	Oryctolagus cuniculus indolethylamine N-methyltransferase (INMT) gene, exon 3 and complete cds	1.4
730	BC006633	Mus musculus, Flt3 interacting zinc finger protein 1, clone MGC:7201 IMAGE:3482191, mRNA, complete cds	1.3
731	AK024670	Homo sapiens cDNA: FLJ21017 fis, clone CAE05907	0.5
732	Z35823	S.cerevisiae chromosome II reading frame ORF YBL062w	1.1
733	Z48636	C.novyi gene for alpha-toxin	0.065

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
734	BC008580	Homo sapiens, clone IMAGE:4179986, mRNA, partial cds	0.71
735	L37746	Homo sapiens lamin B1 gene, exon 10	0.11
736	AF142372	Anolis roquet cytochrome b gene, partial cds; mitochondrial gene for mitochondrial product	0.95
737	AF107454	Homo sapiens clone cD622 mRNA sequence	0.48
738	XM_010112	Homo sapiens solute carrier family 6 (neurotransmitter transporter), member 14 (SLC6A14), mRNA	0.5
739	AF188067	Arabidopsis thaliana clone AtDP5 isopentenyl pyrophosphate:dimethyllallyl pyrophosphate isomerase (ipiAt2) mRNA, partial cds	1.6
740	X90383	A.thaliana DNA for Y13 gene	0.034
741	AE004309	Vibrio cholerae chromosome I, section 217 of 251 of the complete chromosome	0.18
742	AF236642	Calothrix parietina clone 102-2A 16S-23S internal transcribed spacer, complete sequence; and tRNA-Ile and tRNA-Ala genes, complete sequence	1.1
744	AF107699	Homo sapiens RING3 protein (RING3) gene, partial cds	0.027
745	XM_035624	Homo sapiens KIAA0876 protein (KIAA0876), mRNA	3.4
746	XM_001795	Homo sapiens lamin B receptor (LBR), mRNA	0.15
747	AF395180	Panteliella bicolor cytochrome oxidase subunit I gene, partial cds;. mitochondrial gene for mitochondrial product	0.093
748	AF262633	Homo sapiens clone NIGMS NA11418 chromosome 15 paralogous sequence variant, genomic sequence	0.27
749	AF086375	Homo sapiens full length insert cDNA clone ZD68B12	0.000003
750	AJ271002	Mus musculus TFF1/pS2 gene for Trefoil Factor1/pS2, exons 1-3	0.8
751	AF063681	Mus musculus type XIII collagen (col13a1) gene, exons 22-27	0.53
752	AL031634	Caenorhabditis elegans cosmid Y32B12C, complete sequence	0.053
753	Y00165	Sus scrofa mRNA for link protein	0.065
754	AP000693	Homo sapiens genomic DNA, chromosome 21q22.2, PCR fragment from BAC clone:KB739C11, CBR1-HLCS region	0.022
755	AK021535	Homo sapiens cDNA FLJ11473 fis, clone HEMBA1001712	0.064
756	AF305539	Mus musculus B lymphocyte induced maturation protein 1 (Prdm1) gene, exon 8 and complete cds	4E-12
757	J05493	S.pombe no message in thiamine protein (nmt1) gene, complete cds	0.55
758	AE001480	Helicobacter pylori, strain J99 section 41 of 132 of the complete genome	0.51
759	AF072685	Bos taurus matrix metalloproteinase 13 (MMP13) mRNA, complete cds	0.072
760	XM_038408	Homo sapiens hypothetical protein FLJ11331 (FLJ11331), mRNA	0.6
761	XM_041148	Homo sapiens hypothetical gene supported by AF037219 (LOC91856), mRNA	1.7
762	AF234897	Haemulon plumieri Hpl224 NADH dehydrogenase I (ND-1) gene, complete cds; mitochondrial gene for mitochondrial product	3

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
763	NM_008399	Mus musculus integrin, alpha E, epithelial-associated (Itgae), mRNA	1.4
764	Z74898	S.cerevisiae chromosome XV reading frame ORF YOL156w	1.8
765	AF280812	Glycine max putative Hs1pro-1-like receptor mRNA, complete cds	0.59
766	AB013615	Broad bean wilt virus 2 genomic RNA, complete sequence of RNA1	0.68
768	AF079169	Nicotiana tabacum feedback-insensitive anthranilate synthase alpha-2 chain (ASA2) gene, promoter region and 5'UTR	5.9
769	AB014079	Homo sapiens genomic DNA, chromosome 6p21.3, HLA class I region, Cosmid clone:TY1E11, complete sequence	0.007
770	XM_012336	Homo sapiens MBIP protein (MBIP), mRNA	0.0003
771	U41509	Caenorhabditis elegans cosmid W03H1, complete sequence	0.18
772	U23478	Dictyostelium discoideum phosphatidylinositol-4,5-diphosphate 3-kinase (PIK3) mRNA, partial cds	0.00002
773	AP000380	Arabidopsis thaliana genomic DNA, chromosome 5, genomic PCR product GA469	0.39
774	AF115772	Danio rerio basic helix-loop-helix transcription factor Ndr1a (ndr1a) mRNA, complete cds	0.2
775	XM_007458	Homo sapiens butyrate response factor 1 (EGF-response factor 1) (BRF1), mRNA	0.42
776	L31955	Human (clone 1NIB-2) normalized cDNA library sequence	1.6
777	D49711	Populus kitakamiensis (P. sieboldii X P. grandidentata) homt3 gene for caffeic acid O-methyltransferase, complete cds (exon1-4)	0.046
778	L49234	Manduca sexta chitinase precursor gene, complete cds	0.05
779	AY008848	Ictalurus punctatus clone Icpu-UA/3 MHC class I antigen gene, complete cds	0.015
780	AB048375	Oserya coulteriana chloroplast matK gene for maturase K, complete cds	1.9
781	XM_010323	Homo sapiens toll-like receptor 7 (TLR7), mRNA	0.21
782	X69121	P.falciparum Pfgrp mRNA for heat shock protein	0.18
783	AE001570	Helicobacter pylori, strain J99 section 131 of 132 of the complete genome	0.05
784	M31756	Human t(9;22) chromosome 9 breakpoint DNA	0.77
785	M37889	Staphylococcus aureus replication (rep), control of replication (cop), and resistance protein (QacC) genes, complete cds	0.2
786	AF091326	Plasmodium falciparum histone deacetylase (HDAC1) mRNA, complete cds	0.19
787	Z74851	S.cerevisiae chromosome XV reading frame ORF YOL109w	0.2
788	Z85396	H.sapiens Ig lambda light chain variable region gene (34-34SWIIF32) rearranged; Ig-Light-Lambda; VLambda	0.56
789	AF075681	Hemorrhagic enteritis virus hexon protein gene, partial cds	2.1
790	AY029613	Mus musculus GTP binding protein 3 gene, complete cds; nuclear gene for mitochondrial product	5.8
791	NC_001338	Sulfolobus virus 1, complete genome	0.63

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
792	U67563	Methanococcus jannaschii section 105 of 150 of the complete genome	0.11
794	U67549	Methanococcus jannaschii section 91 of 150 of the complete genome	0.21
795	AF293450	Canis familiaris BPAG1-like gene sequence	0.53
797	XM_029942	Homo sapiens KIAA0877 protein (KIAA0877), mRNA	1.4
798	BC009775	Homo sapiens, Similar to hypothetical protein FLJ10842, clone MGC:13398 IMAGE:4092662, mRNA, complete cds	0.061
799	NM_008399	Mus musculus integrin, alpha E, epithelial-associated (Itgae), mRNA	0.24
800	NC_001733	Methanococcus jannaschii small extra-chromosomal element, complete sequence	2
801	Z98532	S.pombe chromosome I cosmid c1B1	0.66
802	AL158132	Human DNA sequence from clone RP3-323A24 on chromosome 4. Contains GSSs and a putative CpG island, complete sequence [Homo sapiens]	0.003
803	XM_007847	Homo sapiens hypothetical protein from clone 24796 (LOC57146), mRNA	5E-32
804	XM_015759	Homo sapiens hypothetical protein MGC2615 (MGC2615), mRNA	1E-48
805	XM_003799	Homo sapiens protocadherin beta 10 (PCDHB10), mRNA	0.71
806	AF098697	Mandarina mandarina from Anijima population 16S ribosomal RNA gene, mitochondrial gene encoding mitochondrial product, partial sequence	0.086
807	AE007509	Streptococcus pneumoniae section 192 of 194 of the complete genome	1.6
808	AY035064	Arabidopsis thaliana unknown protein (T20O10_100/AT3g63000) mRNA, complete cds	0.2
809	AE000595	Helicobacter pylori 26695 section 73 of 134 of the complete genome	0.046
810	Z75093	S.cerevisiae chromosome XV reading frame ORF YOR185c	0.11
811	M30825	Drosophila melanogaster ovarian tumor protein isoforms (otu) gene, complete cds, alternatively spliced	0.11
812	Y17004	Suberites domuncula mRNA for monoubiquitin	0.005
813	BC005104	Homo sapiens, Similar to RIKEN cDNA 5830420C20 gene, clone IMAGE:3633379, mRNA, partial cds	1.7
814	XM_029941	Homo sapiens cadherin-like 22 (CDH22), mRNA	0.0006
815	NM_003246	Homo sapiens thrombospondin 1 (THBS1), mRNA	0.23
816	U38414	Canis familiaris junctional sarcoplasmic reticulum protein mRNA, complete cds	0.21
817	XM_004000	Homo sapiens chromodomain helicase DNA binding protein 1 (CHD1), mRNA	0.63
818	AF006062	Cryptococcus neoformans var. grubii strain H99 urease (URE1) gene, complete cds	1.7
819	XM_018303	Homo sapiens hypothetical protein FLJ11565 (FLJ11565), mRNA	0.07

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
820	AE001164	Borrelia burgdorferi (section 50 of 70) of the complete genome	1.6
821	AF022969	Caenorhabditis elegans cosmid C29G2	0.2
822	AK021462	Homo sapiens cDNA FLJ11400 fis, clone HEMBA1000673	1.6
823	Y10908	B.cereus cysA and wapA genes	0.0003
824	U36892	Triticum aestivum clone AC29 microsatellite sequence	3.4
825	AF258615	Dictyostelium discoideum LagC protein (lagC) gene, complete cds	0.011
826	Z99763	Flaveria pringlei gdcsH gene	0.023
827	X71543	B.taurus microsatellite sequence INRA118	7E-15
828	AF349526	Arabidopsis thaliana putative 60S ribosomal protein (T6C23.18) mRNA, complete cds	1.7
829	D87001	Homo sapiens immunoglobulin lambda gene locus DNA, clone:47H9 downstream contig	0.007
830	XM_006470	Homo sapiens radixin (RDX), mRNA	2.4
831	AF191609	Homo sapiens filamin (FLNB) gene, exon 21	e-140
832	AF064754	Homo sapiens nuclear inhibitor of protein phosphatase-1 (PPP1R8) gene, exon 4	5.5
833	NC_001438	Bean golden mosaic virus A component DNA, complete sequence	0.57
834	D14567	Penicillium urticae mitochondrial l-rRNA (large rRNA) gene and its flanking region	0.23
835	AP000301	Homo sapiens genomic DNA, chromosome 21q22.1, D21S226-AML region, clone:D16B8, complete sequence	0.5
836	NM_014147	Homo sapiens HSPC047 protein (HSPC047), mRNA	1E-90
837	AF296100	Porcine teschovirus strain DS 562/91 polyprotein gene, complete cds	1.3
838	AK020740	Mus musculus adult male spinal cord cDNA, RIKEN full-length enriched library, clone:A330106M24, full insert sequence	1.6
839	XM_045585	Homo sapiens hypothetical protein FLJ11085 (KIAA1434), mRNA	3E-16
840	AF115104	Homo sapiens glutaredoxin (GLRX) gene, exon 1	1.3
841	AF094673	Mus musculus Sos1 gene, intron	3E-26
842	AK025101	Homo sapiens cDNA: FLJ21448 fis, clone COL04473	5E-93
843	M85276	Homo sapiens NKG5 gene, complete cds	0.039
844	AK022390	Homo sapiens cDNA FLJ12328 fis, clone MAMMA1002145	0.018
845	AF269767	Staphylococcus epidermidis strain SR1 clone step.1023b06 genomic sequence	0.47
846	NM_005916	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 7 (MCM7), mRNA	4.5
847	AF209976	Rattus norvegicus stromal cell-derived factor 1 (SDF-1) mRNA, complete cds	1.3
848	NM_017078	Rattus norvegicus Acetylcholine receptor alpha 5 (Chrna5), mRNA	0.95
849	AF269324	Staphylococcus epidermidis strain SR1 clone step.1002a12 genomic sequence	0.16

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
850	AK008669	Mus musculus adult male stomach cDNA, RIKEN full-length enriched library, clone:2210008F06, full insert sequence	4.3
851	XM_044217	Homo sapiens Ran binding protein 11 (LOC51194), mRNA	0.44
852	XM_011510	Homo sapiens CDC5 (cell division cycle 5, S. pombe, homolog)-like (CDC5L), mRNA	0.056
853	AF068574	Arabidopsis thaliana ferulate-5-hydroxylase (F5H) gene, complete cds	0.042
854	AE003072	Drosophila melanogaster genomic scaffold 142000013386025, complete sequence	1.4
855	AF159462	Escherichia coli EHEC factor for adherence (efa1) gene, complete cds	0.42
856	AF110797	Rattus norvegicus GABAB1 receptor (GABABR1) gene, exons 10 through 20 and alternatively spliced products, complete cds	1.6
857	AF319172	Homo sapiens cGMP-specific phosphodiesterase type 5A (PDE5A) gene, partial cds	0.6
858	U90299	Human chromosome 10 duplicated adrenoleukodystrophy (ALD) gene, 3' breakpoint sequence	0.0000003
859	AL050065	Homo sapiens mRNA; cDNA DKFZp566M043 (from clone DKFZp566M043)	0.006
860	U32802	Haemophilus influenzae Rd section 117 of 163 of the complete genome	1.4
861	AK001127	Homo sapiens cDNA FLJ10265 fis, clone HEMBB1001014	0.17
862	AB042995	Plecoglossus altivelis DNA, microsatellite, clone:Pal-3*	0.45
863	NM_004668	Homo sapiens maltase-glucoamylase (alpha-glucosidase) (MGAM), mRNA	0.001
864	NM_021697	Rattus norvegicus neuronal potassium channel alpha subunit (Kv8.1), mRNA	0.19
865	Z28173	S.cerevisiae chromosome XI reading frame ORF YKL173w	0.035
866	XM_051783	Homo sapiens hypothetical protein FLJ11712 (FLJ11712), mRNA	1.1
867	X92498	M.musculus fkh-6 gene	0.99
868	XM_041339	Homo sapiens similar to phosphodiesterase 4D interacting protein (myomegalin) (H. sapiens) (LOC91892), mRNA	1.5
869	AL590401	Human DNA sequence from clone RP11-466P12 on chromosome 6, complete sequence [Homo sapiens]	0.16
870	Z68758	Human DNA sequence from clone LL22NC03-85E10 on chromosome 22 Contais GSSs, complete sequence [Homo sapiens]	0.021
871	Z34916	O.aries DNA for natural resistance associated macrophage protein	4.6
872	NM_009253	Mus musculus serine protease inhibitor-2 related sequence 1 (Spi2-rs1), mRNA	1.5
873	AY024283	Oryza sativa microsatellite MRG6608 containing (TGTA)X6, genomic sequence	3.8
874	Z36108	S.cerevisiae chromosome II reading frame ORF YBR239c	1.6
875	XM_008791	Homo sapiens hypothetical protein (LOC51320), mRNA	0.14

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
876	X89383	R.norvegicus mRNA for SNF1-related kinase	0.18
877	XM_002378	Homo sapiens uncharacterized hypothalamus protein HT010 (HT010), mRNA	0
879	XM_047537	Homo sapiens DKFZP434C153 protein (DKFZP434C153), mRNA	0.003
880	XM_006700	Homo sapiens checkpoint with forkhead and ring finger domains (CHFR), mRNA	4E-27
881	NC_002756	Mertensiella luschani mitochondrion, complete genome	2.1
882	M90915	Human immunodeficiency virus type 1, viral sample LC01.DA11, V3 region	0.019
883	AB011534	Rattus norvegicus mRNA for MEGF8, partial cds	0.19
885	AF364468	Simian-Human immunodeficiency virus clone 201/26w 1 envelope glycoprotein (env) gene, partial cds	1.4
886	XM_005320	Homo sapiens cerberus 1 (Xenopus laevis) homolog (cysteine knot superfamily) (CER1), mRNA	0.63
887	AC079875	Homo sapiens clone CTD-2333B13, complete sequence	0.024
888	NM_032394	Mus musculus myosin VIIb (Myo7b), mRNA	6.6
889	AF209448	Borrelia hermsii plasmid cp32-like EcoRI-cut fragment #3	1.8
890	AK008242	Mus musculus adult male small intestine cDNA, RIKEN full-length enriched library, clone:2010015A19, full insert sequence	0.065
891	AF305851	Homo sapiens clone 16 ribosomal RNA intergenic spacer region, partial sequence	2
892	XM_047604	Homo sapiens coproporphyrinogen oxidase (coproporphyria, harderoporphyria) (CPO), mRNA	0.22
893	AF211133	Carsonella ruddii natural-host Ctenarytaina eucalypti tryptophanyl-tRNA synthetase (trpS) gene, partial cds; 16S ribosomal RNA, 23S ribosomal RNA, and 5S ribosomal RNA genes, complete sequence; transaldolase (tal) and alkyl hydroperoxide reductase smal>	0.2
894	AY047513	Drosophila melanogaster GH01880 full length cDNA	8.8
896	AL158132	Human DNA sequence from clone RP3-323A24 on chromosome 4. Contains GSSs and a putative CpG island, complete sequence [Homo sapiens]	0.0001
897	Z21978	B.napus Myr2.Bn1 gene encoding myrosinase, thioglucoside glucohydrolase	1.4
898	X95904	L.esculentum mRNA for 14-3-3 protein, TFT6	0.81
899	Z48930	C.caldarium mitochondrial genes (10kb)	0.27
900	XM_038535	Homo sapiens KIAA1074 protein (KIAA1074), mRNA	0.4
901	AF016898	Homo sapiens B-ATF gene, complete cds	0.002
902	XM_051951	Homo sapiens similar to PRO0097 protein (H. sapiens) (LOC93544), mRNA	0.003
903	X89383	R.norvegicus mRNA for SNF1-related kinase	0.23
904	AF056336	Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds	0.002
905	U34339	Protopterus aethiopicus 28S ribosomal RNA gene, partial sequence	1E-09

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
906	XM_041974	Homo sapiens hypothetical gene supported by AK025102 (LOC91974), mRNA	0.06
907	D14567	Penicillium urticae mitochondrial l-rRNA (large rRNA) gene and its flanking region	0.26
908	AL035632	Drosophila melanogaster BAC clone BACN32G11	0.52
909	AF220354	Drosophila melanogaster mitotic kinesin-like motor protein CENP-ana (cana) mRNA, complete cds	0.86
910	U67484	Methanococcus jannaschii section 26 of 150 of the complete genome	2.6
911	Y13853	Drosophila erecta clone Er1 inactive Bari-1 family transposon	0.17
912	AL137643	Homo sapiens mRNA; cDNA DKFZp586A2324 (from clone DKFZp586A2324)	1.3
913	AE006618	Streptococcus pyogenes M1 GAS strain SF370, section 147 of 167 of the complete genome	1.4
914	Z46663	M.musculus DNA for growth hormone gene and promoter	0.005
915	AF197225	Emericella nidulans TUPA (tupA) gene, complete cds	0.65
916	L20594	Human annexin III (ANX3) gene, exon 4	0.028
917	AB040730	Clostridium haemolyticum genes for 16S rRNA, tRNA-Ala, tRNA-Ile, 23S rRNA, partial and complete sequence	0.31
918	L10162	Human variable number tandem repeat (VNTR) region, allele 13R4 3' to collagen type II (COL2A1) gene	0.19
919	L35061	Bacteriophage phi-41 orfs L1-12, complete cds's, orf 13, 5' end	0.75
920	AK018618	Mus musculus adult male cecum cDNA, RIKEN full-length enriched library, clone:9130014E20, full insert sequence	0.72
921	AC024865	Caenorhabditis elegans cosmid Y74C10AL, complete sequence	0.083
922	Z65965	H.sapiens CpG island DNA genomic Mse1 fragment, clone 69g7, reverse read cpg69g7.rt1b	0.46
923	AF364335	Influenza A virus (A/Goose/Guangdong/3/97(H5N1)) segment 6 neuraminidase (NA) gene, complete cds	0.46
924	M83534	A.thaliana isocitrate lyase gene, 5' end	0.003
925	AE001390	Plasmodium falciparum chromosome 2, section 27 of 73 of the complete sequence	0.0001
926	AK023864	Homo sapiens cDNA FLJ13802 fis, clone THYRO1000186	0
927	XM_010575	Homo sapiens LOC87729 (LOC87729), mRNA	1.3
928	L16771	Drosophila simulans suppressor of forked (su(f)) gene sequence	0.17
931	BC001815	Homo sapiens, clone IMAGE:2989261, mRNA	2E-33
932	BC008580	Homo sapiens, clone IMAGE:4179986, mRNA, partial cds	1.4
933	D32063	Human gene for 2-oxoglutarate dehydrogenase, exon 14, 15, 16, 17, 18 and 19 sequence	0.058
934	XM_028551	Homo sapiens hypothetical gene supported by AK026706 (LOC90063), mRNA	0.003
935	M87298	Chicken neuropeptide Y gene, exons 1-3	2.1
936	AE006100	Pasteurella multocida PM70 section 67 of 204 of the complete genome	1.5
937	L77040	Homo sapiens (subclone 8_c11 from P1 H22) DNA sequence	9E-14

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
938	AF016349	Homo sapiens hexokinase I (HK1) gene, exon 1R and exon 1, alternatively spliced	2
939	BC001393	Homo sapiens, hypothetical protein, clone MGC:782 IMAGE:3051397, mRNA, complete cds	0.054
940	AK024092	Homo sapiens cDNA FLJ14030 fis, clone HEMBA1004086	0.025
941	AJ244013	Ectromelia virus proviral spi-3 gene for serine proteinase inhibitor, strain Hampstead (egg)	4.3
942	AK000184	Homo sapiens cDNA FLJ20177 fis, clone COL09966, highly similar to Y08136 H	0
943	U67528	Methanococcus jannaschii section 70 of 150 of the complete genome	0.22
944	AF065599	Schistosoma mansoni annexin mRNA, complete cds	0.64
945	AK020851	Mus musculus adult retina cDNA, RIKEN full-length enriched library, clone:A930013F10, full insert sequence	2.7
946	AF067228	Buchnera aphidicola bacterioferritin comigratory protein (bcp) gene, partial cds; chorismate synthase (aroC), ATP phosphoribosyltransferase (hisG), histidinol dehydrogenase (hisD), histidinolphosphate aminotransferase (hisC), imidazoleglycerolphosphate>	0.021
947	XM_049755	Homo sapiens hypothetical gene supported by AL137578 (LOC93193), mRNA	0.19
948	M14657	Bovine thrombomodulin mRNA, 3' end	0.004
949	AF312917	Plasmodium falciparum reticulocyte binding protein 2 homolog B gene, complete cds	4.6
950	U13067	Drosophila melanogaster Twin of m4 (Tom) gene, complete cds; and Brd gene, promoter region and 5'UTR, partial sequence	0.025
951	AL113476	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation	4.1
952	XM_048492	Homo sapiens talin 1 (TLN1), mRNA	5E-50
953	M19686	Bovine interstitial retinol binding protein (IRBP) mRNA, 3' flank	0.0003
954	M69188	Cotton legumin A D-genome alloallele gene, complete cds	0.072
955	AK016519	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4932411G06, full insert sequence	0.65
956	X53545	T. cruzi mRNA for SA85-1.1 protein	0.023
957	U67557	Methanococcus jannaschii section 99 of 150 of the complete genome	0.015
958	AL136165	Human DNA sequence from clone RP5-863M11 on chromosome 6, complete sequence [Homo sapiens]	7E-12
959	AE006697	Sulfolobus solfataricus section 56 of 272 of the complete genome	2
960	AB056323	Macaca fascicularis brain cDNA, clone:QflA-10392	0.56
961	XM_015216	Homo sapiens cytochrome b5 outer mitochondrial membrane precursor (CYB5-M), mRNA	0.25
962	U88513	Flexamia pyrops NADH dehydrogenase 1 gene, mitochondrial gene encoding mitochondrial protein, complete cds	0.025
963	NM_007869	Mus musculus DnaJ-like protein 1 (Dnajl1), mRNA	1.5
964	AE002349	Chlamydia muridarum, section 76 of 85 of the complete genome	0.51

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
965	AF039714	Caenorhabditis elegans cosmid T13E5	1.8
966	AF111813	Plasmodium falciparum 1-deoxy-D-xylulose 5-phosphate reductoisomerase (dxr) gene, complete cds	1.3
967	AE000425	Escherichia coli K12 MG1655 section 315 of 400 of the complete genome	0.002
968	AF108658	Homo sapiens p5327 mRNA, complete cds	0.57
969	X82329	A.hypogaea chi2.1 gene for chitinase (class II)	3.6
970	AK026575	Homo sapiens cDNA: FLJ22922 fis, clone KAT06722	1.5
971	AB016605	Bombyx mori gene for peptidoglycan recognition protein, complete cds	0.0002
972	AB009629	Avian rotavirus RNA for VP1, complete cds	1.4
973	AK020413	Mus musculus 12 days embryo embryonic body between diaphragm region and neck cDNA, RIKEN full-length enriched library, clone:9430013L14, full insert sequence	0.095
974	AF013754	Gallus gallus transcription factor RREB-1 (rreb-1) mRNA, complete cds	3.4
975	V01390	Trypanosoma brucei kinetoplast DNA maxicircle fragment encoding two very small ribosomal RNAs, a 12S rRNA homologous to E.coli 23S rRNA and a 9S rRNA homologous to 16S rRNA	0.18
976	AL112360	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation	0.22
977	AF389904	Danaus chrysippus orientis 12S ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	0.022
979	X96999	P.vulgaris Ypr10 gene	1.5
980	AL110480	Caenorhabditis elegans cosmid Y24F12A, complete sequence	0.16
981	AJ387746	Weldenia candida chloroplast tRNA-Leu intron and trnL-F intergenic spacer	1.8
982	AE001377	Plasmodium falciparum chromosome 2, section 14 of 73 of the complete sequence	0.002
983	U26946	Gallus gallus inhibin beta A subunit mRNA, complete cds	2.1
984	AC091651	Homo sapiens clone RP11-17D6, complete sequence	2E-76
985	AF143382	Arabidopsis lyrata pistillata gene, complete cds	0.02
986	Z29969	E.histolytica plasmid genes for ribosomal RNA and hemolysins HLY1, HLY5mc1 HLY5mc2 HLY4	0.02
987	XM_001301	Homo sapiens KIAA0469 gene product (KIAA0469), mRNA	0.022
988	AB007638	Bacillus subtilis genomic DNA containing gutA to cotA region, 48 degree	0.021
989	XM_012394	Homo sapiens myosin IXA (MYO9A), mRNA	7E-09
990	AF258322	Zenaida galapagoensis beta fibrinogen gene, intron 7 and partial cds	5
991	XM_048778	Homo sapiens similar to coagulation factor VIII, procoagulant component (hemophilia A) (H. sapiens) (LOC93021), mRNA	0.73
992	AB056815	Macaca fascicularis brain cDNA clone:QflA-15307, full insert sequence	6.4

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
993	AJ403948	Homo sapiens partial SLC22A3 gene for organic cation transporter 3, exons 3-4	0.008
994	AF069188	Ephedrus laevicollis NADH dehydrogenase 1 gene, mitochondrial gene encoding mitochondrial protein, partial cds	0.082
995	AF282920	Staphylococcus aureus quinone oxidoreductase and glycine betaine transporter genes, complete cds	6.6
996	AB031325	Homo sapiens gene for calcium-sensing receptor, exons, promoter region	0.081
997	AE001421	Plasmodium falciparum chromosome 2, section 58 of 73 of the complete sequence	0.74
998	AF323615	Rattus norvegicus phosphoinositide-specific phospholipase C epsilon mRNA, complete cds	2.3
999	AF305103	Picea abies clone 1PABC5D3 hypermethylated genomic sequence	0.25
1000	AY022117	Oryza sativa microsatellite MRG4442 containing (TC)X17, closest to marker RG450, genomic sequence	0.7
1001	NM_023324	Mus musculus pellino 1 (Peli1), mRNA	0.26
1002	X06329	Mouse repetitive sequence L1Md-F type 5 'end (1G-6)	0.73
1003	AE001173	Borrelia burgdorferi (section 59 of 70) of the complete genome	0.24
1004	AK021535	Homo sapiens cDNA FLJ11473 fis, clone HEMBA1001712	0.25
1005	U90529	Plasmodium vivax SV-5 Pv200 high-binding region I gene, partial cds	0.24
1006	XM_003560	Homo sapiens MAD2 (mitotic arrest deficient, yeast, homolog)-like 1 (MAD2L1), mRNA	4E-26
1007	AF315106	Homo sapiens isolate HERV-H-PA9 long terminal repeat, partial sequence	0.000001
1008	U25177	Helobdella robusta cyclin A mRNA, partial cds	0.025
1009	NM_021401	Mus musculus secreted and transmembrane 1 (Sectm1), mRNA	0.084
1010	AF339813	Homo sapiens clone IMAGE:297403, mRNA sequence	2
1011	AF020599	Equus caballus insulin-like growth factor 2 (IGF2) gene, partial cds	0.38
1012	BC001815	Homo sapiens, clone IMAGE:2989261, mRNA	7E-43
1013	AJ297945	Frankia sp. ArI3 cryptic plasmid pFQ31 ORF AF, korSAF gene, ORF CrF, ORF DrF, repF gene, ORF FrF, ORF GF, ORF HF, ORF JF, ORF KrF, ORF LrF, ORF MF, ORF NrF, ORF OF, ORF PrF, parAF gene and ORF SrF	0.64
1014	Z71327	S.cerevisiae chromosome XIV reading frame ORF YNL051w	0.61
1015	XM_031156	Homo sapiens hypothetical gene supported by AB007970 (LOC90360), mRNA	0.003
1016	XM_007274	Homo sapiens hypothetical protein FLJ10242 (FLJ10242), mRNA	0.029
1017	AE001495	Helicobacter pylori, strain J99 section 56 of 132 of the complete genome	0.076
1018	AK024606	Homo sapiens cDNA: FLJ20953 fis, clone ADSE01979	e-109
1019	AF049434	Melaleuca lateritia 5S ribosomal RNA gene, partial sequence; and 5S ribosomal RNA intergenic spacer, complete sequence	1.9

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
1020	AF078543	Pestivirus type 4 strain MN fetus polymerase (NS5b) gene, partial cds	0.68
1021	M63636	Streptococcus thermophilus beta-D-galactosidase (lacZ) gene, complete cds	0.6
1022	AJ270226	Entodinium caudatum partial mRNA for putative glycosyltransferase, clone L48	0.67
1023	M59429	T. thermophila F-antigen (tfa) gene, complete cds	0.009
1024	X77801	S.beecheyi genomic DNA with direct repeats and integrated Hepatitis B virus	1.9
1025	AL590109	Human DNA sequence from clone RP11-405J10 on chromosome 10, complete sequence [Homo sapiens]	6E-84
1026	AF269904	Staphylococcus epidermidis strain SR1 clone step.1029h10 genomic sequence	0.076
1027	AL591343	Human DNA sequence from clone RP11-260H5 on chromosome 6, complete sequence [Homo sapiens]	0.22
1028	Z12986	O.aries rearranged T-cell receptor delta	0.78
1029	AY042836	Arabidopsis thaliana Unknown protein mRNA, complete cds	0.25
1030	X00117	Galago Alu repeat type I, GAL9	0.0001
1031	XM_015858	Homo sapiens Werner syndrome (WRN), mRNA	6.6
1032	M27444	Bos taurus (clone pTKD7) dopamine and cyclic AMP-regulated neuronal phosphoprotein (DARPP-32) mRNA, complete cds	0.63
1033	AF272852	Arabidopsis thaliana beta 1,2-xylosyltransferase mRNA, complete cds	0.77
1034	L08174	Romanomermis culicivorax mitochondrial NADH dehydrogenase subunits 6 and 3 (ND6, ND3) cytochrome P450-like protein genes, complete CDS	0.084
1035	AF387598	Nicotiana tabacum EPSP synthase 1 (EPSPS1) gene, partial cds	0.007
1036	AF157094	Sarcophilus harrisii mitochondrial DNA control region, partial sequence	0.23
1037	XM_046761	Homo sapiens hypothetical gene supported by AK000735 (LOC92705), mRNA	0.66
1038	AF348479	Bos taurus myostatin gene, partial cds	6.1
1039	XM_050269	Homo sapiens solute carrier family 1 (glial high affinity glutamate transporter), member 3 (SLC1A3), mRNA	0.21
1040	AF164967	Canine distemper virus strain A75/17, complete genome	7.1
1041	AB028634	Flammulina velutipes mitochondrial gene for RNA polymerase, DNA polymerase, complete and partial cds	0.086
1042	AF312925	Homo sapiens cryptic (CFC1) gene, complete cds	0.000004
1043	U67596	Methanococcus jannaschii section 138 of 150 of the complete genome	0.26
1044	L04631	Human cholesterol 7 alpha-hyroxylase (CYP7) gene, exon 3	0.009
1045	U50336	Mus musculus Ah receptor gene, promoter region and exon 1, partial sequence	2.1
1046	AF105001	Mus musculus Fab1098 immunoglobulin light chain variable region mRNA, partial cds	0.8

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
1047	U55276	Rattus norvegicus microtubule-associated protein 1B gene, promoter region	0.79
1048	AF056302	Drosophila melanogaster eIF-2alpha kinase (GCN2) mRNA, complete cds	0.63
1049	NC_001322	Drosophila yakuba mitochondrion, complete genome	0.24
1050	AF097036	Oreina coerulea cytochrome oxidase subunit I gene, partial cds; mitochondrial gene for mitochondrial product	0.23
1051	L12148	Pasteurella haemolytica-like sp. pllktC, pllktB, pllktD, and leukotoxin structural protein (pllktA) genes, complete cds	0.21
1052	AB005153	Mus musculus DNA for DNA dependent protein kinase catalytic subunit, exon 5, 6, 7	0.006
1053	AF126733	Brassica oleracea var. italica floral homeotic protein pseudogene, partial sequence	2.1
1054	AF090900	Homo sapiens clone HQ0189 PRO0189 mRNA, complete cds	0.000001
1055	AJ223260	Chromodoris purpurea mitochondrial COI gene, partial	0.007
1056	AF089052	Pseudoleistes virescens cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds	0.77
1057	AL138748	Human DNA sequence from clone RP4-732E19 on chromosome Xq21.1-21.33 Contains GSSs, complete sequence [Homo sapiens]	0.59
1058	AL132767	Human DNA sequence from clone RP5-819L10 on chromosome 6q12-13. Contains GSSs, complete sequence [Homo sapiens]	5
1059	AF032670	Lucilia cuprina Notch homolog (Scl) gene, exon B	0.055
1060	AE001371	Plasmodium falciparum chromosome 2, section 8 of 73 of the complete sequence	0.062
1061	AY039845	Arabidopsis thaliana At1g35160/T32G9_30 mRNA, complete cds	4.6
1062	AF365189	Sindoropsis le-testui tRNA-Leu (trnL) gene, partial intron sequence; chloroplast gene for chloroplast product	0.11
1063	U60591	Drosophila melanogaster kuzbanian (kuz) mRNA, complete cds	0.41
1064	AJ297052	Homo sapiens SDS-stable vimentin-bound DNA fragment HEF42VIM12	4E-09
1065	AB023191	Homo sapiens mRNA for KIAA0974 protein, partial cds	0.23
1066	AK021989	Homo sapiens cDNA FLJ11927 fis, clone HEMBB1000402	0.33
1067	XM_038524	Homo sapiens hypothetical protein FLJ23059 (FLJ23059), mRNA	e-169
1068	XM_045967	Homo sapiens estrogen receptor 1 (ESR1), mRNA	4.9
1069	AF354258	Homo sapiens polynucleotide kinase-3'-phosphatase (PNKP) gene, complete cds	0.66
1070	AJ404320	Posidonia oceanica medium repetitive sequence, clone pPopm6	0.038
1071	NC_002756	Mertensiella luschani mitochondrion, complete genome	4.9
1072	Z68886	Human DNA sequence from cosmid L21F12, Huntington's Disease Region, chromosome 4p16.3	2E-10
1073	AE001370	Plasmodium falciparum chromosome 2, section 7 of 73 of the complete sequence	0.025

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
1074	XM_033521	Homo sapiens hypothetical protein FLJ10357 (FLJ10357), mRNA	1.5
1075	U02239	Mycoplasma genitalium random genomic clone xd5, partial cds	0.006
1076	AE006395	Lactococcus lactis subsp. lactis IL1403 section 157 of 218 of the complete genome	0.32
1077	AY023826	Oryza sativa microsatellite MRG6151 containing (ATAC)X8, genomic sequence	0.031
1079	X63213	B.taurus CI-B12 mRNA for ubiquinone oxidoreductase complex	7
1080	AK021648	Homo sapiens cDNA FLJ11586 fis, clone HEMBA1003720	3E-13
1081	AF246689	Dictyostelium discoideum ABC transporter mdrA1 (MDRA1) and ABC transporter mdrA2 (MDRA2) genes, complete cds	0.67
1082	AB016100	Oryza sativa LINE retrotransposon, endonuclease region of RILN5	0.068
1083	U93157	Orestias species mitochondrial control region, allele SRT1, partial sequence	6.9
1084	AF173373	Caenorhabditis elegans transmembrane protein NDG-4 (ndg-4) mRNA, complete cds	1.8
1086	AJ310640	Turkey coronavirus genomic RNA for partial spike glycoprotein (s gene), 3a protein (gene 3), 3b protein (gene 3), E protein (gene 3) and partial M protein (gene 4), strain turkey/UK/412/00	2
1087	M21953	Duck hepatitis B virus, complete genome	0.086
1088	AF332583	Homo sapiens stratum corneum chymotryptic enzyme (KLK7) gene, complete cds, alternative transcripts	2.1
1089	AY037894	Glomus intraradices phosphate transporter mRNA, partial cds	0.084
1091	NM_020078	Rattus norvegicus a disintegrin and metalloproteinase domain 1 (fertilin alpha) (Adam1), mRNA	0.51
1092	AF282531	Homo sapiens clone 18qtel_c30t7 sequence	0.003
1093	AF324424	Ichthyophthirius multifiliis immobilization antigen isoform (IAG52A) gene, complete cds	0.56
1094	AJ404320	Posidonia oceanica medium repetitive sequence, clone pPopm6	0.075
1096	Z46803	V.narbonensis mRNA for legumin A precursor	2.2
1097	XM_050195	Homo sapiens similar to hypothetical protein FLJ14751 (H. sapiens) (LOC93274), mRNA	5.7
1098	AJ246004	Homo sapiens RET gene, 5' genomic fragment	0.00004
1099	AY031051	HIV-1 isolate NC4057-1999 from USA pol polyprotein (pol) gene, partial cds	0.23
1100	AE002146	Ureaplasma urealyticum section 47 of 59 of the complete genome	0.26
1101	Z23650	H. sapiens (D1S436) DNA segment containing (CA) repeat; clone AFM217zc3; single read	0.001
1102	D73382	Sugarbeet mitochondrial gene for ORFB, complete cds	0.73
1103	U67503	Methanococcus jannaschii section 45 of 150 of the complete genome	0.69
1104	AL590376	Human DNA sequence from clone RP11-22P2 on chromosome Xq23-24, complete sequence [Homo sapiens]	0
1106	D14636	Mouse mRNA for PEBP2a1 protein, complete cds	0.61

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
1107	Y14622	Mus musculus Tnfr2 gene, exon 4 to exon 8	0.71
1108	AF130049	Homo sapiens clone FLB3411 PRO0852 mRNA, complete cds	0.065
1109	AJ011009	Glycine max cytosolic glutamine synthetase (gs15) gene promoter	0.007
1110	XM_043523	Homo sapiens Rho guanine exchange factor (GEF) 11 (ARHGEF11), mRNA	0.7
1111	Z77974	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA5D12	0.001
1112	AJ002513	Schizosaccharomyces pombe cmb1 gene	8.2
1113	AF098878	Homo sapiens APAF1 gene, exons 6 and 7	1.9
1114	M14080	Herpesvirus saimiri thymidylate synthase gene, complete cds	0.023
1115	U44838	Glycine max extensin (SbHRGP3) gene, complete cds	0.76
1116	Y15491	Pongo pygmaeus gene encoding fertilin alpha	2.1
1117	U43145	Plasmodium chabaudi repeat organellar protein gene, complete cds	0.25
1118	Z81524	Caenorhabditis elegans cosmid F32H5, complete sequence	0.009
1119	AF052957	Homo sapiens type XV collagen (COL15A1) gene, exons 3 and 4	2.2
1120	U67523	Methanococcus jannaschii section 65 of 150 of the complete genome	0.001
1121	AL121807	S.pombe chromosome III cosmid c132	0.19
1122	X59280	S.douglasii gene for cytochrome b	0.29
1123	XM_030915	Homo sapiens KIAA0673 protein (KIAA0673), mRNA	5E-19
1124	X99254	P.falciparum gene encoding primase, small subunit	0.084
1125	AC004214	Homo sapiens clone UWGC:m32agap from 6p21, complete sequence	0.009
1126	AF061244	Agrocybe aegerita B type DNA polymerase (Mtpol) gene, complete cds; tRNA-Asn gene, complete sequence; and unknown genes, mitochondrial genes for mitochondrial products	0.001
1127	AK001125	Homo sapiens cDNA FLJ10263 fis, clone HEMBB1000991	0
1128	L41046	Pisum sativum endo-1,4-beta-glucanase (EGL1) gene, complete cds	0.0001
1129	XM_008099	Homo sapiens integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide) (ITGAL), mRNA	2E-18
1130	AE000049	Mycoplasma pneumoniae M129 section 31 of 63 of the complete genome	0.75
1131	AY019627	Oryza sativa microsatellite MRG1952 containing (AT)X40, closest to marker L128, genomic sequence	0.024
1132	Z46383	Bovine herpesvirus type 4 DNA for nonconserved region A	4.3
1133	Y07893	S.cerevisiae DNA fragment, right arm of chromosome VII	4.2
1134	XM_040867	Homo sapiens sperm acrosome associated 1 (SPACA1), mRNA	0.003
1135	XM_038693	Homo sapiens solute carrier family 9 (sodium/hydrogen exchanger), isoform 2 (SLC9A2), mRNA	2
1136	NM_033074	Mus musculus DNA segment, Chr 15, Wayne State University 59, expressed (D15Wsu59e), mRNA	0.64

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
1137	M97168	Homo sapiens X (inactive)-specific transcript (XIST) complete exon	3.4
1138	D13973	Dictyostelium discoideum DNA for Dp87 protein, complete cds	0.075
1139	AF303254	Caenorhabditis elegans gene XL153 mRNA, complete cds	2
1140	AB009926	Cyphonocerus ruficollis mitochondrial DNA for 16S rRNA, partial sequence	0.24
1141	NC_002660	Cochliomyia hominivorax mitochondrion, complete genome	0.0009
1142	AL096756	Human DNA sequence from clone RP3-477J10 on chromosome 22q13.31-13.33 Contains a GSS, complete sequence [Homo sapiens]	0.26
1143	XM_031937	Homo sapiens hypothetical protein FLJ11183 (FLJ11183), mRNA	2.2
1144	AE003025	Drosophila melanogaster genomic scaffold 142000013385389, complete sequence	0.22
1145	Z11702	V.faba mRNA for polyphenol oxidase	0.76
1146	XM_049924	Homo sapiens calcium binding protein 5 (CABP5), mRNA	5.6
1147	XM_047707	Homo sapiens KIAA1265 protein (KIAA1265), mRNA	1.6
1148	AY005256	Xylocopa erythrina cytochrome b (cytb) gene, partial cds; mitochondrial gene for mitochondrial product	0.086
1151	Z96679	H.sapiens telomeric DNA sequence, clone 7PTEL026, read 7PTELOO026.seq	9E-34
1152	AJ001677	Branchiostoma floridae mRNA for phenylalanine hydroxylase, partial	0.067
1153	J03252	Human alkaline phosphatase (ALPP) gene, complete cds	0.65
1154	AK007179	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:1700112J16, full insert sequence	0.24
1155	AK004093	Mus musculus 18 days embryo cDNA, RIKEN full-length enriched library, clone:1110034K09, full insert sequence	6.7
1156	AF370142	Arabidopsis thaliana unknown protein (T5I7.1/At2g39710) mRNA, complete cds	1.7
1157	AF053649	Homo sapiens cellular apoptosis susceptibility protein (CSE1) gene, exons 15 and 16	0.006
1158	AL080199	Homo sapiens mRNA; cDNA DKFZp434E082 (from clone DKFZp434E082)	0.081
1159	AF267225	Candidatus Carsonella ruddii natural-host Tainarys sordida ATP synthase alpha subunit (atpA) gene, partial cds; ATP synthase gamma subunit (atpG) gene, complete cds; and ATP synthase beta subunit (atpD) gene, partial cds	0.15
1160	AE000654	Helicobacter pylori 26695 section 132 of 134 of the complete genome	0.51
1161	AK007179	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:1700112J16, full insert sequence	0.25
1162	NM_008787	Mus musculus pericentrin (Pcnt), mRNA	1.7
1163	AK024592	Homo sapiens cDNA: FLJ20939 fis, clone ADSE01583	0.077
1164	D13197	Mouse gene for immunoglobulin diversity region D1	0.076

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
1165	AE001381	Plasmodium falciparum chromosome 2, section 18 of 73 of the complete sequence	0.073
1166	X68360	M.fascicularis gene for apolipoprotein A-II	0.0009
1167	X73032	B.juncea ribosomal intergenic spacer	0.023
1168	XM_037745	Homo sapiens hypothetical gene supported by AL137266 (LOC91332), mRNA	0.21
1169	NM_017755	Homo sapiens hypothetical protein FLJ20303 (FLJ20303), mRNA	0.58
1170	XM_045819	Homo sapiens cofilin 2 (muscle) (CFL2), mRNA	2
1171	AE006349	Lactococcus lactis subsp. lactis IL1403 section 111 of 218 of the complete genome	0.12
1172	XM_030637	Homo sapiens G protein-coupled receptor kinase 7 (GPRK7), mRNA	1.6
1173	AK017298	Mus musculus 6 days neonate head cDNA, RIKEN full-length enriched library, clone:5430411K23, full insert sequence	0.18
1174	AF154915	Homo sapiens transcription factor HOXD12 (HOXD12) and transcription factor HOXD11 (HOXD11) genes, complete cds	0.52
1175	AF143066	Lepidopilum scabrisetum ribosomal protein system 4 (rps4) gene, partial cds	0.51
1176	AL391814	Human DNA sequence from clone RP11-49A4 on chromosome 6, complete sequence [Homo sapiens]	0.06
1177	AF003511	Toxoneuron sp. 16S ribosomal RNA gene, partial sequence	0.0000001
1178	AK022350	Homo sapiens cDNA FLJ12288 fis, clone MAMMA1001783	0.00002
1180	AF307986	Mus musculus small inducible cytokine A21b (Scya21b) gene, complete cds	0.021
1181	NM_022242	Rattus norvegicus niban protein (Niban), mRNA	5
1182	Z57380	H.sapiens CpG island DNA genomic Mse1 fragment, clone 173c2, forward read cpg173c2.ft1a	0.13
1183	XM_043937	Homo sapiens hypothetical protein MGC13033 (MGC13033), mRNA	6.4
1184	L15439	Geukensia demissa neuropeptide mRNA, complete cds	0.24
1185	AJ251399	Proechimys cayennensis mitochondrial cytb gene for cytochrome b (specimen voucher V-815)	0.7
1186	U00053	Caenorhabditis elegans cosmid K03F8	0.62
1187	J00277	Human (genomic clones lambda-[SK2-T2, HS578T]; cDNA clones RS-[3,4, 6]) c-Ha-ras1 proto-oncogene, complete coding sequence	7E-55
1189	X70677	X.laevis XFG 5-1 mRNA for zinc finger protein	0.23
1190	AJ223323	Saccharomyces cerevisiae mitochondrial tRNA-Tyr, tRNA-Asn, & tRNA-Met genes	0.083
1191	XM_030479	Homo sapiens KIAA1462 protein (KIAA1462), mRNA	0.76
1192	AK016425	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4931403E03, full insert sequence	0.00003
1193	AF092854	Saguinus mystax visual pigment gene, P562 allele, intron 4	0.0001
1194	AC025732	Homo sapiens BAC clone RP11-116J19 from Y, complete sequence	1.7

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
1195	AE002177	Chlamydophila pneumoniae AR39, section 13 of 94 of the complete genome	0.011
1196	M94732	Plasmodium falciparum 15 kDa vesicular-like antigen gene, exons 1 through 4	0.009
1197	X76311	H.sapiens endothelial nitric oxidase synthase gene, exons 15 and 16	0.6
1198	L81756	Homo sapiens (subclone 1_g5 from P1 H16) DNA sequence, complete sequence	0.061
1199	Z82625	R.prowazekii genomic DNA fragment (clone A396F)	0.76
1200	XM_012528	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA	2.1
1201	M27082	S.cerevisiae GCN2 gene (which couples GCN4 expression to amino acid availability), complete cds	0.21
1202	AK007856	Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810054D07, full insert sequence	6E-73
1203	M69188	Cotton legumin A D-genome alloallele gene, complete cds	0.076
1204	AB043132	Thunnus thynnus DNA, microsatellite Ttho-6*, partial sequence	0.001
1205	AF019084	Homo sapiens keratin 2e (KRT2E) gene, complete cds	6
1206	U32784	Haemophilus influenzae Rd section 99 of 163 of the complete genome	0.026
1207	XM_004699	Homo sapiens ubiquitin-conjugating enzyme E2H (homologous to yeast UBC8) (UBE2H), mRNA	2
1208	AF375643	Pongo pygmaeus HERV-K-GC1 preintegration site sequence	2.2
1209	AK007179	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:1700112J16, full insert sequence	0.22
1210	AF182214	Glycine max glutamine synthetase gamma 2 subunit gene, 5'-flanking region and partial cds	0.23
1211	AF170224	Alloplectus meridensis ribulose 1,5-bisphosphate carboxylase large subunit gene, partial cds; chloroplast gene for chloroplast product	6.5
1212	NM_022978	Homo sapiens small EDRK-rich factor 1B (centromeric) (SERF1B), mRNA	0.23
1213	U17787	Gromphadorhina portentosa mitochondrion 16S ribosomal RNA, partial sequence	0.027
1214	AF144086	Papio hamadryas anubis chromosome 13 repeat region	0.25
1215	XM_010106	Homo sapiens DKFZP586N0819 protein (DKFZP586N0819), mRNA	0.73
1216	AF198964	Arabidopsis thaliana ATP sulfurylase gene, complete cds	0.072
1217	AJ298866	Xenopus laevis mRNA for winged helix transcription factor (foxd3b gene)	0.2
1218	AF069111	Uroleucon obscurum large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence	0.003
1219	X16715	D. melanogaster gene for chorion protein s16	0.23
1220	AF245117	Mus musculus leukocyte cell-surface molecule (Ly9) gene, exon 1	0.024

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
1221	AP001310	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:MUO22	0.23
1222	AF092375	Rivulus gransabanae tRNA-Ile, tRNA-Gln, and tRNA-Met genes, complete sequence; NADH dehydrogenase subunit II gene, complete cds; tRNA-Trp, tRNA-Ala, tRNA-Asn, tRNA-Cys, and tRNA-Tyr genes, complete sequence; and cytochrome c oxidase subunit I gene, par>	0.26
1223	U84864	HIV-1 strain M14 from USA, envelope glycoprotein (env) gene, partial cds	0.76
1224	XM_051684	Homo sapiens similar to estrogen-related receptor alpha; estrogen receptor-like 1 (H. sapiens) (LOC93491), mRNA	0.57
1225	AF282391	Cucumis sativus clone B99 mitochondrial genomic sequence	2.2
1226	AK026459	Homo sapiens cDNA: FLJ22806 fis, clone KAIA2845	0.024
1227	AJ003131	Spodoptera littoralis nuclear polyhedrosis virus fgf, egt genes and 3 ORFs	0.022
1228	XM_028308	Homo sapiens helicase-moi (KIAA0928), mRNA	1.8
1229	AF219168	Fritillaria camtschatcensis clone cam36 retrotransposon TfcI, partial sequence	2
1230	AF325699	Homo sapiens ataxia-telangiectasia and Rad3 related protein (ATR) gene, partial cds, alternatively spliced	0.069
1231	AE007433	Streptococcus pneumoniae section 116 of 194 of the complete genome	7.9
1232	XM_007429	Homo sapiens CGI-35 protein (LOC51077), mRNA	1E-08
1233	AF021084	Dianous nitidulus cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds	0.07
1234	Z97349	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-06, complete sequence	2.1
1235	XM_038588	Homo sapiens like-glycosyltransferase (LARGE), mRNA	5.5
1236	X95276	P.falciparum complete gene map of plastid-like DNA (IR-B)	0.008
1237	U88570	Drosophila melanogaster CREB-binding protein homolog mRNA, complete cds	1.7
1238	AK024332	Homo sapiens cDNA FLJ14270 fis, clone PLACE1004491	0.68
1239	AC006678	Caenorhabditis elegans cosmid R05G9, complete sequence	1.8
1240	AF250958	Lycopersicon esculentum peptide deformylase-like protein mRNA, complete cds	0.076
1241	M26650	Human islet amyloid polypeptide (hIAPP) gene, complete cds	1.9
1242	XM_037062	Homo sapiens DKFZP564G202 protein (DKFZP564G202), mRNA	0.61
1243	AE003025	Drosophila melanogaster genomic scaffold 142000013385389, complete sequence	0.027
1244	U39701	Mycoplasma genitalium section 23 of 51 of the complete genome	2.1
1245	AE000036	Mycoplasma pneumoniae M129 section 44 of 63 of the complete genome	8.2
1246	AE000830	Methanobacterium thermoautotrophicum from bases 394245 to 404874 (section 36 of 148) of the complete genome	0.67

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
1247	AL358951	Human DNA sequence from clone RP3-456L16 on chromosome 6, complete sequence [Homo sapiens]	0.64
1248	XM_045757	Homo sapiens chloride channel 4 (CLCN4), mRNA	0.56
1249	U59683	Nicotiana tabacum squalene synthase (TSS) gene, complete cds	0.005
1250	AK010434	Mus musculus ES cells cDNA, RIKEN full-length enriched library, clone:2410006O21, full insert sequence	4.9
1251	XM_045757	Homo sapiens chloride channel 4 (CLCN4), mRNA	0.61
1252	AE000717	Aquifex aeolicus section 49 of 109 of the complete genome	0.024
1253	AC024780	Caenorhabditis elegans cosmid Y43B11AR, complete sequence	0.027
1254	AF343030	Human herpesvirus 7 isolate CR18 glycoprotein H gene, complete cds	0.009
1255	AK022153	Homo sapiens cDNA FLJ12091 fis, clone HEMBB1002582	0.0000001
1256	AF309947	Dictyostelium discoideum Rac1A (rac1A) gene, complete cds; and unknown gene	0.009
1257	AB051519	Homo sapiens mRNA for KIAA1732 protein, partial cds	0.25
1258	AC006681	Caenorhabditis elegans clone R13H9, complete sequence	2.2
1260	Y11648	Campylobacter jejuni waaC, galE, wla[B,C,D,E,F,G,H,I,K,L,M], cheY genes and orf1	0.25
1261	AB009592	Oryza sativa gene for cytosolic glutathione reductase, complete cds	2.1
1262	X83997	C.parasitica eapC gene	0.22
1263	AJ404320	Posidonia oceanica medium repetitive sequence, clone pPopm6	0.034
1264	AF038620	Caenorhabditis elegans cosmid H10D12	0.063
1265	U05822	Human proto-oncogene BCL3 gene, exon 2	0.0000001
1266	Z79343	H.sapiens flow-sorted chromosome 6 TaqI fragment, SC6pA4G2	0.13
1267	S60289	LeB4=legumin {5' region} [Vicia faba, Genomic, 1222 nt]	0.0003
1268	AE006303	Lactococcus lactis subsp. lactis IL1403 section 65 of 218 of the complete genome	1.9
1269	AE001410	Plasmodium falciparum chromosome 2, section 47 of 73 of the complete sequence	0.008
1270	X96972	D.buzzatii copia element DNA	0.2
1271	AB042973	Nicotiana tabacum wizz gene, 5' flanking region, partial cds	0.073
1272	Z95309	Caenorhabditis elegans cosmid H36L18, complete sequence	3.5
1273	AF091745	Homo sapiens exonuclease I (EXOI) gene, exon 5	0.2
1274	AF386945	Arabidopsis thaliana Rubisco subunit binding-protein beta subunit (T5A14.11) mRNA, complete cds	0.7
1275	AF269376	Staphylococcus epidermidis strain SR1 clone step.1002h01 genomic sequence	0.076
1276	AK012864	Mus musculus 10, 11 days embryo cDNA, RIKEN full-length enriched library, clone:2810036I15, full insert sequence	0.028
1277	Z74204	S.cerevisiae chromosome IV reading frame ORF YDL156w	0.18
1278	AB049851	Macaca fascicularis brain cDNA, clone:QnpA-18831	2E-91
1279	AE001761	Thermotoga maritima section 73 of 136 of the complete genome	0.19
1280	AE002102	Ureaplasma urealyticum section 3 of 59 of the complete genome	5.5
1281	AK021982	Homo sapiens cDNA FLJ11920 fis, clone HEMBB1000312	0.006

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
1282	AE007504	Streptococcus pneumoniae section 187 of 194 of the complete genome	0.21
1283	X79095	F.trinervia pdk gene for pyruvate,orthophosphate dikinase	0.22
1284	AE007413	Streptococcus pneumoniae section 96 of 194 of the complete genome	1.7
1285	AB050513	Macaca fascicularis brain cDNA, clone:QnpA-17049	0.41
1286	AF339809	Homo sapiens clone IMAGE:274150, mRNA sequence	0.52
1287	AF074991	Homo sapiens full length insert cDNA YH88A03	4E-09
1288	AF277581	Campostoma anomalum microsatellite CA9 sequence	1.6
1289	AF035245	Bacillus lynceorum strain pVIL31 Bag320 satellite DNA	0.23
1291	AF298208	Dictyostelium discoideum transposon thug-T, complete sequence	0.028
1292	AL133656	Homo sapiens mRNA; cDNA DKFZp434O2017 (from clone DKFZp434O2017)	0.021
1293	AK024666	Homo sapiens cDNA: FLJ21013 fis, clone CAE05223	9E-34
1294	U55367	Caenorhabditis elegans cosmid C55H1, complete sequence	2.1
1295	X16715	D. melanogaster gene for chorion protein s16	0.25
1296	AC001080	Homo sapiens (subclone 3_g7 from PAC H74) DNA sequence, complete sequence	0.69
1297	XM_051200	Homo sapiens hypothetical protein MGC5149 (MGC5149), mRNA	0.58
1298	AE000016	Mycoplasma pneumoniae M129 section 1 of 63 of the complete genome	0.026
1299	AF264059	Homo sapiens RAPD fragment lost in a grade 2 astrocytoma	0.73
1300	AE002308	Chlamydia muridarum, section 39 of 85 of the complete genome	0.078
1301	U58745	Caenorhabditis elegans cosmid C10G6, complete sequence	0.26
1302	XM_007768	Homo sapiens KIAA1018 protein (KIAA1018), mRNA	2.2
1303	AC000102	Homo sapiens Chromosome 22q11.2 BAC Clone 60b5 In GNAZ-BCR Region, complete sequence	0.17
1304	AF338734	Homo sapiens hypothetical PHD zinc finger protein XAP135 pseudogene, complete sequence	2.3
1305	AF211141	Carsonella ruddii natural-host Pachypsylla celtidis tryptophanyl-tRNA synthetase (trpS) gene, partial cds; 16S ribosomal RNA, 23S ribosomal RNA, and 5S ribosomal RNA genes, complete sequence; transaldolase (tal) and alkyl hydroperoxide reductase small >	0.087
1306	L81391	Homo sapiens (subclone 2_a6 from P1 H39) DNA sequence, complete sequence	0.18
1307	AB013613	Oryza sativa DNA, centromere sequence RCB11	0.085
1308	U03906	Macroscelides proboscideus aldehyde dehydrogenase I, eta-crystallin mRNA, complete cds	0.26
1309	L13470	Human thyroxine-binding globulin gene, complete cds	0.21
1310	AK026225	Homo sapiens cDNA: FLJ22572 fis, clone HSI02313	3E-27
1311	XM_030391	Homo sapiens dJ467N11.1 protein (DJ467N11.1), mRNA	0.001
1312	XM_017923	Homo sapiens hypothetical protein FLJ12660 (FLJ12660), mRNA	2E-32

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
1313	M57256	B.hermsii vmp21 gene encoding Vmp21 outer membrane lipoprotein	0.58
1314	Y14051	Staphylococcus aureus mecA, mecR1, mecI genes and ORF168, ORF142, ORF44, ORF145 and ORF224	0.081
1315	XM_032018	Homo sapiens similar to RIKEN cDNA 2310040G17 gene (M. musculus) (LOC90480), mRNA	0.027
1316	AF227514	Octodon lunatus cytochrome b gene, partial cds; mitochondrial gene for mitochondrial product	1.9
1317	AE001414	Plasmodium falciparum chromosome 2, section 51 of 73 of the complete sequence	0.73
1318	Z21622	S.cerevisiae RIB7 gene encoding HTP reductase	0.77
1319	XM_040462	Homo sapiens ATP-binding cassette, sub-family D (ALD), member 3 (ABCD3), mRNA	1.8
1320	Z65229	H.sapiens CpG island DNA genomic Mse1 fragment, clone 28a8, forward read cpg28a8.ft1a	0.23
1321	XM_040095	Homo sapiens hypothetical protein (DKFZP434G0310), mRNA	2.3
1322	XM_027314	Homo sapiens hypothetical protein FLJ22351 (FLJ22351), mRNA	1E-14
1323	AF282064	Homo sapiens clone 2qtel_edc17iF-c17jF sequence	3E-88
1324	AF101098	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 38	1.3
1325	AB050093	Neoceratodus forsteri mRNA for pituitary glycoprotein hormone alpha subunit, complete cds	0.009
1326	AL591507	Human DNA sequence from clone RP11-289C14 on chromosome 6, complete sequence [Homo sapiens]	0.026
1327	AJ400873	Homo sapiens partial GPLD1 gene for glycosylphosphatidylinositol phospholipase D, exons 15-20	1.9
1328	AF378831	Mus musculus orphan G protein-coupled receptor (Raig2) mRNA, complete cds	1.9
1329	XM_030116	Homo sapiens hypothetical protein MGC3077 (MGC3077), mRNA	0
1330	X54806	R.norvegicus mRNA for cytokeratin type I (3' end)	0.77
1331	XM_013141	Homo sapiens ATPase, Cu++ transporting, alpha polypeptide (Menkes syndrome) (ATP7A), mRNA	0.72
1332	NM_026428	Mus musculus RIKEN cDNA 1810027P18 gene (1810027P18Rik), mRNA	0.019
1333	U85448	Actinidia deliciosa sucrose-phosphate synthase (KSPS-1) mRNA, partial cds	0.001
1334	AK013974	Mus musculus 13 days embryo head cDNA, RIKEN full-length enriched library, clone:3110002D09, full insert sequence	0.74
1335	U25641	Tetrahymena thermophila telomerase component p80 mRNA, complete cds	0.008
1336	NC_002102	Lactobacillus helveticus plasmid pLH1, complete sequence	0.78
1337	M14292	Human L1Heg repetitive element from the intergenic region of the epsilon and G-gamma globin genes	5E-08

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
1338	AF239910	Petunia axillaris haplotype S15 self-incompatibility ribonuclease mRNA, complete cds	2.1
1339	AF116872	Candida albicans alternative oxidase (AOX2) gene, complete cds	0.25
1340	XM_035344	Homo sapiens KIAA1688 protein (KIAA1688), mRNA	1.6
1341	XM_046636	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA	6E-74
1342	AF292561	Strongyloides stercoralis G protein alpha subunit 2 (gpa-2) gene, complete cds	0.76
1343	AF008597	Catharanthus roseus desacetoxyvindoline-4-hydroxylase (CRSD4H) gene, complete cds	0.26
1344	AF347671	Equine rhinitis A virus isolate PERV/62 P1 (P1) gene, partial cds	6.9
1345	U89019	Hepatitis C virus polyprotein gene, complete cds	0.27
1346	XM_043815	Homo sapiens hypothetical protein FLJ21736 (FLJ21736), mRNA	2.2
1347	L39930	Podocoryne carnea fibrillin mRNA, partial cds	0.7
1348	Z21512	K.lactis GAL80 gene encoding KlGAL80 protein	0.075
1349	AC001490	Homo sapiens (subclone 2_c10 from P1 H32) DNA sequence, complete sequence	2E-11
1350	L36891	Saccharomyces cerevisiae mitochondrion transfer RNA-fMet (tRNA-fMet) gene; transfer RNA-Pro (tRNA-Pro) gene; 9S ribosomal RNA (9S rRNA) gene	0.025
1351	AK017200	Mus musculus 11 days pregnant adult female ovary and uterus cDNA, RIKEN full-length enriched library, clone:5033428C03, full insert sequence	6.2
1352	AB003286	Homo sapiens DNA for choline kinase like protein and muscle type carnitine palmitoyltransferase I, partial and complete cds	0.069
1353	AF312917	Plasmodium falciparum reticulocyte binding protein 2 homolog B gene, complete cds	0.081
1354	M65060	M.thermoautotrophicum trpE, trpG, trpC, trpF, trpB, trpA, trpD genes, complete cds	0.26
1355	AB025642	Arabidopsis thaliana genomic DNA, chromosome 5, BAC clone:T32G24	0.34
1356	L24957	Zygosaccharomyces cidri alpha-galactosidase gene, complete cds	0.08
1357	L38437	Rattus norvegicus NADH ubiquinone oxidoreductase subunit (IP13) gene, complete cds	0.27
1358	AJ301686	Polystoma sp. DNA-25 ITS 1, isolate DNA-25	2.2
1359	AB002805	Homo sapiens OS-9 gene, 5' upstream region and partial cds	0.0004
1361	XM_030723	Homo sapiens CGI-107 protein (LOC51012), mRNA	3.1
1362	NM_031881	Mus musculus neural precursor cell expressed, developmentally down-regulated gene 4b (Nedd4b), mRNA	3.8
1363	AC008855	Homo sapiens chromosome 5 clone CTD-2178M23, complete sequence	0.72
1364	NC_002660	Cochliomyia hominivorax mitochondrion, complete genome	0.074
1365	AF072589	Python regius alpha enolase mRNA, complete cds	1.4
1366	AJ243461	Vicia faba nod-CCP1 gene, exons 1 and 2	0.017

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
1367	XM_011052	Homo sapiens 28kD interferon responsive protein (IFRG28), mRNA	1.6
1368	AL390157	Homo sapiens mRNA; cDNA DKFZp434D179 (from clone DKFZp434D179)	0.0005
1369	AL023822	Caenorhabditis elegans cosmid Y102A5A, complete sequence	0.046
1370	U36918	Mesocricetus auratus mucin (MUC1) mRNA, complete cds	4.4
1371	AF081786	Homo sapiens lysyl hydroxylase 1 gene, promoter region and partial cds	0.18
1372	XM_035682	Homo sapiens similar to hypothetical protein FLJ22639 (H. sapiens) (LOC91047), mRNA	8E-08
1373	Z54645	H.sapiens CpG island DNA genomic Mse1 fragment, clone 14h7, reverse read cpg14h7.rt1b	0.027
1374	AB012135	Schizosaccharomyces pombe gene for catalytic subunit (C5) of proteasome, complete cds	1.9
1375	L47352	Brassica napus (clone Sta 39-4) arabinogalactan protein mRNA, complete cds	0.73
1376	AB036993	Homo sapiens RHAG gene for Rh50 glycoprotein, partial cds	0.0000001
1377	U67535	Methanococcus jannaschii section 77 of 150 of the complete genome	0.03
1378	AF203637	*Myotis myotis* microsatellite A2 sequence	0.017
1379	XM_004748	Homo sapiens hypothetical protein FLJ11110 (FLJ11110), mRNA	1.1
1380	AJ249744	Campylobacter jejuni cjaE gene for putative membrane protein CjaE	0.69
1381	AL591033	Human DNA sequence from clone RP11-94L3 on chromosome 6, complete sequence [Homo sapiens]	1.7
1382	AJ242625	Mus musculus Dmp-1 gene, exons 1-6	0.71
1383	AB036851	Ciona intestinalis mRNA for pellino, complete cds	0.23
1384	XM_012972	Homo sapiens transmembrane phosphatase with tensin homology (TPTE), mRNA	2E-09
1385	AF175313	Oncorhynchus mykiss cardiac sodium-calcium exchanger (NCX) mRNA, complete cds	0.47
1386	AF283669	Homo sapiens kallikrein 14 (KLK14) gene, complete cds	0.44
1387	AY018560	Oryza sativa microsatellite MRG0885 containing (AT)X18, genomic sequence	0.63
1388	AK027272	Homo sapiens cDNA FLJ14366 fis, clone HEMBA1001020	0.019
1389	XM_003052	Homo sapiens roundabout (axon guidance receptor, Drosophila) homolog 1 (ROBO1), mRNA	1E-49
1390	AF208532	Homo sapiens fatty acid omega-hydroxylase CYP4A11 (CYP4A11) gene, complete cds	0.69
1391	AF233326	Mus musculus tumor necrosis factor receptor-associated factor (Traf2) gene, exons 2, 3, and 4	0.72
1392	AE001413	Plasmodium falciparum chromosome 2, section 50 of 73 of the complete sequence	0.15
1394	X54889	Sea urchin developmentally regulated ectodermal gene	0.023

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
1395	AF378868	Arabidopsis thaliana AT5g11200/F2I11_90 mRNA, complete cds	2.5
1396	AF328539	Homo sapiens clone 12qtel_c64t3 sequence	0.0003
1397	AE006450	Lactococcus lactis subsp. lactis IL1403 section 212 of 218 of the complete genome	0.47
1398	Z12840	O.cuniculus mRNA for protein of unknown function	2E-97
1399	U31165	Rattus norvegicus SH3 domain binding protein (CR16) gene, exon 6	1.9
1400	Y15005	Bison bonasus mitochondrial cytB gene	1.8
1401	AC091267	Caenorhabditis elegans cosmid Y37B11A, complete sequence	3.7
1402	AB055364	Macaca fascicularis brain cDNA, clone:QflA-12522	e-119
1403	NC_001610	Didelphis virginiana mitochondrion, complete genome	0.006
1404	AF362372	Dictyostelium discoideum histidine kinase DhkJ (dhkJ) gene, complete cds	0.055
1405	AF027164	Homo sapiens type II integral membrane protein (NKG2-E) gene, partial cds; and type II integral membrane protein (NKG2-F) gene, complete cds	3.6
1406	M76376	Human cysteine-rich protein (CRP) gene, exon 2	0.027
1407	D31863	Mouse Pig-a gene for GPI-anchor biosynthesis (PIG-A protein), exon 6 and complete cds	0.026
1408	XM_031315	Homo sapiens hypothetical protein FLJ14033 similar to hypoxia inducible factor 3, alpha subunit (FLJ14033), mRNA	0.000007
1409	AY019369	Oryza sativa microsatellite MRG1694 containing (AT)X32, genomic sequence	0.0001
1410	AF067610	Caenorhabditis elegans cosmid F41A4	0.084
1411	AJ401391	Drosophila melanogaster mRNA for PDGF/VEGF-like protein (CG7103 gene)	0.18
1412	XM_008417	Homo sapiens hypothetical protein FLJ20694 (FLJ20694), mRNA	0.0000001
1413	AF242195	Homo sapiens KLK15 (KLK15) gene, complete cds, alternatively spliced	e-160
1414	Y14077	Bacillus subitlis 10.6 Kb chromosomal DNA: glyB-prsA region	0.008
1415	AE006802	Sulfolobus solfataricus section 161 of 272 of the complete genome	0.057
1416	AY007149	Homo sapiens clone CDABP0086 mRNA sequence	0.092
1417	K02628	Oxytricha nova (hypotrichous ciliate) (clones LMiC2-(5,6,8)) micronuclear DNA, C2 gene (version 3), complete cds	0.063
1419	X14260	Xenopus tropicalis alpha-globin gene	1.7
1420	AJ401391	Drosophila melanogaster mRNA for PDGF/VEGF-like protein (CG7103 gene)	0.15
1421	XM_032580	Homo sapiens nebulette (NEBL), mRNA	1.3
1422	XM_008060	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 5 (SLC7A5), mRNA	2E-12
1424	AF035820	Hordeum vulgare gibberellin action negative regulator SPY mRNA, complete cds	2.1

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
1425	AL353672	Human DNA sequence from clone RP1-241K1 on chromosome 6, complete sequence [Homo sapiens]	3.8
1426	AF070565	Homo sapiens clone 24425 mRNA sequence	0.2
1427	AK026914	Homo sapiens cDNA: FLJ23261 fis, clone COL05862	0.009
1428	X14735	Podospora anserina mtDNA for large subunit rRNA	0.21
1429	XM_004081	Homo sapiens aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase) (ALDH5A1), mRNA	1.4
1430	Y10687	Sulfolobus acidocaldarius gene encoding purine NTPase	0.019
1431	AF168678	Drosophila melanogaster adenylyl cyclase 78C-s mRNA, complete cds	0.13
1432	AC006666	Caenorhabditis elegans cosmid H31G24, complete sequence	0.014
1433	X02473	Calf mRNA for delta subunit of muscle acetylcholine receptor	1.1
1434	AF270148	Staphylococcus epidermidis strain SR1 clone step.1051c08 genomic sequence	0.006
1435	XM_008084	Homo sapiens hypothetical protein LOC55565 (LOC55565), mRNA	3E-36
1436	AF007876	Homo sapiens Na,K-ATPase beta 2 subunit gene, complete cds	0.008
1437	AK016592	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4933400F21, full insert sequence	0.61
1438	AB023053	Homo sapiens genomic DNA, chromosome 6p21.3, HLA class I region, clone:53L9, complete sequence	2E-10
1439	XM_035837	Homo sapiens cAMP responsive element modulator (CREM), mRNA	1.7
1440	Y12710	A.thaliana gene encoding shaggy-like kinase gamma	0.068
1441	AF351620	Homo sapiens lipocalin-1 interacting membrane receptor (LIMR) gene, complete cds	0.028
1442	U67560	Methanococcus jannaschii section 102 of 150 of the complete genome	2.1
1443	NM_002251	Homo sapiens potassium voltage-gated channel, delayed-rectifier, subfamily S, member 1 (KCNS1), mRNA	1.9
1444	XM_027341	Homo sapiens similar to retinoblastoma inhibiting gene 1 (M. musculus) (LOC89932), mRNA	0.0008
1446	AF039373	Arabidopsis thaliana ecotype RLD chromomethylase (CMT1) gene, complete cds	1.9
1447	U29397	Rattus norvegicus plasma membrane Ca2+ ATPase isoform 3 (PMCA3) gene, 5' flanking region	0.008
1448	XM_036536	Homo sapiens hypothetical protein FLJ10402 (FLJ10402), mRNA	4.1
1449	AK000677	Homo sapiens cDNA FLJ20670 fis, clone KAIA4743	1E-09
1450	AJ243538	Glomus mosseae fox2 gene for Fox2 protein	0.018
1451	AJ296103	Staphylococcus aureus repNVH99 gene for replication protein and smr gene	0.23
1452	AF084911	Bombus ternarius cytochrome b gene, partial cds; mitochondrial gene for mitochondrial product	1.4
1453	AC001080	Homo sapiens (subclone 3_g7 from PAC H74) DNA sequence, complete sequence	0.72

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
1454	AF213160	Gallus gallus microsatellite C-MNT-7 sequence	0.019
1455	AB056366	Macaca fascicularis brain cDNA, clone:QflA-14203	0.024
1456	AF129515	Paramecium tetraurelia SEC7-related protein (SEC7) mRNA, complete cds	0.055
1457	XM_037469	Homo sapiens similar to spastic ataxia of Charlevoix-Saguenay (sacsin) (H. sapiens) (LOC91290), mRNA	1.8
1458	AK005404	Mus musculus adult female placenta cDNA, RIKEN full-length enriched library, clone:1600009D24, full insert sequence	4.8
1459	AE001397	Plasmodium falciparum chromosome 2, section 34 of 73 of the complete sequence	4.2
1460	AF161253	Dictyostelium discoideum protein phosphatase 4 catalytic subunit (pppC) mRNA, complete cds	0.77
1461	X74912	M.hominis lysS gene	0.19
1462	AF027148	Homo sapiens myogenic determining factor 3 (MYOD1) gene, complete cds	0.45
1463	BC003261	Mus musculus, serine/threonine kinase 5, clone MGC:5803 IMAGE:3501444, mRNA, complete cds	0.21
1464	AC079143	Homo sapiens Xp BAC RP11-346D13 (Roswell Park Cancer Institute Human BAC Library) complete sequence	2
1465	Y07829	Homo sapiens RFB30 gene for RING finger protein	4.5
1466	BC006448	Homo sapiens, clone IMAGE:3637085, mRNA	1.9
1467	X05287	Locusta migratoria mitochondrial gene for 16S rRNA	0.19
1468	XM_052063	Homo sapiens hypothetical protein DKFZp547A023 (DKFZp547A023), mRNA	0
1469	AF113952	Campylobacter jejuni multidrug-efflux transporter gene, complete cds; and unknown genes	0.066
1470	AE006680	Sulfolobus solfataricus section 39 of 272 of the complete genome	5.2
1471	AY045578	Arabidopsis thaliana AT4g37000/C7A10_360 mRNA, complete cds	2.2
1472	AF269209	Takifugu rubripes clone FTCRAV4S1 T cell receptor V alpha chain gene, partial cds	1.9
1473	XM_027952	Homo sapiens dihydrofolate reductase (DHFR), mRNA	1.3
1474	U80449	Caenorhabditis elegans cosmid R10A10	1.8
1475	X15634	C. elegans core histone genes H4(his-10) and H3(his-9)	0.025
1476	Z16938	H. sapiens (D19S218) DNA segment containing (CA) repeat; clone AFM207wc3; single read	0.02
1477	X96783	H.sapiens Syt V gene (genomic and cDNA sequence)	0.0007
1478	Y08924	P.falciparum mRNA for AARP2 protein	0.003
1479	XM_036181	Homo sapiens RAN binding protein 2-like 1 (RANBP2L1), mRNA	0.21
1480	AL390874	Human DNA sequence from clone RP11-238K16 on chromosome 9, complete sequence [Homo sapiens]	0.002
1481	AL133157	S.pombe chromosome I cosmid c1B2	0.38
1482	U67598	Methanococcus jannaschii section 140 of 150 of the complete genome	0.37

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
1483	AJ242525	Chlamydomonas reinhardtii partial dhc10 gene for 1 beta dynein heavy chain, exons 16-53	5.8
1484	L19842	Daltonia sp. mitochondrial NADH dehydrogenase, and cytochrome b genes, 3' end, and transfer RNA-Ser gene	0.001
1485	AJ239534	Canis familiaris tRNA-derived SINE element, clone D254UC12	0.009
1486	AF044206	Homo sapiens cyclooxygenase (COX-2) gene, promoter and exon 1	0.2
1487	AB035880	Chaitoregma tattakana mitochondrial genes for small subunit rRNA, tRNA-Val, large subunit rRNA, partial and complete sequences	0.23
1488	AE006205	Pasteurella multocida PM70 section 172 of 204 of the complete genome	0.26
1489	XM_011446	Homo sapiens hypothetical protein FLJ10775 (FLJ10775), mRNA	6E-16
1490	NM_030714	Mus musculus deltex 3 homolog (Drosophila) (Dtx3), mRNA	0.39
1491	AE001407	Plasmodium falciparum chromosome 2, section 44 of 73 of the complete sequence	0.001
1492	BC005530	Mus musculus, clone IMAGE:3495762, mRNA	6.4
1493	XM_017183	Homo sapiens hypothetical protein FLJ22474 (FLJ22474), mRNA	0.0007
1494	AF198964	Arabidopsis thaliana ATP sulfurylase gene, complete cds	0.057
1495	AK026781	Homo sapiens cDNA: FLJ23128 fis, clone LNG08384	0.0002
1496	AF307860	Homo sapiens CYR61 protein (CYR61) gene, complete cds	3.9
1497	AL591667	Human DNA sequence from clone RP11-389N9 on chromosome 6, complete sequence [Homo sapiens]	0.004
1498	XM_002800	Homo sapiens kinesin-like protein 2 (hklp2), mRNA	2E-53
1499	M90970	Atriplex nummularia DNA sequence	4.8
1500	D34630	Arabidopsis thaliana mRNA for acetyl-CoA carboxylase, complete cds	0.22
1501	AC004498	Homo sapiens chromosome 5, P1 clone 1209C1 (LBNL H104), complete sequence	3E-13
1502	AF104350	Dictyostelium discoideum prespore-specific protein (pspC) gene, partial cds; and unknown gene	0.017
1503	XM_028059	Homo sapiens KIAA1681 protein (KIAA1681), mRNA	0.35
1504	U83462	Mus musculus serotonin N-acetyltransferase (AANAT) gene, complete cds	0.017
1505	AD001534	Borrelia afzelli (isolate UMO1), sequence fragment	0.7
1506	AF092379	Rivulus haraldsiolii tRNA-Ile, tRNA-Gln, and tRNA-Met genes, complete sequence; NADH dehydrogenase subunit II gene, complete cds; tRNA-Trp, tRNA-Ala, tRNA-Asn, tRNA-Cys, and tRNA-Tyr genes, complete sequence; and cytochrome c oxidase subunit I gene, pa>	0.002
1507	AF397158	Homo sapiens clone 11 pur alpha-associated ribosomal RNA gene, partial sequence	1E-39
1509	AF370352	Arabidopsis thaliana putative ribosomal protein (AT4g16720) mRNA, complete cds	1.2

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
1510	AF286240	HIV-1 isolate 97CDKFE4 from Republic of the Congo gag protein (gag) and pol protein (pol) genes, partial cds	1.2
1511	L29256	Human dinucleotide repeat polymorphism at the DXS1690 locus	5E-50
1512	AF214115	Peromyscus maniculatus H19 mRNA, complete cds	2.1
1513	XM_003799	Homo sapiens protocadherin beta 10 (PCDHB10), mRNA	0.57
1514	AF387030	Homo sapiens DNA polymerase epsilon subunit B (POLE2) gene, exons 14 and 15	0.72
1515	M27054	Homo sapiens asparagine synthetase (TS11) gene, exons 1-3 and promoter region	0.2
1516	XM_051852	Homo sapiens mesoderm development candidate 2 (MESDC2), mRNA	5.9
1517	XM_052004	Homo sapiens heterogeneous nuclear protein similar to rat helix destabilizing protein (FBRNP), mRNA	0.00009
1518	XM_046730	Homo sapiens hypothetical gene supported by L27560 (LOC92701), mRNA	0.53
1519	AF136179	Mus musculus spermine synthase gene, partial cds	0.063
1520	U19360	Onchocerca volvulus nuclear hormone receptor-like peptide, complete cds	1.6
1521	AY039907	Arabidopsis thaliana AT5g41810/K16L22_9 mRNA, complete cds	5.9
1522	D86573	Plasmodium falciparum DNA for flavoprotein subunit of succinate dehydrogenase, complete cds	0.009
1523	NC_002548	Acute bee paralysis virus, complete genome	0.07
1524	U33959	Macaca fascicularis fertilin beta mRNA, complete cds	0.3
1525	AF270048	Staphylococcus epidermidis strain SR1 clone step.1043h07 genomic sequence	0.76
1526	AB047239	Staphylococcus aureus DNA, complete structure of cassette chromosome(SCC)-like element, strain:ATCC25923	0.72
1527	U39684	Mycoplasma genitalium section 6 of 51 of the complete genome	0.21
1528	XM_030430	Homo sapiens hypothetical protein (FLJ11127), mRNA	2
1529	D38148	Rotavirus strain A5-13 NSP1 gene, complete cds	0.68
1530	AK020846	Mus musculus adult retina cDNA, RIKEN full-length enriched library, clone:A930011E06, full insert sequence	0.2
1531	AF130049	Homo sapiens clone FLB3411 PRO0852 mRNA, complete cds	0.067
1532	AF332140	Mus musculus c-Fos (Fos) gene, 5' flanking and promoter regions	1.8
1533	AF231842	Jasminum odoratissimum tRNA-Leu (trnL) gene, partial intron and 3' exon, and trnL-trnF spacer region; chloroplast gene for chloroplast product	1.3
1534	NC_001560	Vesicular stomatitis virus, complete genome	0.35
1535	AF213897	Homo sapiens cAMP responsive element modulator (CREM) gene, exon C	0.24
1536	XM_049251	Homo sapiens KIAA0903 protein (KIAA0903), mRNA	0.22
1537	AK027713	Homo sapiens cDNA FLJ14807 fis, clone NT2RP4001760, weakly similar to PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR	1E-36

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
1538	AF268091	Chloris gayana phosphoenolpyruvate carboxylase (ppc) mRNA, complete cds	6.1
1539	AC023351	Homo sapiens clone RP11-637J20, complete sequence	1E-49
1540	NC_002161	Bovine parainfluenza virus 3, complete genome	6.4
1541	AE001092	Archaeoglobus fulgidus section 15 of 172 of the complete genome	0.15
1542	AF044202	Drosophila melanogaster glutamate receptor DGluRIIB mRNA, complete cds	0.008
1543	Z72767	S.cerevisiae chromosome VII reading frame ORF YGL245w	1.8
1544	AJ277899	Nicotiana tabacum drepp4 gene, exons 1-4	0.24
1545	XM_005131	Homo sapiens chromatin accessibility complex 1 (CHRAC1), mRNA	0.71
1546	AF270048	Staphylococcus epidermidis strain SR1 clone step.1043h07 genomic sequence	0.67
1547	AL112743	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation	0.076
1548	S68847	YAP2=AP-1-like stress-induced transcriptional activator [Saccharomyces cerevisiae, W303, Genomic, 2181 nt]	0.21
1549	AF176634	Reldia sp. Amaya and Smith 578 NADH dehydrogenase subunit F (ndhF) gene, partial cds; chloroplast gene for chloroplast product	0.54
1551	X79988	H.sapiens HIP gene, exon 1	0.21
1552	AK015054	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930402M22, full insert sequence	2.2
1553	U07731	Human quinone oxidoreductase2 (NQO2) gene, introns 1 and 2 and exon 2	0.42
1554	AE001370	Plasmodium falciparum chromosome 2, section 7 of 73 of the complete sequence	0.02
1555	AF222996	Danio rerio nocA-like Zn-finger protein (nlz) mRNA, complete cds	0.59
1556	AJ000080	Trypanosoma brucei hsp100 and gpi-plc genes	0.00004
1557	D30745	Xenopus laevis MRP RNA gene	5
1558	X17256	Yeast THR4 gene for threonine synthase (EC 4.2.99.2)	0.64
		HIV-1 clone LTNP1-85V3 from USA envelope glycoprotein V3	

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
1568	Z29373	H.sapiens gene for neural cell adhesion molecule L1	0.85
1569	AF138876	Bacillus thuringiensis isolate M15 insertion sequence IS231N	0.48
1570	AF043087	Hordeum vulgare dehydrin 1 (dhn1) gene, complete cds	2.1
1571	AE002293	Chlamydia muridarum, section 25 of 85 of the complete genome	0.57
1572	AB017043	Rattus norvegicus gene for hepatocyte nuclear factor 3 gamma, partial cds	3.7
1573	XM_038951	Homo sapiens hypothetical protein MGC15875 (MGC15875), mRNA	0.43
1574	AF244979	Mus musculus galectin-11 mRNA, variant b, complete cds, alternatively spliced	0.24
1575	XM_006069	Homo sapiens wee1+ (S. pombe) homolog (WEE1), mRNA	6E-10
1576	AK025037	Homo sapiens cDNA: FLJ21384 fis, clone COL03354	1.7
1577	Z71443	S.cerevisiae chromosome XIV reading frame ORF YNL167c	0.014
1578	AF263518	Arabidopsis thaliana protein synthesis initiation factor 4G (EIF4G) gene, complete cds	0.59
1579	AE000680	Aquifex aeolicus section 12 of 109 of the complete genome	1.2
1580	AE001404	Plasmodium falciparum chromosome 2, section 41 of 73 of the complete sequence	1.5
1581	AJ390510	Candida albicans partial mRNA for serine/threonine kinase (sha3 gene)	0.18
1582	AC004173	Homo sapiens clone UWGC:y23x011 from 6p21, complete sequence	0.002
1583	Z71687	S.cerevisiae chromosome XIV reading frame ORF YNR072w	2.1
1585	X95065	H.sapiens dinucleotide repeat (GT) from chromosome 13q (229bp)	0.18
1586	Z24310	H. sapiens (D10S593) DNA segment containing (CA) repeat; clone AFM311yb1; single read	0.002
1587	Y18476	Trichophyton rubrum mitochondrial cytb gene and NADH1 to NADH5 genes	6.9
1588	Z47046	Human cosmid QLL2C9 from Xq28	0.00007
1589	Z71687	S.cerevisiae chromosome XIV reading frame ORF YNR072w	1.6
1590	XM_005485	Homo sapiens KIAA0414 protein (KIAA0414), mRNA	0.002
1591	NM_024364	Rattus norvegicus hairless (hr), mRNA	0.22
1593	AF136150	Caenorhabditis elegans homogentisate 1,2-dioxygenase (hgo) gene, complete cds	1.6
1594	XM_033896	Homo sapiens insulin-like growth factor 2 receptor (IGF2R), mRNA	1.4
1595	AJ404228	Saccharomyces douglasii mitochondrial tRNA gene cluster	0.008
1596	BC007460	Homo sapiens, acid phosphatase, prostate, clone MGC:12236 IMAGE:3951204, mRNA, complete cds	0.029
1597	NM_024201	Mus musculus RIKEN cDNA 0610011N22 gene (0610011N22Rik), mRNA	5.3
1598	U88166	Caenorhabditis elegans cosmid M01A12	0.61
1599	AE001394	Plasmodium falciparum chromosome 2, section 31 of 73 of the complete sequence	2

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
1600	AJ306417	Corynebacterium glutamicum partial nrdF gene for ribonucleotide reductase beta-subunit and ctaD gene for cytochrome aa3 oxidase subunit I	1.9
1601	AF287270	Homo sapiens mucolipin (MCOLN1) gene, complete cds	6
1602	AE002207	Chlamydophila pneumoniae AR39, section 37 of 94 of the complete genome	0.083
1603	AK003449	Mus musculus 18 days embryo cDNA, RIKEN full-length enriched library, clone:1110004P21, full insert sequence	0.2
1604	AB008103	Arabidopsis thaliana AtERF-1 mRNA for ethylene responsive element binding factor 1, complete cds	0.79
1605	AE006406	Lactococcus lactis subsp. lactis IL1403 section 168 of 218 of the complete genome	0.18
1606	BC008122	Homo sapiens, clone MGC:18053 IMAGE:4148889, mRNA, complete cds	1.5
1607	D28598	Chicken mRNA for c-maf proto-oncogene product c-Maf long form, complete cds	0.44
1608	X97314	M.sativa mRNA for cdc2 kinase homologue, cdc2MsC	1.5
1609	AP001407	Homo sapiens genomic DNA, chromosome 21q22.2, clone:10C6, LB7T-ERG region, complete sequence	1.1
1611	XM_017891	Homo sapiens similar to heterogeneous nuclear ribonucleoprotein L (H. sapiens) (LOC91538), mRNA	1.4
1612	U48562	Corrigiola littoralis ORF2280 gene homolog, chloroplast gene encoding chloroplast protein, partial cds	0.074
1613	XM_036274	Homo sapiens similar to tumor protein p53-binding protein (H. sapiens) (LOC65591), mRNA	2
1614	AJ271039	Plasmodium yoelii yoelii partial mrk gene for MO15-related kinase	0.001
1615	AB016467	Datisca cannabina chloroplast gene for maturase K, partial cds	0.25
1616	AF027807	Homo sapiens beta-casein (CSN2) gene, complete cds	0.074
1617	AK002822	Mus musculus adult male kidney cDNA, RIKEN full-length enriched library, clone:0610039A20, full insert sequence	0.55
1618	U67580	Methanococcus jannaschii section 122 of 150 of the complete genome	0.032
1619	U89140	Mus musculus aldose reductase gene, promoter region and exon 1	0.48
1620	AE002799	Drosophila melanogaster genomic scaffold 142000013385566, complete sequence	0.17
1621	L14855	Bos taurus neurexin I-alpha mRNA, complete cds	0.48
1622	AF379854	Cloning vector pVLH/hsp, complete sequence	2
1623	Z11883	S.tuberosum U1snRNA variant genes U1-1, U1-2, U1-3, U1-4, U1-5 and U1-6	0.54
1624	AJ294727	Mus musculus ILTIFa gene for IL-TIF alpha protein (IL-22), exons 1a-5	0.011
1625	XM_043073	Homo sapiens hypothetical protein DKFZp434A1319 (DKFZP434A1319), mRNA	1.9

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
1626	M84732	Plasmodium yoelii sporozoite surface protein 2 gene , complete cds	0.007
1627	M83304	G.hirsutum late embryogenesis-abundant protein 2-D (LeaA2-D) mRNA, complete cds	9.8
1628	U32725	Haemophilus influenzae Rd section 40 of 163 of the complete genome	0.14
1629	AF185589	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region	0.027
1630	AL591667	Human DNA sequence from clone RP11-389N9 on chromosome 6, complete sequence [Homo sapiens]	0.15
1631	AB058397	Oryza sativa CHS gene for chalcone synthase, complete cds	0.16
1632	M11043	Mouse DNA fragment that hybridizes to HSV-1 SmaI A fragment	1.5
1633	AF145699	Staphylococcus aureus putative membrane protein MprF (mprF) gene, complete cds; and unknown gene	1.5
1634	AF088902	Mus musculus SLIT1 protein (Slit1) mRNA, partial cds	0.5
1635	AB048882	Macaca fascicularis brain cDNA, clone:QnpA-16525	0.21
1636	X98369	M.musculus mRNA for SOX15 protein	0.24
1637	AF131767	Homo sapiens clone 24900 mRNA sequence	0.25
1638	AL117657	Homo sapiens mRNA; cDNA DKFZp586F1924 (from clone DKFZp586F1924)	1.9
1639	AB042973	Nicotiana tabacum wizz gene, 5' flanking region, partial cds	0.072
1640	AJ272083	Staphylococcus aureus empbp gene for extracellular matrix and plasma binding protein, strain SA 113	0.008
1641	BC009423	Homo sapiens, clone MGC:15151 IMAGE:3538202, mRNA, complete cds	1.9
1642	AF114905	Saccharomyces sp. CID1 ATP synthase subunit 8 (ATP8) gene, mitochondrial gene encoding mitochondrial protein, complete cds	0.18
1643	AF270417	Staphylococcus epidermidis strain SR1 clone step.4052d03a genomic sequence	0.063
1644	X91340	G.hybrida chs-like gene	0.51
1645	AF097026	Homo sapiens autosomal highly conserved protein (AHCP) gene, complete cds	0.008
1646	XM_028810	Homo sapiens 67292 (KIAA1755), mRNA	5.5
1647	AL049339	Homo sapiens mRNA; cDNA DKFZp564P046 (from clone DKFZp564P046)	2.1
1648	AE001398	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence	0.13
1649	M55171	Mouse opsin (MOPS) gene, complete cds	0.52
1650	AB008103	Arabidopsis thaliana AtERF-1 mRNA for ethylene responsive element binding factor 1, complete cds	0.66
1651	AL589705	Human DNA sequence from clone RP11-64M7 on chromosome 6, complete sequence [Homo sapiens]	0.5
1652	X79559	T.trypanoides (R1) 18S rRNA gene	0.069
1653	XM_048416	Homo sapiens PRO0478 protein (PRO0478), mRNA	0.0001

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
1654	AF082761	Dasyurus maculatus isolate QM.E1 mitochondrial D-loop, partial sequence	0.063
1655	AF282568	Homo sapiens clone 20ptel_c15bt7 sequence	4E-39
1656	AB027617	Pyrus pyrifolia gene for UDP-glucose pyrophosphorylase, complete cds	0.19
1657	AK023864	Homo sapiens cDNA FLJ13802 fis, clone THYRO1000186	0.2
1658	NM_009905	Mus musculus CDC-like kinase (Clk), mRNA	1.7
1659	AL023846	Caenorhabditis elegans cosmid Y52B11C, complete sequence	2.3
1660	AF334780	Homo sapiens pregnancy-induced growth inhibitor OKL38 gene, partial cds	0.73
1661	XM_042066	Homo sapiens mitogen-activated protein kinase kinase kinase 1 (MAP3K1), mRNA	1.9
1662	XM_034872	Homo sapiens KIAA0202 protein (KIAA0202), mRNA	0.23
1663	AC002252	Homo sapiens (subclone 1_g7 from BAC H76) DNA sequence, complete sequence	3E-14
1664	AK023113	Homo sapiens cDNA FLJ13051 fis, clone NT2RP3001447	2E-20
1665	BC003552	Homo sapiens, calnexin, clone MGC:1196 IMAGE:3546389, mRNA, complete cds	0.076
1666	AF097142	Tapinaspis sp. 12S small subunit ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	1.5
1667	AL117103	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation	6.1
1668	NM_013825	Mus musculus lymphocyte antigen 75 (Ly75), mRNA	0.74
1669	NM_007043	Homo sapiens HIV-1 rev binding protein 2 (HRB2), mRNA	7E-22
1670	Z27359	G.hirsutum (AD52) copia-like reverse transcriptase fragments	0.24
1671	AK021535	Homo sapiens cDNA FLJ11473 fis, clone HEMBA1001712	0.25
1672	Y00145	Dictyostelium discoideum UDP glucose pyrophosphorylase gene (UDPGP; EC 2.7.7.9)	0.22
1673	M63291	Drosophila silvestris alcohol dehydrogenase gene, complete cds	0.028
1674	AF100401	Influenza B virus B/Guangdong/5/94 segment 8 nonstructural protein (NS1) and nonstructural protein (NS2) genes, complete cds	0.2
1675	U80449	Caenorhabditis elegans cosmid R10A10	1.6
1676	X15634	C. elegans core histone genes H4(his-10) and H3(his-9)	0.022
1677	XM_050366	Homo sapiens zinc finger protein, X-linked (ZFX), mRNA	0.23
1678	AE007046	Mycobacterium tuberculosis CDC1551, section 132 of 280 of the complete genome	0.062
1679	XM_008207	Homo sapiens glucose-6-phosphatase, catalytic (glycogen storage disease type I, von Gierke disease) (G6PC), mRNA	4E-18
1680	AB049118	Hemicentrotus pulcherrimus mRNA for transcription factor HpLim1, complete cds	0.21
1681	XM_002421	Homo sapiens hypothetical protein FLJ20254 (FLJ20254), mRNA	4.1
1682	X96783	H.sapiens Syt V gene (genomic and cDNA sequence)	0.000004

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
1683	U79732	Plasmodium berghei extrachromosomal plastid PB-2, tRNA-Pro, tRNA-Glu, tRNA-Lys, tRNA-Asp, tRNA-Ser, tRNA-Tyr, tRNA-Met, tRNA-Leu, tRNA-Cys, and tRNA-His genes, complete sequence, rps4 gene, complete cds, tRNA-Thr gene, complete sequence, and large subu>	0.001
1684	NC_002619	Pteropus scapulatus mitochondrion, complete genome	6.3
1685	L16679	Caenorhabditis elegans cosmid K07D8, complete sequence	1.8
1686	Y08924	P.falciparum mRNA for AARP2 protein	0.003
1687	U32760	Haemophilus influenzae Rd section 75 of 163 of the complete genome	2.2
1688	AF298624	Dictyostelium discoideum chromosome 2 repeat region	0.009
1689	XM_031155	Homo sapiens RAS protein activator like 2 (RASAL2), mRNA	0.33
1690	AE006899	Sulfolobus solfataricus section 258 of 272 of the complete genome	5
1691	U67556	Methanococcus jannaschii section 98 of 150 of the complete genome	0.42
1692	AK012631	Mus musculus 10, 11 days embryo cDNA, RIKEN full-length enriched library, clone:2810001G20, full insert sequence	0.064
1693	BC007399	Homo sapiens, clone MGC:16308 IMAGE:3836116, mRNA, complete cds	0.022
1694	AL389897	Human DNA sequence from clone RP11-110C10 on chromosome 20. Contains GSSs, complete sequence [Homo sapiens]	1E-26
1695	Z62421	H.sapiens CpG island DNA genomic Mse1 fragment, clone 68h2, forward read cpg68h2.ft1a	4E-70
1696	BC010535	Homo sapiens, clone IMAGE:3456494, mRNA	0.002
1697	Z68319	Caenorhabditis elegans cosmid T23G7, complete sequence	0.18
1698	U48363	Mus musculus transcriptional activator alpha-NAC (Naca) gene, complete cds	0.058
1699	AF135430	Ustilago nuda 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	1.4
1701	XM_007461	Homo sapiens similar to enhancer of rudimentary (Drosophila) homolog (H. sapiens) (LOC65719), mRNA	0.18
1702	NM_025083	Homo sapiens hypothetical protein FLJ21128 (FLJ21128), mRNA	e-124
1703	XM_050592	Homo sapiens uncharacterized hematopoietic stem/progenitor cells protein MDS032 (MDS032), mRNA	0.068
1704	AF277167	Homo sapiens Makorin RING zinc-finger protein 2 (MKRN2) gene, exon 4	2
1705	AE001433	Plasmodium falciparum chromosome 2, section 70 of 73 of the complete sequence	0.67
1706	AF075003	Homo sapiens full length insert cDNA YH97B03	0.001
1707	NM_011378	Mus musculus transcriptional regulator, SIN3A (yeast) (Sin3a), mRNA	0.62

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
1708	AE001321	Chlamydia trachomatis section 48 of 87 of the complete genome	0.026
1709	XM_046388	Homo sapiens similar to elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1 (H. sapiens) (LOC92652), mRNA	6.1
1710	S55685	MOR6.5=ouabain resistance gene {repeat sequence} [mice, Genomic, 6395 nt]	5.7
1711	AB055378	Macaca fascicularis brain cDNA, clone:QflA-13294	0.22
1712	XM_043597	Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA	1E-20
1713	AE007426	Streptococcus pneumoniae section 109 of 194 of the complete genome	0.32
1714	AK016519	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4932411G06, full insert sequence	e-129
1715	AL122033	S.pombe chromosome II cosmid c1921	0.53
1716	AK012960	Mus musculus 10, 11 days embryo cDNA, RIKEN full-length enriched library, clone:2810401G03, full insert sequence	0.075
1717	AL590123	Human DNA sequence from clone RP11-473J14 on chromosome X, complete sequence [Homo sapiens]	0.19
1718	D17343	Rattus norvegicus cytochrome P450 2B15 gene, exon 1	0.66
1719	XM_028703	Homo sapiens KIAA0889 protein (KIAA0889), mRNA	0.00004
1720	AB060865	Macaca fascicularis brain cDNA clone:QtrA-11953, full insert sequence	2.3
1721	AL133397	Human DNA sequence from clone RP1-213J1p on chromosome 22q11.21-12.2, complete sequence [Homo sapiens]	0.083
1722	X58913	Mitochondrion Drosophila eugracilis ND2 and COI genes (partial) and genes for tRNA-Trp, tRNA-Tyr, and tRNA-Cys	0.074
1723	AC002359	Homo sapiens Xp22 Cosmid U239B3 (from Lawrence Livermore X library) complete sequence	0.0008
1724	AE006322	Lactococcus lactis subsp. lactis IL1403 section 84 of 218 of the complete genome	1.8
1725	Z71290	S.cerevisiae chromosome XIV reading frame ORF YNL014w	0.67
1726	XM_005723	Homo sapiens hypothetical protein PRO2859 (PRO2859), mRNA	0.014
1727	AF123488	South River virus polyprotein mRNA, complete cds	0.57
1728	D78176	Mouse DNA for primary transcript of atrial natriuretic clearance receptor	0.061
1730	XM_006871	Homo sapiens ethanolamine kinase (EKI1), mRNA	4.1
1731	AL078640	Human DNA sequence from clone 536P6 on chromosome 22. Contains an EST, complete sequence [Homo sapiens]	0.07
1732	AC092030	Homo sapiens clone RP11-636I12, complete sequence	0.029
1733	AK003349	Mus musculus 18 days embryo cDNA, RIKEN full-length enriched library, clone:1110003F05, full insert sequence	0.16
1734	AF131767	Homo sapiens clone 24900 mRNA sequence	0.2
1735	Z74246	S.cerevisiae chromosome IV reading frame ORF YDL198c	0.023
1736	NM_021401	Mus musculus secreted and transmembrane 1 (Sectm1), mRNA	0.069
1737	AF213931	Buchnera aphidicola DNA polymerase III beta subunit (dnaN) gene, complete cds	0.68

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
1738	AF288892	Homo sapiens clone 20r DH4-17/BCL-1 gene fusion reciprocal breakpoint sequence	2
1739	X99719	S.enterica hsdM, hsdS & hsdR genes	0.23
1740	XM_041866	Homo sapiens KIAA1468 protein (KIAA1468), mRNA	5.9
1741	AY010113	Homo sapiens unknown mRNA sequence	0.64
1742	AK009187	Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310006I24, full insert sequence	4E-23
1743	AF130074	Homo sapiens clone FLB9348 PRO2523 mRNA, complete cds	0.14
1744	AJ249165	Plasmodium falciparum gc-beta gene, exons 1-13	0.002
1745	AK014565	Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched library, clone:4632411B12, full insert sequence	0.54
1746	M15058	Vaccinia virus (strain WR) HindIII D fragment DNA, complete	0.15
1747	Z16416	M.pulmonis DNA for insertion sequence IS1138 encoding putative transposase	0.026
1748	XM_047638	Homo sapiens Fzr1 protein (FZR1), mRNA	1.2
1750	U21853	Anabaena sp. phycobilisome core component (apcF) gene, complete cds, and glutamine synthetase (glnA) gene, partial cds	0.076
1751	AF169454	Neisseria meningitidis strain Z2491 clone Cm045 unknown sequence	0.19
1752	AF102750	Apanteles canarsiae 16S large subunit ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	0.066
1753	AF034389	Plasmodium falciparum sexual stage antigen (s16) gene, promoter and partial cds	0.18
1754	AB047239	Staphylococcus aureus DNA, complete structure of cassette chromosome(SCC)-like element, strain:ATCC25923	1.5
1755	X98669	A.thaliana zat1 gene	0.023
1756	X16619	Chlamydomonas reinhardtii ARG7 gene for argininosuccinate lyase	1.5
1757	XM_005488	Homo sapiens KIAA0354 gene product (KIAA0354), mRNA	0.063
1758	AF110966	HIV-1 isolate C-96BW04.10 country Botswana, complete genome	1.1
1759	AF247193	Mus musculus endobrevin (Vamp8) gene, exon 1	5.4
1760	XM_045302	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 5 (PSMD5), mRNA	0.0008
1761	AE006350	Lactococcus lactis subsp. lactis IL1403 section 112 of 218 of the complete genome	0.69
1762	AJ247001	Anguilla anguilla mitochondrial DNA for partial tRNA-Thr and tRNA-Pro genes and D-loop, isolate RM11	0.052
1763	AB024996	Cicer arietinum mRNA for rac-type small GTP-binding protein, complete cds	1.6
1764	M13945	Mus musculus pim-1 protein kinase gene, complete cds	5.7
1765	AF106842	Platanus racemosa PlaraLFY protein (PlaraLFY) gene, complete cds	0.22
1766	AF269822	Staphylococcus epidermidis strain SR1 clone step.1024f03 genomic sequence	7.5
1767	AF256830	Salmo salar clone BHMS549 microsatellite sequence	1.8

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
1768	AE007395	Streptococcus pneumoniae section 78 of 194 of the complete genome	1.6
1769	AB028896	Streptococcus agalactiae type-specific capsular polysaccharide biosynthesis gene region (cpsIaA to ung gene), complete cds	0.025
1770	AL583831	Human DNA sequence from clone RP11-469L10 on chromosome 6, complete sequence [Homo sapiens]	0.15
1771	AL354683	Human DNA sequence from clone RP11-259K11 on chromosome 20, complete sequence [Homo sapiens]	0.21
1772	XM_047524	Homo sapiens procollagen (type III) N-endopeptidase (PCOLN3), mRNA	4.6
1773	AC084500	Caenorhabditis briggsae cosmid G13G15, complete sequence	0.076
1774	M13945	Mus musculus pim-1 protein kinase gene, complete cds	6.1
1775	L27474	Human arginase (ARG1) gene dinucleotide repeat polymorphism, intron 5	0.21
1776	Z79696	Caenorhabditis elegans cosmid F54F3, complete sequence	1.9
1777	AY018282	Oryza sativa microsatellite MRG0607 containing (AT)X14, closest to marker C132, genomic sequence	0.071
1778	AF114938	Saccharomyces sp. IFO 1815 small subunit ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, complete sequence	0.078
1779	AF170085	Homo sapiens Charcot-Leyden crystal protein gene, partial sequence	6E-18
1780	Y08919	P.flesus mRNA for p53 protein	0.082
1781	L46868	Trypanosoma brucei dominant expression site (DES) gene, promoter region	2.2
1782	AF157008	Prunus dulcis self-incompatibility associated ribonuclease gene, complete cds	0.44
1783	AB017459	Carabus sylvestris mitochondrial ND5 gene, isolate: Baumgartner Austria, partial cds	0.029
1784	AJ294714	Pichia anomala leu2 gene for beta-isopropylmalate dehydrogenase	0.26
1785	AF125972	Caenorhabditis elegans cosmid H25P19	0.64
1786	AB015413	Helicobacter pylori cagA gene, complete cds, strain ATCC43526	1.5
1787	AK021477	Homo sapiens cDNA FLJ11415 fis, clone HEMBA1000942	7E-12
1788	AC006812	Caenorhabditis elegans cosmid Y64H9A, complete sequence	0.63
1789	XM_004181	Homo sapiens megakaryocyte-enhanced gene transcript 1 protein (MEGT1), mRNA	7E-66
1790	AJ236640	Homo sapiens chromosome 22 CpG island DNA, genomic Mse1 fragment, clone 22CGIB49A20 , complete read	9E-19
1791	XM_041751	Homo sapiens discoidin domain receptor family, member 1 (DDR1), mRNA	3.5
1792	AL034546	Human DNA sequence from clone RP5-898I4 on chromosome 22q13.33 Contains a GSS and a putative CpG island, complete sequence [Homo sapiens]	0.000005
1793	AJ006873	Buchnera aphidicola plasmid pBUs1, repA2 gene, leuA gene and ORF1	0.23

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
1794	X79779	S.tuberosum KST1 mRNA	0.67
1795	AF371373	Cricetulus griseus hypothetical protein A1-3 mRNA, complete cds	0.61
1796	AF165082	Pollachius virens cytochrome b gene, partial cds; mitochondrial gene for mitochondrial product	0.53
1797	AE007418	Streptococcus pneumoniae section 101 of 194 of the complete genome	0.027
1798	X67082	H.sapiens AMBP gene transcription regulatory region	0.006
1799	AL117655	Homo sapiens mRNA; cDNA DKFZp586E2024 (from clone DKFZp586E2024)	5.2
1800	AB048972	Macaca fascicularis brain cDNA, clone:QnpA-12040	0.53
1801	XM_030865	Homo sapiens M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein) (MPHOSPH10), mRNA	0.18
1802	AF123488	South River virus polyprotein mRNA, complete cds	0.49
1803	AB027590	Pachliopta aristolochiae mitochondrial mRNA for NADH dehydrogenase subunit 5, partial cds	0.024
1804	J00889	Chicken cellular myc proto-oncogene, complete cds	0.008
1805	XM_030024	Homo sapiens similar to protein kinase C binding protein 1 (H. sapiens) (LOC90218), mRNA	0.009
1806	AB023486	Homo sapiens gene for histamine H2 receptor, promoter region and complete cds	0.064
1807	D21196	Dictyostelium discoideum mitochondrial DNA	0.21
1808	AY035029	Arabidopsis thaliana putative dihydroorotate dehydrogenase (MEB5.3/AT3g17810) mRNA, complete cds	5.3
1809	AB047389	Clostridium difficile purL gene for formylglycinamidine ribonucleotide synthetase (FGAM synthetase), complete cds	0.019
1810	AK012033	Mus musculus 10 days embryo cDNA, RIKEN full-length enriched library, clone:2610315E15, full insert sequence	2.2
1811	AF044202	Drosophila melanogaster glutamate receptor DGluRIIB mRNA, complete cds	0.008
1812	AK026967	Homo sapiens cDNA: FLJ23314 fis, clone HEP11989	0.66
1813	AB050432	Macaca fascicularis brain cDNA, clone:QnpA-21861	0.4
1814	X16871	Human DNA for elongation factor 1-alpha (clone lambda-4)	4.7
1815	AE000001	Mycoplasma pneumoniae M129 section 16 of 63 of the complete genome	1.9
1816	AK002671	Mus musculus adult male kidney cDNA, RIKEN full-length enriched library, clone:0610025N14, full insert sequence	0.052
1817	AF202903	Sporopachydermia cereana var. D77-321B internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence	0.5
1819	L42167	Mus musculus (clone R24) rds gene, partial cds	0.16
1820	XM_027078	Homo sapiens ATPase, Class V, type 10D (ATP10D), mRNA	0.16
1821	L27619	Macaca nemestrina T-cell receptor beta chain V region (Vb15.1) gene, partial cds	0.016

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
1822	BC003900	Mus musculus, Similar to hypothetical protein 384D8_6, clone MGC:6766 IMAGE:3601298, mRNA, complete cds	0.51
1823	XM_050561	Homo sapiens KIAA0700 protein (KIAA0700), mRNA	0.51
1824	S66407	FLT4=receptor tyrosine kinase isoform FLT4 long {3' region, alternatively spliced} [human, mRNA Partial, 216 nt]	8E-36
1825	AY008805	Equus caballus retinoblastoma (RB1) gene, partial cds	0.058
1826	AJ276629	Rattus norvegicus Sacm21/RT1-A intergenic region, haplotype RT1n and partial RT1-A gene for MHC Class I antigen	3.7
1827	AF029975	Eucalyptus grandis MADS box protein (EGM1) mRNA, complete cds	1.2
1828	AL109708	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 254679	0.019
1829	AF270353	Staphylococcus epidermidis strain SR1 clone step.4025a02 genomic sequence	0.051
1831	U72236	Dictyostelium discoideum ModA (modA) gene, complete cds	0.5
1832	L15234	Mycoplasma pneumoniae Cys-tRNA, Pro-tRNA, Met-tRNA, Ile-tRNA, Ser-tRNA, fMet-tRNA, Asp-tRNA and Phe-tRNA genes	1.1
1833	XM_012722	Homo sapiens RNA (guanine-7-) methyltransferase (RNMT), mRNA	0.5
1834	AF108228	Ginkgo biloba GinLFY protein (GinLFY) gene, complete cds	4.2
1836	XM_049943	Homo sapiens topoisomerase (DNA) II alpha (170kD) (TOP2A), mRNA	0.47
1837	NC_002674	Aulopus japonicus mitochondrion, complete genome	3.1
1838	AE001399	Plasmodium falciparum chromosome 2, section 36 of 73 of the complete sequence	0.008
1839	U53695	Leishmania enriettii multidrug resistance (lemdr1) gene, 5' UTR	0.5
1840	AF257022	Salmo salar clone BHMS7-009 microsatellite sequence	0.7
1841	AF239571	Acineta superba tRNA-Leu (trnL) gene, partial sequence; and trnL-F intergenic spacer region, complete sequence; chloroplast gene for chloroplast product	5.4
1842	AL032651	Caenorhabditis elegans cosmid Y6D1A, complete sequence	0.019
1844	XM_034229	Homo sapiens similar to hypothetical protein FLJ14260 (H. sapiens) (LOC90803), mRNA	0.068
1845	AL137121	Human DNA sequence from clone RP11-122K21 on chromosome 13, complete sequence [Homo sapiens]	e-147
1846	AF137535	Danio rerio clone Dare-DAXX DAXX protein mRNA, partial cds	1.7
1847	AK023539	Homo sapiens cDNA FLJ13477 fis, clone PLACE1003638	0.21
1848	AF218799	Gallus gallus clone LDH-BT1 lactate dehydrogenase B mRNA, complete cds	6.4
1849	AF250345	Xenopus laevis early growth response protein mRNA, complete cds	0.52
1850	BC006858	Mus musculus, clone IMAGE:3594635, mRNA	1.5
1852	XM_006782	Homo sapiens cyclin T1 (CCNT1), mRNA	0.092
1853	J03883	Rabbit zeta-1 globin processed pseudogene, complete cds	1.5

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
1854	AF349951	Homo sapiens HP95 mRNA, complete cds	3E-09
1855	AF268062	Candidatus Carsonella ruddii natural-host Bactericera cockerelli RNA polymerase beta subunit (rpoB) and RNA polymerase beta-prime subunit (rpoC) genes, partial cds	0.17
1856	AF114508	Uncultured gamma proteobacterium SUR-ATT-8 16S ribosomal RNA gene, complete sequence	1.5
1857	AE006785	Sulfolobus solfataricus section 144 of 272 of the complete genome	0.091
1858	AF078684	Psoroptes ovis glutathione S-transferase mRNA, complete cds	0.0006
1859	BC004671	Mus musculus, FK506 binding protein 1a (12 kDa), clone MGC:6253 IMAGE:3498682, mRNA, complete cds	0.12
1860	NM_025083	Homo sapiens hypothetical protein FLJ21128 (FLJ21128), mRNA	e-121
1861	BC004161	Homo sapiens, transmembrane 4 superfamily member (tetraspan NET-7), clone MGC:2447 IMAGE:2958221, mRNA, complete cds	0.051
1862	BC009855	Homo sapiens, Similar to nucleolin, clone MGC:16354 IMAGE:3926227, mRNA, complete cds	e-171
1863	AK016507	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4931439C15, full insert sequence	0.019
1864	AF334756	Homo sapiens interleukin-1 HY2 (IL1HY2) gene, complete cds	1.5
1865	Z68881	Human DNA sequence from cosmid L118G10, Huntington's Disease Region, chromosome 4p16.3	0.005
1866	AJ277737	Homo sapiens partial POLR2J2 gene for RPB11b1 protein, intron 4 (1824 BP)	0.0000001
1867	XM_051572	Homo sapiens heat shock transcription factor 2 (HSF2), mRNA	1E-11
1868	AF256918	Salmo salar clone BHMS267 microsatellite sequence	0.11
1869	AE000557	Helicobacter pylori 26695 section 35 of 134 of the complete genome	0.17
1870	XM_050469	Homo sapiens ferritin, light polypeptide (FTL), mRNA	0.081
1871	XM_042818	Homo sapiens homeo box D4 (HOXD4), mRNA	0.24
1872	AB035093	Petunia x hybrida mRNA for lateral shoot inducing factor, complete cds	1.9
1873	AE006184	Pasteurella multocida PM70 section 151 of 204 of the complete genome	5.6
1874	AE006880	Sulfolobus solfataricus section 239 of 272 of the complete genome	3.3
1875	NC_002669	Bacteriophage bIL310, complete genome	4.7
1876	AK012924	Mus musculus 10, 11 days embryo cDNA, RIKEN full-length enriched library, clone:2810048H02, full insert sequence	1.8
1877	XM_032188	Homo sapiens cell division cycle 27 (CDC27), mRNA	5.5
1878	M33662	Hamster G-o protein alpha subunit 2 mRNA, complete cds	5.8
1879	Y00478	L.esculentum LEACO2 gene	0.28
1880	XM_050519	Homo sapiens annexin A2 (ANXA2), mRNA	8E-34
1881	AF054822	Drosophila melanogaster activin beta precursor, gene, partial cds	0.43

	Table 3A Nearest Neighbor (BlastN vs. Genbank)		
SEQ ID NO	ACCESSN	DESCRIP	P VALUE
1882	AB062967	Macaca fascicularis brain cDNA clone:QmoA-10357, full insert sequence	1.7
1883	D87001	Homo sapiens immunoglobulin lambda gene locus DNA, clone:47H9 downstream contig	0.64
1884	AF378137	Plasmodium falciparum clone g2-4-4#5 MB2 gene, partial cds	0.081
1885	XM_011791	Homo sapiens laminin, gamma 3 (LAMC3), mRNA	3E-58
1886	XM_007214	Homo sapiens hypothetical protein FLJ10956 (FLJ10956), mRNA	e-119
1887	AF227741	Rattus norvegicus protein kinase WNK1 (WNK1) mRNA, complete cds	0.96
1888	AL359578	Homo sapiens mRNA; cDNA DKFZp547N163 (from clone DKFZp547N163)	0.063
1889	AE002841	Drosophila melanogaster genomic scaffold 142000013385478, complete sequence	0.19
1890	X01121	Mycoplasma capricolum genes for ribosomal proteins S8 and L6	0.5
1892	AF082924	Trissolcus basalis cytochrome oxidase II gene, partial cds; and tRNA-Asp and tRNA-Lys genes, complete sequence; mitochondrial genes for mitochondrial products	0.02
1893	BC005693	Mus musculus, Similar to RIKEN cDNA 1110002A15 gene, clone MGC:11574 IMAGE:3597594, mRNA, complete cds	1.4
1894	U29721	Entamoeba histolytica p21racB (Eh racB) gene, partial cds	0.15
1895	AK023959	Homo sapiens cDNA FLJ13897 fis, clone THYRO1001706	0.17
1896	XM_038475	Homo sapiens DKFZP564J102 protein (DKFZP564J102), mRNA	6E-33
1897	AL010164	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-95, complete sequence	1.1
1898	AF176059	Helcon sp. 16S ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	0.009
1899	L34640	Homo sapiens platelet/endothelial cell adhesion molecule-1 (PECAM-1) gene, exons 7, 8 and 9	0.007
1901	AC026061	Homo sapiens BAC clone RP11-223K9 from Y, complete sequence	1.5
1902	AF188516	Staphylococcus aureus Bmr-like protein SblA (sblA) gene, complete cds	0.08
1903	AL360177	Human DNA sequence from clone RP11-86K9 on chromosome 10, complete sequence [Homo sapiens]	0.077
1904	L76261	Meloidogyne javanica mitochondrial transfer RNA His, 16S ribosomal RNA (16S rRNA) genes, ND3 gene, complete cds, and cytochrome b gene, 5' end of CDS	0.17
1905	XM_042904	Homo sapiens mitochondrial ribosomal protein S25 (MRPS25), mRNA	2
1906	XM_051831	Homo sapiens similar to CYTOCHROME P450 51 (CYPL1) (P450L1) (STEROL 14-ALPHA DEMETHYLASE) (LANOSTEROL 14-ALPHA DEMETHYLASE) (LDM) (P450-14DM) (H. sapiens) (LOC93525), mRNA	0.66

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
1907	XM_012289	Homo sapiens cytoskeleton associated protein 2 (CKAP2), mRNA	2
1908	U44391	Human Down Syndrome region of chromosome 21, clone A12H1-1B2	0.008
1909	L04961	Mouse nuclear-localized inactive X-specific transcript (Xist) mRNA	1.8
1910	X61202	Methanococcus voltae fruA, fruB, fruG genes for subunits of F420-reducing hydrogenase and fruD orf	0.078
1911	AP000242	Homo sapiens genomic DNA, chromosome 21q22.1, clone:f43D11, SOD-AML region, complete sequence	0.0001
1912	AL023777	S.pombe chromosome III cosmid c1827	0.66
1913	XM_038450	Homo sapiens hypothetical protein FLJ20694 (FLJ20694), mRNA	0
1914	AF129510	Mus musculus DACH protein (Dach) mRNA, complete cds	2.1
1915	AE001405	Plasmodium falciparum chromosome 2, section 42 of 73 of the complete sequence	0.18
1916	XM_039566	Homo sapiens KIAA0948 protein (KIAA0948), mRNA	6.8
1917	AP001431	Homo sapiens genomic DNA, chromosome 21q22.2, clone:T1492, LB7T-ERG region, complete sequence	0.074
1918	AF329137	Camelus bactrianus microsatellite Cms1 sequence	0.008
1919	NM_003816	Homo sapiens a disintegrin and metalloproteinase domain 9 (meltrin gamma) (ADAM9), mRNA	1E-17
1920	AE001414	Plasmodium falciparum chromosome 2, section 51 of 73 of the complete sequence	0.001
1921	U95074	Caenorhabditis elegans protein disulphide isomerase isoform I (pdi-1) and cyclophilin isoform 9 (cyp-9) genes, complete cds	0.029
1922	AB019534	Homo sapiens gene for cathepsin L2, complete cds	0.07
1923	AJ133777	Arabidopsis thaliana mRNA for gamma-adaptin 2	6.6
1924	XM_001304	Homo sapiens cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4) (CDKN2C), mRNA	0.25
1925	AB037166	Clostridium botulinum genes for ORF-22, HA-70, HA-17, HA-33, NTNHA, neurotoxin, complete cds	0.2
1926	Z48243	A.thaliana PARP mRNA for PARP protein	0.081
1927	XM_041006	Homo sapiens choreoacanthocytosis gene; KIAA0986 protein (KIAA0986), mRNA	0.25
1928	XM_050592	Homo sapiens uncharacterized hematopoietic stem/progenitor cells protein MDS032 (MDS032), mRNA	0.083
1929	U34610	Mus musculus alpha-1(XVIII) collagen (COL18A1) gene, exon 6 and 7	0.008
1930	BC007658	Homo sapiens, clone MGC:747 IMAGE:3343994, mRNA, complete cds	6E-50
1931	AL451135	Human DNA sequence from clone RP11-45G20 on chromosome 6, complete sequence [Homo sapiens]	2
1932	AB004883	Marchantia paleacea mRNA for ribulose 1,5-bisphosphate carboxylase/oxygenase small subunit, complete cds	0.26

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
1933	AF019973	Rattus norvegicus neuron-specific enolase (NSE) mRNA, complete cds	0.22
1934	AF231684	Drosophila melanogaster outstretched (os) gene, complete cds	0.75
1935	AC079136	Homo sapiens clone RP11-153L12, complete sequence	0.75
1936	AE006611	Streptococcus pyogenes M1 GAS strain SF370, section 140 of 167 of the complete genome	1.5
1937	AE007418	Streptococcus pneumoniae section 101 of 194 of the complete genome	0.029
1938	L26949	Simian immunodeficiency virus (T5) surface envelope glycoprotein proviral gene, 5' end	0.027
1939	AF343914	Campylobacter jejuni NCTC 11828 LOS biosynthesis cluster, partial sequence	0.58
1940	Z69925	Human DNA sequence from clone LL22NC03-116A5 on chromosome 22 Contains GSSs, complete sequence [Homo sapiens]	6.2
1941	U96876	Homo sapiens insulin induced protein 1 (INSIG1) gene, complete cds	0.78
1942	XM_030024	Homo sapiens similar to protein kinase C binding protein 1 (H. sapiens) (LOC90218), mRNA	0.009
1943	AF226993	Rattus norvegicus selective LIM binding factor mRNA, complete cds	0.7
1944	AF033037	Plasmodium falciparum merozoite surface protein 4, merozoite surface protein 5, merozoite surface protein 2, and adenylosuccinate lyase genes, complete cds	0.69
1945	AB053087	Human immunodeficiency virus type 1 pol gene, reverse transcriptase amino terminal part, partial cds, 99JP-NH3-II plasma virus clone:NH3RT-V3-2-9	0.028
1946	XM_033335	Homo sapiens hypothetical protein PRO2389 (PRO2389), mRNA	0.0001
1947	XM_010334	Homo sapiens transducin (beta)-like 1 (TBL1), mRNA	2.2
1948	AK003943	Mus musculus 18 days embryo cDNA, RIKEN full-length enriched library, clone:1110028F11, full insert sequence	2E-10
1949	AF085600	Drosophila melanogaster inorganic pyrophosphatase NURF-38 (Nurf-38) gene, complete cds	0.78
1950	U79731	Plasmodium berghei extrachromosomal plastid PB-1, ORF470 gene, partial cds, tRNA-Thr, large subunit ribosomal RNA, tRNA-Met, tRNA-Arg, tRNA-Val, tRNA-Arg, tRNA-Leu, tRNA-Asn, tRNA-Ala, and small subunit ribosomal RNA genes, complete sequences	0.72
1951	AK022877	Homo sapiens cDNA FLJ12815 fis, clone NT2RP2002546	0.003
1952	M62755	Potato 4-coumarate--CoA ligase (St4C1-1) gene, complete cds	0.085
1953	AK017902	Mus musculus adult male thymus cDNA, RIKEN full-length enriched library, clone:5830406J20, full insert sequence	2.3
1954	AF164418	Sorghum bicolor maturase (matK) gene, complete cds; chloroplast gene for chloroplast product	0.078
1955	X54567	Human MFD22 dinucleotide repeat DNA	3E-13

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
1956	AB056832	Macaca fascicularis brain cDNA clone:QflA-14079, full insert sequence	0.00009
1957	XM_034132	Homo sapiens ubiquitously transcribed tetratricopeptide repeat gene, Y chromosome (UTY), mRNA	7
1958	L09706	Homo sapiens complement component 2 (C2) gene allele b, exons 1 through 8	0.24
1959	XM_017231	Homo sapiens hypothetical protein FLJ23342 (FLJ23342), mRNA	8E-76
1960	X83989	P.palustris chloroplast rbcL gene, promoter region	0.003
1961	AK025090	Homo sapiens cDNA: FLJ21437 fis, clone COL04285	0
1962	AK013805	Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched library, clone:2900079F10, full insert sequence	0.14
1963	AE006210	Pasteurella multocida PM70 section 177 of 204 of the complete genome	0.042
1964	AF075080	Homo sapiens full length insert cDNA YQ80D07	0.000001
1965	D42118	Tobacco gene for parAs protein, promoter region and partial cds	0.009
1966	AF269350	Staphylococcus epidermidis strain SR1 clone step.1002d12 genomic sequence	2.3
1967	AF068904	Staphylococcus aureus cell division protein FtsZ (ftsZ) gene, partial cds; YlmD (ylmD), YlmE (ylmE), YlmF (ylmF), YlmG (ylmG), and YlmH (ylmH) genes, complete cds; and cell division protein DivIVA (divIVA) gene, partial cds	0.19
1968	AL589920	Human DNA sequence from clone RP11-117A20 on chromosome 6, complete sequence [Homo sapiens]	0.003
1969	AF027688	Mus musculus survival motor neuron (Smn) gene, promoter region and partial cds	0.56
1970	AL049340	Homo sapiens mRNA; cDNA DKFZp564P056 (from clone DKFZp564P056)	0.25
1971	AJ223385	Fowlpox virus strain HP-440 DNA, isolate FP9, 14.6 kb fragment	0.25
1972	U25354	Human mitochondrial DNA control region, Indonesian, sequence 1 of 60	3E-65
1973	AF269868	Staphylococcus epidermidis strain SR1 clone step.1027g02 genomic sequence	0.083
1974	AE003326	Drosophila melanogaster genomic scaffold 142000013385598, complete sequence	0.087
1975	XM_050217	Homo sapiens RNA binding protein (LOC84549), mRNA	2.1
1976	AE001402	Plasmodium falciparum chromosome 2, section 39 of 73 of the complete sequence	0.026
1977	XM_001935	Homo sapiens forkhead box D2 (FOXD2), mRNA	2.1
1978	AL590384	Human DNA sequence from clone RP11-349A16 on chromosome Xq22.3-24, complete sequence [Homo sapiens]	0.008
1979	AL117050	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation	2.2
1980	XM_037529	Homo sapiens KIAA0410 gene product (KIAA0410), mRNA	2.3
1981	X56212	C.elegans gene for vitellogenin	1.8

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
1982	AF231684	Drosophila melanogaster outstretched (os) gene, complete cds	0.7
1983	AB032264	Danio rerio mRNA for glycogen synthase kinase 3 alpha, complete cds	2.2
1984	AK022877	Homo sapiens cDNA FLJ12815 fis, clone NT2RP2002546	0.009
1985	U89140	Mus musculus aldose reductase gene, promoter region and exon 1	0.69
1986	M37036	Rat nucleolar proteins B23.1 and B23.2	0.086
1987	XM_035498	Homo sapiens amiloride-sensitive cation channel 2, neuronal (ACCN2), mRNA	0.25
1988	U40944	Caenorhabditis elegans cosmid PDB1, complete sequence	0.025
1989	AF102762	Dasylagon n. sp. 'Mardulyn & Whitfield' 16S large subunit ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	0.24
1990	AF247631	Maoricicada iolanthe cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial gene for mitochondrial product	0.026
1991	Z81538	Caenorhabditis elegans cosmid F45H10, complete sequence	6.2
1992	Z72516	Caenorhabditis elegans cosmid T25G3, complete sequence	0.75
1993	AE002201	Chlamydophila pneumoniae AR39, section 32 of 94 of the complete genome	6.6
1994	NM_003816	Homo sapiens a disintegrin and metalloproteinase domain 9 (meltrin gamma) (ADAM9), mRNA	2E-17
1995	AL158132	Human DNA sequence from clone RP3-323A24 on chromosome 4. Contains GSSs and a putative CpG island, complete sequence [Homo sapiens]	0.074
1996	NM_023122	Mus musculus glycoprotein m6b (Gpm6b), mRNA	5.7
1997	AF014502	*Glycine max seed coat peroxidase precursor (Ep) gene, complete cds*	1.8
1998	AJ270226	Entodinium caudatum partial mRNA for putative glycosyltransferase, clone L48	2.1
1999	AF159913	Euplotes crassus transposon Tec1 clone Tec1-2 orf 2 and orf 3 pseudogenes, complete sequence	0.011
2000	AF101309	Caenorhabditis elegans cosmid H24G06, complete sequence	2.2
2001	AB021240	Hypseleotris compressus mitochondrial gene for Cytochrome b, complete cds	0.022
2002	AC078798	Homo sapiens 3 BAC PAC-56F11 (Roswell Park Cancer Institute Human BAC Library) complete sequence	0.001
2003	AK021504	Homo sapiens cDNA FLJ11442 fis, clone HEMBA1001327	0.76
2004	AF314531	Chilli leaf curl virus A component, complete sequence	0.23
2005	XM_047794	Homo sapiens KIAA1641 protein (KIAA1641), mRNA	e-123
2006	AC079136	Homo sapiens clone RP11-153L12, complete sequence	0.65
2007	AE001422	Plasmodium falciparum chromosome 2, section 59 of 73 of the complete sequence	0.001
2009	AJ306692	Drosophila virilis ORF1, rpL14 gene and ORF2	0.26
2010	AC084242	Arabidopsis thaliana chromosome 1 BAC T24P22 genomic sequence, complete sequence	0.72

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
2011	Z16768	H. sapiens (D12S90) DNA segment containing (CA) repeat; clone AFM172xd8; single read	0.058
2012	AF311633	Eimeria nieschulzi ORF470 gene, partial cds; apicoplast gene for apicoplast product	1.9
2013	XM_012933	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA	2.5
2014	AB035190	Homo sapiens RHD gene, intron 2, complete sequence	1.6
2015	NC_002135	Pleurotus ostreatus mitochondrial plasmid mlp1, complete sequence	0.22
2016	AF085619	Elgaria paucicarinata NADH dehydrogenase subunit I (ND1) gene, partial cds; tRNA-Ile, tRNA-Gln, and tRNA-Met genes, complete sequence; NADH dehydrogenase subunit II (ND2) gene, complete cds; tRNA-Trp, tRNA-Ala, tRNA-Asn, tRNA-Cys, and tRNA-Tyr genes, c>	2.3
2017	D85424	Homo sapiens gene for alphaS1-casein, 5'flanking region	0.077
2018	AE001138	Borrelia burgdorferi (section 24 of 70) of the complete genome	0.026
2019	BC007114	Homo sapiens, clone IMAGE:4295422, mRNA	0.23
2020	AF080510	Homo sapiens mannose-binding protein gene, exon 4 and complete cds	0.00001
2022	XM_027941	Homo sapiens hypothetical protein DKFZp761J139 (DKFZp761J139), mRNA	0.003
2023	Z68996	H.sapiens mRNA for immunoglobulin kappa light chain VJ region (ID POM021)	0.15
2024	AB049191	Mus musculus DNA, clone:lambda4/6, endogenous mouse mammary tumor virus LTR region	0.15
2025	U62057	Mycoplasma capricolum NADH oxidase (naox) gene, partial cds, and lipoate-protein ligase (lpla), pyruvate dehydrogenase EI alpha subunit (odpa), pyruvate dehydrogenase EI beta subunit (odpb), pyruvate dehydrogenase EII (odp2), dihydrolipoamide dehydroge>	3
2026	AY018527	Oryza sativa microsatellite MRG0852 containing (AT)X17, genomic sequence	0.0003
2027	AF266084	Phyllopetalia apicalis large subunit ribosomal RNA gene, partial sequence; tRNA-Valine gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence; mitochondrial genes for mitochondrial products	0.009
2028	AF249912	Cucumis melo galactinol synthase (GAS1) gene, upstream sequence and partial cds	0.021
2029	XM_048172	Homo sapiens hypothetical protein DKFZp434F1017 (DKFZP434F1017), mRNA	6.5
2030	AF367436	Erysimum cheiri chloroplast outer envelope membrane protein mRNA, complete cds	1.2
2031	AF135026	Homo sapiens kallikrein-like protein 3 (KLK9) gene, complete cds, alternatively spliced	0.76
2032	Z69782	A.thermophilum xylR gene, xynA gene and alfA gene	0.0004

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
2033	NM_013730	Mus musculus signaling lymphocyte activation molecule (Slam), mRNA	6.4
2034	NC_002811	Tarsius bancanus mitochondrion, complete genome	0.69
2035	AF184822	Arabidopsis thaliana inhibitor tagged site ITS55 genomic sequence	0.24
2036	AE006626	Streptococcus pyogenes M1 GAS strain SF370, section 155 of 167 of the complete genome	5.4
2037	AF324424	Ichthyophthirius multifiliis immobilization antigen isoform (IAG52A) gene, complete cds	0.003
2038	AL391223	Human chromosome 14 DNA sequence Partial sequence from BAC R-325N7_PCR1 of library RPCI-11 from chromosome 14 of Homo sapiens (Human), complete sequence	6.3
2040	AF369348	Rabies virus V231.RB phosphoprotein (P) gene, complete cds	1.4
2041	AF023666	Apis mellifera sn-glycerol-3-phosphate dehydrogenase (Gpdh) gene, complete cds	0.25
2042	XM_011553	Homo sapiens aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid-5-beta-reductase) (AKR1D1), mRNA	0.001
2043	XM_004530	Homo sapiens nuclear receptor subfamily 2, group E, member 1 (NR2E1), mRNA	5E-41
2044	AJ277602	Gallus gallus partial mRNA for initiation of translation factor 2 (clF2 gene)	0.72
2045	XM_041537	Homo sapiens echinoderm microtubule-associated protein-like (EMAPL), mRNA	1.7
2046	AE001429	Plasmodium falciparum chromosome 2, section 66 of 73 of the complete sequence	0.57
2047	L03188	Saccharomyces cerevisiae integrin analogue gene, complete cds	0.23
2048	XM_034810	Homo sapiens similar to ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY (H. sapiens) (LOC90908), mRNA	2E-25
2049	AE006570	Streptococcus pyogenes M1 GAS strain SF370, section 99 of 167 of the complete genome	0.64
2050	AY023977	Oryza sativa microsatellite MRG6302 containing (ATTA)X6, closest to marker R1674, genomic sequence	0.6
2051	M91384	Dictyostelium discoideum thioredoxin (TRX1) mRNA, complete cds	0.68
2052	XM_032748	Homo sapiens KIAA1634 protein (KIAA1634), mRNA	0.066
2053	AB004814	Oryza sativa DNA for NLS receptor, complete cds	0.009
2054	AF130049	Homo sapiens clone FLB3411 PRO0852 mRNA, complete cds	0.078
2055	Y19213	Homo sapiens putative psihHbA pseudogene for hair keratin, exons 2 to 7	0.038
2056	AF305146	Picea abies clone 1PABCA3F hypomethylated genomic sequence	1.8
2057	Z67997	Human DNA sequence from cosmid L206D7, Huntington's Disease Region, chromosome 4p16.3	0.0001
2058	U51024	Human Down Syndrome region of chromosome 21 DNA	0.0008
2059	AC092063	Homo sapiens clone RP11-745H7, complete sequence	0

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
2060	AE002123	Ureaplasma urealyticum section 24 of 59 of the complete genome	1.8
2061	Z68019	HIV-1 DNA V3 region (homosexual H1031, seroconversion sample 1987)	0.25
2062	XM_006487	Homo sapiens spectrin, beta, non-erythrocytic 2 (SPTBN2), mRNA	0.000003
2063	AF329716	Oncorhynchus mykiss clone OSU9 T cell receptor beta chain variable region gene, partial cds	0.0008
2064	AC024773	Caenorhabditis elegans cosmid Y40C7A, complete sequence	0.035
2065	XM_032748	Homo sapiens KIAA1634 protein (KIAA1634), mRNA	0.079
2066	M58526	Human alpha-5 collagen type IV (COL4A5) mRNA, 3' end	2.1
2068	X56697	B.thuringiensis gene for sigma factor 35	0.59
2069	D00768	Pig pituitary glycoprotein hormone alpha subunit gene, exons 3 and 4 and 3'flank	1.6
2070	AF110621	Boophilus microplus 12S ribosomal RNA gene, partial sequence; tRNA-Ile, tRNA-Gln, and tRNA-Phe genes, complete sequence; and NADH dehydrogenase subunit 5 (ND5) gene, partial cds, mitochondrial genes for mitochondrial products	0.21
2071	AC024779	Caenorhabditis elegans cosmid Y43B11AL, complete sequence	0.24
2072	AK023589	Homo sapiens cDNA FLJ13527 fis, clone PLACE1006076	0
2073	X77691	W.suaveolens mitochondrial DNA intergenic region between ORF1 and 15S rRNA genes	0.24
2074	Z68749	Caenorhabditis elegans cosmid F56H11, complete sequence	1.4
2075	AF302113	Solanum tuberosum glutamine synthetase GS2 (gln) mRNA, partial cds; nuclear gene for plastid product	1.4
2076	U27078	Trichaptum abietinum mitochondrial small subunit ribosomal RNA, mitochondrial gene, partial sequence	0.64
2077	XM_012456	Homo sapiens golgin-67 (KIAA0855), mRNA	2.2
2078	AB032960	Homo sapiens mRNA for KIAA1134 protein, partial cds	1E-36
2079	XM_052376	Homo sapiens hypothetical gene supported by AF106046; AK000332 (LOC93587), mRNA	0.66
2080	AB021866	Homo sapiens KIP gene, complete cds	1.3
2081	XM_029213	Homo sapiens hypothetical protein DKFZp564O0523 (DKFZP564O0523), mRNA	0.38
2082	AF384143	Triticum aestivum pathogenesis-related protein 1 mRNA, complete cds	0.0003
2083	AE002368	Neisseria meningitidis serogroup B strain MC58 section 10 of 206 of the complete genome	0.71
2084	AE006662	Sulfolobus solfataricus section 21 of 272 of the complete genome	0.63
2085	AY020760	Oryza sativa microsatellite MRG3085 containing (TA)X13, closest to marker R2976, genomic sequence	6.9
2086	AF161419	Homo sapiens HSPC301 mRNA, partial cds	1.8
2087	AJ249838	Gallus gallus mRNA for radixin (rdx gene)	2.1
2088	U43536	Corynebacterium glutamicum heat shock, ATP-binding protein (clpB) gene, complete cds	0.22
2089	XM_037588	Homo sapiens KIAA0874 protein (KIAA0874), mRNA	2E-34

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
2090	NC_002697	Chrysomya chloropyga mitochondrion, complete genome	0.077
2091	AF332207	Caenorhabditis elegans clone yk509b7 nuclear receptor NHR-57 gene, partial cds	0.45
2092	U39886	Bos taurus Y-chromosome specific genomic sequence	0.2
2093	Z19055	B.aphidicola tryptophan operon	0.26
2094	AJ290309	Simethis mattiazzii chloroplast trnL-trnF intergenic spacer	0.57
2095	AK013631	Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched library, clone:2900041A09, full insert sequence	0.18
2096	AF015468	Plasmodium falciparum microsatellite LT103 sequence	0.11
2097	AJ277734	Sus scrofa microsatellite sequence S0601	0.4
2098	AF203341	Glycine max chloroplast carboxyl transferase alpha subunit (accA-4) nuclear pseudogene, partial sequence; and putative steroid reductase gene, complete cds	0.001
2099	XM_052597	Homo sapiens KIAA1350 protein (KIAA1350), mRNA	0
2100	Z96649	H.sapiens telomeric DNA sequence, clone 6QTEL010, read 6QTELOO010.seq	0.007
2101	BC009105	Mus musculus, Harvey rat sarcoma oncogene, subgroup R, clone MGC:6162 IMAGE:3483313, mRNA, complete cds	4.1
2102	AF245117	Mus musculus leukocyte cell-surface molecule (Ly9) gene, exon 1	0.025
2103	AL023810	Caenorhabditis elegans cosmid C16D2, complete sequence	0.008
2104	X17051	E.gracilis DNA for ribosomal protein operon	0.21
2105	AF005392	Homo sapiens alpha tubulin (TUBA2) gene, partial cds	0.63
2106	AE002798	Drosophila melanogaster genomic scaffold 142000013385466, complete sequence	0.025
2107	AE002114	Ureaplasma urealyticum section 15 of 59 of the complete genome	0.074
2108	L48039	Fibrobacter succinogenes endo-1,4-beta-D-glucanase gene, complete cds, endo-1,4-beta-D-glucanase gene, 5' end of cds	2
2109	D87922	Rat DNA for 3'UTR of skeletal muscle sodium channel, partial sequence	0.71
2110	AF157137	Gongronella butleri 18S ribosomal RNA gene, partial sequence	0.24
2111	Z92970	Caenorhabditis elegans cosmid H06O01, complete sequence	0.24
2112	AB035494	Alternaria alternata gene for Akt3-2, complete cds	0.61
2113	M38351	Rat embryonic glutamic acid decarboxylase gene, embryonic stop (ES) exon	0.67
2114	X16715	D. melanogaster gene for chorion protein s16	0.21
2115	U16271	Homo sapiens AMP deaminase isoform L (AMPD2) gene, exons 1A and 1B	0.07
2116	AF317672	Helicobacter pylori isolate 4424 vacuolating cytotoxin VacA (vacA) gene, partial cds	0.24
2117	NM_010250	Mus musculus gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 1 (Gabra1), mRNA	0.76
2118	BC010786	Mus musculus, Similar to CREB/ATF family transcription factor, clone MGC:18836 IMAGE:4211480, mRNA, complete cds	0.69

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
2119	U67482	Methanococcus jannaschii section 24 of 150 of the complete genome	0.24
2120	U73373	HIV-1 clone 1063-2-VPR vpr gene, complete cds	2
2121	AE007370	Streptococcus pneumoniae section 53 of 194 of the complete genome	0.68
2122	AL449163	Human DNA sequence from clone RP11-533E16 on chromosome 6, complete sequence [Homo sapiens]	2E-11
2123	X63382	Antithamnion sp. rhodoplast genes atpI, atpH, atpG, atpF, atpD, atpA, orf1, orf2 and orf3	0.081
2124	AF186797	Homo sapiens RalGDS-like (RGL) gene, exon 17	0.009
2125	AF110796	Rattus norvegicus GABAB1 receptor (GABABR1) gene, exons 1 through 9	4.2
2126	XM_038798	Homo sapiens KIAA1457 protein (KIAA1457), mRNA	2E-96
2127	U96998	Homo sapiens MET proto-oncogene, intron 19, 3' end	0.67
2128	AE006410	Lactococcus lactis subsp. lactis IL1403 section 172 of 218 of the complete genome	0.084
2129	AB050422	Macaca fascicularis brain cDNA, clone:QnpA-21421	6.9
2130	AF375597	Mus musculus medium and short chain L-3-hydroxyacyl-Coenzyme A dehydrogenase (Mschad) gene, exons 2 through 8, and complete cds; nuclear gene for mitochondrial product	2.2
2131	AE002758	Drosophila melanogaster genomic scaffold 142000013385931, complete sequence	0.26
2132	AJ008105	Chrysolina timarchoides COI gene, partial CDS	0.031
2133	U67526	Methanococcus jannaschii section 68 of 150 of the complete genome	2
2134	AJ223966	Mus musculus NAGA gene	0.63
2135	AF016986	Callicebus moloch gamma1-globin gene, complete cds	0.68
2136	U66872	Danio rerio enhancer of rudimentary homolog mRNA, complete cds	0.029
2137	AJ271220	Homo sapiens partial gene for dystrophin, intron 49	0.009
2138	AF075602	Canis familiaris prostaglandin E2 receptor subtype EP2 mRNA, complete cds	0.23
2139	XM_045015	Homo sapiens hypothetical protein FLJ00052 (FLJ00052), mRNA	0.75
2140	AY034614	Danio rerio Sec61 alpha form B mRNA, complete cds	0.1
2141	XM_028150	Homo sapiens similar to MACROPHAGE MANNOSE RECEPTOR PRECURSOR (H. sapiens) (LOC90010), mRNA	1.9
2142	M24026	Rat MHC class I RT1 (RT44) mRNA (u haplotype), 3' end	0.24
2143	AK010194	Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310076E16, full insert sequence	2
2144	AF165062	Hepatitis C virus strain MD9-2 complete genome	1.2
2145	AE007469	Streptococcus pneumoniae section 152 of 194 of the complete genome	2.1
2146	Z97349	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-06, complete sequence	0.046
2147	NM_010161	Mus musculus ecotropic viral integration site 2 (Evi2), mRNA	0.02

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
2148	AE005586	Escherichia coli O157:H7 EDL933 genome, contig 3 of 3, section 205 of 290	1.2
2149	AF332928	Psacothea hilaris isolate HA15 16S ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	0.069
2150	D49504	Borrelia garinii gene for outer surface protein C, complete cds	0.37
2151	L25647	Homo sapiens fibroblast growth factor receptor gene (located in the central MHC) signal peptide and consecutive exon	0.05
2152	AB040746	Carassius auratus gene for c-MYC, complete cds	0.063
2153	X55978	T. brucei ESAG 8 gene for a leucine-rich repeat family protein	0.12
2154	AB010426	Phytoplasma sp. gene for AL1 like protein, complete cds	0.009
2155	XM_005841	Homo sapiens cdk inhibitor p21 binding protein (TOK-1), mRNA	5.8
2156	AK025222	Homo sapiens cDNA: FLJ21569 fis, clone COL06508	1E-33
2157	AF234652	Mesembryanthemum crystallinum protein kinase MK5 mRNA, complete cds	0.2
2158	AE006513	Streptococcus pyogenes M1 GAS strain SF370, section 42 of 167 of the complete genome	9.2
2159	XM_003660	Homo sapiens calcium modulating ligand (CAMLG), mRNA	0.023
2160	AF003490	Mesostoa kerri 16S ribosomal RNA gene, partial sequence	0.000004
2161	XM_048768	Homo sapiens tetratricopeptide repeat domain 3 (TTC3), mRNA	6.7
2162	AF323442	Plasmodium yoelii yoelii clone 10 235 kDa rhoptry protein (IIIa.1) gene, partial cds	0.019
2163	AK016560	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4932441H21, full insert sequence	4.7
2164	Y12332	E.tenella plastid genes rps12, rps7, tuf, ORF45, and tRNA-Phe	0.003
2165	AL114081	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation	0.002
2166	AF332207	Caenorhabditis elegans clone yk509b7 nuclear receptor NHR-57 gene, partial cds	0.49
2167	AF102263	Helicoverpa zea clone S211 cytochrome P450 (CYP6B8) mRNA, complete cds	0.074
2168	AL133397	Human DNA sequence from clone RP1-213J1p on chromosome 22q11.21-12.2, complete sequence [Homo sapiens]	0.039
2169	AL157423	Homo sapiens mRNA; cDNA DKFZp761O0511 (from clone DKFZp761O0511)	7E-15
2170	AF282578	Homo sapiens clone 20ptel_c1622_12_3.3f sequence	9E-17
2171	AB022280	Oryzias latipes gene for soluble guanylyl cyclase alpha subunit, complete cds	3.7
2172	AF052744	Homo sapiens transcriptional repressor p54 gene, promoter region and partial cds	2
2173	XM_007685	Homo sapiens MAGE-like 2 (MAGEL2), mRNA	0.008
2174	AK019539	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4921514G21, full insert sequence	1.6
2175	AE007472	Streptococcus pneumoniae section 155 of 194 of the complete genome	6.2
2176	AL162381	Human DNA sequence from clone RP11-174B19 on chromosome 6, complete sequence [Homo sapiens]	0.059

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
2177	M21836	Mouse extra-embryonic endodermal cytokeratin type II (EndoA) mRNA, complete cds	e-138
2178	X06292	Human c-fes/fps proto-oncogene	1.7
2179	AF360278	Arabidopsis thaliana putative MLH1 protein (AT4g09140) mRNA, complete cds	0.0001
2180	X78548	G.max gene encoding epoxide hydrolase	0.68
2181	Z56222	H.sapiens CpG island DNA genomic Mse1 fragment, clone 97b6, reverse read cpg97b6.rt1a	5E-60
2182	AF200412	Wiebesia brusi cytochrome oxidase subunit I (COI) gene, partial cds; tRNA-Leu gene, complete sequence; and cytochrome oxidase subunit II (COII) gene gene, partial cds; mitochondrial genes for mitochondrial products	0.084
2183	AF360327	Arabidopsis thaliana putative metal-binding protein (MLE2.16/AT5g63530) mRNA, complete cds	0.014
2184	XM_005837	Homo sapiens CUG triplet repeat, RNA-binding protein 2 (CUGBP2), mRNA	0.22
2185	BC008152	Mus musculus, caspase 1, clone MGC:6106 IMAGE:3583883, mRNA, complete cds	1.9
2186	U41289	Dictyostelium discoideum K7 kinesin-like protein mRNA, complete cds	0.66
2187	AF163863	Mustela vison tyrosine aminotransferase gene, complete cds	0.23
2188	XM_017198	Homo sapiens hypothetical protein FLJ12085 (FLJ12085), mRNA	4E-36
2189	D16180	Human PMP2 gene for peripheral myelin protein 2, exon 2 and 3	0.68
2190	AB037920	Clostridium botulinum genes for ORF-22, HA-70, HA-17, HA-33, NTNHA, neurotoxin, complete cds	0.083
2191	AE006703	Sulfolobus solfataricus section 62 of 272 of the complete genome	1.6
2192	AB047401	Periplaneta americana Vg-2 mRNA for vitellogenin-2, complete cds	0.25
2193	U11491	Human rotavirus M37 non-structural protein NSP1 mRNA, complete cds	0.17
2194	AF338818	Mus musculus flavohemoprotein b5/b5R mRNA, complete cds	2.3
2195	AP001290	Mus musculus genomic DNA, chromosome 7, clone:B118_5, complete sequence	0.56
2196	XM_010940	Homo sapiens putative GR6 protein (GR6), mRNA	2E-61
2197	AF119554	Plasmodium falciparum para-aminobenzoic acid synthetase gene, complete cds	0.009
2198	AY035995	Streptococcus pneumoniae strain SPN1506 topoisomerase IV subunit A (parC) gene, complete cds	1.2
2199	XM_006892	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2), mRNA	0.049
2200	X87127	Borrelia burgdorferi repeated DNA element, 30.5 kb circular plasmid copy	0.46
2201	AB010958	Clostridium thermocellum xynA and xynB genes for xylanase, complete cds	0.23

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
2202	AE003004	Drosophila melanogaster genomic scaffold 142000013385492, complete sequence	0.23
2203	U63418	Mus musculus uncoupling protein (Ucp) gene, nuclear gene encoding mitochondrial protein, complete cds	0.23
2204	AJ243265	Homo sapiens partial PGM1 gene for phosphoglucomutase 1, exons 5-7	e-135
2205	X13883	Yersinia pseudotuberculosis virulence plasmid pIBI yopA gene for Yop1 protein	2.1
2206	XM_011639	Homo sapiens KIAA0535 gene product (KIAA0535), mRNA	8E-22
2207	AF098990	Caenorhabditis elegans cosmid H35N03	2.2
2208	AB037920	Clostridium botulinum genes for ORF-22, HA-70, HA-17, HA-33, NTNHA, neurotoxin, complete cds	0.2
2209	AB053087	Human immunodeficiency virus type 1 pol gene, reverse transcriptase amino terminal part, partial cds, 99JP-NH3-II plasma virus clone:NH3RT-V3-2-9	0.028
2210	NM_008989	Mus musculus purine rich element binding protein A (Pura), mRNA	0.028
2211	U97291	Equus caballus random genomic clone JH226	0.008
2212	AK001699	Homo sapiens cDNA FLJ10837 fis, clone NT2RP4001260, highly similar to Homo sapiens mRNA for KIAA0875 protein	0.016
2213	U84532	Human dystrobrevin (DTN) gene, exon 4	0.23
2214	Z54522	H.sapiens CpG island DNA genomic Mse1 fragment, clone 12b6, forward read cpg12b6.ft1c	1.5
2215	Z69666	Human DNA sequence from cosmid 24F8 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs, repeat polymorphism and CpG island	6.5
2216	M69205	Ockelbo virus complete genome	2.2
2217	AF202552	Homo sapiens DNA methyltransferase (DNMT1) gene, exons 2, 3, and 4	0.24
2218	D16541	Chicken DNA for connectin(titin), partial sequence	0.064
2220	AC023351	Homo sapiens clone RP11-637J20, complete sequence	1E-59
2221	AL512305	Human DNA sequence from clone RP11-85E24 on chromosome 6, complete sequence [Homo sapiens]	0.002
2222	U67581	Methanococcus jannaschii section 123 of 150 of the complete genome	5
2223	AE007428	Streptococcus pneumoniae section 111 of 194 of the complete genome	1.9
2224	AK023601	Homo sapiens cDNA FLJ13539 fis, clone PLACE1006640	1.7
2225	AF375468	Homo sapiens endothelial protein C receptor (PROCR) gene, complete cds	0.016
2226	AF350726	Symphyglossum sanguineum chloroplast tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence	1.4
2227	NM_008308	Mus musculus 5-hydroxytryptamine (serotonin) receptor 1A (Htr1a), mRNA	0.23
2228	Z62421	H.sapiens CpG island DNA genomic Mse1 fragment, clone 68h2, forward read cpg68h2.ft1a	4E-68

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
2229	AF210834	Homo sapiens HARP (HARP) gene, exons 3 and 4	0.008
2230	L81672	Homo sapiens (subclone 2_b12 from P1 H49) DNA sequence, complete sequence	0.13
2231	XM_008431	Homo sapiens integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3), mRNA	1.8
2232	AE006295	Lactococcus lactis subsp. lactis IL1403 section 57 of 218 of the complete genome	0.19
2233	U39693	Mycoplasma genitalium section 15 of 51 of the complete genome	0.21
2234	AL032629	Caenorhabditis elegans cosmid Y102F5A, complete sequence	0.46
2235	AF029114	Ascogaster sp. 16S ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence	0.076
2236	AF150036	Hyalomma dromedarii 12S small ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	0.63
2237	AF013711	Homo sapiens 22 kDa actin-binding protein (SM22) gene, complete cds	0.6
2238	XM_035961	Homo sapiens hypothetical protein FLJ10849 (FLJ10849), mRNA	0.77
2239	AJ290957	Drosophila erecta partial eIF2g gene for eukaryotic translation initiation factor 2 gamma and Su(var)3-9 gene for heterochromatin protein	0.24
2240	AF282004	Homo sapiens clone 15qtel_c366at7 sequence	8.2
2241	AF104915	Plasmodium falciparum protein serine/threonine kinase-1 (psk1) gene, complete cds	0.009
2242	M22064	Mouse MHC class I Lyt-2-a gene encoding lyt-2.1 T-cell surface alloantigen, complete cds	0.049
2243	AF265368	Hypseleotris compressa 12S ribosomal RNA gene, complete sequence; mitochondrial gene for mitochondrial product	0.21
2245	AE001397	Plasmodium falciparum chromosome 2, section 34 of 73 of the complete sequence	0.024
2246	AK004676	Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200009I24, full insert sequence	0.56
2247	XM_002436	Homo sapiens sterile-alpha motif and leucine zipper containing kinase AZK (ZAK), mRNA	0.67
2248	AE006324	Lactococcus lactis subsp. lactis IL1403 section 86 of 218 of the complete genome	0.47
2249	XM_042833	Homo sapiens KIAA0295 protein (KIAA0295), mRNA	5.1
2250	X63412	B.burgdorferi plasmid ospA gene for outer surface protein A	0.36
2251	AK024235	Homo sapiens cDNA FLJ14173 fis, clone NT2RP2002755	1.8
2252	U69826	Eryx miliaris nogajorum cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds	5.9
2254	AF038086	HIV-1 isolate TZB0036 from Tanzania, gp120 C2-C4 region (env) gene, partial cds	0.077
2255	AF317082	Adoncholaimus thalassophygas isolate Sou39 large subunit ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	0.003
2256	NM_005386	Homo sapiens neuronatin (NNAT), mRNA	0.6

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
2257	XM_037301	Homo sapiens hypothetical protein FLJ12697 (FLJ12697), mRNA	2E-61
2258	XM_028046	Homo sapiens KIAA0220 protein (KIAA0220), mRNA	5E-61
2259	U94520	Lactococcus lactis plasmid pND861 abortive phage resistance proteins (abiLi) and (abiLii) genes, complete cds	0.81
2260	U00037	Caenorhabditis elegans cosmid T20H4	0.081
2261	Z74866	S.cerevisiae chromosome XV reading frame ORF YOL124c	0.55
2262	Z92779	Caenorhabditis elegans cosmid C44E1, complete sequence	0.7
2263	V00694	Saccharomyces cerevisiae mitochondrion COX/OXI3 gene encoding for cytochrome oxidase subunit 1	0.021
2264	AC010728	Homo sapiens BAC clone RP11-258E22 from Y, complete sequence	3E-30
2265	AJ406392	Beta vulgaris partial En/Spm-like transposon, clone 44.9	0.054
2266	AE001430	Plasmodium falciparum chromosome 2, section 67 of 73 of the complete sequence	0.064
2267	AF378270	Pangasius sp. ZZSH-2001 microsatellite PSP-G 456 sequence	1.1
2268	XM_047227	Homo sapiens hypothetical gene supported by AL122112 (LOC92776), mRNA	0.38
2269	AE002758	Drosophila melanogaster genomic scaffold 142000013385931, complete sequence	0.2
2270	AL115861	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation	0.14
2271	AE006407	Lactococcus lactis subsp. lactis IL1403 section 169 of 218 of the complete genome	1.8
2272	XM_049351	Homo sapiens KIAA1600 protein (KIAA1600), mRNA	0.0007
2273	AE005977	Caulobacter crescentus section 303 of 359 of the complete genome	5.2
2274	XM_007057	Homo sapiens chromosome 12 open reading frame 5 (C12orf5), mRNA	0.63
2275	XM_031923	Homo sapiens hypothetical gene supported by AK023761 (LOC90466), mRNA	0.0000007
2276	AJ005330	pGAII(-) SK positive selection cloning vector gltS gene	3E-21
2277	XM_029246	Homo sapiens collagen, type I, alpha 2 (COL1A2), mRNA	0.051
2278	AF185279	Homo sapiens polymerase delta small subunit (POLD2) gene, partial sequence	0.002
2279	AF080592	Mus musculus centrin (Cetn2) gene, complete cds	1.8
2280	XM_033626	Homo sapiens nucleoporin-like protein 1 (NLP_1), mRNA	3.6
2281	AB011667	Ipomoea purpurea genes for dihydroflavonol 4-reductase, complete cds	0.25
2282	AB011667	Ipomoea purpurea genes for dihydroflavonol 4-reductase, complete cds	0.25
2283	XM_002698	Homo sapiens LOC89635 (LOC89635), mRNA	6.3
2284	BC009385	Homo sapiens, clone IMAGE:4127835, mRNA	0.61
2285	U39718	Mycoplasma genitalium section 40 of 51 of the complete genome	3.4
2286	AB036755	Schizosaccharomyces pombe spo14/stl1 gene for Sec12-like protein, complete cds	0.079

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
2287	AF369960	Sepiella maindroni isolate c 16S ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	0.22
2288	AE005360	Escherichia coli O157:H7 EDL933 genome, contig 2 of 3, section 29 of 55	0.6
2289	U01034	Eastern equine encephalomyelitis virus North American antigenic variety nonstructural polyprotein and structural polyprotein genes, complete cds	1.7
2290	AF355103	Pleurotus ostreatus linear mitochondrial plasmid mlp2, partial sequence	5.7
2291	AC000043	Homo sapiens Chromosome 22q13 Cosmid Clone p74a8, complete sequence	0.085
2292	X89398	H.sapiens ung gene for uracil DNA-glycosylase	0.71
2293	AY008264	Yersinia enterocolitica phage shock protein locus, complete sequence	2.2
2294	AJ011320	Drosophila melanogaster Su(P) and anon-73B1 genes and partial o25 gene and Pros26 gene	6.5
2295	XM_040290	Homo sapiens glutamate receptor, ionotropic, AMPA 1 (GRIA1), mRNA	4
2296	AJ293578	Homo sapiens partial MOCS1 gene, exons 2-8	6.3
2297	BC007051	Homo sapiens, clone MGC:12465 IMAGE:3683051, mRNA, complete cds	7E-32
2298	M23103	B.subtilis spoIVCB gene, complete cds	0.2
2299	AF280606	Triticum aestivum omega gliadin pseudogene, complete sequence	0.24
2300	AF266095	Platycnemis pennipes large subunit ribosomal RNA gene, partial sequence; tRNA-Valine gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence; mitochondrial genes for mitochondrial products	0.077
2301	AF114927	Saccharomyces pastorianus CBS1538 small subunit ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, complete sequence	0.23
2302	M68901	P.multocida adenylate cyclase (cya) gene, complete cds	0.23
2303	AJ235878	Amorphophallus kiusiuensis chloroplast atpB-rbcL spacer, isolate PL1	0.23
2304	NM_016158	Homo sapiens erythrocyte transmembrane protein (LOC51145), mRNA	5E-34
2305	Y17254	Euplotes octocarinatus gamma-tubulin 2 micronuclear gene	2.3
2306	X99872	Sulfolobus acidocaldarius pyrB gene	0.033
2307	X81001	H.sapiens HCG II mRNA	0.001
2308	Z80213	Caenorhabditis elegans cosmid C09E9, complete sequence	0.025
2309	AF257022	Salmo salar clone BHMS7-009 microsatellite sequence	0.74
2310	AL138748	Human DNA sequence from clone RP4-732E19 on chromosome Xq21.1-21.33 Contains GSSs, complete sequence [Homo sapiens]	0.21
2311	AJ409108	Entamoeba histolytica rpl27a-2 gene for ribosomal protein large subunit 27a-2, exons 1-2	0.009
2312	U26556	Human ferritin H (FTHL13) pseudogene	0.008

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
2313	AF126320	Protoclythia modesta 12S ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	0.26
2314	AL137590	Homo sapiens mRNA; cDNA DKFZp434K0610 (from clone DKFZp434K0610)	2
2315	Z81471	Caenorhabditis elegans cosmid C14B4, complete sequence	0.029
2316	AE001567	Helicobacter pylori, strain J99 section 128 of 132 of the complete genome	0.028
2317	U47913	Tribolium freemani Woot retrotransposon, partial sequence and 3' insertion junction F3(1)	0.081
2318	XM_037521	Homo sapiens centrosomal P4.1-associated protein; uncharacterized bone marrow protein BM032 (BM032), mRNA	2.2
2319	AF269701	Staphylococcus epidermidis strain SR1 clone step.1017g02 genomic sequence	0.7
2320	AF378183	Oryza sativa cultivar Milyang23 cytosolic fructose-1 mRNA, partial cds	6.9
2321	AY019090	Oryza sativa microsatellite MRG1415 containing (AT)X26, genomic sequence	0.085
2322	AL449163	Human DNA sequence from clone RP11-533E16 on chromosome 6, complete sequence [Homo sapiens]	0.00004
2323	M19540	Adenovirus type 41 DNA-binding protein (DBP) gene, exons 2 and 3, 23K protease, complete cds, hexon and 100K protein genes, last exons	0.026
2324	AJ272029	Homo sapiens partial CD30 gene for cytokine receptor CD30 and promoter region	0.003
2325	AF082966	Homo sapiens genomic sequence	0.75
2326	AE002940	Drosophila melanogaster genomic scaffold 142000013385820, complete sequence	0.028
2327	Z54147	Human DNA sequence from cosmid L129H7, Huntington's Disease Region, chromosome 4p16.3 contains CpG island	0.001
2328	D12590	Rattus norvegicus DNA, RFLP marker at locus A403	0.077
2329	XM_035524	Homo sapiens KIAA1201 protein (KIAA1201), mRNA	0.025
2330	XM_003575	Homo sapiens soluble liver antigen/liver pancreas antigen (LOC51091), mRNA	4E-27
2331	BC009503	Homo sapiens, G1 to S phase transition 1, clone MGC:1735 IMAGE:2822947, mRNA, complete cds	0.69
2332	BC005572	Mus musculus, golgi vesicular membrane trafficking protein p18, clone MGC:11601 IMAGE:3967968, mRNA, complete cds	0.78
2333	U39726	Mycoplasma genitalium section 48 of 51 of the complete genome	0.086
2334	XM_039942	Homo sapiens Meis (mouse) homolog 3 (MEIS3), mRNA	0.72
2335	X67506	C.thermocellum ancA gene	0.084
2336	AL117553	Homo sapiens mRNA; cDNA DKFZp564F1171 (from clone DKFZp564F1171)	0.22
2337	AF115574	Pisum sativum pathogenesis-related protein (DRR206-c) gene, complete cds	0.009
2338	Y11874	M.musculus uPA gene, promoter sequence	2.3

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
2339	BC008277	Mus musculus, Similar to Endothelin receptor type A, clone MGC:6567 IMAGE:2812426, mRNA, complete cds	2.2
2340	XM_009543	Homo sapiens transcription factor AP-2 gamma (activating enhancer-binding protein 2 gamma) (TFAP2C), mRNA	0.21
2341	NM_015809	Mus musculus keratin-associated protein 5-4 (Krtap5-4), mRNA	0.42
2342	AE000813	Methanobacterium thermoautotrophicum from bases 206991 to 217929 (section 19 of 148) of the complete genome	5.2
2343	XM_034632	Homo sapiens hypothetical protein PRO2832 (PRO2832), mRNA	0.0000005
2344	XM_034229	Homo sapiens similar to hypothetical protein FLJ14260 (H. sapiens) (LOC90803), mRNA	0.069
2345	XM_033361	Homo sapiens 62537 (FLJ00024), mRNA	0.008
2346	BC005332	Homo sapiens, Similar to immunoglobulin kappa constant, clone MGC:12418 IMAGE:3934658, mRNA, complete cds	3E-33
2347	AF321120	Mus musculus gap junction membrane channel protein alpha 8 (Gja8) gene, complete cds	2.1
2348	AB054512	Berardius bairdii DNA, SINE flanking sequence Tuti35 locus	0.77
2349	Z98549	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-14, complete sequence	0.029
2351	XM_033483	Homo sapiens hypothetical gene supported by L39957; L43086; M85256; M99603; S56182; S73911; U07989; U79763; U96290; U96294; U96397; X58082; Z18327; AB006847; AB027436; AB027438; AF007572; AF035035; AF052535; AF099196; AF103384; AF103390; AF103466; AF10>	8E-33
2352	XM_033483	Homo sapiens hypothetical gene supported by L39957; L43086; M85256; M99603; S56182; S73911; U07989; U79763; U96290; U96294; U96397; X58082; Z18327; AB006847; AB027436; AB027438; AF007572; AF035035; AF052535; AF099196; AF103384; AF103390; AF103466; AF10>	1E-27
2353	XM_033483	Homo sapiens hypothetical gene supported by L39957; L43086; M85256; M99603; S56182; S73911; U07989; U79763; U96290; U96294; U96397; X58082; Z18327; AB006847; AB027436; AB027438; AF007572; AF035035; AF052535; AF099196; AF103384; AF103390; AF103466; AF10>	8E-33
2354	XM_043728	Homo sapiens hypothetical gene supported by AF074988 (LOC92227), mRNA	0.001
2355	AE001425	Plasmodium falciparum chromosome 2, section 62 of 73 of the complete sequence	6.4
2356	XM_033483	Homo sapiens hypothetical gene supported by L39957; L43086; M85256; M99603; S56182; S73911; U07989; U79763; U96290; U96294; U96397; X58082; Z18327; AB006847; AB027436; AB027438; AF007572; AF035035; AF052535; AF099196; AF103384; AF103390; AF103466; AF10>	9E-14
2357	AF184072	Homo sapiens target of methylation-induced silencing 1 (TMS1) gene, complete cds	6.6

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
2358	XM_032347	Homo sapiens region containing TLS-associated serine-arginine protein 1; TLS-associated serine-arginine protein 2; TLS-associated serine-arginine protein 2; TLS-associated serine-arginine protein 2; TLS-associated serine-arginine protein 1; TLS-associa>	0
2360	X54807	Human CYP2C8 gene for cytochrome P-450, 5' flank and exon 1	0.00003
2361	X67506	C.thermocellum ancA gene	0.054
2362	AL513350	Human DNA sequence from clone RP11-509D8 on chromosome 9, complete sequence [Homo sapiens]	0.003
2363	AF020663	Homo sapiens myotubularin (MTM1) gene, promoter and exon 1	0.068
2364	U43626	Human chromosome 15q11-q13 putative DNA replication origin in the g-aminobutyric acid receptor b3 and a5 gene cluster	0.059
2365	AY019090	Oryza sativa microsatellite MRG1415 containing (AT)X26, genomic sequence	0.081
2366	U27586	Cytophaga heparina heparinase III (HepC) gene, complete cds	0.38
2367	XM_047192	Homo sapiens similar to MYOSIN HEAVY CHAIN, CARDIAC MUSCLE ALPHA ISOFORM (MYHC-ALPHA) (M. musculus) (LOC92771), mRNA	e-133
2368	M20319	S.cerevisiae ATR1 gene conferring aminotriazole resistance, complete cds	1.3
2369	XM_051036	Homo sapiens carbohydrate (keratan sulfate Gal-6) sulfotransferase 1 (CHST1), mRNA	4.6
2370	AB062951	Macaca fascicularis brain cDNA clone:QmoA-12201, full insert sequence	1.5
2371	U29335	Pisum sativum clone MFRTPCR62 wound-inducible cytochrome P450 mRNA, partial cds	0.41
2372	AF272630	Ureaplasma urealyticum serovar 14 23S ribosomal RNA and 5S ribosomal RNA genes, complete sequence; and dihydrofolate reductase (folA) gene, partial cds	0.061
2373	AF179375	Mycoplasma fermentans orfD1 gene, Insertion sequence IS1630D, orfD2 gene	0.61
2374	X16876	Soybean ENOD2B gene for Ngm-75	0.96
2375	AF263831	Homo sapiens chromosome 11 DNaseI hypersensitive region	2.7
2376	AF157162	Syzygites megalocarpus 18S ribosomal RNA gene, partial sequence	5.4
2377	AJ308588	Medicago truncatula partial mRNA for nodulin 25 (nod25 gene), clone 3	4.6
2378	X02870	Bovine gene for cytokeratin VIb	0.053
2379	AL590157	Human DNA sequence from clone RP13-420K18 on chromosome X, complete sequence [Homo sapiens]	4E-08
2380	AF282242	Plasmodium falciparum strain Dd2 chloroquine resistance marker protein gene, complete cds	4.2
2381	Z24745	A.thaliana 2S albumin gene isoforms 1 and 2, complete CDS's	0.6

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
2382	AL035418	Human DNA sequence from clone RP1-141I3 on chromosome 22q13.1-13.33 Contains a GSS, complete sequence [Homo sapiens]	1.6
2383	Y17968	Gallus gallus mRNA for high mobility group 1 protein	1.5
2384	XM_034735	Homo sapiens similar to hypothetical protein FLJ21463 (H. sapiens) (LOC90883), mRNA	5.6
2385	AF001415	Arabidopsis thaliana 14-3-3-like protein GF14 upsilon (GRF5) gene, complete cds	1.3
2386	XM_009026	Homo sapiens retinol dehydrogenase 8 (all-trans) (RDH8), mRNA	1.9
2387	XM_003095	Homo sapiens zinc finger protein 288 (ZNF288), mRNA	1.8
2388	AE003083	Drosophila melanogaster genomic scaffold 142000013385449, complete sequence	0.51
2389	AE002798	Drosophila melanogaster genomic scaffold 142000013385466, complete sequence	0.018
2390	AL359506	Human DNA sequence from clone CTD-2007A7 on chromosome 20. Contains GSSs, complete sequence [Homo sapiens]	0.28
2391	U32726	Haemophilus influenzae Rd section 41 of 163 of the complete genome	0.3
2392	AB010468	Cyprinus carpio mRNA for CXC chemokine receptor-1, complete cds	0.9
2393	AE006886	Sulfolobus solfataricus section 245 of 272 of the complete genome	0.19
2394	M19810	Human apolipoprotein B-100 (apoB) gene, exon 4	0.43
2395	AB005548	Homo sapiens gene for squamous cell carcinoma antigen 2, partial cds	0.0004
2396	AJ318337	Plasmodium falciparum krueppel1 gene for Krueppel-like protein	0.62
2397	U01102	Human lung Clara cells 10 kda secretory protein (CC10) gene, satellite and Alu repeat sequences, complete cds	3.8
2398	AK017766	Mus musculus 8 days embryo cDNA, RIKEN full-length enriched library, clone:5730512J02, full insert sequence	1.7
2399	AE000032	Mycoplasma pneumoniae M129 section 48 of 63 of the complete genome	0.55
2400	AF333234	Homo sapiens receptor activator of nuclear factor kappa B ligand (RANKL) gene, promoter region	0.22
2401	BC010652	Homo sapiens, clone MGC:9753 IMAGE:3855206, mRNA, complete cds	1.8
2402	AK007856	Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810054D07, full insert sequence	2E-94
2403	AF172723	Homo sapiens integrin alpha 10 subunit (ITGA10) gene, exons 7 through 17 and partial cds	0.21
2404	NM_026570	Mus musculus glioma-amplified sequence-41 (Gas41-pending), mRNA	1.1
2405	U78770	Mus musculus spasmolytic polypeptide (mSP) gene, complete cds	1.8

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
2406	U26729	Human neprilysin gene, non-coding exon 3	0.92
2407	AE006346	Lactococcus lactis subsp. lactis IL1403 section 108 of 218 of the complete genome	2
2408	AF258783	Felis catus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds	0.23
2409	AC007280	Homo sapiens BAC clone RP11-332C7 from 7p11.2-p21, complete sequence	0.39
2410	D13065	Mycoplasma capricolum mcs4 gene for MCS4 RNA	0.062
2411	AF196058	Drosophila pseudoobscura strain PSU606 period (per) gene, intron 4, partial sequence	1.5
2412	AF370534	Arabidopsis thaliana Putative L-ascorbate peroxidase (AT4g09010) mRNA, complete cds	1.8
2413	AF084197	Pongo pygmaeus gamma-aminobutyric acid receptor A5 subunit duplicated gene, 5'UTR region	0.00009
2414	Y17045	Plasmodium falciparum gltS gene	0.063
2415	AL021177	Caenorhabditis elegans cosmid Y1A5A, complete sequence	0.22
2416	AJ238847	Drosophila melanogaster mRNA for drosophila dodeca-satellite protein 1 (DDP-1)	0.22
2417	AB056333	Macaca fascicularis brain cDNA, clone:QflA-13486	e-126
2418	AF104821	Danio rerio Hlx2 gene, promoter region	0.056
2419	AF138960	Neospora caninum ycf24 protein (ycf24) gene, partial cds; DNA dependent RNA polymerase beta subunit (rpoB) gene, complete cds; and DNA dependent RNA polymerase beta subunit' (rpoC1) gene, partial cds, plastid genes for plastid products	0.21
2420	AF338712	Emeus crassus mitochondrion, partial genome	1.3
2421	Z82625	R.prowazekii genomic DNA fragment (clone A396F)	0.46
2422	XM_015945	Homo sapiens hypothetical protein FLJ13842 (FLJ13842), mRNA	6E-62
2423	X57010	Human COL2A1 gene for collagen II alpha 1 chain, exons E2-E15	0.63
2424	AF283525	Homo sapiens FIP2 gene, exons 11, 12 and 13	4E-71
2425	AK013530	Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched library, clone:2900012M01, full insert sequence	5.3
2426	D86077	Homo sapiens DNA for cyclin G, partial cds	0.02
2427	X94208	H.sapiens TPR gene (1121bp)	0.19
2428	AF211528	Nicotiana tabacum Avr9/Cf-9 rapidly elicited protein 4 (ACRE4) mRNA, complete cds	0.22
2430	L35688	Homo sapiens (subclone H9 10_d10 from P1 LBL#3) DNA sequence	5E-08
2431	U59711	Cavia porcellus seminal vesicle secretory protein SVP-1/-3/-4 gene, complete cds	0.14
2432	AK023305	Homo sapiens cDNA FLJ13243 fis, clone OVARC1000622	0.002
2433	AB048868	Macaca fascicularis brain cDNA, clone:QnpA-10055	0.044
2434	AF167585	Homo sapiens clone C13 immunoglobulin heavy chain variable region gene, partial cds	0.13
2435	AB013796	Ceratopteris richardii mRNA for CRHB6, complete cds	0.024

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
2436	AF071481	Homo sapiens potassium channel (KCNQ3) gene, exon 4	1.9
2437	AF282242	Plasmodium falciparum strain Dd2 chloroquine resistance marker protein gene, complete cds	0.22
2438	AY018307	Oryza sativa microsatellite MRG0632 containing (AT)X14, genomic sequence	0.073
2439	Z74273	S.cerevisiae chromosome IV reading frame ORF YDL225w	0.028
2440	AY021257	Oryza sativa microsatellite MRG3582 containing (TA)X22, genomic sequence	0.018
2441	XM_012164	Homo sapiens STE20-like kinase (JIK), mRNA	0.27
2442	XM_036587	Homo sapiens hypothetical protein DKFZp564B1023 (DKFZP564B1023), mRNA	0.008
2443	AL112743	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation	0.069
2444	AB020575	Conocephalum conicum psbA gene, complete cds, strain J type	0.074
2445	BC001772	Homo sapiens, Similar to glutaminyl-tRNA synthetase, clone MGC:1525 IMAGE:3543728, mRNA, complete cds	5.5
2446	AF289113	Drosophila montana clone mon 10 transposon Penelope gene sequence	0.064
2447	XM_015806	Homo sapiens hypothetical protein FLJ22621 (FLJ22621), mRNA	0
2448	AY047559	Drosophila melanogaster GH07383 full length cDNA	0.92
2449	XM_052662	Homo sapiens amino-terminal enhancer of split (AES), mRNA	0.59
2450	AL138723	Human DNA sequence from clone RP11-446N1 on chromosome 6, complete sequence [Homo sapiens]	0.008
2451	AF151389	Dermatobia hominis strain Ponta Grossa tRNA-Ile gene, partial sequence; D-loop, complete sequence; and 12S ribosomal RNA, partial sequence; mitochondrial genes for mitochondrial products	0.46
2452	NM_018123	Homo sapiens hypothetical protein FLJ10517 (FLJ10517), mRNA	0.21
2453	XM_042803	Homo sapiens hypothetical gene supported by AL359651 (LOC92091), mRNA	1.9
2454	AE001397	Plasmodium falciparum chromosome 2, section 34 of 73 of the complete sequence	5
2455	AF017996	Mus musculus lysosomal acid lipase gene, promoter region	0.022
2456	XM_028409	Homo sapiens KIAA1871 protein (KIAA1871), mRNA	0.0003
2457	XM_051692	Homo sapiens KIAA1705 protein (KIAA1705), mRNA	0.0003
2458	U00037	Caenorhabditis elegans cosmid T20H4	0.073
2459	AL138748	Human DNA sequence from clone RP4-732E19 on chromosome Xq21.1-21.33 Contains GSSs, complete sequence [Homo sapiens]	0.2
2460	AF052744	Homo sapiens transcriptional repressor p54 gene, promoter region and partial cds	1.8
2461	XM_007006	Homo sapiens KIAA0985 protein (KIAA0985), mRNA	1.7
2462	AF303046	Homo sapiens prostinogen mRNA, complete cds	0.44
2463	AK023562	Homo sapiens cDNA FLJ13500 fis, clone PLACE1004693	e-116

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
2464	AF076692	Aspergillus fumigatus aureobasidin-resistance protein (aur1) mRNA, complete cds	3.2
2465	AF054616	Glossina morsitans morsitans thrombin inhibitor precursor (TTI) mRNA, complete cds	0.44
2466	Z54147	Human DNA sequence from cosmid L129H7, Huntington's Disease Region, chromosome 4p16.3 contains CpG island	4E-09
2467	XM_040290	Homo sapiens glutamate receptor, ionotropic, AMPA 1 (GRIA1), mRNA	4
2468	AY026512	Rattus norvegicus dynein-associated protein RKM23 (km23) mRNA, complete cds	1.5
2469	AY033091	Plasmodium berghei Pbs36 gene, complete cds	0.0008
2470	XM_051572	Homo sapiens heat shock transcription factor 2 (HSF2), mRNA	2E-42
2471	AF287003	Floriceps minacanthus 18S ribosomal RNA gene, complete sequence	1.8
2472	X99872	Sulfolobus acidocaldarius pyrB gene	0.2
2473	U49451	Bombina orientalis SAP bombesin preprohormone mRNA, complete cds	0.56
2474	AC024819	Caenorhabditis elegans cosmid Y55B1AL, complete sequence	6.9
2475	AF282602	Litoria subglandulosa strain SAMA_R51051 NADH dehydrogenase subunit 4 (ND4) gene, partial cds; mitochondrial gene for mitochondrial product	0.073
2476	AL591343	Human DNA sequence from clone RP11-260H5 on chromosome 6, complete sequence [Homo sapiens]	0.24
2477	Z69375	Human DNA sequence from cosmid L174G8, Huntington's Disease Region, chromosome 4p16.3	3E-16
2478	U32174	Dictyostelium discoideum spore lysis A (splA) gene, complete cds	0.25
2479	XM_045095	Homo sapiens KIAA1320 protein (KIAA1320), mRNA	0.53
2480	AY035224	Gallus gallus cardiac muscle factor 1 gene, partial cds	0.78
2481	D14567	Penicillium urticae mitochondrial l-rRNA (large rRNA) gene and its flanking region	0.25
2482	AF119218	HIV-1 strain 96CG38.10 from Republic of the Congo, envelope glycoprotein, C2-C4 region (env) gene, partial cds	0.002
2483	AF386963	Arabidopsis thaliana Unknown protein mRNA, complete cds	0.057
2484	Z19595	C.elegans her-1 gene	0.19
2485	AE006341	Lactococcus lactis subsp. lactis IL1403 section 103 of 218 of the complete genome	6.1
2486	AL583831	Human DNA sequence from clone RP11-469L10 on chromosome 6, complete sequence [Homo sapiens]	0.23
2487	NC_001617	Human rhinovirus 89	0.078
2488	X65859	H.sapiens pseudogene for the low affinity IL-8 receptor	5.7
2489	AE007508	Streptococcus pneumoniae section 191 of 194 of the complete genome	0.63
2490	AF199367	Entamoeba histolytica cdc48-like protein gene, complete cds	0.56
2491	AF211160	Pseudonaja textilis tissue-type liver phospholipase A2 inhibitor beta subunit isoform PTI-2B mRNA, complete cds	2.2

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
2492	AE000813	Methanobacterium thermoautotrophicum from bases 206991 to 217929 (section 19 of 148) of the complete genome	5.5
2493	U67604	Methanococcus jannaschii section 146 of 150 of the complete genome	1
2494	D16253	Pichia canadensis mitochondrial gene for NADH dehydrogenase subunit 5, complete cds	0.006
2495	NC_001530	Human papillomavirus type 47, complete genome	5.4
2496	AF286437	Pseudavenzoaria ochropodis from host Tringa ochropus 16S ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	0.4
2497	XM_006069	Homo sapiens wee1+ (S. pombe) homolog (WEE1), mRNA	3E-26
2498	AF314019	Rana boylii NADH dehydrogenase subunit I (ND1) gene, partial cds; tRNA-Ile, tRNA-Gln, and tRNA-Met genes, complete sequence; NADH dehydrogenase subunit II (ND2) gene, complete cds; tRNA-Trp, tRNA-Ala, tRNA-Asn, tRNA-Cys, and tRNA-Tyr genes, complete se>	1.4
2499	AJ314911	Dictyostelium discoideum DrnA gene for putative RNaseIII, exons 1-3	0.51
2500	M35228	Vesicular stomatitis virus (strain 86-GM-B) glycoprotein gene, complete cds	0.45
2501	AB021290	Homo sapiens gene for chondromodulin-1, promoter and partial cds	0.72
2502	AJ307807	Astrammina rara partial 18S rRNA gene, isolate A44	3.5
2503	AB005148	Bos taurus mRNA for IL-1 receptor antagonist, complete cds	0.84
2504	AE002687	Drosophila melanogaster genomic scaffold 142000013385743, complete sequence	0.23
2505	AF053496	Caenorhabditis elegans beta chain spectrin homolog Sma1 (sma1) mRNA, complete cds	5.9
2506	X59611	E.coli IncFV plasmid pED208 oriT region with genes traM, traJ and traY (part.)	0.043
2507	XM_051897	Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA	3E-66
2508	AJ132890	Bos taurus mRNA for acetyl-CoA-carboxylase	0.18
2509	Y13537	Homo sapiens LAG-3 gene, 3' region	1.7
2510	AE002149	Ureaplasma urealyticum section 50 of 59 of the complete genome	0.027
2511	AF170573	Influenza C virus C/Johannesburg/1/66 segment 5 nucleoprotein (NP) gene, partial cds	2.4
2512	AK016507	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4931439C15, full insert sequence	6.8
2513	AL354664	Human DNA sequence from clone RP11-209D8 on chromosome 6. Contains ESTs and GSSs. Contains part of the COL12A1 gene for collagen type XII, alpha 1, complete sequence [Homo sapiens]	0.082
2514	AB042531	Pisum sativum PsEXT mRNA for xyloglucan endotransglycosylase, complete cds	2E-12

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
2515	AL590371	Human DNA sequence from clone RP11-295H23 on chromosome 6, complete sequence [Homo sapiens]	1.5
2516	AF334780	Homo sapiens pregnancy-induced growth inhibitor OKL38 gene, partial cds	0.8
2517	AF362371	Dictyostelium discoideum histidine kinase DhkI (dhkI) gene, complete cds	0.021
2518	NM_012608	Rattus norvegicus Membrane metallo-endopeptidase (neutral endopeptidase/enkephalinase) (Mme), mRNA	2
2519	BC007173	Mus musculus, clone IMAGE:3493127, mRNA, partial cds	5E-53
2520	Y13870	Homo sapiens mRNA containing (CAG)6 repeat, clone CZ-CAG-12	0.06
2521	AF051769	Homo sapiens hyaluronidase-like pseudogene 1 (HYALP1), partial sequence	0.009
2522	AF309947	Dictyostelium discoideum Rac1A (rac1A) gene, complete cds; and unknown gene	0.77
2523	AF128392	Arabidopsis thaliana BAC F15P23	0.22
2524	AK020739	Mus musculus adult male spinal cord cDNA, RIKEN full-length enriched library, clone:A330106L17, full insert sequence	7.2
2525	Y09472	B.taurus gene encoding preprododecapeptide	0.24
2526	D87922	Rat DNA for 3'UTR of skeletal muscle sodium channel, partial sequence	0.4
2527	U70865	Carassius auratus CCK8 precursor, mRNA, complete cds	0.67
2528	AB012624	Homo sapiens FLI1 gene for ERGB transcription fuctor, intron 4 and partial cds	0.054
2529	AF180492	Crocuta crocuta microsatellite Ccr12 sequence	0.083
2530	AL078640	Human DNA sequence from clone 536P6 on chromosome 22. Contains an EST, complete sequence [Homo sapiens]	2E-11
2531	Z63184	H.sapiens CpG island DNA genomic Mse1 fragment, clone 7a1, forward read cpg7a1.ft1d	6E-22
2532	AL162055	Homo sapiens mRNA; cDNA DKFZp761M2223 (from clone DKFZp761M2223)	0.022
2533	AE001392	Plasmodium falciparum chromosome 2, section 29 of 73 of the complete sequence	6.5
2535	AF202903	Sporopachydermia cereana var. D77-321B internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence	0.14
2536	U59487	Borrelia burgdorferi P35 antigen protein gene, and 7.5 kDa lipoprotein gene, complete cds	0.029
2537	XM_030999	Homo sapiens KIAA0444 protein (KIAA0444), mRNA	0.012
2538	AF302838	Mus musculus putative tumor suppressor LEU2 gene, exons 1 and 2	0.63
2539	AF125423	Bresiliidae gen. sp. LSP21-1 cytochrome oxidase I gene, partial cds; mitochondrial gene for mitochondrial product	0.66
2540	AP001348	Homo sapiens genomic DNA, chromosome 21q21.1-q21.2 clone:f39G8, LL56-APP region, complete sequence	0.42

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
2541	XM_028324	Homo sapiens hypothetical protein FLJ14195; KIAA1714 protein (FLJ14195), mRNA	8E-98
2542	AF238860	Streptococcus mutans mutacin I biosynthesis gene cluster, partial sequence	4.6
2543	AE005391	Escherichia coli O157:H7 EDL933 genome, contig 3 of 3, section 10 of 290	1.6
2544	AK024518	Homo sapiens cDNA: FLJ20865 fis, clone ADKA01850	0.06
2545	AK026595	Homo sapiens cDNA: FLJ22942 fis, clone KAT08170, highly similar to HUMMHBW62 Homo sapiens (clone pMF18) MHC class I HLA-Bw62 mRNA	4E-39
2546	AL449163	Human DNA sequence from clone RP11-533E16 on chromosome 6, complete sequence [Homo sapiens]	2.3
2547	AJ305053	Caprine arthritis-encephalitis virus proviral partial pol gene for Pol protein (reverse transcriptase), isolate CAEV Br/UFRGS-2/C767	0.69
2548	AF283067	Homo sapiens clone 3ptel_c11bt3 sequence	1E-41
2549	AF286431	Bychovskiata intermedia from host Charadrius leschenaulti 16S ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	0.94
2550	L35232	Schizosaccharomyces pombe deoxyribonuclease (exo2) gene, exons 1-3, complete cds	0.93
2551	AF319044	Methanosarcina acetivorans strain C2A MtaF (mtaF) and MtaG (mtaG) genes, complete cds	0.034
2552	XM_018334	Homo sapiens hypothetical protein FLJ22418 (FLJ22418), mRNA	0.013
2553	U35862	Visna virus clone 678 env3.2 envelope polyprotein (env) gene, partial cds	0.17
2554	M20005	N.crassa conidation-specific protein genes con-10 (complete cds.) and con-13 (3' flank)	0.079
2555	AB050531	Macaca fascicularis brain cDNA, clone:QnpA-20907	1.4
2556	AB009693	Mus musculus gene for mafG, complete cds	5.6
2557	U67593	Methanococcus jannaschii section 135 of 150 of the complete genome	0.024
2558	XM_028292	Homo sapiens x 009 protein (MDS009), mRNA	4
2559	U67578	Methanococcus jannaschii section 120 of 150 of the complete genome	1.8
2560	AE001759	Thermotoga maritima section 71 of 136 of the complete genome	1.9
2561	AF363230	Phascolion strombi homeodomain transcription factor Gsx (Gsx) gene, partial cds	0.59
2562	NM_019211	Rattus norvegicus RAS guanyl releasing protein 1 (Rasgrp), mRNA	2.5
2563	U60070	Solanum tuberosum disease resistance homolog (St121) gene, partial cds	0.68
2564	AE006593	Streptococcus pyogenes M1 GAS strain SF370, section 122 of 167 of the complete genome	0.062

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
2565	AF147231	Wilkesia gymnoxiphium ASAPETALA1-A (ASAP1-A) gene, exons 3 through 8, partial cds	0.026
2566	AK018656	Mus musculus adult male cecum cDNA, RIKEN full-length enriched library, clone:9130402C12, full insert sequence	0.74
2567	X65859	H.sapiens pseudogene for the low affinity IL-8 receptor	5.4
2568	XM_030855	Homo sapiens similar to KIAA1361 protein (H. sapiens) (LOC90315), mRNA	0.65
2569	XM_031726	Homo sapiens hypothetical protein FLJ12577 (FLJ12577), mRNA	2.1
2570	Z68749	Caenorhabditis elegans cosmid F56H11, complete sequence	0.025
2571	AE000020	Mycoplasma pneumoniae M129 section 60 of 63 of the complete genome	0.17
2572	U63091	Oryctolagus cuniculus beta-globin-like gene cluster locus control region	0.13
2573	BC001339	Homo sapiens, clone IMAGE:3461987, mRNA, partial cds	1E-31
2574	U86962	Dictyostelium discoideum MigA (migA) gene, complete cds	0.9
2575	AY021629	Oryza sativa microsatellite MRG3954 containing (TA)X30, genomic sequence	6.5
2576	AB063077	Macaca fascicularis brain cDNA clone:QtrA-13349, full insert sequence	0.59
2577	XM_044332	Homo sapiens piwi (Drosophila)-like 1 (PIWIL1), mRNA	4E-28
2578	Z97185	S.pombe chromosome I cosmid c16A10	1.5
2579	L43603	Gallus gallus Na+/K+-ATPase alpha-1 subunit gene, promoter region	0.7
2580	AC016645	Homo sapiens chromosome 5 clone RP11-54A24, complete sequence	0.0001
2581	AE001408	Plasmodium falciparum chromosome 2, section 45 of 73 of the complete sequence	0.25
2582	AF067699	Ischnura prognata cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds	0.45
2583	AC026061	Homo sapiens BAC clone RP11-223K9 from Y, complete sequence	2E-15
2584	Y13537	Homo sapiens LAG-3 gene, 3' region	0.24
2585	AE005977	Caulobacter crescentus section 303 of 359 of the complete genome	5.5
2586	U13190	Angiostrongylus cantonensis clone G-2 retrotransposable element AcT-1	0.077
2587	AF364550	Drosophila melanogaster transposon cruiser, complete sequence	0.07
2588	XM_034146	Homo sapiens CD36 antigen (collagen type I receptor, thrombospondin receptor) (CD36), mRNA	0.62
2589	AF014580	Gonioctena viminalis 12S ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence	2.1
2590	XM_042643	Homo sapiens hypothetical protein DKFZp434G131 (DKFZP434G131), mRNA	0.68
2591	BC004324	Homo sapiens, ribosomal protein S16, clone MGC:10931 IMAGE:3628799, mRNA, complete cds	0.006

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
2592	U42430	Mesocricetus auratus CD36 mRNA, complete cds	0.71
2593	U16137	Saccharomyces cerevisiae Mvp1p (MVP1) gene, complete cds	4.7
2594	AB047954	Macaca fascicularis brain cDNA, clone:QnpA-12630	0.65
2595	AF261697	Homo sapiens clone 17ptel_c39t3 sequence	0.024
2596	AF162598	Drosophila virilis strain w159 zeste protein (z) gene, partial cds	0.063
2597	U40255	Peromyscus sejugis ND3 and ND4L genes, complete cds, tRNA(arg) gene, complete sequence, tRNA(gly) gene, partial sequence, and ND4 gene, partial cds, mitochondrial genes encoding mitochondrial products	0.67
2598	Z63251	H.sapiens CpG island DNA genomic Mse1 fragment, clone 7h10, forward read cpg7h10.f1a	0.003
2599	U68150	Chelonus sp. 16S mitochondrial ribosomal RNA, mitochondrial gene, partial sequence	0.003
2600	AF138281	Arabidopsis thaliana phospholipase D-gamma-2 mRNA, complete cds	0.071
2601	AF069985	Mus musculus nitrilase homolog 1 (Nit1) gene, alternatively spliced product, complete cds	0.39
2602	M83134	Human germline IgH chain (hv3005) V3-region	0.35
2603	AF275245	Trama rara 12S small subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and 16S large subunit ribosomal RNA gene, partial sequence; mitochondrial genes for mitochondrial products	0.59
2604	X93302	S.cerevisiae mRNA for Msn5 protein	0.05
2605	AK015536	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930470H18, full insert sequence	0.7
2606	AC087735	Caenorhabditis elegans cosmid Y35H6, complete sequence	0.022
2607	AJ271002	Mus musculus TFF1/pS2 gene for Trefoil Factor1/pS2, exons 1-3	0.73
2608	NM_019664	Mus musculus potassium inwardly-rectifying channel, subfamily J, member 15 (Kcnj15), mRNA	5.8
2609	AL450330	Human DNA sequence from clone RP11-162H13 on chromosome 6 Contains GSSs, complete sequence [Homo sapiens]	0.25
2610	Z24671	H. sapiens (D1S514) DNA segment containing (CA) repeat; clone AFMa151za5; single read	0.007
2611	AE000773	Aquifex aeolicus section 105 of 109 of the complete genome	0.34
2612	X93508	E.histolytica mRNA for 170kDa subunit of galactose/N-acetylgalactosamine binding lectin	0.054
2613	AK003780	Mus musculus 18 days embryo cDNA, RIKEN full-length enriched library, clone:1110018I21, full insert sequence	0.15
2614	L81687	Homo sapiens (subclone 1_c12 from P1 H54) DNA sequence, complete sequence	5.2
2615	M10090	Human myoglobin gene, exon 1	0.13
2616	NC_002670	Bacteriophage bIL311, complete genome	0.061
2617	AB016259	Oryzias latipes gene for cardiac muscle actin, complete cds	0.19
2618	U67578	Methanococcus jannaschii section 120 of 150 of the complete genome	2

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
2619	AF186258	Homo sapiens sulfotransferase 1C1 (SULT1C1) gene, exons 2 and 3	0.002
2620	X79777	P.furiosus aor, cmo and ado-hcy genes	6.1
2621	XM_042013	Homo sapiens cell division cycle 34 (CDC34), mRNA	1.5
2622	AB044879	Equus caballus DNA, microsatellite TKY379	0.18
2623	AF117951	Mus musculus lysyl oxidase-like protein 2 mRNA, partial cds	0.015
2624	AF310887	Dictyostelium discoideum RacB (racB) gene, partial cds; and unknown gene	0.17
2625	XM_034353	Homo sapiens KIAA1500 protein (KIAA1500), mRNA	4E-89
2626	AK021859	Homo sapiens cDNA FLJ11797 fis, clone HEMBA1006182	0
2627	AF280894	Pongo pygmaeus clone 3458 chromosome Xq genomic sequence	0.0002
2628	AE001396	Plasmodium falciparum chromosome 2, section 33 of 73 of the complete sequence	0.074
2629	XM_046097	Homo sapiens similar to RIKEN cDNA 2610307I21 gene; hypothetical protein, MNCb-4273 (M. musculus) (LOC92606), mRNA	0.58
2630	X02438	Leishmania tarentolae maxicircle DNA fragment	6.2
2631	AF181582	Bombus terrestris 16S large subunit ribosomal RNA gene, partial sequence	0.2
2632	M34149	S.cerevisiae mitochondrial gap 12 sequence	0.64
2633	AJ400612	Trioxys angelicae partial mitochondrial ATPase 6 gene for ATPase 6 subunit	0.65
2634	AB021290	Homo sapiens gene for chondromodulin-1, promoter and partial cds	0.75
2635	AJ133756	Drosophila melanogaster mRNA for jim zinc finger protein	0.028
2636	AL121589	Human DNA sequence from clone RP5-1140M3 on chromosome 20. Contains GSSs, complete sequence [Homo sapiens]	0.002
2637	XM_040430	Homo sapiens hypothetical protein FLJ10599 (FLJ10599), mRNA	0.24
2638	AB015484	Dugesia japonica mRNA for myosin heavy chain, complete cds	0.2
2639	XM_008161	Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA	0.075
2640	AF024621	Mus musculus gamma-aminobutyric acid receptor rho2 subunit mRNA, complete cds	6.8
2641	L78777	Homo sapiens (subclone 2_b8 from P1 H49) DNA sequence	8E-11
2642	AE001028	Archaeoglobus fulgidus section 79 of 172 of the complete genome	2
2643	AB013796	Ceratopteris richardii mRNA for CRHB6, complete cds	0.028
2644	X03848	Chlorella ellipsoidea chloroplast 16S-23S DNA spacer and ORF1 to ORF4 DNA	0.086
2645	Z21938	B.aphidicola trpE and trpG genes for anthranilate synthase, components I and II	0.74
2646	XM_039805	Homo sapiens hypothetical protein MGC3040 (MGC3040), mRNA	2.1

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
2647	AF267217	Candidatus Carsonella ruddii natural-host Pachypsylla celtidis ATP synthase alpha subunit (atpA) gene, partial cds; ATP synthase gamma subunit (atpG) gene, complete cds; and ATP synthase beta subunit (atpD) gene, partial cds	0.71
2648	L39786	Lupinus angustifolius conglutin gamma gene, complete cds	0.084
2649	AB049879	Macaca fascicularis brain cDNA, clone:QnpA-18812	0.74
2650	AE002648	Drosophila melanogaster genomic scaffold 142000013385436, complete sequence	2.1
2651	XM_032228	Homo sapiens hypothetical gene supported by AL080068 (LOC90510), mRNA	2.4
2652	XM_044529	Homo sapiens calcium and integrin binding protein (DNA-dependent protein kinase interacting protein) (SIP2-28), mRNA	0.76
2653	AB035494	Alternaria alternata gene for Akt3-2, complete cds	0.7
2654	AE001381	Plasmodium falciparum chromosome 2, section 18 of 73 of the complete sequence	0.27
2655	XM_013145	Homo sapiens Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region, gene 1 (AMMECR1), mRNA	0.65
2656	NM_007976	Mus musculus coagulation factor V (F5), mRNA	0.077
2657	U47913	Tribolium freemani Woot retrotransposon, partial sequence and 3' insertion junction F3(1)	0.087
2658	D10331	Pneumonia virus of mice mRNA for nonstructural proteins and major nucleocapsid protein, complete cds	0.084
2659	AL390874	Human DNA sequence from clone RP11-238K16 on chromosome 9, complete sequence [Homo sapiens]	0.003
2660	AF020282	Dictyostelium discoideum DG2033 gene, partial cds	2.3
2661	AF393505	Mus musculus potential meiotic DNA repair locus	2.2
2663	U12186	Oryctolagus cuniculus sodium/dicarboxylate cotransporter mRNA, partial cds	2.3
2664	AJ305053	Caprine arthritis-encephalitis virus proviral partial pol gene for Pol protein (reverse transcriptase), isolate CAEV Br/UFRGS-2/C767	0.78
2665	AE006628	Streptococcus pyogenes M1 GAS strain SF370, section 157 of 167 of the complete genome	2.4
2666	L76504	Cronartium arizonicum isolate FSprP-1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 26S ribosomal RNA gene, partial sequence	0.79
2667	XM_032307	Homo sapiens neuronal thread protein (AD7C-NTP), mRNA	7.2
2668	XM_010126	Homo sapiens stromal antigen 2 (STAG2), mRNA	e-123
2670	AB018798	Plasmodium yoelii gene for P-Type ATPase, complete cds	0.029
2671	Z24358	H. sapiens (D2S377) DNA segment containing (CA) repeat; clone AFM319zf9; single read	0.0004
2672	AE000878	Methanobacterium thermoautotrophicum from bases 976801 to 992232 (section 84 of 148) of the complete genome	6.2

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
2673	AL137717	Homo sapiens mRNA; cDNA DKFZp434J1630 (from clone DKFZp434J1630)	2E-31
2674	X61377	S.cerevisiae XYK gene for xylulokinase	2.4
2675	XM_034353	Homo sapiens KIAA1500 protein (KIAA1500), mRNA	4E-89
2676	J01268	Slime mold (D.discoideum) actin 2 (sub 2) pseudogene 5' end	0.085
2677	AF113932	Carios puertoricensis 16S ribosomal RNA, partial sequence	0.079
2678	XM_028752	Homo sapiens ribophorin II (RPN2), mRNA	2.1
2679	BC003254	Mus musculus, Similar to dentatorubral pallidoluysian atrophy, clone MGC:5758, mRNA, complete cds	0.78
2680	NC_001871	Feline foamy virus, complete genome	0.27
2681	AF188115	Simian immunodeficiency virus Gag protein gene, complete cds; Pol protein gene, partial cds; Vif protein (Vif), Vpr protein (Vpr), truncated Tat protein (Tat), Rev protein (Rev), Env protein (Env), and Nef protein (Nef) genes, complete cds; and long te>	0.77
2682	AE007382	Streptococcus pneumoniae section 65 of 194 of the complete genome	0.73
2683	AF190869	Gorilla gorilla X chromosome clone 1, partial sequence	0.082
2685	AK004792	Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200015I07, full insert sequence	1E-15
2686	AE001387	Plasmodium falciparum chromosome 2, section 24 of 73 of the complete sequence	0.063
2687	AB051438	Homo sapiens mRNA for KIAA1651 protein, partial cds	e-141
2688	AY047509	Drosophila melanogaster GH01721 full length cDNA	0.21
2689	AK016678	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4933405P16, full insert sequence	0.21
2690	Z19055	B.aphidicola tryptophan operon	0.077
2691	XM_047737	Homo sapiens ubiquitin specific protease 25 (USP25), mRNA	9E-56
2692	U13190	Angiostrongylus cantonensis clone G-2 retrotransposable element AcT-1	0.26
2693	X00858	H.sapiens DHFR gene, exon 5	0.27
2695	AK026620	Homo sapiens cDNA: FLJ22967 fis, clone KAT10573, highly similar to AF151892 Homo sapiens CGI-134 protein mRNA	0.077
2696	D87001	Homo sapiens immunoglobulin lambda gene locus DNA, clone:47H9 downstream contig	0.25
2697	U93276	Mus musculus glucokinase gene, intron 1 and hypersensitive site VII region	0.73
2698	AE006705	Sulfolobus solfataricus section 64 of 272 of the complete genome	1.2
2699	AE001423	Plasmodium falciparum chromosome 2, section 60 of 73 of the complete sequence	2.2
2700	X76799	H.sapiens genomic DNA dinucleotide (AC) repeat clone a10	6.4
2701	Z93324	L.major DNA containing open reading frame	0.23
2702	AJ251163	Dictyostelium discoideum dymB gene for dynamin B homologue	6.3
2703	AK020562	Mus musculus adult male urinary bladder cDNA, RIKEN full-length enriched library, clone:9530018H14, full insert sequence	0.76

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
2704	AF116983	Stenomesson variegatum ribulose 1,5-bisphosphate carboxylase large subunit (rbcL) gene, partial cds; chloroplast gene for chloroplast product	6.4
2706	XM_051524	Homo sapiens archain 1 (ARCN1), mRNA	0.66
2707	AF351620	Homo sapiens lipocalin-1 interacting membrane receptor (LIMR) gene, complete cds	0.084
2708	AF180472	Homo sapiens aryl-hydrocarbon interacting protein-like 1 (AIPL1) gene, complete cds	5.9
2709	AY008848	Ictalurus punctatus clone Icpu-UA/3 MHC class I antigen gene, complete cds	0.025
2710	NM_016862	Mus musculus vesicle transport through interaction with t-SNAREs 1 homolog (Vti1-pending), mRNA	0.65
2711	AE004023	Xylella fastidiosa 9a5c, section 169 of 229 of the complete genome	3.9
2712	XM_037239	Homo sapiens actin, beta (ACTB), mRNA	1E-49
2713	AE001404	Plasmodium falciparum chromosome 2, section 41 of 73 of the complete sequence	0.7
2714	XM_050114	Homo sapiens TERA protein (TERA), mRNA	5.9
2715	AK001082	Homo sapiens cDNA FLJ10220 fis, clone HEMBA1007342	0.56
2716	AF380155	Ctenopharyngodon idella c-Fos (c-fos) mRNA, complete cds	3.2
2717	AB027352	Cordyceps sp. 97003 mitochondrial DNA for small subunit ribosomal RNA	0.47
2718	AB033220	Lactococcus lactis gadB gene, untranslated by upstream frameshift, strain:01-1	1.9
2719	U01841	Mus musculus B6/CBAF1J peroxisome proliferator activated receptor gamma (ppar) mRNA, complete cds	0.009
2720	AL023814	Caenorhabditis elegans cosmid H08J19, complete sequence	0.021
2721	XM_047737	Homo sapiens ubiquitin specific protease 25 (USP25), mRNA	5E-56
2723	AF389403	Takifugu rubripes pericentriolar material 1 protein (PCM1) mRNA, complete cds	1.9
2724	AE006369	Lactococcus lactis subsp. lactis IL1403 section 131 of 218 of the complete genome	0.21
2726	AF367865	Mesembryanthemum crystallinum potassium transporter HAK2p (HAK2) mRNA, complete cds	0.39
2727	XM_043040	Homo sapiens hypothetical protein MGC2718 (MGC2718), mRNA	1E-09
2728	AE001392	Plasmodium falciparum chromosome 2, section 29 of 73 of the complete sequence	0.0000004
2729	U31371	Bovine herpesvirus 4 1.7-kb late RNA (L1.7) mRNA, repeat region	1.9
2730	AF195728	Libellula flavida 16S ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	0.025
2731	AK024658	Homo sapiens cDNA: FLJ21005 fis, clone CAE03745	0.64
2732	AK025613	Homo sapiens cDNA: FLJ21960 fis, clone HEP05517	1.4
2733	L11016	Homo sapiens lymphotoxin-beta gene, complete cds	0.0001
2734	Y14422	M.musculus DNA for retinal protein	1.2

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
2735	X83757	E.histolytica 170 kDa lectin gene, 5' region	0.64
2736	AK017535	Mus musculus 8 days embryo cDNA, RIKEN full-length enriched library, clone:5730409K12, full insert sequence	0.64
2737	AY047509	Drosophila melanogaster GH01721 full length cDNA	0.21
2738	AB019433	Homo sapiens gene for T-cell nuclear receptor NOT (Nurr1), complete cds	0.024
2739	U58731	Caenorhabditis elegans cosmid W09B12	0.61
2740	U35620	Nicotiana tabacum ribulose-1,5 bisphosphate carboxylase/oxygenase large subunit N-methyltransferase (rbcmtT) mRNA, complete cds	1
2741	AF181720	Homo sapiens RU2AS (RU2) gene, complete cds; and RU2S (RU2) gene, partial cds	5.4
2742	AE006560	Streptococcus pyogenes M1 GAS strain SF370, section 89 of 167 of the complete genome	0.24
2743	AF346287	Gonioctena pallida haplotype 61 mitochondrial control region, partial sequence	5
2744	L05617	Dictyostelium purpureum (Dpp5) DNA sequence, repeat region	0.021
2745	AK021104	Mus musculus adult male corpus striatum cDNA, RIKEN full-length enriched library, clone:C030026M15, full insert sequence	1
2746	L08174	Romanomermis culicivorax mitochondrial NADH dehydrogenase subunits 6 and 3 (ND6, ND3) cytochrome P450-like protein genes, complete CDS	1.6
2747	AB006130	Mesocricetus auratus mRNA for haptoglobin, complete cds	0.24
2748	AK001448	Homo sapiens cDNA FLJ10586 fis, clone NT2RP2003986	0.0008
2749	M95192	Drosophila melanogaster hairless protein (H) mRNA, complete cds	3.6
2750	X53426	Nicotiana sylvestris NySS41 and partial NySS42 genes for RUBISCO small subunit (SSU)	0.63
2751	NC_001336	Methanobacterium thermoautotrophicum plasmid pFV1, complete sequence	0.074
2752	NM_011595	Mus musculus tissue inhibitor of metalloproteinase 3 (Timp3), mRNA	0.012
2753	AF299340	Homo sapiens CD164 gene, complete cds, alternatively spliced	0.074
2754	AL121765	S.pombe chromosome I cosmid c1786	0.025
2755	U27078	Trichaptum abietinum mitochondrial small subunit ribosomal RNA, mitochondrial gene, partial sequence	0.44
2756	AF279292	Mycoplasma hyopneumoniae strain ISU 232 YX1 (yx1) gene, partial cds; p110 membrane protein precursor, gene, complete cds; and YX2 (yx2) gene, partial cds	0.024
2757	AL590371	Human DNA sequence from clone RP11-295H23 on chromosome 6, complete sequence [Homo sapiens]	0.61
2758	XM_041904	Homo sapiens cathepsin S (CTSS), mRNA	6
2759	D63170	Gallus domesticus DNA for the terminal heterochromatic region of the Z chromosome	1.4
2760	NM_023197	Mus musculus RIKEN cDNA 2310008H09 gene (2310008H09Rik), mRNA	0.025

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
2761	BC007150	Mus musculus, dystroglycan 1, clone MGC:6651 IMAGE:3496914, mRNA, complete cds	0.18
2762	BC000480	Homo sapiens, amyloid beta precursor protein-binding protein 1, 59kD, clone MGC:8690 IMAGE:2964638, mRNA, complete cds	8E-65
2764	XM_036683	Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 3 (ADAMTS3), mRNA	3E-46
2765	AJ005581	Encephalitozoon cuniculi complete rDNA unit (16S, 5.8S, 23S, ITS1 and IGS)	0.42
2766	AE005227	Escherichia coli O157:H7 EDL933 genome, contig 1 of 3, section 51 of 155	0.007
2767	XM_048172	Homo sapiens hypothetical protein DKFZp434F1017 (DKFZP434F1017), mRNA	3.8
2769	AF129087	Medicago sativa mitogen-activated protein kinase homologue (TDY1) gene, complete cds	0.66
2770	XM_008176	Homo sapiens MYB binding protein (P160) 1a (MYBBP1A), mRNA	5.2
2771	AC024865	Caenorhabditis elegans cosmid Y74C10AL, complete sequence	0.039
2772	XM_036164	Homo sapiens RAN binding protein 2 (RANBP2), mRNA	1E-59
2773	AL023816	Caenorhabditis elegans cosmid T05G11, complete sequence	0.64
2774	XM_004980	Homo sapiens cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7) (CFTR), mRNA	0.016
2775	XM_032209	Homo sapiens hypothetical gene supported by AK023337 (LOC90509), mRNA	0.018
2776	Z69650	Human DNA sequence from cosmid L69F7B, Huntington's Disease Region, chromosome 4p16.3 contains Huntington Disease (HD) gene	0.64
2777	AJ305053	Caprine arthritis-encephalitis virus proviral partial pol gene for Pol protein (reverse transcriptase), isolate CAEV Br/UFRGS-2/C767	0.46
2778	AK017531	Mus musculus 8 days embryo cDNA, RIKEN full-length enriched library, clone:5730409F18, full insert sequence	0.67
2779	AF028784	Rattus norvegicus glial fibrillary acidic proteins alpha and delta (GFAP) gene, alternatively spliced products, complete cds	0.11
2780	AF101236	Naja sputatrix neutral phospholipase A2 (NPLA2) gene, complete cds	0.054
2781	U71280	Mesocricetus auratus cytochrome P450 aldosterone synthase (CYP11B2) gene, complete cds	0.023
2782	X80007	P.sativum gene for chalcone synthase	0.15
2783	AF171040	Anopheles funestus clone AF10 microsatellite sequence	2
2784	XM_011464	Homo sapiens hypothetical protein FLJ20170 (FLJ20170), mRNA	0.21
2785	Y18929	Homo sapiens wild type AF-4/FEL gene, part of intron 3, individual PB	3
2786	L81581	Homo sapiens (subclone 4_a4 from P1 H11) DNA sequence, complete sequence	0.024

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
2787	NM_024381	Rattus norvegicus ATP-stimulated glucocorticoid-receptor translocaton promoter (Gyk), mRNA	0.17
2788	X72688	L.stagnalis LS-rab1 mRNA	0.2
2789	XM_033154	Homo sapiens syntrophin, gamma 1 (SNTG1), mRNA	0.021
2790	AB017186	Clostridium perfringens genes of hem operon, complete cds	1.4
2791	U47416	Solanum allophyllum NADH dehydrogenase subunit (ndhF) gene, chloroplast gene encoding chloroplast protein, partial cds	0.2
2792	M21258	Human small nuclear ribonucleoprotein (snRNP) E gene, exon 5 and Alu repeats copy N and O	0.051
2793	L05004	Staphylococcus aureus dehydroquinate synthase (aroB) gene, 3' end cds; 3-phosphoshikimate-1-carboxyvinyltransferase (aroA) gene, complete cds; ORF3, complete cds	0.21
2794	AF302005	Uma scoparia isolate ROM3406 cytochrome b gene, partial cds; mitochondrial gene for mitochondrial product	2
2795	AF288209	Homo sapiens beta galactosyltransferase bGalT7 mRNA, complete cds	2
2796	AB048897	Macaca fascicularis brain cDNA, clone:QnpA-17253	1.7
2797	AK025054	Homo sapiens cDNA: FLJ21401 fis, clone COL03678	0.071
2798	U39886	Bos taurus Y-chromosome specific genomic sequence	0.002
2799	AJ277649	Caenorhabditis elegans mRNA for CHE-14 protein	0.6
2800	AF058764	Xenopus laevis bone morphogenetic protein 4 (BMP-4) gene, complete cds	0.56
2801	AE001398	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence	0.15
2802	AF079456	O'nyong-nyong virus strain SG650, complete genome	0.003
2803	AF087913	Human endogenous retrovirus HERV-P-T47D	6
2804	AB005053	Anomala cuprea entomopoxvirus gene for spheroidin, complete cds	1.8
2805	AF027656	Homo sapiens cholesteryl ester transfer protein gene, promoter region	0.004
2806	XM_031478	Homo sapiens vacuolar protein sorting protein 18 (VPS18), mRNA	1.7
2807	XM_001718	Homo sapiens KIAA0475 gene product (KIAA0475), mRNA	0.023
2808	L21906	Human troponin I, slow-twitch isoform (TNNI1) gene, exons 2-4	1.5
2809	NM_006633	Homo sapiens IQ motif containing GTPase activating protein 2 (IQGAP2), mRNA	5E-39
2810	AE001541	Helicobacter pylori, strain J99 section 102 of 132 of the complete genome	0.2
2811	M63577	S.cerevisiae SFP1 gene, complete cds	0.023
2812	XM_004980	Homo sapiens cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7) (CFTR), mRNA	0.013
2813	AJ305053	Caprine arthritis-encephalitis virus proviral partial pol gene for Pol protein (reverse transcriptase), isolate CAEV Br/UFRGS-2/C767	0.5

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
2814	AK014450	Mus musculus 18 days pregnant adult female placenta and extra embryonic tissue cDNA, RIKEN full-length enriched library, clone:3830422A13, full insert sequence	0.075
2815	X99691	B.taurus DNA for agouti gene	2
2816	Z64630	H.sapiens CpG island DNA genomic Mse1 fragment, clone 152h5, forward read cpg152h5.ft1a	0.14
2817	AF357971	Ovine pulmonary adenocarcinoma virus, complete sequence; and flanking Ovis aries sequence	4.9
2818	AE003336	Drosophila melanogaster genomic scaffold 142000013385800, complete sequence	0.16
2819	U72236	Dictyostelium discoideum ModA (modA) gene, complete cds	0.61
2820	XM_018110	Homo sapiens gap junction protein, beta 3, 31kD (connexin 31) (GJB3), mRNA	5.1
2821	AJ005588	Capsicum annuum gene encoding 5-epi-aristolochene synthase, exons 1 to 7	0.23
2822	AK022842	Homo sapiens cDNA FLJ12780 fis, clone NT2RP2001813	0.074
2823	AF138281	Arabidopsis thaliana phospholipase D-gamma-2 mRNA, complete cds	0.071
2824	AB040882	Homo sapiens mRNA for KIAA1449 protein, partial cds	0.18
2825	AB022156	Mus musculus Cctb gene for chaperonin containing TCP-1 beta subunit, complete cds	0.5
2826	BC005516	Mus musculus, RIKEN cDNA 1200007D18 gene, clone MGC:7601 IMAGE:3494155, mRNA, complete cds	0.51
2827	AK025207	Homo sapiens cDNA: FLJ21554 fis, clone COL06330	4.4
2828	NM_018798	Mus musculus ubiquilin 2 (Ubqln2), mRNA	0.043
2829	Z23770	H. sapiens (D17S842) DNA segment containing (CA) repeat; clone AFM240xe5; single read	0.00004
2830	BC005762	Mus musculus, Similar to proteasome (prosome, macropain) subunit, alpha type 1, clone MGC:6546 IMAGE:2655483, mRNA, complete cds	0.67
2831	AB047932	Macaca fascicularis brain cDNA, clone:QnpA-10158	0.68
2832	U19765	Human nucleic acid binding protein gene, complete cds	0.18
2833	AF200327	Plasmodium chabaudi unknown genes	0.028
2834	U67544	Methanococcus jannaschii section 86 of 150 of the complete genome	0.14
2835	BC010357	Homo sapiens, Similar to hypothetical protein, clone MGC:13367 IMAGE:4249317, mRNA, complete cds	2E-55
2836	AE007471	Streptococcus pneumoniae section 154 of 194 of the complete genome	5.2
2837	AJ320185	Solanum tuberosum sn1 gene for snakin-1, exons 1-2	0.44
2838	AF039954	Homo sapiens CC chemokine LCC-1 precursor, gene, complete cds	0.002
2839	Y13631	Clostridium botulinum P-21, P-47 ntnh, bonT genes	0.14
2840	AL390181	Homo sapiens mRNA; cDNA DKFZp547J125 (from clone DKFZp547J125)	0.019

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
2841	AF366200	Diadema antillarum isolate dmid3 tRNA-Lys gene, partial sequence; ATPase 8 gene, complete cds; and ATPase 6 gene, partial cds; mitochondrial genes for mitochondrial products	6.1
2842	AJ237688	Canis familiaris polymorphic marker clone XA07	0.53
2843	AF244979	Mus musculus galectin-11 mRNA, variant b, complete cds, alternatively spliced	0.25
2844	AL390174	Homo sapiens mRNA; cDNA DKFZp547J184 (from clone DKFZp547J184)	0.21
2845	U80230	Human clotting factor VIII gene, junction regions of the deletion of exons 15 through 20 and LINE-1-like repeat region	2E-09
2846	U31086	Gallus gallus neuron-glia adhesion molecule (Ng-CAM) gene, partial cds, exons 1 and 2	0.064
2847	D16685	Rice gene for lactate dehydrogenase, complete cds	0.003
2848	AB007459	Chara corallina ccm1 mRNA for myosin, complete cds	0.067
2849	U63328	Pissodes strobi vitellogenin (Vtg) mRNA, partial cds	0.68
2850	U50727	Human p40-phox (NCF4) gene, exon 8	0.023
2851	NM_017190	Rattus norvegicus Myelin-associated glycoprotein (Mag), mRNA	6.5
2852	AF361105	Homo sapiens interleukin 9 (IL9) gene, complete cds	0.37
2853	AP001416	Homo sapiens genomic DNA, chromosome 21q22.2, clone:D34, LB7T-ERG region, complete sequence	1.5
2854	Y16771	Phylica pubescens chloroplast partial trnL gene & intergenic spacer	0.6
2855	AE005624	Escherichia coli O157:H7 EDL933 genome, contig 3 of 3, section 243 of 290	0.075
2856	AF159568	Microbotryum violaceum ammonium transporter MEPa (MEPa) mRNA, complete cds	0.7
2857	M34149	S.cerevisiae mitochondrial gap 12 sequence	0.51
2858	D16541	Chicken DNA for connectin(titin), partial sequence	0.064
2859	AC007039	Homo sapiens BAC clone RP11-263A15 from Y, complete sequence	e-149
2860	AJ294714	Pichia anomala leu2 gene for beta-isopropylmalate dehydrogenase	0.056
2861	XM_051160	Homo sapiens KIAA1463 protein (KIAA1463), mRNA	0.22
2862	XM_031527	Homo sapiens leucine-rich PPR-motif containing (LRPPRC), mRNA	0.0003
2863	AF323443	Plasmodium yoelii yoelii clone 11 235 kDa rhoptry protein (IIa.2) gene, partial cds	0.02
2864	Y14324	Staphylococcus aureus partial ORF292 and ORF271, ORF331 and ORF314	0.62
2865	BC007568	Homo sapiens, clone IMAGE:3028427, mRNA, partial cds	0.16
2866	U67518	Methanococcus jannaschii section 60 of 150 of the complete genome	0.67
2867	AJ133742	Sus scrofa ryr3 gene (partial), exon 2	0.68
2868	AF116520	Mus musculus periplakin (ppl) gene, exons 2-14	0.083
2869	D38044	Human gene for Ah-receptor, exon 7-9	0.25

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
2870	XM_010162	Homo sapiens methyl CpG binding protein 2 (Rett syndrome) (MECP2), mRNA	1.7
2871	AF303030	Lavatera phoenicea isolate 804 internal transcribed spacer 1, partial sequence, 5.8S ribosomal RNA, complete sequence and internal transcribed spacer 2, partial sequence	0.01
2872	AE002274	Chlamydia muridarum, section 6 of 85 of the complete genome	1.8
2873	AB062056	Homo sapiens p53DINP1 gene for p53DINP1a, p53DINP1b, complete cds, alternative splicing	8E-26
2874	AF150965	Bacillus anthracis plasmid pXO1 resolvase X (resX) and transposase X (traX) genes, complete cds	1.6
2875	U90292	Human chromosome 16 duplicated adrenoleukodystrophy (ALD) gene, 5' breakpoint sequence	3E-41
2876	U75361	Rattus norvegicus Munc13-3 mRNA, complete cds	3E-18
2877	AF006686	Plecotus auritus clone Paur06 microsatellite sequence	5E-10
2878	NM_009694	Mus musculus apolipoprotein B editing complex 2 (Apobec2), mRNA	0.00009
2879	AF315316	Vigna radiata ACC oxidase gene, complete cds	0.003
2880	AE005714	Caulobacter crescentus section 40 of 359 of the complete genome	1.5
2881	AL451135	Human DNA sequence from clone RP11-45G20 on chromosome 6, complete sequence [Homo sapiens]	1.9
2882	AF315316	Vigna radiata ACC oxidase gene, complete cds	0.003
2883	NM_009694	Mus musculus apolipoprotein B editing complex 2 (Apobec2), mRNA	0.00008
2884	AB047932	Macaca fascicularis brain cDNA, clone:QnpA-10158	0.16
2885	U18671	Human Stat2 gene, complete cds	0.23
2886	AB040670	Bombyx mori copg2 mRNA for nonclathrin coat protein gamma2-COP, partial cds	0.074
2887	AK017987	Mus musculus adult male thymus cDNA, RIKEN full-length enriched library, clone:5830443J22, full insert sequence	0.035
2889	AE001419	Plasmodium falciparum chromosome 2, section 56 of 73 of the complete sequence	0.12
2890	AF275225	Eriosoma lanigerum 12S small subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and 16S large subunit ribosomal RNA gene, partial sequence; mitochondrial genes for mitochondrial products	0.35
2891	AF372971	Arabidopsis thaliana AT3g23580/MDB19_7 mRNA, complete cds	0.53
2892	AJ404851	Homo sapiens partial ARNT gene for aryl hydrocarbon receptor nuclear translocator, exon 4	3.7
2893	AJ012380	Fugu rubripes partial rara gene, exons 4-10	1.4
2894	AB064593	Escherichia coli icdA gene for isocitrate dehydrogenase, complete cds	0.027
2895	AF182444	Drosophila melanogaster disco-interacting protein (dip1) gene, alternatively spliced products, complete cds; and TO42 gene, partial cds	1.6

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
2896	AY020760	Oryza sativa microsatellite MRG3085 containing (TA)X13, closest to marker R2976, genomic sequence	0.007
2897	AE006318	Lactococcus lactis subsp. lactis IL1403 section 80 of 218 of the complete genome	0.53
2898	X01973	Mouse gene for interferon alpha 4 (Mu IFN-alpha 4)	3.9
2899	AF176677	Candida albicans gamma-glutamylcysteine synthetase (GCS1) gene, complete cds	0.07
2900	AF109009	Prolaupala kukui clone 1092 transposon Lau1 sequence	3.6
2901	D49739	Chicken mRNA for leucine zipper protein, complete cds	2.4
2902	U34610	Mus musculus alpha-1(XVIII) collagen (COL18A1) gene, exon 6 and 7	0.006
2903	AK026763	Homo sapiens cDNA: FLJ23110 fis, clone LNG07802	0.34
2904	AF343914	Campylobacter jejuni NCTC 11828 LOS biosynthesis cluster, partial sequence	0.024
2905	AE002722	Drosophila melanogaster genomic scaffold 142000013385665, complete sequence	0.007
2906	XM_027242	Homo sapiens KIAA0805 protein (KIAA0805), mRNA	1.1
2907	Y15082	Homo sapiens p14.5 gene, partial exon 1 and promoter; hPOP1 gene exon 1 and promoter and bidirectional promoter region	0.67
2908	XM_009536	Homo sapiens GTPase GES; REM protein (REM), mRNA	5.9
2909	XM_036351	Homo sapiens nuclear transcription factor Y, alpha (NFYA), mRNA	1E-32
2910	AB037851	Homo sapiens mRNA for KIAA1430 protein, partial cds	0.58
2911	XM_002943	Homo sapiens similar to PRO0327 protein (H. sapiens) (LOC92570), mRNA	2.4
2912	AF069179	Lysiphlebus cardui NADH dehydrogenase 1 gene, mitochondrial gene encoding mitochondrial protein, partial cds	0.008
2913	AJ243545	Arabidopsis thaliana gene for 67 kD chloroplastic RNA-binding protein, P67	0.54
2914	AJ295795	Isolepis producta chloroplast trnL gene intron	2.2
2915	AJ311050	Medicago sativa pr10.2 gene for class 10 PR protein	0.26
2916	AK021512	Homo sapiens cDNA FLJ11450 fis, clone HEMBA1001432	0.25
2917	AK002979	Mus musculus adult male brain cDNA, RIKEN full-length enriched library, clone:0710001P07, full insert sequence	0.023
2918	AY007505	Streptococcus mitis phage SM1 PblA (pblA) and PblB (pblB) genes, complete cds; lysin (lys) gene, partial cds; and unknown genes	0.026
2919	AK022043	Homo sapiens cDNA FLJ11981 fis, clone HEMBB1001317	0.69
2920	AF162969	Mycoplasma capricolum capricolum strain 960038 fructose biphosphate aldolase gene, partial cds	0.064
2921	XM_051364	Homo sapiens similar to immediate early protein (H. sapiens) (LOC93434), mRNA	0.086
2922	XM_027642	Homo sapiens KIAA0349 protein (KIAA0349), mRNA	0.24
2923	XM_045819	Homo sapiens cofilin 2 (muscle) (CFL2), mRNA	1.9
2924	AF146362	Drosophila melanogaster Huntington disease protein homolog (Hsap\HD) mRNA, complete cds	0.23

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
2925	U91993	Solanum chacoense transposable element Sch2, sequence	0.027
2926	AK021782	Homo sapiens cDNA FLJ11720 fis, clone HEMBA1005293	2.3
2927	AF274444	Carsonella ruddii ribosomal protein L11 (rpL11), ribosomal protein L1 (rpL1), ribosomal protein L10 (rpL10), ribosomal protein L7/L12 (rpL7/L12), beta subunit of RNA polymerase (rpoB), beta-prime subunit of RNA polymerase (rpoC), ribosomal protein S12 >	2
2928	AF003047	Simian immunodeficiency virus isolate P2S1 patient P2, gp120 (env) gene, partial cds	0.064
2929	AK022102	Homo sapiens cDNA FLJ12040 fis, clone HEMBB1001944	0
2930	AC004239	Homo sapiens BAC clone CTB-34F8 from 7p15-p21, complete sequence	0.001
2931	AF104819	Strumaria truncata trnL gene, partial sequence; chloroplast gene for chloroplast product	0.25
2932	AF171916	Trimeresurus flavomaculatus cytochrome b (cytb) gene, partial cds; mitochondrial gene for mitochondrial product	0.21
2933	AJ011596	Homo sapiens trapped 3' terminal exon, clone B2E8	0.0003
2934	AF269137	Homo sapiens GABAA receptor gamma 3 subunit (GABRG3) gene, exon 3	0.8
2935	AB030586	Arabidopsis thaliana AATL1 gene for amino acid transporter-like protein 1, complete cds	1.9
2936	L76484	Cronartium appalachianum isolate Ca-1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 26S ribosomal RNA gene, partial sequence	0.71
2937	AF366570	Trypanosoma congolense calreticulin mRNA, complete cds	0.084
2938	NM_004682	Homo sapiens PC4 and SFRS1 interacting protein 1 (PSIP1), mRNA	2
2939	AL050219	Homo sapiens mRNA; cDNA DKFZp586J1623 (from clone DKFZp586J1623)	1.8
2940	AF275687	Plasmodium falciparum knob-associated histidine-rich protein (KAHRP) gene, complete cds	0.009
2941	AF142701	Vigna umbellata maturase-like protein (matK) gene, complete cds; chloroplast gene for chloroplast product	0.56
2942	AF226775	Mitthyridium undulatum small ribosomal protein 4 (rps4) gene, partial cds; chloroplast gene for chloroplast product	0.073
2943	XM_034735	Homo sapiens similar to hypothetical protein FLJ21463 (H. sapiens) (LOC90883), mRNA	0
2944	AK017899	Mus musculus adult male thymus cDNA, RIKEN full-length enriched library, clone:5830405M20, full insert sequence	0.28
2945	Y10159	D.discoideum racGAP gene	6.2
2946	XM_011562	Homo sapiens hypothetical gene supported by NM_000181 (LOC92707), mRNA	0.025
2947	AF191257	Trichuris trichiura microsatellite ttstr14	0.078
2948	Y08449	E.caballus DNA segment containing CA microsatellite VHL137	0.00003

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
2949	AK003959	Mus musculus 18 days embryo cDNA, RIKEN full-length enriched library, clone:1110029G12, full insert sequence	0.077
2950	NM_012779	Rattus norvegicus Aquaporin 5 (Aqp5), mRNA	2.2
2951	AJ404295	Borelis schlumbergeri 18S rRNA gene, isolate 191	0.25
2952	AE001365	Plasmodium falciparum chromosome 2, section 2 of 73 of the complete sequence	0.49
2954	Y13434	Ovis aries mRNA for thyroid stimulating hormone receptor	1.8
2955	AB026906	Homo sapiens SDHD gene for small subunit of cytochrome b of succinate dehydrogenase, complete cds	0.001
2956	BC010367	Homo sapiens, hypothetical protein FLJ20534, clone MGC:13432 IMAGE:4334172, mRNA, complete cds	4
2957	AJ251957	Ciona intestinalis mRNA for nuclear lamin (lamin L2 gene)	2
2958	AK016695	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4933406J08, full insert sequence	2E-14
2959	Z13985	M.musculus control region sequence DNA	0.072
2960	AL591590	Human DNA sequence from clone CTD-2053G21 on chromosome Xq13.3-21.2, complete sequence [Homo sapiens]	0.007
2961	AB002807	Glycine max DNA for nodulin 35, partial cds	0.24
2962	AE001399	Plasmodium falciparum chromosome 2, section 36 of 73 of the complete sequence	0.003
2963	AF298224	Homo sapiens RPCI-II 289E13 CD21 gene, partial cds	0.00001
2964	XM_018458	Homo sapiens similar to hypothetical protein PRO2822 (H. sapiens) (LOC93537), mRNA	0.21
2965	AF288778	Homo sapiens erythroleukemia translocation breakpoint region	0.068
2966	AF073994	Drosophila melanogaster gamma-tubulin (GTUB) gene, partial cds; and recombination repair protein 1 (RRP1) and thymidylate synthase (TS) genes, complete cds; and RNA-binding protein (RBP9) gene, partial sequence	0.14
2967	AL121822	Human DNA sequence from clone 346P11 on chromosome Xq21.2-21.33, complete sequence [Homo sapiens]	0.0000001
2968	U31284	Mesotaenium caldariorum clone mesphy1b phytochrome gene, complete cds	0.59
2969	XM_008806	Homo sapiens mitogen-activated protein kinase 4 (MAPK4), mRNA	1.8
2970	XM_027307	Homo sapiens KIAA1209 protein (KIAA1209), mRNA	0.001
2971	AF179711	Hylobates sp. RH50 glycoprotein (RHAG) gene, intron 9	0.56
2972	BC007133	Mus musculus, apoptosis inhibitory protein 5, clone MGC:5830 IMAGE:3594358, mRNA, complete cds	5.4
2973	AF282018	Homo sapiens clone 15qtel_ctg0082_c262bt3_c290bt3 sequence	2E-53
2974	AE004790	Pseudomonas aeruginosa PA01, section 351 of 529 of the complete genome	1.8
2975	XM_003050	Homo sapiens similar to seven transmembrane domain orphan receptor (H. sapiens) (LOC63108), mRNA	0.27
2976	AF353728	Mus musculus myo-inositol monophosphatase 1 (Impa1) gene, exons 1 through 7	1.2

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
2977	AK005535	Mus musculus adult female placenta cDNA, RIKEN full-length enriched library, clone:1600025H15, full insert sequence	0.55
2978	AJ002479	Medicago truncatula ENBP1 gene, exons 1 to 12	0.64
2979	AF154836	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2	0.000001
2981	AF260819	Plasmodium falciparum CG1 protein gene, complete cds	0.73
2982	AE006714	Sulfolobus solfataricus section 73 of 272 of the complete genome	0.02
2984	NM_004114	Homo sapiens fibroblast growth factor 13 (FGF13), mRNA	6.7
2985	AF155369	Buthus martensii putative potassium ion channel blocker TXKs1 mRNA, complete cds	0.72
2986	XM_041836	Homo sapiens similar to MHC class I region ORF (H. sapiens) (LOC91955), mRNA	0.18
2987	AF153668	Microcephala discoidea NADH dehydrogenase (ndhF) gene, partial cds; chloroplast gene for chloroplast product	1.7
2988	AF216211	Drosophila buzzatii alpha-esterase 3 (aE3) and alpha-esterase 4b (aE4b) genes, complete cds	0.073
2989	AF352244	Dermatophagoides farinae paramyosin-like allergen mRNA, partial cds	0.025
2990	XM_007409	Homo sapiens alkylation repair; alkB homolog (ABH), mRNA	0.21
2991	AF005779	Sus scrofa neuropeptide Y Y1 receptor mRNA, complete cds	0.66
2992	AF264749	Arabidopsis thaliana hydrophobic protein RCI2B (RCI2B) and hydrophobic protein RCI2A (RCI2A) genes, complete cds	0.022
2994	AL162033	Homo sapiens mRNA; cDNA DKFZp434F1872 (from clone DKFZp434F1872)	0.69
2995	AK013593	Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched library, clone:2900024O09, full insert sequence	0.7
2996	AF222716	Plasmodium falciparum clone 3D7 unconventional myosin PfM-B gene, complete cds	0.027
2997	AK006599	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:1700034J06, full insert sequence	2.2
2998	AF010509	Plasmodium falciparum microsatellite TA39 sequence	0.001
2999	AF070566	Homo sapiens clones 24611 and 24705 mRNA sequence	0.000003
3000	AF181676	Homo sapiens clone 204I12 polymorphic microsatellite sequence	0.074
3001	M17169	Chinese hamster glucose-regulated protein GRP78 mRNA, complete cds	0.008
3002	NM_031236	Rattus norvegicus alpha 1,2-fucosyltransferase (Fut1), mRNA	0.69
3003	XM_016321	Homo sapiens region containing TBX3-iso protein; T-box 3 (ulnar mammary syndrome) (LOC82353), mRNA	0.73
3004	BC005379	Homo sapiens, Similar to plasminogen, clone MGC:12496 IMAGE:3934860, mRNA, complete cds	0.000001
3005	AF276176	Scaphirhynchus platorynchus microsatellite Spl-107 sequence	0.009
3006	XM_010048	Homo sapiens like mouse brain protein E46 (E46L), mRNA	0.47
3007	NC_001807	Human mitochondrion, complete genome	1E-10
3008	AE006103	Pasteurella multocida PM70 section 70 of 204 of the complete genome	0.4

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
3009	AE006266	Lactococcus lactis subsp. lactis IL1403 section 28 of 218 of the complete genome	0.2
3010	AF022812	Dehalospirillum multivorans GTP cyclohydrolase II (ribA) gene, partial cds; and 3,4-dihydroxy-2-butanone-4-phosphate synthase (ribB), riboflavin synthase (ribH), tetrachloroethene reductive dehalogenase catalytically active subunit (pceA), and tetrachl>	0.21
3011	AJ243901	Mycoplasma hominis p75 gene, strain PG21	1.4
3013	XM_027894	Homo sapiens hypothetical protein DKFZp761C121 (DKFZp761C121), mRNA	5E-33
3014	AJ390525	Candida albicans ORF DNA, clone 64gB	0.52
3015	AJ006873	Buchnera aphidicola plasmid pBUs1, repA2 gene, leuA gene and ORF1	0.013
3016	L07898	Entamoeba histolytica alpha-1 tubulin (tub1) gene, complete cds	0.024
3017	L25107	Human LIS mRNA	1.2
3018	AL122122	Homo sapiens mRNA; cDNA DKFZp434L098 (from clone DKFZp434L098)	0.007
3019	V01270	Rattus norvegicus genes for 18S, 5.8S, and 28S ribosomal RNAs	2E-10
3020	AK023061	Homo sapiens cDNA FLJ12999 fis, clone NT2RP3000324	0.12
3021	U80449	Caenorhabditis elegans cosmid R10A10	0.29
3022	AF355473	Oryzias latipes germ cell-less protein (gcl) mRNA, complete cds	2.3
3023	XM_037811	Homo sapiens hypothetical gene supported by AL117650 (LOC91349), mRNA	0.39
3024	AK016492	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4931430N09, full insert sequence	0.004
3025	XM_011189	Homo sapiens similar to DKFZP564K247 protein (H. sapiens) (LOC91537), mRNA	4
3026	BC010710	Mus musculus, Similar to ribosomal protein L19, clone MGC:6500 IMAGE:2648593, mRNA, complete cds	5.1
3027	XM_017923	Homo sapiens hypothetical protein FLJ12660 (FLJ12660), mRNA	4.1
3028	AC016671	Homo sapiens BAC clone RP11-12J24 from Y, complete sequence	0.012
3029	L13662	Campylobacter jejuni major cell-binding factor (peb1) and receptor genes, complete cds	0.044
3030	X77172	M.musculus pF2 genomic DNA, homology with mouse repetitive elements B1, B2 and human Alu	0.008
3031	AF074841	Campylobacter lari tRNA-Ala and tRNA-Ile genes, complete sequence	0.016
3032	AF272846	Homo sapiens Fanconi anemia complementation group D2 protein (FANCD2) gene, exon 1	0.065
3033	D50090	Drosophila americana texana G-3-P dehydrogenase (alphaGpdh) gene, exon1-8, complete cds	0.13
3034	AE001417	Plasmodium falciparum chromosome 2, section 54 of 73 of the complete sequence	0.15
3035	AK002007	Homo sapiens cDNA FLJ11145 fis, clone PLACE1006626, highly similar to Homo sapiens mRNA for KIAA0928 protein	0.026

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
3036	AL512432	Human DNA sequence from clone RP11-245H22 on chromosome 6 Contains GSSs, complete sequence [Homo sapiens]	0.00003
3037	AB030490	Glycine max SG-05 gene for thiamin biosynthetic enzyme, complete cds	0.003
3038	U05820	Saccharomyces cerevisiae DA-box protein Smc2p (SMC2) gene, complete cds, and assimilatory sulfite reductase (MET10) gene, partial cds	1.7
3039	AF098761	Gracilaria gracilis microsatellite Gg155R sequence	0.07
3041	AF045595	Carassius auratus clone gf-40 glutamic acid decarboxylase isoform 67 (GAD67) mRNA, complete cds	2
3042	AJ404308	Sorites marginalis 18S rRNA gene, isolate 836	0.009
3043	AE006495	Streptococcus pyogenes M1 GAS strain SF370, section 24 of 167 of the complete genome	6
3044	XM_030781	Homo sapiens enigma (LIM domain protein) (ENIGMA), mRNA	3E-18
3045	AC024748	Caenorhabditis elegans cosmid Y110A2AR, complete sequence	0.15
3046	AL512282	Human DNA sequence from clone XXyac-BA141F18 on chromosome X, complete sequence [Homo sapiens]	0.06
3047	AF009980	Otolemur garnetti color vision opsin gene, exons 5 and 6, and complete cds	0.17
3048	AF284953	Carex exsiccata tRNA-Thr, partial sequence; trnT-trnL intergenic spacer, tRNA-Leu, and trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe, partial sequence; chloroplast genes for chloroplast products	0.23
3049	AE004036	Xylella fastidiosa 9a5c, section 182 of 229 of the complete genome	4.3
3050	X94767	H.sapiens RP3 gene (XLRP gene 2)	0.002
3051	AF279135	Dictyostelium discoideum spore coat structural protein SP65 (cotE) gene, complete cds	0.003
3052	AF277452	Rattus norvegicus Pkd1 mRNA, partial cds	0.12
3053	AF327114	Homo sapiens clone 8qtel_c19t7 sequence	8E-17
3054	AB052201	Macaca fascicularis brain cDNA, clone:QnpA-20394	0.59
3055	AJ235314	Antilocapra americana mitochondrial DNA for D-loop	0.17
3056	AF361481	Homo sapiens mitochondrial GTP-binding protein 1 (GTPBP3) gene, complete cds; nuclear gene for mitochondrial product	0.009
3057	AE006879	Sulfolobus solfataricus section 238 of 272 of the complete genome	1.6
3058	AJ277756	Legionella pneumophila ORF X (partial), recA gene, recX gene and sya gene (partial)	0.21
3059	U73044	Schizosaccharomyces pombe ARS binding protein 2 (abp2) mRNA, complete cds	0.058
3060	AF043123	Homo sapiens interleukin-7 receptor precursor (IL7R) gene, exon 1	0.2
3061	L43603	Gallus gallus Na+/K+-ATPase alpha-1 subunit gene, promoter region	0.48

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
3062	X68976	N.viridescens mRNA for Hoxd-10	0.092
3063	AF001454	Helianthus annuus Dc3 promoter-binding factor-2 (DPBF-2) mRNA, complete cds	0.18
3064	AF086062	Homo sapiens full length insert cDNA clone YZ06B11	3E-24
3065	U67234	Human clone HS5.29 Alu-Ya5 sequence	0.087
3066	AF030199	Mus musculus type 1 sigma receptor gene, complete cds	0.45
3067	J05544	Plasmodium falciparum glucosephosphate isomerase (ggi.R1) gene, complete cds	0.2
3068	X17455	Rat Bmyc gene 5'-fragment	0.003
3069	AF298207	Dictyostelium discoideum transposon thug-S, complete sequence	0.003
3070	NM_030238	Mus musculus dynein, cytoplasmic, heavy chain 1 (Dnchc1), mRNA	1.7
3071	AB032151	Homo sapiens BABP gene for bile acid-binding protein [AKR 1C2], exon 1 to 7	0.28
3072	NC_001481	Feline calicivirus, complete genome	1.9
3073	U49266	Mus musculus growth hormone receptor/binding protein gene, exons 9-10, and partial cds	0.13
3074	Z24279	H. sapiens (D1S489) DNA segment containing (CA) repeat; clone AFM309ve9; single read	0.16
3075	AF228724	Rhagoletis conversa NADH-dehydrogenase subunit 4 (ND4) gene, partial sequence; NADH-dehydrogenase subunit 4L (ND4L) gene, complete sequence; and tRNA-Thr gene, partial sequence; mitochondrial genes for mitochondrial products	0.048
3076	U72723	Oryza longistaminata receptor kinase-like protein (Xa21) gene, complete cds and family member C, pseudogene	0.21
3077	U55184	Human G protein Golf alpha gene, exon 12 and complete cds	1E-16
3078	AC006119	Mus musculus clone UWGC:mbac10gap from 14D1-D2 (T-Cell Receptor Alpha Locus), complete sequence	0.00004
3079	AK015900	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930526F13, full insert sequence	0.76
3080	AL133637	Homo sapiens mRNA; cDNA DKFZp434J1618 (from clone DKFZp434J1618); partial cds	0.071
3081	S74063	c-raf=raf protein [Xenopus laevis, mRNA, 2736 nt]	0.56
3082	NM_014498	Homo sapiens type II Golgi membrane protein (GPP130), mRNA	1.9
3083	AF238234	Entamoeba histolytica diaphanous protein (dia) gene, partial cds	2.1
3084	XM_010729	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily f, member 1 (SMARCF1), mRNA	0.65
3085	AK007542	Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810019D05, full insert sequence	0.62
3086	AF228977	Human T-cell lymphotropic virus type 1 isolate ATLL long terminal repeat, partial sequence	0.0003
3087	AC091698	Homo sapiens clone RP11-596J6, complete sequence	0.073
3088	AF233882	Homo sapiens plakoglobin (JUP) gene, exons 1 through 7	4E-88

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
3089	U29468	Drosophila koepferae KO4 San Luis, Argentina, Gandalf transposable element DNA< partial sequence	0.2
3090	AF279292	Mycoplasma hyopneumoniae strain ISU 232 YX1 (yx1) gene, partial cds; p110 membrane protein precursor, gene, complete cds; and YX2 (yx2) gene, partial cds	0.2
3091	AF391284	Homo sapiens 11p15.5 clone LOH11A, partial sequence	0.007
3092	AF259737	Ovis aries microsatellite MNS-64 sequence	0.66
3093	NM_030261	Mus musculus hypothetical protein MGC7182 (MGC7182), mRNA	6E-36
3094	AB047879	Macaca fascicularis brain cDNA, clone:QnpA-14270	0.00003
3095	X65607	H.sapiens MT1X gene for metallothionein 1X	0.023
3096	AF231164	Pseudosymblepharis schimperiana tRNA-Leu, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe, partial sequence; chloroplast genes for chloroplast products	0.06
3097	AF290431	Mus musculus sequence downstream of Hyal1; and Fus2 gene, 5' UTR and exon 1	1.3
3098	X96762	C.elegans mRNA for DNA topoisomerase I	0.028
3099	AB036229	Salganea nigrita mitochondrial COII gene for cytochrome oxidase II, partial cds, collection_site:Lake Danao, Leyte, Philippines	0.53
3100	AJ309183	Staphylococcus aureus partial coa gene for coagulase, type F, isolate rs59	0.07
3101	AF240785	Homo sapiens glutathione-S-transferase GSTT1 deletion/junction region sequence	0.000004
3102	XM_031737	Homo sapiens synaptosomal-associated protein, 23kD (SNAP23), mRNA	0.0000004
3103	AY035097	Arabidopsis thaliana putative proline-rich protein (F23H24.15) mRNA, complete cds	0.18
3104	AF121069	Anopheles farauti 3 12S small subunit ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	0.065
3105	NM_016701	Mus musculus nestin (Nes), mRNA	0.23
3106	L41893	Homo sapiens retinoblastoma susceptibility protein (RB1) gene, exon 5, bases 44452-44939 in L11910	0.008
3107	Z78623	H.sapiens flow-sorted chromosome 6 TaqI fragment, SC6pA12B7	2E-21
3108	XM_041367	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4 (15kD, B15) (NDUFB4), mRNA	2E-24
3109	AL117617	Homo sapiens mRNA; cDNA DKFZp564H0764 (from clone DKFZp564H0764)	0.17
3110	AK023907	Homo sapiens cDNA FLJ13845 fis, clone THYRO1000815	7E-42
3111	M95396	Yeast putative transcriptional activator (ADA2) gene, complete cds	3.8
3112	NC_002670	Bacteriophage bIL311, complete genome	0.073
3113	XM_037870	Homo sapiens desmoplakin (DPI, DPII) (DSP), mRNA	2.2
3114	NM_032276	Homo sapiens hypothetical protein DKFZp547E052 (DKFZp547E052), mRNA	0.43

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
3115	AB048877	Macaca fascicularis brain cDNA, clone:QnpA-16414	3E-30
3116	AK014209	Mus musculus 13 days embryo head cDNA, RIKEN full-length enriched library, clone:3110053B16, full insert sequence	0.029
3117	XM_037053	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA	9E-47
3118	AF156197	Cinara pseudotaxifolia cytochrome oxidase II gene, partial cds; mitochondrial gene for mitochondrial product	0.18
3119	AK022006	Homo sapiens cDNA FLJ11944 fis, clone HEMBB1000684	0.003
3120	U23175	Caenorhabditis elegans cosmid F57F10, complete sequence	0.022
3121	AF267198	Candidatus Carsonella ruddii natural-host Arytaina genistae ATP synthase alpha subunit (atpA) gene, partial cds; ATP synthase gamma subunit (atpG) gene, complete cds; and ATP synthase beta subunit (atpD) gene, partial cds	0.019
3122	AY026461	Homo sapiens CUB domain containing protein 1 (CDCP1) mRNA, complete cds	0.5
3123	NC_002471	Typhlonectes natans mitochondrion, complete genome	0.45
3125	AF328531	Homo sapiens clone 9qtel_c10t7 sequence	0.00001
3126	AF397158	Homo sapiens clone 11 pur alpha-associated ribosomal RNA gene, partial sequence	2E-37
3127	AF110970	HIV-1 isolate C-96BW11.06 country Botswana, complete genome	5.3
3128	AJ237690	Canis familiaris polymorphic marker clone XC08	1.3
3129	AE001176	Borrelia burgdorferi (section 62 of 70) of the complete genome	0.084
3130	AJ271333	Campylobacter hyoilei ORF1, ORF2, ORF3 and ORF4	6.7
3131	AF112247	Merluccius productus Mpro-1 mitochondrial control region, partial sequence	0.0008
3132	XM_002378	Homo sapiens uncharacterized hypothalamus protein HT010 (HT010), mRNA	4E-28
3133	AJ242726	Xenopus laevis mRNA for p21 activated kinase 2 (PAK2 gene)	0.25
3134	AF049711	Petunia x hybrida pollen-specific 1-aminocyclopropane-1-carboxylate synthase (ACS2) gene, complete cds	0.24
3135	XM_003091	Homo sapiens KIAA0001 gene product; putative G-protein-coupled receptor; G protein coupled receptor for UDP-glucose (KIAA0001), mRNA	2.2
3136	Z33368	M.capricolum DNA for CONTIG MCABF	0.001
3137	AE001433	Plasmodium falciparum chromosome 2, section 70 of 73 of the complete sequence	0.001
3138	AK017235	Mus musculus adult male pituitary gland cDNA, RIKEN full-length enriched library, clone:5330405D10, full insert sequence	0.7
3139	Z57308	H.sapiens CpG island DNA genomic Mse1 fragment, clone 170g9, reverse read cpg170g9.rt1a	0.023
3140	AC005485	Homo sapiens PAC clone RP5-998M2 from 7q33-q35, complete sequence	5.4
3141	AF118654	Leishmania donovani ATPase 6 gene; kinetoplast gene for kinetoplast product	0.66

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
3142	AJ271879	Uncultured eubacterium plasmid pIE1130 DNA for repA gene, repC gene, repB gene, mobA gene, mobB gene, mobC gene, cac gene, catIII gene, sulII gene, strA gene, strB gene and aph(3')-I gene	0.26
3143	Y00165	Sus scrofa mRNA for link protein	0.079
3144	AF283982	Caenorhabditis elegans transcription enhancer factor-1-like protein EGL-44 (egl-44) gene, complete cds	0.0007
3145	AE004926	Pseudomonas aeruginosa PA01, section 487 of 529 of the complete genome	0.44
3146	AE004738	Pseudomonas aeruginosa PA01, section 299 of 529 of the complete genome	1.4
3147	AC083824	Homo sapiens clone RP11-91J18, complete sequence	0.59
3148	AY023127	Oryza sativa microsatellite MRG5452 containing (GCA)X9, closest to marker C402, genomic sequence	0.77
3149	XM_002943	Homo sapiens similar to PRO0327 protein (H. sapiens) (LOC92570), mRNA	0.073
3150	D88151	Clostridium perfringens DNA for D-alanine:D-alanine ligase, cortical fragment-lytic enzyme	0.057
3151	XM_009013	Homo sapiens similar to tumor necrosis factor (ligand) superfamily, member 14 (H. sapiens) (LOC63472), mRNA	1.7
3152	NM_012702	Rattus norvegicus Carcinoembryonic antigen gene family (CGM1) (Cgm1), mRNA	1.5
3153	AJ131041	Clogmia albipunctata mRNA for Hunchback protein, partial	0.019
3154	AE000720	Aquifex aeolicus section 52 of 109 of the complete genome	5.3
3155	X74789	Potato leaf roll virus RNA sequence	0.47
3156	AF064478	Homo sapiens natural resistance-associated macrophage protein 2 (NRAMP2) gene, exons 4 and 5	0.021
3157	M84761	Rat fatty acid synthase gene, complete cds	0.25
3158	AF239566	Polycycnis ornata tRNA-Leu (trnL) gene, partial sequence; and trnL-F intergenic spacer region, complete sequence; chloroplast gene for chloroplast product	0.007
3159	AF343914	Campylobacter jejuni NCTC 11828 LOS biosynthesis cluster, partial sequence	0.025
3160	AL137443	Homo sapiens mRNA; cDNA DKFZp566G184 (from clone DKFZp566G184)	0.99
3161	X54452	D.discoideum culmination spiA (Dd31) gene	0.71
3162	X80908	L.esculentum gene for fruit ripening polygalacturonase	0.069
3163	XM_007838	Homo sapiens nuclear factor of activated T-cells 5, tonicity-responsive (NFAT5), mRNA	0.5
3164	AF119385	Mus musculus KvLQT1 gene, KvLQT1-AS allele, partial intron sequence	0.17
3165	X86449	E.caballus DNA segment containing microsatellite	1E-25
3166	Z22800	H.sapiens microsatellite repeat	0.000004
3167	U22842	Lagos bat virus nucleoprotein gene, partial cds	0.027

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
3168	AF108897	Campylobacter jejuni PglB (pglB) gene, partial cds; and PglA (pglA), PglC (pglC), PglD (pglD), PglE (pglE), PglF (pglF), and PglG (pglG) genes, complete cds	0.73
3169	AE000556	Helicobacter pylori 26695 section 34 of 134 of the complete genome	0.016
3170	AK024295	Homo sapiens cDNA FLJ14233 fis, clone NT2RP4000049	0.46
3171	U13835	Mus musculus c-abl protein (c-abl) gene, exons 1 and 1B, alternatively spliced	4.5
3172	AJ132887	Homo sapiens telomere-junction DNA sequence, haplotype B	6E-13
3173	XM_007277	Homo sapiens hypothetical protein DKFZp761F2014 (DKFZp761F2014), mRNA	1.9
3174	L40470	Pisum sativum (clone HW39-4) gene fragment	0.05
3175	AF206594	Lacerta vivipara 12S ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and 16S ribosomal RNA gene, partial sequence; mitochondrial genes for mitochondrial products	0.69
3176	XM_037847	Homo sapiens neurexophilin 3 (NXPH3), mRNA	6.7
3177	AY026945	Rattus norvegicus T:G mismatch thymine glycosylase mRNA, complete cds	1.6
3178	XM_028009	Homo sapiens KIAA1563 protein (KIAA1563), mRNA	2E-71
3179	AF250386	Carsonella ruddii RNA polymerase beta subunit (rpoB) and RNA polymerase beta-prime subunit (rpoC) genes, partial cds	0.65
3180	AB038968	Homo sapiens CFLAR gene, exon 5, exon 6	0.24
3182	AK023569	Homo sapiens cDNA FLJ13507 fis, clone PLACE1005085	2E-64
3183	AF240176	Mus Mus musculus MRP13 mRNA	2
3184	U20230	Human guanyl cyclase C gene, partial cds	0.2
3185	L18959	Ovis aries T cell receptor gene V-region, exons 1 (3' end) and 2 (5' end)	0.64
3186	U36785	Rattus norvegicus putative pheromone receptor VN1 mRNA, complete cds	0.73
3187	AF270614	Homo sapiens clone 5qtel_c93t7 sequence	0.075
3188	NM_004114	Homo sapiens fibroblast growth factor 13 (FGF13), mRNA	6.7
3189	AJ403239	M.musculus DNA for vimentin-binding fragment VimE7	0.076
3190	BC010716	Mus musculus, clone MGC:6551 IMAGE:2655861, mRNA, complete cds	4.9
3191	AF270162	Staphylococcus epidermidis strain SR1 clone step.1051e05 genomic sequence	0.56
3192	XM_046992	Homo sapiens hypothetical gene supported by AL137734 (LOC92742), mRNA	1.5
3193	AE003909	Xylella fastidiosa 9a5c, section 55 of 229 of the complete genome	6.3
3194	AF240176	Mus Mus musculus MRP13 mRNA	1.5
3195	L08174	Romanomermis culicivorax mitochondrial NADH dehydrogenase subunits 6 and 3 (ND6, ND3) cytochrome P450-like protein genes, complete CDS	0.5

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
3196	AK021098	Mus musculus adult male corpus striatum cDNA, RIKEN full-length enriched library, clone:C030021G16, full insert sequence	6.5
3197	AF311637	Eimeria separata ORF470 gene, partial cds; apicoplast gene for apicoplast product	0.079
3198	D84549	Candida tropicalis DNA for carnitine acetyltransferase, complete cds	0.057
3199	XM_045864	Homo sapiens KIAA1804 protein (KIAA1804), mRNA	0
3200	XM_010334	Homo sapiens transducin (beta)-like 1 (TBL1), mRNA	1.9
3201	AL133154	S.pombe chromosome I cosmid c1751	0.15
3202	S75898	aromatase [Poephila guttata=zebra finches, ovary, mRNA, 3188 nt]	0.49
3203	AF047669	Homo sapiens dystrophin (DMD) gene, deletion junction 8 between introns 7 and 20	0.001
3204	AB042652	Bos taurus mRNA for zona pellucida glycoprotein ZPB, complete cds	0.58
3205	AF147082	Homo sapiens gamma-glutamyl hydrolase gene, exons 3 through 7	0.028
3206	AE006252	Lactococcus lactis subsp. lactis IL1403 section 14 of 218 of the complete genome	0.07
3207	Z99773	Caenorhabditis elegans cosmid H06A10, complete sequence	0.7
3208	NC_001328	Caenorhabditis elegans mitochondrion, complete genome	0.025
3209	AY037251	Arabidopsis thaliana AT4g30750/T10C21_100 mRNA, complete cds	5.9
3210	Z12834	L.esculentum gene for polyphenol oxidase	0.75
3211	AL391057	Human DNA sequence from clone RP11-533B2 on chromosome 10, complete sequence [Homo sapiens]	0.07
3212	AF001454	Helianthus annuus Dc3 promoter-binding factor-2 (DPBF-2) mRNA, complete cds	0.21
3213	AF295925	Streptococcus pneumoniae transposon Tn5252 Orf28, Orf27, Orf26, Orf25, Orf24, Orf23, Orf22, Orf21, and Orf20 genes, complete cds	0.019
3214	AC024821	Caenorhabditis elegans cosmid Y55B1AR, complete sequence	1.7
3215	AC018655	Homo sapiens 12q BAC RP11-946G22 (Roswell Park Cancer Institute Human BAC Library) complete sequence	0.0000001
3216	XM_043524	Homo sapiens cadherin 17, LI cadherin (liver-intestine) (CDH17), mRNA	2E-52
3217	XM_051566	Homo sapiens phosphoinositide-3-kinase, catalytic, beta polypeptide (PIK3CB), mRNA	0.025
3218	X84742	M.musculus GPX3 gene	0.079
3219	AL445527	Human DNA sequence from clone RP11-115C2 on chromosome 1, complete sequence [Homo sapiens]	5.4
3220	AF254792	Danio rerio Period3 circadian clock protein (Per3) mRNA, complete cds	3.8
3221	AE002225	Chlamydophila pneumoniae AR39, section 53 of 94 of the complete genome	0.12

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
3222	XM_048692	Homo sapiens similar to hypothetical protein (H. sapiens) (LOC92998), mRNA	2E-15
3223	AF335456	Clavulina cinerea 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	0.037
3224	AF335589	Glycine max chitinase class I (Chia1) and hypothetical protein genes, complete cds	3.3
3225	AE005230	Escherichia coli O157:H7 EDL933 genome, contig 1 of 3, section 54 of 155	5.2
3226	AB010822	Homo sapiens MASP gene for mannose binding protein-associated protease, exon 1	7E-13
3227	XM_052139	Homo sapiens interleukin 13 receptor, alpha 1 (IL13RA1), mRNA	0.007
3228	AF293654	Toxoplasma gondii TgMIC10 precursor (MIC10) mRNA, complete cds	0.15
3229	AJ388514	Canis familiaris mRNA for partial Ribosomal protein S14	0.38
3230	U80814	Caenorhabditis elegans cosmid B0547, complete sequence	0.22
3231	NM_013890	Mus musculus f-box and WD-40 domain protein 2 (Fbxw2), mRNA	0.29
3232	AB042411	Homo sapiens strg gene for striatum-specific G potein-coupled receptor, complete cds	0.000009
3233	AF151527	Hyphantria cunea serpin gene, complete cds	0.001
3234	X78305	M. musculus (SRP9) signal recognition particle subunit mRNA, 1116bp	0.047
3235	NM_018830	Mus musculus N-acylsphingosine amidohydrolase 2 (Asah2), mRNA	0.18
3236	AF302060	Apocryptophagus sp. MSPAR4 cytochrome oxidase I (COI) gene, partial cds; mitochondrial gene for mitochondrial product	0.007
3237	AB024025	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K16F13	0.012
3238	U25810	Bos taurus lysozyme (LZ) gene, complete cds	0.004
3239	X95363	C.annuum gamma thionin gene	0.15
3240	AF286897	Plasmodium berghei carbamoyl phosphate synthetase II gene, partial cds	0.15
3241	AF290920	Procambarus clarkii microsatellite PclG-03 sequence	3.7
3242	AE006380	Lactococcus lactis subsp. lactis IL1403 section 142 of 218 of the complete genome	2.2
3243	U66913	Dictyostelium discoideum ORF DG1040 gene, partial cds	0.22
3244	Y00460	Mouse genes for transfer RNA-Ala, tRNA-Ile, tRNA-Pro and tRNA-Lys	0.026
3245	L08052	Fruitfly myosin alkali light chain (Mlc1) gene `supercontractile/tubular muscle and indirect flight muscle isoforms'; complete cds's	0.67
3246	AF076597	Dictyostelium discoideum ubiquitin-conjugating enzyme protein UbcC (ubcC) mRNA, complete cds	0.58

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
3247	U67518	Methanococcus jannaschii section 60 of 150 of the complete genome	0.003
3248	AF362370	Dictyostelium discoideum histidine kinase DhkH (dhkH) gene, partial cds	6
3249	AF146688	Fugu rubripes sex comb on midleg-like 2 protein (SCML2) gene, complete cds	0.026
3250	AK009952	Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310057C01, full insert sequence	0.07
3251	AB005803	Homo sapiens DNA for histidine-rich glycoprotein, complete cds	0.078
3252	AY021484	Oryza sativa microsatellite MRG3809 containing (TA)X27, closest to marker G227, genomic sequence	2.2
3253	AD000833	Homo sapiens DNA from chromosome 19-cosmid f19399 (~17 kb EcoRI restriction fragment)	0.024
3254	AB048982	Macaca fascicularis brain cDNA, clone:QnpA-13067	0.38
3255	AL023839	Caenorhabditis elegans cosmid Y39A1C, complete sequence	0.026
3256	NC_002052	Tomato spotted wilt virus RNA-L, complete sequence	0.22
3257	AK022137	Homo sapiens cDNA FLJ12075 fis, clone HEMBB1002425	0.64
3258	U44047	Xenopus laevis MCM2 mRNA, complete cds	0.24
3259	Z61385	H.sapiens CpG island DNA genomic Mse1 fragment, clone 51d3, forward read cpg51d3.ft1a	5E-21
3260	AF163151	Homo sapiens dentin sialophosphoprotein precursor (DSPP) gene, complete cds	0.003
3261	L11194	Montinia caryophyllacea ribulose 1,5-bisphosphate carboxylase large subunit (rbcL) gene, partial cds; chloroplast gene for chloroplast product	6.4
3262	BC002928	Homo sapiens, clone MGC:11357 IMAGE:3954507, mRNA, complete cds	3E-46
3263	XM_002837	Homo sapiens acid phosphatase, prostate (ACPP), mRNA	2.3
3264	AF189787	Hordeum vulgare putative c-myb-like transcription factor (MYB3R-1) gene, partial cds	0.61
3266	AB048353	Paramecium caudatum mRNA for hsp60, partial cds	1.8
3267	U75274	Arabidopsis thaliana acyl-CoA binding protein (ACBP) gene, complete cds	0.69
3268	AF034077	Equus caballus alpha-1-antitrypsin (Spi2) gene, complete cds	0.077
3269	AL031426	Human DNA sequence from clone CTA-191D12 on chromosome 22q13.1 Contains two exons of the APOL2 gene for apolipoprotein L 2, ESTs and GSSs, complete sequence [Homo sapiens]	0.000001
3270	AJ007958	Thiobacillus sp. plasmid pT3.2I including adh and repA genes, partial	0.001
3271	NM_025978	Mus musculus RIKEN cDNA 2700016E08 gene (2700016E08Rik), mRNA	1E-17
3272	XM_018403	Homo sapiens similar to gene with multiple splice variants near HD locus on 4p16.3 (H. sapiens) (LOC91016), mRNA	5.5
3273	AJ238613	Gallus gallus mRNA for teneurin-1	0.57
3274	XM_033841	Homo sapiens FGFR1 oncogene partner (FOP), mRNA	0.55

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
3275	NM_014601	Homo sapiens EH-domain containing 2 (EHD2), mRNA	0.065
3276	AK021659	Homo sapiens cDNA FLJ11597 fis, clone HEMBA1003856	9E-13
3277	AB054644	Sarcophaga peregrina gene for lectin, 5' upstream region and partial cds	0.045
3278	AK010362	Mus musculus ES cells cDNA, RIKEN full-length enriched library, clone:2410003J06, full insert sequence	5.5
3279	AF282974	Plasmodium falciparum cysteine protease falcipain-3 gene, complete cds	1.8
3280	U60135	Arabidopsis thaliana serine/threonine protein phosphatase 2A-3 catalytic subunit gene, complete cds	0.024
3281	AF365086	Martiodendron parviflorum tRNA-Leu (trnL) gene, partial intron sequence; chloroplast gene for chloroplast product	6.5
3282	AE002140	Ureaplasma urealyticum section 41 of 59 of the complete genome	0.22
3283	Z49124	S.oleracea chloroplast secA mRNA	0.074
3284	AE002353	Chlamydia muridarum, section 80 of 85 of the complete genome	4.4
3285	XM_011989	Homo sapiens ELKL motif kinase (EMK1), mRNA	7E-54
3286	AJ252287	Plasmodium falciparum partial msp3 gene for merozoite surface protein 3	0.68
3287	AK018224	Mus musculus adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:6330531I01, full insert sequence	2
3288	X91123	Homo sapiens partial SLC6A2 gene for norepinephrine transporter, exon 5	7.5
3289	AB045007	Mus musculus GNB2 gene for guanine nucleotide binding protein beta2 subunit, complete cds	0.67
3290	AY017272	Peromyscus difficilis isolate TK32541 mys-9 retrotransposon and LTR, 5' sequence	5.4
3291	AL590902	S.pombe chromosome I cosmid pB8E5	0.077
3292	XM_003311	Homo sapiens surfactant protein A binding protein (SPAR), mRNA	0.38
3293	AK027388	Homo sapiens cDNA FLJ14482 fis, clone MAMMA1002362	0.007
3294	AB043885	Homo sapiens BHLHB2 gene for bHLH transcriptional factor DEC1, complete cds	0.068
3295	XM_028213	Homo sapiens up-regulated by BCG-CWS (LOC64116), mRNA	0.073
3296	XM_039789	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 2 (SLC2A2), mRNA	9.2
3297	AK021841	Homo sapiens cDNA FLJ11779 fis, clone HEMBA1005921	0.65
3298	M11815	Plasmid pGKL1 from killer yeast (K.lactis), complete	0.008
3299	AF166527	Zea mays flowering-time protein isoforms alpha and beta (ZmLD) gene, alternatively spliced products, complete cds	0.074
3300	XM_040556	Homo sapiens similar to hypothetical protein FLJ20127 (H. sapiens) (LOC91775), mRNA	0.22
3301	AB001569	Carrot DNA for transposon Tdc1	0.17
3302	AF326737	Mus musculus sclerostin gene, complete cds	4.7
3303	AF272001	Ebola virus subtype Zaire strain Mayinga complete genome	1.9

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
3304	XM_034863	Homo sapiens similar to hypothetical protein FLJ22294 (H. sapiens) (LOC90918), mRNA	0.2
3305	AC006654	Caenorhabditis elegans cosmid H09I01, complete sequence	0.023
3306	AK008812	Mus musculus adult male stomach cDNA, RIKEN full-length enriched library, clone:2210403E17, full insert sequence	6.1
3307	AF151387	Lucilia eximia tRNA-Ile gene, partial sequence; D-loop, complete sequence; and 12S ribosomal RNA, partial sequence; mitochondrial genes for mitochondrial products	0.077
3308	S53497	immunoglobulin epsilon chain constant region=secreted form {3' region} [human, B cell myeloma U-266, Genomic, 3198 nt]	5.5
3309	XM_010126	Homo sapiens stromal antigen 2 (STAG2), mRNA	e-115
3310	D10500	Homo sapiens MAT gene for mitochondrial acetoacetyl-CoA thiolase, exon 1	1.9
3311	AF293900	Paraflabellula reniformis small subunit ribosomal RNA gene, complete sequence	0.092
3312	NC_001530	Human papillomavirus type 47, complete genome	0.67
3313	Z85396	H.sapiens Ig lambda light chain variable region gene (34-34SWIIF32) rearranged; Ig-Light-Lambda; VLambda	0.71
3314	NC_001566	Apis mellifera ligustica mitochondrion, complete genome	0.015
3315	AF103869	Plasmodium yoelii blood-stage membrane protein Ag-1 mRNA, complete cds	1.5
3316	XM_007957	Homo sapiens hypothetical protein (LOC57019), mRNA	3E-27
3317	XM_012723	Homo sapiens chromosome 18 open reading frame 1 (C18orf1), mRNA	2.7
3318	XM_046956	Homo sapiens Kallmann syndrome 1 sequence (KAL1), mRNA	4.5
3319	AE000614	Helicobacter pylori 26695 section 92 of 134 of the complete genome	0.068
3320	NM_017932	Homo sapiens hypothetical protein FLJ20700 (FLJ20700), mRNA	1.7
3321	AK017541	Mus musculus 8 days embryo cDNA, RIKEN full-length enriched library, clone:5730410F24, full insert sequence	4.8
3322	AK016519	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4932411G06, full insert sequence	1.9
3323	U38184	Trypanosoma cruzi kinetoplast minicircle ATPase subunit 6 mRNA, complete cds	0.0003
3324	Z54181	M.catarrhalis bla gene for BRO-2	0.069
3325	U43961	Oryza sativa 3-hydroxy-3-methylglutaryl-CoA reductase gene, promoter region and complete cds	0.17
3326	AK025166	Homo sapiens cDNA: FLJ21513 fis, clone COL05778	0.23
3327	AF158727	Homo sapiens truncated properdin (PFC) gene, exons 1 and 2	0.73
3328	AL116536	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation	0.57
3329	NC_001712	Locusta migratoria mitochondrion, complete genome	0.061

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
3330	AY028779	Staphylococcus epidermidis plasmid pST6 beta-lactamase repressor BlaI (blaI) gene, partial cds; resolvase/integrase BinR (binR), recombinase Sin (sin), repressor QacR (qacR), and transport protein QacB (qacB) genes, complete cds; and unknown gene	0.23
3331	AF346992	*Homo sapiens mitochondrion*, complete genome	1.7
3332	NM_031389	Mus musculus ribonuclease/angiogenin inhibitor 2 (Rnh2), mRNA	1.9
3333	AC079918	Homo sapiens BAC clone RP11-114K13 from 7, complete sequence	0.0002
3335	AF298207	Dictyostelium discoideum transposon thug-S, complete sequence	0.15
3336	L36903	Saccharomyces cerevisiae mitochondrion 21S ribosomal RNA (21S rRNA) gene, 21S R2 ribosomal RNA (21S R2 rRNA) gene, and ORF RI	0.024
3337	AF239663	Prunus persica ACC synthase gene, partial cds	0.066
3338	AJ223690	H.sapiens D2-1-K2G7np gene for immunoglobulin kappa chain variable region	0.026
3339	AC084157	Caenorhabditis elegans cosmid Y46E12BR, complete sequence	4.4
3340	M58606	B.subtilis threonine deaminase (ILVA) gene, complete cds	0.62
3341	NC_001648	Cassava vein mosaic virus, complete genome	0.008
3342	U09277	Caenorhabditis elegans Bristol N2 synaptic vesicle acetylcholine transporter (unc-17) gene, complete cds	0.024
3343	U52821	Mus musculus prion (PrP) gene, exons 1 and 2	1.9
3344	AK014936	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4921521D15, full insert sequence	2
3345	AE007447	Streptococcus pneumoniae section 130 of 194 of the complete genome	5
3346	AK005820	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:1700010F03, full insert sequence	0.18
3347	AB011681	Danio rerio mRNA for ZOR-2, complete cds	1.9
3348	AB030616	Mus musculus Chetk-alpha gene for choline/ethanolamine kinase-alpha, exon 1 and 5'-flanking region	2E-10
3349	AF269359	Staphylococcus epidermidis strain SR1 clone step.1002e12 genomic sequence	0.53
3350	AF063004	Trypanosoma rotatorium trans-spliced leader gene, partial sequence	1.9
3351	AE001411	Plasmodium falciparum chromosome 2, section 48 of 73 of the complete sequence	0.008
3352	AF240496	Mus musculus clone 148d4 Naip5 gene, partial sequence	0.56
3353	XM_004722	Homo sapiens hypothetical protein FLB6421 (FLB6421), mRNA	2.2
3354	AF100324	Mycoplasma fermentans DNA polymerase III subunit (dnaH), YabC protein (yabC), orf550, lipoprotein MALP-404 precursor (malP), insertion sequence IS1630 transposase (tnpA) genes, complete cds; P78 ATP-binding cassette transport operon, complete sequence;>	2.1
3355	NM_019684	Mus musculus serine/threonine kinase 23 (Stk23), mRNA	0.23

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
3356	AB004856	Buchnera aphidicola mRNA for homoserine kinase, partial cds	1.9
3357	AF328428	Homo sapiens clone 1ptel_2109Bf&Br sequence	2E-11
3358	XM_041166	Homo sapiens hypothetical gene supported by AF308287; BC009516 (LOC91860), mRNA	0.024
3359	AE006429	Lactococcus lactis subsp. lactis IL1403 section 191 of 218 of the complete genome	0.24
3360	U95455	HIV-1 clone 8 isolate BV from Milan, envelope glycoprotein, V1-V5 region (env) gene, partial cds	0.026
3361	XM_001775	Homo sapiens PEF protein with a long N-terminal hydrophobic domain (peflin) (PEF), mRNA	0.45
3362	AF100670	Caenorhabditis elegans cosmid M4	0.072
3363	AB036737	Homo sapiens mRNA for RERE, complete cds	0.21
3364	AE001030	Archaeoglobus fulgidus section 77 of 172 of the complete genome	1.5
3365	XM_046602	Homo sapiens hypothetical gene supported by AK027658 (LOC92679), mRNA	2
3366	XM_005889	Homo sapiens kinesin-like 1 (KNSL1), mRNA	0.21
3367	AF275345	Lycopersicon esculentum MADS-box transcription factor jointless gene, complete cds	1.2
3368	NC_000857	Ceratitis capitata complete mitochondrial genome	0.022
3369	AC002048	Human PCR Fragment of Cosmid g1346a274 from 7q31.3, complete sequence [Homo sapiens]	1E-16
3371	AB016611	Enterobacter cloacae ampC gene, complete cds	0.62
3372	NM_026040	Mus musculus RIKEN cDNA 2810036K01 gene (2810036K01Rik), mRNA	e-138
3373	AJ252860	Human immunodeficiency virus type 1, partial proviral POL gene, rt region, isolate CL	0.25
3374	XM_043434	Homo sapiens villin-like (VILL), mRNA	1.8
3375	AE002776	Drosophila melanogaster genomic scaffold 142000013385952, complete sequence	0.19
3376	XM_030198	Homo sapiens tumor necrosis factor receptor superfamily, member 8 (TNFRSF8), mRNA	0.76
3377	X65450	C.canis mRNA for chloride channel	6.3
3378	NM_032248	Homo sapiens hypothetical protein DKFZp434F1719 (DKFZp434F1719), mRNA	1E-47
3379	L47121	Carnobacterium piscicola transposase, bacteriocin, histidine protein kinase, ATP dependent transloactor, accessory protein, and carnobacteriocin B2 genes, complete cds	0.18
3380	L26287	Schistosoma mansoni SMDR2 gene, complete cds	0.66
3381	AF125130	Nemadactylus macropterus clone 15.1 microsatellite sequence	0.072
3383	AB040099	Oryzias latipes olgc4 gene for membrane guanylyl cyclase OlGC4, 5' flanking sequence and partial cds	0.22
3384	AF375398	Arabidopsis thaliana At1g51660/F19C24_26 gene, complete cds	6
3385	AF391256	HIV-1 clone TV004G24 from South Africa gag protein (gag) gene, complete cds	0.23
3386	X91865	A.thaliana asp5 gene	2.1

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
3387	XM_047084	Homo sapiens human immunodeficiency virus type I enhancer-binding protein 2 (HIVEP2), mRNA	0.21
3388	AF115469	Arabidopsis thaliana cultivar Landsberg erecta Arac2 (Arac2) gene, complete cds	2.3
3389	Z48051	H.sapiens gene for myelin oligodendrocyte glycoprotein (MOG)	0.008
3390	U49259	Arabidopsis thaliana isopentenyl diphosphate:dimethylallyl diphosphate isomerase (IPP2) mRNA, complete cds	2.2
3391	AF032124	Homo sapiens RET proto-oncogene (RET) gene, 5' flanking region and partial cds	0.079
3392	AE001420	Plasmodium falciparum chromosome 2, section 57 of 73 of the complete sequence	0.067
3393	XM_005555	Homo sapiens UDP-glucose ceramide glucosyltransferase (UGCG), mRNA	0.076
3394	Z81014	Human DNA sequence from cosmid U65A4, between markers DXS366 and DXS87 on chromosome X *	2.1
3395	XM_002056	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA	0.26
3396	AF339787	Homo sapiens clone IMAGE:205688, mRNA sequence	2
3397	AP000145	Homo sapiens genomic DNA, chromosome 21q21.2, LL56-APP region, clone B2291C14-R44F3, segment 10/10, complete sequence	0.026
3398	AF261936	Homo sapiens clone 11ptel_c3t7 sequence	0.00002
3399	AF193615	Homo sapiens G-protein-coupled inward rectifying K+ channel KCNJ9 (KCNJ9) gene, complete cds	0.009
3400	AK009952	Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310057C01, full insert sequence	0.079
3401	AF091779	Oncorhynchus mykiss non-classical MHC class I antigen (Onmy-UAA) gene, Onmy-UAA*0101 allele, complete cds	2.3
3402	AB001735	Mus musculus DNA for ADAMTS-1, complete cds	2.3
3403	AK000589	Homo sapiens cDNA FLJ20582 fis, clone KAT12156	1E-13
3404	U55243	Dictyostelium discoideum glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, partial cds	0.24
3405	AF110612	Boophilus microplus cytochrome b apoenzyme (Cytb) gene, partial cds; tRNA-Ser, tRNA-Leu, tRNA-Cys, and tRNA-Met genes, complete sequence; and NADH dehydrogenase subunit 2 (ND2) gene, partial cds, mitochondrial genes for mitochondrial products	0.077
3406	AF060542	Haemophilus influenzae biogroup aegyptius HaeIV restriction/modification system (HaeIVRM) gene, complete cds	0.75
3407	AF303391	Homo sapiens meiotic recombination 11 (MRE11A) gene, exon 16	1.7
3408	AF269359	Staphylococcus epidermidis strain SR1 clone step.1002e12 genomic sequence	0.22
3409	AF327975	Hentzia palmarum 16S ribosomal RNA, partial sequence; mitochondrial gene for mitochondrial product	0.57

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
3410	XM_047898	Homo sapiens variable charge protein on X with eight repeats (VCX-8r), mRNA	5.9
3411	XM_047003	Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, B, 150kD (TAF2B), mRNA	0.7
3412	D86566	Human DNA for NOTCH4, partial cds	0.025
3413	AF360301	Arabidopsis thaliana unknown protein (T8B10_70/AT3g60410) mRNA, complete cds	0.64
3414	AJ404228	Saccharomyces douglasii mitochondrial tRNA gene cluster	0.002
3415	XM_037369	Homo sapiens hypothetical protein FLJ20693 (FLJ20693), mRNA	9E-14
3416	AE005230	Escherichia coli O157:H7 EDL933 genome, contig 1 of 3, section 54 of 155	6.2
3417	AL121778	Human DNA sequence from clone RP5-839B11 on chromosome 20. Contains the first coding exon of the gene for a novel protein with a Kunitz/Bovine pancreatic trypsin inhibitor domain and WAP-type (Whey Acidic Protein) 'four-disulfide core' domains and an e>	0.08
3418	AY020760	Oryza sativa microsatellite MRG3085 containing (TA)X13, closest to marker R2976, genomic sequence	6.8
3419	AL122122	Homo sapiens mRNA; cDNA DKFZp434L098 (from clone DKFZp434L098)	1.8
3420	AF250346	Xenopus laevis early growth response protein 1 (egr1) gene, partial cds	0.077
3421	XM_044852	Homo sapiens KIAA1572 protein (KIAA1572), mRNA	0.7
3422	XM_049057	Homo sapiens G protein-coupled receptor 49 (GPR49), mRNA	7
3423	AJ223690	H.sapiens D2-1-K2G7np gene for immunoglobulin kappa chain variable region	0.028
3424	AJ314752	Anas platyrhynchos mIgM gene (partial), mIgA gene (partial) and IgA gene (partial), clone 13.1	0.072
3425	U51739	Ipomoea trifida secreted glycoprotein 2 (ISG2) mRNA, complete cds	0.64
3426	S66752	coagulation factor IX {3' region} [human, Genomic Mutant, 3130 nt]	0.026
3427	AE001122	Borrelia burgdorferi (section 8 of 70) of the complete genome	0.72
3428	AJ233850	Rattus norvegicus microsatellite sequence clone 27E9	2.1
3429	L35664	Homo sapiens (subclone H8 8_f5 from P1 35 H5 C8) DNA sequence	0.079
3430	U97029	Callithrix geoffroyi epsilon-globin gene, partial cds	2.1
3431	Z82181	Human DNA sequence from clone LL22NC01-86D10 on chromosome 22 Contains part of the SYN3 gene for synapsin III and ESTs, complete sequence [Homo sapiens]	0.71
3432	AB066544	Macaca fascicularis brain cDNA clone:QtrA-10780, full insert sequence	0.62
3433	L77039	Homo sapiens (subclone 2_e8 from P1 H22) DNA sequence	0.0000002
3434	AL590650	Human DNA sequence from clone RP11-334F20 on chromosome 6, complete sequence [Homo sapiens]	1.9

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
3435	U93519	Kladothrips rugosus cytochrome oxidase subunit I (COI) gene, mitochondrial gene encoding mitochondrial protein, partial cds	0.77
3437	U23451	Caenorhabditis elegans cosmid ZK75	0.48
3438	BC003415	Homo sapiens, clone IMAGE:3451161, mRNA	0.41
3439	AK024526	Homo sapiens cDNA: FLJ20873 fis, clone ADKA02669	3.3
3440	AE002548	Neisseria meningitidis serogroup B strain MC58 section 190 of 206 of the complete genome	0.6
3441	AF116832	Anopheles minimus strain PT1 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial gene for mitochondrial product	1.5
3442	AB055323	Macaca fascicularis brain cDNA, clone:QflA-10308	1.6
3443	AK014667	Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched library, clone:4833408P15, full insert sequence	7E-25
3444	U80753	Homo sapiens CAGL79 mRNA, partial cds	0.048
3445	AJ275304	Cicer arietinum mRNA for putative ABA-responsive protein	1.4
3446	AF336131	Lumpy skin disease virus strain Neethling, 3' partial sequence	0.3
3447	U11476	HIV-1 isolate LBLA010 from Liberty City, Florida, envelope glycoprotein (env) gene, partial cds	1.6
3448	XM_045582	Homo sapiens hypothetical gene supported by AL137476 (LOC92530), mRNA	6E-13
3449	AF030199	Mus musculus type 1 sigma receptor gene, complete cds	0.63
3450	AF345926	Myzopoda aurita 12S ribosomal RNA gene, complete sequence; tRNA-Val gene, complete sequence; and 16S ribosomal RNA gene, complete sequence; mitochondrial genes for mitochondrial products	0.13
3451	NM_008715	Mus musculus Notch2-like (Notch2l), mRNA	0.17
3452	AF067794	Nicotiana tabacum meristem-specific promoter sequence	0.1
3453	AJ287175	Mucor indicus partial act-1 gene for actin	2
3454	U89439	Bos taurus ubiquitin-like protein mRNA, complete cds	0.000003
3455	AF250346	Xenopus laevis early growth response protein 1 (egr1) gene, partial cds	0.072
3456	Z73587	S.cerevisiae chromosome XVI reading frame ORF YPL231w	0.19
3457	AB055310	Macaca fascicularis brain cDNA, clone:QflA-14233	0.21
3458	Y16090	Daucus carota Susy*Dc1 gene	0.13
3459	AE003868	Xylella fastidiosa 9a5c, section 14 of 229 of the complete genome	0.16
3460	AF281912	Homo sapiens clone 16qtel_c89bt7 sequence	5E-36
3461	AF126541	Ateline herpesvirus 3 H-DNA terminal repeat unit, complete sequence	0.023
3462	AK011178	Mus musculus 10 days embryo cDNA, RIKEN full-length enriched library, clone:2600010E01, full insert sequence	1.5
3463	AF370226	Arabidopsis thaliana unknown protein (F1B16.11) mRNA, complete cds	0.4
3464	X94768	H.sapiens RP3 gene (XLRP gene 3)	0.21
3465	AB029068	Mus musculus gene for Ser/Thr kinase KKIAMRE, exon 1, 2, 3, 4, 5	0.57

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
3466	X84742	M.musculus GPX3 gene	0.038
3467	BC010011	Homo sapiens, Similar to RIKEN cDNA 4931428D14 gene, clone MGC:15407 IMAGE:4309613, mRNA, complete cds	0.22
3468	AF288536	Legionella longbeachae spectinomycin 3' adenylyltransferase (aadA), possible transcriptional regulatory protein (lrpR), and possible sensor kinase protein (lskS) genes, complete cds; and unknown genes	1
3469	AF288536	Legionella longbeachae spectinomycin 3' adenylyltransferase (aadA), possible transcriptional regulatory protein (lrpR), and possible sensor kinase protein (lskS) genes, complete cds; and unknown genes	1.8
3470	AB013150	Papilio machaon mitochondrial ND5 gene for NADH dehydrogenase subunit 5, partial cds	5.9
3471	XM_028011	Homo sapiens CGI-145 protein (LOC51028), mRNA	0.63
3472	XM_052069	Homo sapiens actin related protein (MGC15664), mRNA	5.7
3473	AL449163	Human DNA sequence from clone RP11-533E16 on chromosome 6, complete sequence [Homo sapiens]	0.00001
3474	X96685	B.burgdorferi cell division genes	1.9
3475	AF179589	Rana tigrina rugulosa glucagon receptor (GluR) mRNA, complete cds	0.19
3476	AJ297549	Homo sapiens partial PIK3CB gene for phosphatidylinositol 3-kinase catalytic subunit p110beta, exons 1-2 and joined CDS	0.87
3477	XM_032707	Homo sapiens KIAA0630 protein (KIAA0630), mRNA	0.2
3478	U25032	Caenorhabditis elegans par-3 mRNA, complete cds	1.3
3479	U89283	Biomphalaria glabrata myoglobin gene, complete cds	3.2
3480	AY029303	Strongylocentrotus purpuratus ADAM precursor, mRNA, complete cds	5.6
3481	AB043223	Mus musculus V186.2 gene for immunoglobulin heavy chain, clone:L1G6001	7.5
3482	AF304130	Danio rerio transmembrane receptor Roundabout1 (robo1) mRNA, complete cds	1.8
3483	AF386077	Homo sapiens interleukin 17B (IL17B) gene, complete cds	0.65
3484	U39889	Bos taurus Y-chromosome specific genomic sequence	0.65
3485	XM_032347	Homo sapiens region containing TLS-associated serine-arginine protein 1; TLS-associated serine-arginine protein 2; TLS-associated serine-arginine protein 2; TLS-associated serine-arginine protein 2; TLS-associated serine-arginine protein 1; TLS-associa>	0
3486	AF120475	Mus musculus myelin-associated oligodendrocytic basic proteins MOBP170 and MOBP69 (Mobp) gene, exons 3 through 5 and complete cds, alternatively spliced	0.0008
3487	U81676	Unidentified eubacterium clone vadinBC27 16S ribosomal RNA gene, partial sequence	0.31
3488	AL596023	Human DNA sequence from clone RP11-142J18 on chromosome X, complete sequence [Homo sapiens]	0.016
3489	U67210	Human clone HS2.16 Alu-Ya5 sequence	0.056

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
3490	XM_007196	Homo sapiens similar to ret finger protein 2; candidate tumor suppressor involved in B-CLL (H. sapiens) (LOC93519), mRNA	0.0000008
3491	AL049568	Human DNA sequence from clone SC22CB-23F1 on chromosome 22q13.31-13.33 Contains a GSS, complete sequence [Homo sapiens]	0.074
3492	X94755	A.thaliana mRNA for SNF1-related ser/thr protein kinase (1852 bp)	0.15
3493	AL392109	Human DNA sequence from clone RP13-459H7 on chromosome 10, complete sequence [Homo sapiens]	1.8
3494	S53497	immunoglobulin epsilon chain constant region=secreted form {3' region} [human, B cell myeloma U-266, Genomic, 3198 nt]	3.2
3495	X16027	R.norvegicus gene encoding alkaline phosphatase, exon 2	0.0009
3496	AF213918	Buchnera aphidicola plasmid pTrpEG isolate Mor26ps anthranilate synthase component I (trpE) pseudogene, partial sequence	0.004
3497	AE006491	Streptococcus pyogenes M1 GAS strain SF370, section 20 of 167 of the complete genome	0.33
3498	Z73587	S.cerevisiae chromosome XVI reading frame ORF YPL231w	0.089
3499	AK023040	Homo sapiens cDNA FLJ12978 fis, clone NT2RP2006321	2E-62
3500	AF062039	Homo sapiens integrin alpha-2 subunit (ITGA2) gene, ITGA2-1 allele, partial cds	0.65
3501	Z77974	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA5D12	0.036
3502	M13934	Human ribosomal protein S14 gene, complete cds	0.54
3503	NM_023220	Mus musculus RIKEN cDNA 2010106G01 gene (2010106G01Rik), mRNA	1.1
3504	AF140513	Homo sapiens clone 254LL2 genomic sequence	0.0004
3505	AL359558	Homo sapiens mRNA; cDNA DKFZp762O1615 (from clone DKFZp762O1615)	0.019
3506	XM_048768	Homo sapiens tetratricopeptide repeat domain 3 (TTC3), mRNA	0.00009
3507	AF074994	Homo sapiens full length insert cDNA YH91C06	0.65
3508	NC_001338	Sulfolobus virus 1, complete genome	0.008
3509	U67502	Methanococcus jannaschii section 44 of 150 of the complete genome	0.21
3510	AY035821	Schizosaccharomyces pombe Byr1-binding protein Bob1 (bob1) gene, complete cds	0.19
3511	AF275842	Plasmodium falciparum clone b.2 PfEMP1 (var) mRNA, partial cds	2
3512	AJ294714	Pichia anomala leu2 gene for beta-isopropylmalate dehydrogenase	0.19
3513	AL391240	Human DNA sequence from clone RP3-397P18 on chromosome 6, complete sequence [Homo sapiens]	3.4
3514	AE002304	Chlamydia muridarum, section 35 of 85 of the complete genome	1.8
3515	AF083830	Homo sapiens dihydropyridine receptor alpha 2 subunit (CACNA2D1) gene, exon 14	0.2

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
3516	AE005222	Escherichia coli O157:H7 EDL933 genome, contig 1 of 3, section 46 of 155	1.7
3517	U04208	Escherichia coli 9142-88 cytolethal distending toxin (cdtA, cdtB, and cdtC) genes, complete cds	0.008
3518	Y07738	M.musculus gene for vimentin	0.65
3519	AF304091	Sotalia fluviatilis alpla lactalbumin gene, partial cds	2
3520	AF270356	Staphylococcus epidermidis strain SR1 clone step.4025c09 genomic sequence	0.52
3521	AF017516	Bombus pascuorum cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds	1.8
3523	AF098919	Gallus gallus alpha-globin gene domain 5' region	2
3524	XM_047517	Homo sapiens Kruppel-like factor 4 (gut) (KLF4), mRNA	1E-39
3525	NC_001626	Petromyzon marinus mitochondrion, complete genome	0.021
3526	AF246647	Bemisia tabaci biotype Q 16S ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	1.9
3527	AL391240	Human DNA sequence from clone RP3-397P18 on chromosome 6, complete sequence [Homo sapiens]	3.1
3528	M32779	AcNPV with an S.frugiperda insertion element IFP2.2	1.9
3529	L44121	Homo sapiens (clone pHK2.1D) CMT1A gene, repeat unit	6E-44
3530	U52350	Arabidopsis thaliana GTP-binding protein (ARAC5) mRNA, complete cds	0.007
3531	X80908	L.esculentum gene for fruit ripening polygalacturonase	0.65
3532	AF267203	Candidatus Carsonella ruddii natural-host Blastopsylla occidentalis ATP synthase alpha subunit (atpA) gene, partial cds; ATP synthase gamma subunit (atpG) gene, complete cds; and ATP synthase beta subunit (atpD) gene, partial cds	0.22
3533	AE001379	Plasmodium falciparum chromosome 2, section 16 of 73 of the complete sequence	0.25
3534	XM_034129	Homo sapiens hypothetical protein DKFZp761J1523 (DKFZp761J1523), mRNA	6
3535	AE002304	Chlamydia muridarum, section 35 of 85 of the complete genome	1.8
3536	AK024082	Homo sapiens cDNA FLJ14020 fis, clone HEMBA1002508	1.7
3537	U67547	Methanococcus jannaschii section 89 of 150 of the complete genome	0.22
3538	AF215629	Crypteronia paniculata chloroplast rpl16 gene, intron sequence	0.024
3539	X03853	Pea chloroplast gene for ribulose 1,5-bisphosphate carboxylase (rbcl)	0.008
3540	X85055	B.taurus cosmid-derived microsatellite DNA (clone IDVGA-40)	0.0009
3541	AK005508	Mus musculus adult female placenta cDNA, RIKEN full-length enriched library, clone:1600021C16, full insert sequence	0.63
3542	Y16262	Daucus carota mRNA for neutral invertase	0.21
3543	AL513491	Human DNA sequence from clone RP11-79A21 on chromosome X, complete sequence [Homo sapiens]	0.56
3544	XM_036298	Homo sapiens hypothetical gene supported by AL442095 (LOC91124), mRNA	0.02
3545	XM_049045	Homo sapiens KIAA0118 protein (KIAA0118), mRNA	0.46

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
3546	AY020760	Oryza sativa microsatellite MRG3085 containing (TA)X13, closest to marker R2976, genomic sequence	5.4
3547	AF198037	Mycoplasma pulmonis LipB (lipB) gene, complete cds; and VsaG (vsaG) and VsaE (vsaE) genes, partial cds	0.008
3548	X62658	E.faecalis plasmid pAD1 sea1 gene and orfy	1.7
3549	AF083468	Emericella nidulans putative zinc finger protein (flbC) gene, complete cds	0.18
3550	AF315801	Homo sapiens chromosome Y AHCP pseudogene, complete sequence	1.9
3551	AC007042	Homo sapiens clone RP11-399H17, complete sequence	6
3552	AF198037	Mycoplasma pulmonis LipB (lipB) gene, complete cds; and VsaG (vsaG) and VsaE (vsaE) genes, partial cds	0.008
3553	AK025090	Homo sapiens cDNA: FLJ21437 fis, clone COL04285	0
3554	X76027	K.lactis APA2 gene for tetraphosphatase, QCR7 gene, bc1 complex subunit VII	0.4
3555	Z78713	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA15A11	0.61
3556	U50357	Streptococcus zooepidemicus zoocin A immunity factor (zif) and zoocin A endopeptidase (zooA) genes, complete cds	0.13
3557	U93721	Homo sapiens green cone photoreceptor pigment gene, 5' flanking region	1.4
3558	AJ291489	Paracentrotus lividus mRNA for fibrosurfin (surfin2656 gene)	3.7
3559	M13820	Plasmid ColIb-p9 colicin Ib structural and immunity genes, complete cds	0.2
3560	Z54147	Human DNA sequence from cosmid L129H7, Huntington's Disease Region, chromosome 4p16.3 contains CpG island	2
3561	AJ301616	Homo sapiens DNC gene for deoxynucleotide carrier, exons 1-9	0.17
3562	U29403	Human immunodeficiency virus type 1 defective gag gene, clone 3-13, truncated cds	0.63
3563	AF090118	Plasmodium falciparum heat shock protein hsp104 (hsp104) gene, partial cds	0.21
3564	Z22707	S.scrofa spI IFN gene	0.57
3565	AF090889	Homo sapiens clone HQ0092	0.62
3566	XM_050705	Homo sapiens GalNAc-4-sulfotransferase 2 (GALNAC4ST-2), mRNA	0.15
3567	XM_016611	Homo sapiens similar to 8-oxoguanine DNA glycosylase (H. sapiens) (LOC93577), mRNA	0.052
3568	Z35914	S.cerevisiae chromosome II reading frame ORF YBR045c	0.59
3569	S69278	CYP1A2=3-methylcholanthrene responsive gene [Oncorhynchus mykiss=rainbow trout, liver, Genomic, 5023 nt]	1.5
3570	X56832	H.sapiens ENO3 gene for muscle specific enolase	0.21
3571	XM_011264	Homo sapiens KIAA0372 gene product (KIAA0372), mRNA	0
3572	NM_022628	Rattus norvegicus nephrin (Nphs1), mRNA	0.017
3573	AJ299718	Homo sapiens partial MASP2 gene, intron 7	6E-33
3574	Z69651	Human DNA sequence from cosmid L75B9, Huntington's Disease Region, chromosome 4p16.3	0.022

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
3575	AF327739	Streptococcus thermophilus Peb1 (peb1), GlnQ (glnQ), response regulator Rr1 (rr1), Hpk2 (hpk2), YycJ-like protein (yycJ), and MurM (murM) genes, complete cds	0.59
3576	AC001656	Drosophila melanogaster (P1 DS00397 (D18)) DNA sequence, complete sequence	0.068
3577	AF262620	Periplaneta americana 16S ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	0.2
3578	L08425	*Zea mays auxin-binding protein* (abp1) gene, exons 1-5 and complete cds	0.64
3579	M97702	Drosophila melanogaster glutathione S-transferase gene	1.8
3580	AF268059	Candidatus Carsonella ruddii natural-host Arytaina geniotae RNA polymerase beta subunit (rpoB) and RNA polymerase beta-prime subunit (rpoC) genes, partial cds	0.063
3581	U30149	Entamoeba histolytica pyruvate:ferredoxin oxidoreductase (pfo1) gene, complete cds	1.9
3582	X88893	C.jacchus intron 4 of visual pigment gene (green allele)	0.00008
3584	AK000939	Homo sapiens cDNA FLJ10077 fis, clone HEMBA1001864	0.19
3585	AL114356	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation	5.6
3586	AF126992	Oxytropis besseyi var. ventosa chloroplast tRNA-Leu (trnL) gene, intron sequence	0.21
3587	Z47046	Human cosmid QLL2C9 from Xq28	5.7
3588	AE006246	*Lactococcus lactis subsp. lactis* IL1403 section 8 of 218 of the complete genome	5.3
3589	AY018921	Oryza sativa microsatellite MRG1246 containing (AT)X23, genomic sequence	0.71
3590	AL589705	Human DNA sequence from clone RP11-64M7 on chromosome 6, complete sequence [Homo sapiens]	0.069
3591	NM_010250	Mus musculus gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 1 (Gabra1), mRNA	3.8
3592	AC024748	Caenorhabditis elegans cosmid Y110A2AR, complete sequence	0.017
3593	AJ002240	Mus musculus minisatellite tandem repeat (MMS9)	1.7
3594	AJ293574	Brassica napus gene for putative corticosteroid binding protein and partial gene for hypothetical protein, cultivar N-o-9	0.21
3596	AF324889	Homo sapiens myosin phosphatase target subunit 2 (MYPT2) gene, exon 1	0.22
3597	S62623	IGF2=insulin-like growth factor 2 {clone PPA1, exon 9} [human, Genomic, 811 nt]	5.4
3598	Z22707	S.scrofa spI IFN gene	0.57
3600	AB030490	Glycine max SG-05 gene for thiamin biosynthetic enzyme, complete cds	0.023
3602	S69278	CYP1A2=3-methylcholanthrene responsive gene [Oncorhynchus mykiss=rainbow trout, liver, Genomic, 5023 nt]	1.7
3603	XM_029148	Homo sapiens hypothetical protein BC004923 (LOC85865), mRNA	0.002

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
3604	AJ002979	L. concinnum chloroplast DNA for intergenic spacer between tRNA-Thr (UGU) and tRNA-Leu (UAA) 5'exon, collected from W. Pakawau, Cape Farewell, South Island, New Zealand	0.067
3605	U36927	Plasmodium yoelii rhoptry protein gene, complete cds	0.2
3606	AK021502	Homo sapiens cDNA FLJ11440 fis, clone HEMBA1001319	0.00001
3607	AB033604	Capra hircus Hsp70-3 gene for 70 kDa heat shock protein, complete cds	0.18
3608	M81651	Human semenogelin II (SEMGII) gene, complete cds	1.8
3609	AB054512	Berardius bairdii DNA, SINE flanking sequence Tuti35 locus	0.49
3610	AF057740	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exon 24 and complete cds	0.018
3611	AJ295158	Homo sapiens gene for thymosin beta-4	1E-48
3612	X79402	B.taurus mRNA for plasminogen	0.21
3613	NC_001807	Human mitochondrion, complete genome	3E-20
3614	X92204	P.hybrida NAM gene	0.049
3616	AB032016	Homo sapiens PDNP1 gene for phosphodiesterase I/nucleotide pyrophosphatase 1, 5' flanking region and partial cds	0.009
3617	AF339159	Macropus rufogriseus mannose-6-phosphate/insulin-like growth factor II receptor (m6p/igf2r) mRNA, partial cds	0.47
3618	AB025285	Homo sapiens c-ERBB-2 gene, exons 1', 2', 3', 4'	0.0000001
3619	AJ002550	Homo sapiens MMP-1 gene, promoter region	3.8
3620	AB004856	Buchnera aphidicola mRNA for homoserine kinase, partial cds	0.79
3621	AB010426	Phytoplasma sp. gene for AL1 like protein, complete cds	1.8
3622	L36903	Saccharomyces cerevisiae mitochondrion 21S ribosomal RNA (21S rRNA) gene, 21S R2 ribosomal RNA (21S R2 rRNA) gene, and ORF RI	0.022
3623	AF267642	Filobasidiella neoformans var. neoformans Myo2p-like protein gene	0.49
3624	XM_044499	Homo sapiens KIAA0484 protein (KIAA0484), mRNA	0.0001
3625	L04550	Homo sapiens DNA fragment	2.6
3626	AF210054	Homo sapiens bone morphogenetic protein 7 (BMP7) gene, promoter region and partial cds	2.5
3627	AL591505	Human DNA sequence from clone RP11-67I12 on chromosome X, complete sequence [Homo sapiens]	0.001
3628	AL049969	Homo sapiens mRNA; cDNA DKFZp564A072 (from clone DKFZp564A072)	0.35
3629	AB055284	Macaca fascicularis brain cDNA, clone:QflA-11654	0.15
3630	AF304448	Homo sapiens vitamin D receptor-interacting protein complex component DRIP150 (DRIP150) mRNA, complete cds	1.3
3631	AL133157	S.pombe chromosome I cosmid c1B2	0.6
3632	AC002475	Homo sapiens Chromosome 22q11.2 PCR Product dgcr-gap1 In DGCR Region, complete sequence	0.005
3633	AK003943	Mus musculus 18 days embryo cDNA, RIKEN full-length enriched library, clone:1110028F11, full insert sequence	4E-18
3634	S78712	hemolin=48 kda C2-type immunoglobulin-like protein [Hyalophora cecropia=giant silkmoths, Genomic, 6622 nt]	3.5

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
3635	AK023897	Homo sapiens cDNA FLJ13835 fis, clone THYRO1000712	2E-98
3636	X55978	T. brucei ESAG 8 gene for a leucine-rich repeat family protein	0.14
3637	XM_031534	Homo sapiens similar to uterine protein (M. musculus) (LOC90410), mRNA	5E-47
3638	AF044287	Drosophila melanogaster delta adaptin subunit of AP-3 (garnet) gene, complete cds	0.004
3639	AB060917	Macaca fascicularis brain cDNA clone:QtrA-14684, full insert sequence	1.1
3640	AK008522	Mus musculus adult male small intestine cDNA, RIKEN full-length enriched library, clone:2010305C02, full insert sequence	0.41
3641	NM_031340	Rattus norvegicus timeless (Drosophila) homolog (Timeless), mRNA	0.18
3642	AF334544	Homo sapiens chromosome Y landmark: proximal chromosome 1 translocation boundary distal to AZFc region	0.19
3643	XM_033642	Homo sapiens nucleophosmin (nucleolar phosphoprotein B23, numatrin) (NPM1), mRNA	1E-66
3645	AE001462	Helicobacter pylori, strain J99 section 23 of 132 of the complete genome	1.3
3646	L81761	Homo sapiens (subclone 6_c10 from P1 H17) DNA sequence, complete sequence	4E-12
3647	AJ271348	Homo sapiens partial DRD3 gene for dopamine D3 receptor, exon 1	0.19
3648	U58991	Simian immunodeficiency virus from African green monkey, tantalus species (SIVtan) proviral DNA, complete genome	0.16
3649	NM_014601	Homo sapiens EH-domain containing 2 (EHD2), mRNA	0.087
3650	NM_032717	Homo sapiens hypothetical protein MGC11324 (MGC11324), mRNA	0.62
3651	XM_004462	Homo sapiens signal sequence receptor, alpha (translocon-associated protein alpha) (SSR1), mRNA	0.79
3652	AY016336	Phragmites australis rpl36-rps8 intergenic spacer, chloroplast sequence	0.69
3653	Z63374	H.sapiens CpG island DNA genomic Mse1 fragment, clone 82b3, forward read cpg82b3.ft1a	0.22
3654	U10927	Staphylococcus aureus M type 1 capsular polysaccharide biosynthesis (capA, capB, capC, capD, capE, capF, capG, capH, capI, capJ, capK, capL, capM) genes, complete cds	0.026
3655	AE007446	Streptococcus pneumoniae section 129 of 194 of the complete genome	0.18
3656	BC006035	Mus musculus, clone IMAGE:3492938, mRNA, partial cds	5.3
3657	AF352740	Oncorhynchus mykiss clone OMM1055 microsatellite sequence	2.1
3658	NM_032141	Homo sapiens hypothetical protein DKFZp434K1421 (DKFZP434K1421), mRNA	0
3659	AF275231	Phloeomyzus passerinii 12S small subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and 16S large subunit ribosomal RNA gene, partial sequence; mitochondrial genes for mitochondrial products	0.077

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
3660	AF017646	Schizosaccharomyces pombe TFIIH subunit p47 (tfh47) gene, complete cds	0.72
3661	AF200526	Zea mays cellulose synthase-2 (CesA-2) mRNA, complete cds	2.2
3662	AJ297654	Sus scrofa AACT2 gene for alpha-1-antichymotrypsin 2, exons 1-5	0.74
3663	XM_018189	Homo sapiens hypothetical protein FLJ13949 (FLJ13949), mRNA	0.74
3664	AE004047	Xylella fastidiosa 9a5c, section 193 of 229 of the complete genome	2.2
3665	XM_003012	Homo sapiens EphB1 (EPHB1), mRNA	6.9
3666	AF083240	Shewanella putrefaciens multi-cytochrome gene cluster, complete sequence; ferrous iron transporter (feoB), deca-heme c-type cytochrome (mtrC), c-type cytochrome precursor (mtrA), and outer membrane protein precursor (mtrB) genes, complete cds	0.085
3667	AF100304	Caenorhabditis elegans cosmid W07B3, complete sequence	0.74
3668	AP001348	Homo sapiens genomic DNA, chromosome 21q21.1-q21.2 clone:f39G8, LL56-APP region, complete sequence	2E-18
3669	AB005039	Alternaria alternata MAT2 gene, complete cds	6.4
3670	NM_009181	Mus musculus sialyltransferase 8 (alpha-2, 8-sialytransferase) B (Siat8b), mRNA	0.22
3671	AB045894	Nepenthes alata NaAP4 mRNA for aspartic proteinase 4, complete cds	7
3672	M74944	Simian immunodeficiency virus (32H Re-isolate of SIVmac 251, clone W9) env gene, complete cds	0.25
3673	AF288211	Danio rerio Nkx5-1 mRNA, complete cds	0.072
3674	AC006753	Caenorhabditis elegans cosmid Y40A1A, complete sequence	0.02
3675	S53497	immunoglobulin epsilon chain constant region=secreted form {3' region} [human, B cell myeloma U-266, Genomic, 3198 nt]	6.8
3676	AL512305	Human DNA sequence from clone RP11-85E24 on chromosome 6, complete sequence [Homo sapiens]	0.009
3677	AF207862	Bos taurus bradykinin receptor B2 (BDKRB2) gene, promoter	5.8
3678	AF269417	Staphylococcus epidermidis strain SR1 clone step.1003e03 genomic sequence	5.1
3679	X53232	Rat mRNA for preoptic regulatory factor-2 (PORF-2)	2
3680	AB005039	Alternaria alternata MAT2 gene, complete cds	6.5
3681	AE003252	Drosophila melanogaster genomic scaffold 142000013385369, complete sequence	1.9
3682	U19744	Caenorhabditis elegans integrin beta pat-3 gene, complete cds	0.083
3683	XM_010829	Homo sapiens potassium channel, subfamily K, member 3 (TASK-1) (KCNK3), mRNA	0.25
3684	AF065853	Homo sapiens OR7E11P pseudogene, partial sequence	0.077
3685	AF325859	Choristoneura fumiferana antifreeze protein (AFP-Lu1) gene, complete cds	2.3
3686	XM_017134	Homo sapiens breast cancer 2, early onset (BRCA2), mRNA	0.23

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
3687	AE002139	Ureaplasma urealyticum section 40 of 59 of the complete genome	0.17
3688	J00241	Human Ig germline kappa-L chain, C region (inv3 allele)	0.22
3689	U23855	Bos taurus von Willebrand factor gene, 5' flanking region and exon 1	0.78
3690	AK015465	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930455H04, full insert sequence	6.2
3691	XM_042056	Homo sapiens LOC86123 (LOC86123), mRNA	2
3692	AL137458	Homo sapiens mRNA; cDNA DKFZp434E2221 (from clone DKFZp434E2221)	0.086
3693	Z81079	Caenorhabditis elegans cosmid F39H11, complete sequence	2
3694	AF142998	Pteronotus parnellii NADH dehydrogenase subunit 1 (ND1) gene, partial cds; mitochondrial gene for mitochondrial product	0.69
3695	AK012282	Mus musculus 11 days embryo cDNA, RIKEN full-length enriched library, clone:2700023I24, full insert sequence	0.75
3696	AB032937	Cucumis sativus CS-ACS1 gene for 1-aminocyclopropane-1-carboxylate synthase, complete cds	1.5
3697	M92295	Gorilla gorilla gamma-1 and gamma-2 globin genes, complete cds	0.029
3698	AF034085	Caenorhabditis elegans UNC-45 (unc-45) gene, complete cds	0.0001
3699	AB048996	Macaca fascicularis brain cDNA, clone:QnpA-14055	0.25
3700	AK024527	Homo sapiens cDNA: FLJ20874 fis, clone ADKA02818	0.000001
3701	AK014489	Mus musculus 14 days embryo liver cDNA, RIKEN full-length enriched library, clone:4432412D04, full insert sequence	4.3
3702	NM_022599	Rattus norvegicus outer membrane protein (Omp25), mRNA	1E-14
3703	AF177242	Bodo saltans clone pBME40 mitocondrial minicircle DNA	0.021
3704	AF183329	Homo sapiens clone NIGMS NA10926D chromosome 10 paralogous sequence variant, genomic sequence	5E-61
3706	AF374728	Saxifragella bicuspidata maturase K (matK) gene, partial cds; chloroplast gene for chloroplast product	0.65
3707	AK010113	Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310068J16, full insert sequence	5E-29
3708	XM_045657	Homo sapiens McKusick-Kaufman syndrome (MKKS), mRNA	1.8
3709	AJ223690	H.sapiens D2-1-K2G7np gene for immunoglobulin kappa chain variable region	0.026
3710	XM_008389	Homo sapiens C1q-related factor (CRF), mRNA	0.026
3711	AF200526	Zea mays cellulose synthase-2 (CesA-2) mRNA, complete cds	2.3
3712	AE000049	Mycoplasma pneumoniae M129 section 31 of 63 of the complete genome	0.68
3713	XM_002495	Homo sapiens cyclic nucleotide gated channel alpha 3 (CNGA3), mRNA	2.1
3714	AF322106	Oncorhynchus mykiss lysozyme II precursor, gene, complete cds	0.7
3715	AK002007	Homo sapiens cDNA FLJ11145 fis, clone PLACE1006626, highly similar to Homo sapiens mRNA for KIAA0928 protein	0.029
3716	Z73978	Caenorhabditis elegans cosmid ZC302, complete sequence	0.23
3717	NM_023979	Rattus norvegicus apoptotic protease activating factor 1 (Apaf1), mRNA	0.52

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
3718	AF335504	Oryza sativa hemoglobin 1 (hb1), hemoglobin 3 (hb3), and hemoglobin 4 (hb4) genes, complete cds	0.077
3719	BC006943	Mus musculus, Similar to RIKEN cDNA 3230401N03 gene, clone MGC:6906 IMAGE:2655807, mRNA, complete cds	2
3720	AK007159	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:1700110I01, full insert sequence	6
3721	AF033002	Cerebratulus lacteus body wall globin gene, complete cds	0.026
3722	X95276	P.falciparum complete gene map of plastid-like DNA (IR-B)	0.2
3723	XM_012629	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 8 (RNA helicase) (DDX8), mRNA	1.4
3724	XM_042643	Homo sapiens hypothetical protein DKFZp434G131 (DKFZP434G131), mRNA	0.69
3725	AF145640	Drosophila melanogaster clone GH07346 BcDNA.GH07346 (BcDNA.GH07346) mRNA, complete cds	2.3
3726	X58823	Bovine COX7cP1 retroposed pseudogene for cytochrome c oxidase subunit VIIc	0.21
3727	XM_052301	Homo sapiens hypothetical protein MGC3199 (MGC3199), mRNA	6E-25
3728	U00176	Dictyostelium mucoroides DMUC2 clone p288m2 G1-like and G5-like ORFs' proteins, complete cds	0.00009
3729	AJ132901	Drosophila guanche mitochondrial A+T-rich region	0.071
3730	AL583762	Human chromosome 14 DNA sequence Partial sequence from BAC R-1109N18_PCR1 of library RPCI-11 from chromosome 14 of Homo sapiens (Human), complete sequence	7E-35
3731	AK021083	Mus musculus adult male corpus striatum cDNA, RIKEN full-length enriched library, clone:C030015A19, full insert sequence	1.5
3732	XM_001934	Homo sapiens PRO0529 protein (PRO0529), mRNA	1.4
3733	AJ235836	Labordia tinifolia chloroplast ndhF gene	2.2
3734	M81855	Rat mdr mRNA sequence	1.9
3735	NM_031649	Rattus norvegicus killer cell lectin-like receptor subfamily G, member 1 (Klrg1), mRNA	4.9
3736	Z78014	Caenorhabditis elegans cosmid F42E8, complete sequence	0.002
3737	XM_045320	Homo sapiens chondroitin sulfate proteoglycan 6 (bamacan) (CSPG6), mRNA	0.0005
3738	AF288788	Staphylococcus aureus rot-like protein Rlp (rlp) gene, complete cds	0.4
3739	D16417	Dictyostelium discoideum mRNA	0.008
3740	X15465	Hamster SPC14 LINE L1 repeat DNA	0.000003
3741	Y14544	Danio rerio mRNA for Hoxc8 protein	0.014
3742	M13897	Rattus norvegicus thyrotropin beta subunit (TSH-beta) gene, complete cds, clones RP100-14 and RP21	3.5
3743	AE001390	Plasmodium falciparum chromosome 2, section 27 of 73 of the complete sequence	0.018
3744	XM_035389	Homo sapiens ribosomal protein, large, P1 (RPLP1), mRNA	9E-36
3745	XM_007409	Homo sapiens alkylation repair; alkB homolog (ABH), mRNA	0.057

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
3746	AE007425	Streptococcus pneumoniae section 108 of 194 of the complete genome	0.15
3747	Z38113	S.cerevisiae chromosome IX lambda clone 4554	4.9
3749	X80491	S.latifolia SLM4 mRNA	0.02
3750	XM_035466	Homo sapiens hBKLF for basic kruppel like factor (LOC51274), mRNA	2E-35
3751	Z75957	Human DNA sequence from cosmid U203H4, between markers DXS366 and DXS87 on chromosome X	0.000001
3752	AE000800	Methanobacterium thermoautotrophicum from bases 58271 to 68710 (section 6 of 148) of the complete genome	0.19
3754	AJ409501	Mus musculus RNA binding site for Dazl protein, clone gf10	0.73
3755	AJ243829	Oryza sativa RPA gene for protein phosphatase 2A A subunit, exons 1-12	3E-25
3756	AK026692	Homo sapiens cDNA: FLJ23039 fis, clone LNG02242	0.022
3757	S81000	{microsatellite regions} [Cryptococcus neoformans=pathogenic yeast, var. gattii, serotype B, UCLA 371-B, human isolate, Genomic, 283 nt]	0.94
3758	AF252420	Bos taurus clone MNB-5 microsatellite sequence	0.074
3759	AF338734	Homo sapiens hypothetical PHD zinc finger protein XAP135 pseudogene, complete sequence	2.1
3760	AJ401038	Human immunodeficiency virus type 1 proviral gp160 gene for envelope protein, strain 97DC.KFE267	0.79
3761	NC_002087	Plasmid pRL765, complete sequence	0.71
3762	AE004161	Vibrio cholerae chromosome I, section 69 of 251 of the complete chromosome	1.9
3763	Z54349	H.sapiens MN/CA9 GENE	0.56
3764	AF372396	HIV-1 isolate CM53658 from Cameroon envelope glycoprotein (env) gene, partial cds	1.8
3765	AY021127	Oryza sativa microsatellite MRG3452 containing (TA)X19, genomic sequence	1.9
3766	AK021485	Homo sapiens cDNA FLJ11423 fis, clone HEMBA1001024	3.4
3767	AF269468	Staphylococcus epidermidis strain SR1 clone step.1005a02 genomic sequence	0.69
3768	AF229080	Rattus norvegicus glucagon receptor gene, promoter and partial cds	0.71
3769	X04384	Sea urchin (L.pictus) gene for testis specific histone H2B-2	0.23
3770	Z36061	S.cerevisiae chromosome II reading frame ORF YBR192w	0.087
3771	AB038488	Halimeda discoidea chloroplast rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial cds	0.25
3772	XM_003759	Homo sapiens leukocyte cell-derived chemotaxin 2 (LECT2), mRNA	0.000001
3773	AF122979	Tridacna maxima 16S ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	0.076
3774	L44120	Homo sapiens (clone pHK1.5D) CMT1A gene, primer binding site	5E-39

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
3775	AC008855	Homo sapiens chromosome 5 clone CTD-2178M23, complete sequence	0.73
3776	AF267225	Candidatus Carsonella ruddii natural-host Tainarys sordida ATP synthase alpha subunit (atpA) gene, partial cds; ATP synthase gamma subunit (atpG) gene, complete cds; and ATP synthase beta subunit (atpD) gene, partial cds	0.024
3777	U67231	Human clone HS4.74 Alu-Ya5 sequence	2E-11
3778	XM_038985	Homo sapiens similar to HYPOTHETICAL PROTEIN KIAA0379 (H. sapiens) (LOC91526), mRNA	0.13
3779	X71625	H.sapiens dinucleotide repeat polymorphism cA14	0.057
3780	BC007480	Mus musculus, clone MGC:7570 IMAGE:3493227, mRNA, complete cds	0.59
3781	U60153	Human immunodeficiency virus type 1 isolate ID4-77, clone 12, from USA, envelope glycoprotein (env) gene, partial cds	0.013
3782	XM_050963	Homo sapiens hypothetical protein DKFZp564O1664 (DKFZP564O1664), mRNA	0
3783	AC024236	Homo sapiens BAC clone RP11-400I17 from Y, complete sequence	0.0001
3784	M17627	Chicken alpha-A-crystallin gene, complete cds and 5' flank	0.077
3785	NM_031557	Rattus norvegicus Prostaglandin I2 (prostacyclin) synthase (Ptgis), mRNA	5.8
3786	Z79647	B.thayeri mitochondrial 16S rRNA gene	0.23
3787	AF032386	Nicotiana tabacum aldose-1-epimerase-like protein (GP40) mRNA, complete cds	0.077
3788	X89568	P.sativum mRNA for HMGI/Y protein	5.8
3789	Z71180	Caenorhabditis elegans cosmid F22E12, complete sequence	0.24
3790	AJ239079	Tetrahymena pyriformis partial gc4 gene for guanylyl cyclase, isoform 4	0.79
3791	AF310890	Dictyostelium discoideum PcmA (pcmA) and RacE (racE) genes, complete cds; tRNA-Phe gene, complete sequence; and unknown gene	0.00003
3792	L22300	Chilo iridescent virus type 6 zinc finger protein and non-histone chromosomal high mobility group protein homolog genes, complete cds	0.021
3793	AF155054	Rickettsia slovaca protein PS 120 (D) gene, partial cds	0.47
3794	X59799	M.musculus S-antigen gene promoter region	0.2
3795	AF330221	Oncorhynchus keta clone Oke4 microsatellite sequence	0.56
3796	XM_043227	Homo sapiens similar to proteasome (prosome, macropain) 26S subunit, non-ATPase, 13 (H. sapiens) (LOC92153), mRNA	6
3797	D17668	Clostridium septicum gene for alpha-toxin, complete cds	0.39
3798	AF165135	Mycoplasma mycoides mycoides SC strain Afade hypothetical proline rich glycoprotein, hypothetical surface-located membrane protein, lipoprotein B precursor (lppB), and hypothetical ABC transporter protein genes, complete cds; hypothetical ABC transport>	1.5

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
3799	AF379892	Rhagigaster sp. M222 16S ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	0.068
3800	NM_024379	Rattus norvegicus glutamate receptor delta-2 subunit (Grid2), mRNA	1.5
3801	AF364550	Drosophila melanogaster transposon cruiser, complete sequence	5.4
3803	AJ315160	Xenopus tropicalis BMP-2 gene for bone morphogenetic protein 2	0.24
3804	AJ293015	Pisum sativum lox1:Ps:7 gene for lipoxygenase, exons 1-8	0.079
3805	Z82768	R.prowazekii genomic DNA fragment (clone A810F)	1.5
3806	NM_013780	Mus musculus neuronal PAS domain protein 3 (Npas3), mRNA	0.72
3807	U56088	Human periodic tryptophan protein 2 (PWP2) gene, exons 3 to 14	0.25
3808	D88987	Mus musculus Ampd3 gene, exon 4	0.18
3809	Z72680	S.cerevisiae chromosome VII reading frame ORF YGL158w	0.73
3810	M17988	Spiroplasma virus 4 (SpV4) replicative form, complete genome	5.3
3811	XM_039684	Homo sapiens putative G-protein coupled receptor (SH120), mRNA	0.17
3812	XM_039684	Homo sapiens putative G-protein coupled receptor (SH120), mRNA	0.19
3813	X60735	S.murinus Dq52 gene and immunoglobulin heavy chain S region gene loci	1.4
3814	XM_045862	Homo sapiens ring finger protein 10 (RNF10), mRNA	5E-14
3815	AB005521	Homo sapiens ppar gamma gene for peroxisome proliferator activated-receptor gamma, exon 1	1.6
3816	AF271964	Bos taurus microsatellite MNB-162 sequence	0.019
3817	AF274307	Zaocys dhumnades creatine kinase mRNA, complete cds	6.1
3818	BC010716	Mus musculus, clone MGC:6551 IMAGE:2655861, mRNA, complete cds	5.5
3819	AE004219	Vibrio cholerae chromosome I, section 127 of 251 of the complete chromosome	5.7
3820	AB060193	Macaca fascicularis brain cDNA clone:QccE-22277, full insert sequence	1.9
3821	AY007106	Homo sapiens clone TCCCIA00427 mRNA sequence	3E-45
3822	X02801	Mouse gene for glial fibrillary acidic protein (GFAP)	0.08
3824	AJ234506	Hordeum vulgare genomic DNA fragment; clone MWG0561.uni	2.1
3825	AK019864	Mus musculus 11 days pregnant adult female ovary and uterus cDNA, RIKEN full-length enriched library, clone:5031405K23, full insert sequence	1.8
3826	AK023304	Homo sapiens cDNA FLJ13242 fis, clone OVARC1000578	6.5
3827	AB062056	Homo sapiens p53DINP1 gene for p53DINP1a, p53DINP1b, complete cds, alternative splicing	0.055
3828	AF379858	Dendrocerus carpenteri 16S ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	0.07
3829	X05621	Chironomus pallidivittatus BR1 gene for giant secretory protein	0.077

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
3830	AF108841	Homo sapiens human endogenous retrovirus HERV-H10 pol protein (pol) gene, partial cds; env pseudogene and 3' LTR, complete sequence	0.009
3831	AF309030	Ixodes scapularis haplotype SSCP NC2_29 16S ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	0.21
3832	AF268055	Candidatus Carsonella ruddii natural-host Glycaspis brimblecombei RNA polymerase beta subunit (rpoB) and RNA polymerase beta-prime subunit (rpoC) genes, partial cds	0.0007
3833	AY021307	Oryza sativa microsatellite MRG3632 containing (TA)X23, genomic sequence	0.009
3834	XM_034551	Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 4 (DYRK4), mRNA	0.00003
3835	AK001647	Homo sapiens cDNA FLJ10785 fis, clone NT2RP4000457, weakly similar to UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 15 (EC 3.1.2.15)	0
3836	XM_043492	Homo sapiens 42259 (KIAA1728), mRNA	5E-19
3837	U22345	Human chromosome 20q12 locus-specific repeat	0.003
3838	J05535	Bovine vascular smooth muscle connexin43 mRNA, complete cds	0.18
3839	AF290221	Cucumis sativus clone B80F mitochondrial genomic sequence	0.065
3840	NM_010059	Mus musculus disrupted meiotic cDNA 1 homolog (Dmc1h), mRNA	5.3
3841	NM_017681	Homo sapiens hypothetical protein FLJ20130 (FLJ20130), mRNA	2
3842	AE002114	Ureaplasma urealyticum section 15 of 59 of the complete genome	1.9
3843	AK022372	Homo sapiens cDNA FLJ12310 fis, clone MAMMA1001970	0.019
3844	U33633	Rice ragged stunt virus minor structural protein gene, complete cds	0.21
3845	AB062993	Macaca fascicularis brain cDNA clone:QmoA-10825, full insert sequence	4E-40
3846	AJ251485	Gorilla gorilla partial lmp7 gene for large multifunctional protease 7, exon 7 and tap2 gene for antigen peptide transporter 2, exons 1-6	0.71
3847	AP000145	Homo sapiens genomic DNA, chromosome 21q21.2, LL56-APP region, clone B2291C14-R44F3, segment 10/10, complete sequence	0.68
3848	XM_046052	Homo sapiens similar to ribosomal protein S3A (H. sapiens) (LOC65465), mRNA	0.017
3849	XM_012036	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 5 (KCNJ5), mRNA	5
3850	AB035883	Pseudoregma bambucicola mitochondrial genes for small subunit rRNA, tRNA-Val, large subunit rRNA, partial and complete sequences, country:Taiwan:Sun Moon Lake	0.077
3851	AB037688	Xenopus laevis Xptch-2 mRNA for patched-2, complete cds	1.8

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
3852	AB041264	Mus musculus pseudogene for GTP-binding protein beta1 subunit	0.53
3853	AF288170	Plasmodium falciparum isolate MM cytoadherence linked asexual protein (clag9) mRNA, partial cds	0.083
3854	AF304321	Neospora caninum RNA polymerase C1 (rpoC1) gene, partial sequence, plastid gene for plastid product	0.002
3855	AF133181	Peziza varia 18S ribosomal RNA gene, and internal transcribed spacer 1, partial sequence	2.1
3856	NM_012694	Rattus norvegicus Solute carrier family 6 (neurotransmitter transporter, dopamine), member 3 (Slc6a3), mRNA	0.56
3857	NM_030261	Mus musculus hypothetical protein MGC7182 (MGC7182), mRNA	6E-36
3858	AF231164	Pseudosymblepharis schimperiana tRNA-Leu, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe, partial sequence; chloroplast genes for chloroplast products	0.059
3859	Z36070	S.cerevisiae chromosome II reading frame ORF YBR201w	0.064
3860	Z24279	H. sapiens (D1S489) DNA segment containing (CA) repeat; clone AFM309ve9; single read	0.2
3861	XM_036937	Homo sapiens KIAA1020 protein (KIAA1020), mRNA	2.1
3862	AB033019	Homo sapiens mRNA for KIAA1193 protein, partial cds	1.6
3864	XM_030075	Homo sapiens hypothetical protein DKFZp434D0513 (DKFZp434D0513), mRNA	2E-74
3865	NM_023979	Rattus norvegicus apoptotic protease activating factor 1 (Apaf1), mRNA	0.59
3866	U50715	Mus musculus alpha-galactosidase A gene, complete cds	0.008
3867	AF078780	Caenorhabditis elegans cosmid C04F2	1.7
3869	L07305	Histoplasma capsulatum (clone pMS3) H-ATPase gene, complete cds	0.46
3870	XM_035796	Homo sapiens hypothetical gene supported by AF001893; AH005586 (LOC91063), mRNA	1.7
3871	NM_025788	Mus musculus RIKEN cDNA 4930511N13 gene (4930511N13Rik), mRNA	5.4
3872	AF339787	Homo sapiens clone IMAGE:205688, mRNA sequence	2
3873	AF028784	Rattus norvegicus glial fibrillary acidic proteins alpha and delta (GFAP) gene, alternatively spliced products, complete cds	0.005
3874	AF328904	Mus musculus lysyl-tRNA synthetase (Kars) gene, exon 14, complete cds; adenosine deaminase tRNA-specific 1 (Adat1) gene, exons EA, 1 and partial cds	0.22
3875	AF033647	Rhytidiadelphus triquetrus 23S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, 4.5S ribosomal RNA gene, internal transcribed spacer 3, and 5S ribosomal RNA gene, complete sequence, chloroplast genes for chloroplast RNAs	2
3876	BC006035	Mus musculus, clone IMAGE:3492938, mRNA, partial cds	5.6
3877	AF311856	Homo sapiens spectrin beta IV (SPTBN3) mRNA, complete cds, alternatively spliced	0.5
3878	AB041327	Anguilla japonica GnRH receptor mRNA for gonadotropin-releasing hormone receptor, complete cds	0.24

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
3879	AF220175	Homo sapiens acid ceramidase (ASAH) gene, exons 5 through 14, and complete cds	0.0009
3880	X89398	H.sapiens ung gene for uracil DNA-glycosylase	0.002
3881	L14017	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	0.56
3882	M97008	Xenopus laevis/gilli hybrid IgM chain gene, clone LG7Gmu	0.007
3883	Z78414	Caenorhabditis elegans cosmid W09D12, complete sequence	0.63
3884	AL512549	S.pombe chromosome I BAC pB2B4	1.9
3885	AB030616	Mus musculus Chetk-alpha gene for choline/ethanolamine kinase-alpha, exon 1 and 5'-flanking region	6.4
3886	AF069535	Bradypus tridactylus 16S ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, complete sequence	1.5
3887	AK023304	Homo sapiens cDNA FLJ13242 fis, clone OVARC1000578	0.056
3888	AB039756	Brassica rapa SP11-32 mRNA for S locus protein 11-32, partial cds, strain:S32(50-11t)	1.9
3889	AL512405	Human DNA sequence from clone RP11-370N21 on chromosome 6, complete sequence [Homo sapiens]	1.6
3890	AF147813	Protrama radicis elongation factor 1 alpha gene, partial cds	0.18
3891	XM_046967	Homo sapiens region containing variable charge protein on X with eight repeats; variable charge protein on X with two repeats; variable charge, X chromosome (LOC92738), mRNA	0.21
3892	XM_037664	Homo sapiens hypothetical protein MGC4090 (MGC4090), mRNA	1.5
3893	AJ296142	Silene foetida partial rpb2 gene for RNA polymerase II, exons 23 and 24	0.16
3894	AF360340	Arabidopsis thaliana putative pectinesterase (K19E1.17/AT5g53370) mRNA, complete cds	2.7
3895	AF327975	Hentzia palmarum 16S ribosomal RNA, partial sequence; mitochondrial gene for mitochondrial product	0.55
3896	Z15140	L.esculentum mRNA for chitinase	2.1
3897	U57326	Chlamydomonas reinhardtii chloroplast complete Eco10 fragment, rpoC2 gene, partial cds	0.001
3898	AK024908	Homo sapiens cDNA: FLJ21255 fis, clone COL01321	0.003
3899	NC_002087	Plasmid pRL765, complete sequence	0.62
3900	AF063220	Papaya ringspot virus isolate P polyprotein gene, partial cds	0.25
3901	AE002173	Chlamydophila pneumoniae AR39, section 9 of 94 of the complete genome	0.25
3902	BC001152	Homo sapiens, growth arrest-specific 7, clone MGC:1347 IMAGE:3353809, mRNA, complete cds	5.9
3903	AB011800	Agrobacterium tumefaciens plasmid pRiA4 gene, virB operon	5.4
3904	BC010389	Homo sapiens, clone MGC:13615 IMAGE:4283814, mRNA, complete cds	0.084
3905	AF091779	Oncorhynchus mykiss non-classical MHC class I antigen (Onmy-UAA) gene, Onmy-UAA*0101 allele, complete cds	2.3
3906	AF222716	Plasmodium falciparum clone 3D7 unconventional myosin PfM-B gene, complete cds	6.2

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
3907	Z48951	S.cerevisiae chromosome XVI cosmid 9723	2.5
3908	XM_040326	Homo sapiens absent in melanoma 1 (AIM1), mRNA	0.056
3909	AF271964	Bos taurus microsatellite MNB-162 sequence	0.019
3910	BC003261	Mus musculus, serine/threonine kinase 5, clone MGC:5803 IMAGE:3501444, mRNA, complete cds	0.056
3911	AJ011641	Arabidopsis thaliana (ecotype Columbia) spl8 gene, exons 1-3	1.7
3912	AK000864	Homo sapiens cDNA FLJ10002 fis, clone HEMBA1000046	0.53
3913	XM_045747	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1), mRNA	2E-33
3914	AF269581	Staphylococcus epidermidis strain SR1 clone step.1011g07 genomic sequence	0.057
3915	XM_042333	Homo sapiens casein kinase 2, beta polypeptide (CSNK2B), mRNA	1.9
3916	AF269810	Staphylococcus epidermidis strain SR1 clone step.1023h06 genomic sequence	0.022
3917	AJ404228	Saccharomyces douglasii mitochondrial tRNA gene cluster	0.21
3918	XM_027223	Homo sapiens hypothetical gene supported by AK021954 (LOC89916), mRNA	0.61
3919	AJ011641	Arabidopsis thaliana (ecotype Columbia) spl8 gene, exons 1-3	2
3920	AF020725	Gallus gallus unoccupied integration site for endogenous ALV-type retroviral element ev-B2	2
3921	AL157825	Human DNA sequence from clone RP11-518C21 on chromosome Xq13.2-21.1, complete sequence [Homo sapiens]	1.2
3922	AF203676	Myotis myotis microsatellite H23 sequence	0.2
3923	XM_010734	Homo sapiens smg GDS-ASSOCIATED PROTEIN (Kifap3), mRNA	0.66
3924	AF056048	Heterodera glycines beta-1,4-endoglucanase-3 precursor (eng-3) gene, promoter and complete cds	0.026
3925	XM_042676	Homo sapiens hypothetical protein MGC4618 (MGC4618), mRNA	2.2
3926	AL359750	Human DNA sequence from clone RP11-24A10 on chromosome 13, complete sequence [Homo sapiens]	0.024
3927	NM_019054	Homo sapiens hypothetical protein MGC5560 (MGC5560), mRNA	2E-31
3928	AL023845	Caenorhabditis elegans cosmid Y51B9A, complete sequence	0.25
3929	BC001781	Homo sapiens, ribosomal protein L44, clone MGC:2064 IMAGE:3353669, mRNA, complete cds	7E-43
3930	AK004553	Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200002O22, full insert sequence	0.51
3932	X17339	Dengue-2 virus NS1 gene for nonstructural protein (patient M2)	0.23
3933	AE004278	Vibrio cholerae chromosome I, section 186 of 251 of the complete chromosome	0.35
3934	U41064	Drosophila melanogaster putative extracellular ligand trunk gene, complete cds	0.53
3935	AF005900	Homo sapiens alpha2B-adrenergic receptor (alpha2C2AR) gene, complete cds	5.2
3936	AK024599	Homo sapiens cDNA: FLJ20946 fis, clone ADSE01819	5

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
3937	K00489	human enkephalin gene, intron c (3' end) and 3' flank	0.24
3938	U92545	Gallus gallus tubby-like protein (TULP1) mRNA, complete cds	1.8
3939	Z69363	Human DNA sequence from cosmid L60G9B, Huntington's Disease Region, chromosome 4p16.3 contains ESTs	0.55
3941	U82516	Dictyostelium discoideum random slug cDNA22 protein (rsc22) mRNA, complete cds	1.8
3942	NM_026077	Mus musculus RIKEN cDNA 3110040N11 gene (3110040N11Rik), mRNA	e-107
3943	AF241235	Homo sapiens Na+,K+-ATPase gamma-subunit (FXYD2) gene, alternatively spliced isoforms 1 and 2, exons 1 through 6 and complete cds	0.00002
3944	M38180	Human 3-beta-hydroxysteroid dehydrogenase/delta-5-delta-4-isomerase (3-beta-HSD) gene, complete cds	0.64
3945	AJ275020	Homo sapiens partial FAH gene for fumarylacatoacetate hydrolase, intron 10	0.71
3946	AB042198	Mus musculus mac25 gene promoter and exon 1, partial cds	1.9
3947	AF082520	Cryptosporidium parvum Hsp60 gene, partial cds	0.68
3948	Z48051	H.sapiens gene for myelin oligodendrocyte glycoprotein (MOG)	0.71
3949	AF269768	Staphylococcus epidermidis strain SR1 clone step.1023b09 genomic sequence	0.59
3950	AK022181	Homo sapiens cDNA FLJ12119 fis, clone MAMMA1000092	0.62
3951	AF186889	Chlosyne janais 16S ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	0.056
3952	AB026544	Hyoscyamus niger tr1 gene for tropinone reductase-I, complete cds	0.17
3954	M32666	Homo sapiens ITGB3 gene, intron 1, partial sequence	2
3955	Z72888	S.cerevisiae chromosome VII reading frame ORF YGR103w	0.009
3956	AB038979	Homo sapiens gene for caspase-10, exon 11 and complete cds	0.001
3958	AF148987	Legionella fallonii macrophage infectivity potentiator (mip) gene, partial cds	0.075
3959	AF159173	Gallus gallus structural muscle protein titin mRNA, partial cds	1.2
3960	U34931	Mycoplasma pulmonis FtsZ (ftsZ) gene, complete cds, methionyl-tRNA synthetase (metG) gene, partial cds	0.21
3961	AF072439	Rattus norvegicus zinc-finger protein-37 mRNA, complete cds	0.58
3962	AF079877	Mus musculus cyclin G2 (Ccng2) gene, complete cds	0.049
3963	X87947	S.cerevisiae ALG2 gene	0.024
3964	BC004730	Mus musculus, proteasome (prosome, macropain) subunit, beta type 10, clone MGC:5837 IMAGE:3583052, mRNA, complete cds	6.8
3965	BC010610	Homo sapiens, clone IMAGE:4214515, mRNA, partial cds	2E-11
3966	AK012050	Mus musculus 10 days embryo cDNA, RIKEN full-length enriched library, clone:2610319A01, full insert sequence	e-144
3967	BC000240	Homo sapiens, chromosome 4 open reading frame 1, clone IMAGE:3352004, mRNA	1.9
3969	AE007346	Streptococcus pneumoniae section 29 of 194 of the complete genome	4.4

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
3970	AK021969	Homo sapiens cDNA FLJ11907 fis, clone HEMBB1000059	0.005
3971	U05765	Human annexin V (ANX5) gene, exon 7	4.9
3972	S68117	rPLP-A=prolactin-like protein A {5' region, exon 1, intron 1} [rats, Genomic, 1187 nt]	0.11
3973	AL358852	Human DNA sequence from clone RP1-317N9 on chromosome 6, complete sequence [Homo sapiens]	0.18
3974	M26221	African green monkey origin of replication (ORS8) region	0.01
3975	M22064	Mouse MHC class I Lyt-2-a gene encoding lyt-2.1 T-cell surface alloantigen, complete cds	0.71
3976	AY039917	Arabidopsis thaliana putative wall-associated kinase 1 (F16F4.6) mRNA, complete cds	3.5
3977	U67488	Methanococcus jannaschii section 30 of 150 of the complete genome	0.021
3979	XM_027089	Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALAD2), mRNA	1E-09
3980	AF062751	Manduca sexta soluble guanylyl cyclase beta-1 subunit mRNA, complete cds	0.53
3981	AP000214	Homo sapiens genomic DNA, chromosome 21q22.1, D21S226-AML region, clone f43D11-119B8, segment 12/12, complete sequence	0.0003
3982	AF360278	Arabidopsis thaliana putative MLH1 protein (AT4g09140) mRNA, complete cds	0.0001
3983	AF187968	2 Homo sapiens concentrative nucleoside transporter (CNT1) gene, exon 2	0.085
3984	AY032741	Drosophila melanogaster H.M.S. Beagle transposon long terminal repeat, complete sequence; and heat shock protein Hsp70Ab gene, promoter and partial cds	0.6
3985	NM_008697	Mus musculus ninein (Nin), mRNA	4
3986	AB055369	Macaca fascicularis brain cDNA, clone:QflA-12661	0
3987	X15999	Kluyveromyces lactis mitochondrial tRNA-Val, COII and COI (partial)	0.023
3988	AC008855	Homo sapiens chromosome 5 clone CTD-2178M23, complete sequence	0.56
3989	X79482	I.punctatus Immunoglobulin mu heavy chain gene	0.00007
3990	AF051289	Dalbulus charlesi NADH dehydrogenase subunit 1 gene, mitochondrial gene encoding mitochondrial protein, complete cds	0.072
3991	BC004382	Homo sapiens, clone IMAGE:3640982, mRNA, partial cds	e-147
3992	XM_041432	Homo sapiens hypothetical gene supported by AL117603 (LOC91908), mRNA	1.3
3993	NM_027142	Mus musculus RIKEN cDNA 2310012P17 gene (2310012P17Rik), mRNA	0.027
3994	AB022673	Oryza sativa rpl12-1 gene for chloroplast ribosomal protein L12, complete cds	0.69
3995	AB009987	Bombyx mori nuclear polyhedrosis virus gene for putative DNA-directed RNA polymerase component lef8, complete cds	0.2
3996	NM_000144	Homo sapiens Friedreich ataxia (FRDA), mRNA	0.008

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
3997	XM_002395	Homo sapiens LBP protein; likely ortholog of mouse CRTR-1 (LBP-9), mRNA	0.58
3998	AF056532	Brassica napus cultivar Darmor AP31 gene, AP31-DN allele, partial cds	2
3999	Z72888	S.cerevisiae chromosome VII reading frame ORF YGR103w	0.008
4000	AL512660	Human DNA sequence from clone RP11-353M9 on chromosome 10, complete sequence [Homo sapiens]	5.3
4001	AF190131	Cloning vector pVO205 hygromycin-B-phosphotransferase (hph) gene, complete cds	1.7
4002	AJ132557	Oryctolagus cuniculus CYP19 gene, ovarian promoter region	0.069
4003	AB001901	Homo sapiens PACE4 gene, exon 4-7	4
4004	AE006784	Sulfolobus solfataricus section 143 of 272 of the complete genome	0.19
4005	XM_049237	Homo sapiens KIAA0841 protein (KIAA0841), mRNA	1.7
4006	AF107676	Aedes aegypti clone 416 Feilai family of SINES	0.54
4007	AB053857	TT virus gene for ORF1, partial cds, clone:Pd-10-3	0.24
4008	AC078798	Homo sapiens 3 BAC PAC-56F11 (Roswell Park Cancer Institute Human BAC Library) complete sequence	5
4009	NM_026040	Mus musculus RIKEN cDNA 2810036K01 gene (2810036K01Rik), mRNA	2E-33
4011	XM_027300	Homo sapiens DKFZP434K114 protein (DKFZP434K114), mRNA	4E-08
4012	AY021973	Oryza sativa microsatellite MRG4298 containing (TA)X104, closest to marker S10620, genomic sequence	0.0009
4013	AB003097	Fruitfly strain g20 mitochondrial DNA, A+T-rich region, partial sequence	0.000003
4014	AJ000682	Bos taurus PPARG gene, intron 1, 5'	0.1
4015	AE001504	Helicobacter pylori, strain J99 section 65 of 132 of the complete genome	0.64
4016	NM_031442	Homo sapiens hypothetical protein DKFZp761J17121 (DKFZP761J17121), mRNA	0.007
4017	U10698	Rattus norvegicus liver microsomal carboxylesterase mRNA, complete cds	0.21
4018	AF009255	Homo sapiens putative chloride channel gene (CLCN6), exons 14, 15, 16, and 17	1.7
4019	NM_010657	Mus musculus kappa B and Rss recognition component (Krc), mRNA	0.17
4020	AY021100	Oryza sativa microsatellite MRG3425 containing (TA)X19, closest to marker L246, genomic sequence	4.7
4021	U43092	Rattus norvegicus surfactant protein-A (SP-A) gene, complete cds	0.9
4022	XM_050127	Homo sapiens oligophrenin 1 (OPHN1), mRNA	0.64
4023	AE005576	Escherichia coli O157:H7 EDL933 genome, contig 3 of 3, section 195 of 290	0.45
4024	AF288693	Mus musculus Ube1l (Ube1l) gene, partial cds	0.0008
4025	AF203748	Taphozous sp. Brca1 (Brca1) gene, partial cds	5.6

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
4026	AF179234	Homo sapiens short-chain dehydrogenase/reductase 1 (SDR1) gene, exon 1	0.56
4027	AF163735	Illicium parviflorum internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence	0.62
4028	NM_026233	Mus musculus RIKEN cDNA 4933434I20 gene (4933434I20Rik), mRNA	6.5
4029	AL031426	Human DNA sequence from clone CTA-191D12 on chromosome 22q13.1 Contains two exons of the APOL2 gene for apolipoprotein L 2, ESTs and GSSs, complete sequence [Homo sapiens]	0.000001
4030	XM_008148	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 6 (MLLT6), mRNA	0.63
4031	AF007904	Chaetopterus variopedatus histone H4 and histone H2A genes, complete cds	0.009
4032	XM_051353	Homo sapiens C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 5 (CLECSF5), mRNA	0.69
4033	U88154	Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds	0.074
4034	AC023838	Arabidopsis thaliana chromosome III P1 MJM20 genomic sequence, complete sequence	0.2
4035	X15894	Sinapsis alba cab-1 gene for chlorophyll a/b-binding polypeptide	0.1
4036	X54742	Nicotiana plumbaginifolia beta-(1,3)-glucanase gene for a vacuolar isoform	1.8
4037	NM_017590	Homo sapiens hypothetical protein DKFZp434K0920 (DKFZp434K0920), mRNA	0.13
4038	U92482	Equus caballus interleukin-1 receptor antagonist (EqIL-1RA) mRNA, complete cds	0.38
4039	U47540	Aspergillus nidulans nitrogen regulatory protein (tamA) gene, complete cds	0.18
4040	AK001076	Homo sapiens cDNA FLJ10214 fis, clone HEMBA1006530	0.0000009
4041	AC002049	Homo sapiens Chromosome 22q11.2 Cosmid Clone 107d7 In BCRL2-GGT Region, complete sequence	1.3
4042	U55243	Dictyostelium discoideum glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, partial cds	0.23
4043	Z16701	H. sapiens (D1S218) DNA segment containing (CA) repeat; clone AFM157xe7; single read	0.002
4044	AB012733	Rhododendron semibarbatum chloroplast matK gene for ribosomal maturase, complete cds	0.024
4045	AF034950	Bos taurus gonadotropin hormone receptor (GnRH) gene, partial cds	0.22
4046	AJ307017	Mus musculus mRNA for putative ubiquitin-specific protease (Usp9y gene)	1.7
4047	AE001159	Borrelia burgdorferi (section 45 of 70) of the complete genome	0.89
4048	AF239215	Forficula auricularia microsatellite FA2 sequence	0.0002

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
4049	AP000249	Homo sapiens genomic DNA, chromosome 21q22.1, D21S226-AML region, clone:B762O15, complete sequence	1E-18
4050	AP000249	Homo sapiens genomic DNA, chromosome 21q22.1, D21S226-AML region, clone:B762O15, complete sequence	2E-18
4051	AF355470	Mus musculus cysteine dioxygenase gene, exon 2	0.61
4052	BC010739	Homo sapiens, hypothetical protein FLJ12612 similar to COP9 (constitutive photomorphogenic), subunit 7b (Arabidopsis), clone MGC:16836 IMAGE:3893022, mRNA, complete cds	4.5
4053	AK016525	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4932415G12, full insert sequence	1.5
4054	AJ237609	Borrelia recurrentis vmpA1 gene, silent copy	1.8
4055	U00038	Caenorhabditis elegans cosmid T21D11, complete sequence	4.3
4056	AF268053	Candidatus Carsonella ruddii natural-host Tainarys sordida RNA polymerase beta subunit (rpoB) and RNA polymerase beta-prime subunit (rpoC) genes, partial cds	0.067
4057	AC016694	Homo sapiens BAC clone RP11-123G1 from Y, complete sequence	0.2
4058	AK019557	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930402H05, full insert sequence	0.15
4059	AF233898	Escherichia coli strain KI1218 BfpA (bfpA) gene, partial cds	0.063
4060	AK026269	Homo sapiens cDNA: FLJ22616 fis, clone HSI05164	5.7
4061	Z80362	H.sapiens HLA-DRB pseudogene, exon 1;	1.7
4062	XM_046282	Homo sapiens hypothetical gene supported by AK026722 (LOC92635), mRNA	0.007
4063	U83303	Human line-1 reverse transcriptase gene, partial cds, and granulocyte chemotactic protein-2 (GCP-2) gene, complete cds	5E-12
4064	AF276169	Scaphirhynchus platorynchus microsatellite Spl-100 sequence	0.074
4065	AF156797	Mus musculus ATP synthase coupling factor 6 gene, 5' UTR; and GABP-alpha subunit gene, promoter and 5' UTR, partial sequence	1.2
4066	AF110420	Mus musculus hoTgN37INRA locus sequence	4E-10
4067	AK021659	Homo sapiens cDNA FLJ11597 fis, clone HEMBA1003856	6E-10
4068	AL512724	Homo sapiens mRNA; cDNA DKFZp547M202 (from clone DKFZp547M202)	0.2
4069	S54531	L-plastin {exon 1, promoter} [human, Genomic, 3231 nt]	0.023
4070	L02110	Mus musculus proviral retroviral insertion in the cGMP-phosphodiesterase (rd beta PDE) gene, intron 1, with the proviral insert encompassing the env pseudogene (3' end) and 3' LTR	2.1
4071	XM_015244	Homo sapiens ring finger protein 21, interferon-responsive (RNF21), mRNA	1.5
4072	AK015420	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930448I18, full insert sequence	0.003
4073	U67583	Methanococcus jannaschii section 125 of 150 of the complete genome	0.021
4074	X05640	Mouse NF-M gene for middle-molecular-mass neurofilament protein	0.072

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
4075	D01021	Anthocidaris crassispina mRNA for dynein beta-heavy chain, complete cds	0.61
4076	XM_029072	Homo sapiens LOC89256 (LOC89256), mRNA	0.006
4077	NM_017757	Homo sapiens hypothetical protein FLJ20307 (FLJ20307), mRNA	0.26
4078	AF145592	Nicotiana tabacum calcium/calmodulin-dependent protein kinase (CCaMK) gene, exons	0.002
4079	AF384970	Arabidopsis thaliana somatic embryogenesis receptor-like kinase 3 (SERK3) mRNA, complete cds	5.3
4080	AF238313	Dictyostelium discoideum developmental protein DG1037 (DG1037) gene, partial cds	0.2
4081	NM_012519	Rattus norvegicus Ca++/calmodulin-dependent protein kinase II, delta subunit (Camk2d), mRNA	0.071
4082	AL590384	Human DNA sequence from clone RP11-349A16 on chromosome Xq22.3-24, complete sequence [Homo sapiens]	0.11
4083	AF391284	Homo sapiens 11p15.5 clone LOH11A, partial sequence	0.17
4086	XM_034197	Homo sapiens KIAA1505 protein (KIAA1505), mRNA	e-153
4087	AE007255	Sinorhizobium meliloti plasmid pSymA section 61 of 121 of the complete plasmid sequence	5.4
4088	AE006586	Streptococcus pyogenes M1 GAS strain SF370, section 115 of 167 of the complete genome	1.6
4089	AF391284	Homo sapiens 11p15.5 clone LOH11A, partial sequence	0.14
4090	U41549	Caenorhabditis elegans cosmid F22F1	0.065
4091	AF231164	Pseudosymblepharis schimperiana tRNA-Leu, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe, partial sequence; chloroplast genes for chloroplast products	0.066
4092	XM_005131	Homo sapiens chromatin accessibility complex 1 (CHRAC1), mRNA	0.39
4093	NM_025929	Mus musculus RIKEN cDNA 2010109I03 gene (2010109I03Rik), mRNA	5.1
4094	X82784	D.discoideum mRNA for calcium binding protein	0.00001
4095	U04524	Caedibacter taeniospiralis 47 R body synthesis and assembly (rebA rebB, rebC, rebD) genes, complete cds	0.58
4096	XM_050063	Homo sapiens B-cell CLL/lymphoma 9 (BCL9), mRNA	0.075
4097	XM_037650	Homo sapiens syndecan 1 (SDC1), mRNA	2
4098	AF286472	Homo sapiens retinitis pigmentosa GTPase regulator (RPGR) gene, exon ORF15 partial cds	0.076
4099	L05466	Pneumocystis carinii beta-tubulin gene, complete cds	0.009
4100	Z69723	Human DNA sequence from cosmid U238E5, between markers DXS6791 and DXS8038 on chromosome X	0.18
4101	D83657	Human DNA for CAAF1 (calcium-binding protein in amniotic fluid 1), complete cds	5E-30
4102	AL117050	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation	2.1
4103	AE004168	Vibrio cholerae chromosome I, section 76 of 251 of the complete chromosome	2.3

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
4104	BC007114	Homo sapiens, clone IMAGE:4295422, mRNA	0.22
4105	D13859	Penicillium chrysogenum mitochondrion genes for rRNA, tRNA and S5 ribosomal protein, complete cds	0.75
4106	AF137068	Canis familiaris cubilin (CUBN) mRNA, complete cds	4.3
4107	AK012387	Mus musculus 11 days embryo cDNA, RIKEN full-length enriched library, clone:2700047H13, full insert sequence	0.38
4108	NC_001942	Mycoplasma arthritidis bacteriophage MAV1, complete genome	0.12
4109	AF333431	Homo sapiens pseudo attP site psiD, partial sequence	0.45
4110	AF305628	Cubitermes subarquatus microsatellite P19 sequence	0.68
4111	D10997	C.ellipsoidea rbcL, rps14, trnM, trnG, trnD, trnS, rps4, atpE, atpB genes, complete cds	1.8
4112	Z99704	Human DNA sequence from clone LL22NC01-75B8 on chromosome 22 Contains GSSs, complete sequence [Homo sapiens]	0.005
4113	XM_016579	Homo sapiens androgen-induced prostate proliferative shutoff associated protein (KIAA0979), mRNA	1.6
4114	NM_008149	Mus musculus glycerol-3-phosphate acyltransferase, mitochondrial (Gpam), mRNA	5.5
4115	XM_036116	Homo sapiens KIAA0594 protein (KIAA0594), mRNA	e-144
4116	XM_030510	Homo sapiens microfibrillar-associated protein 2 (MFAP2), mRNA	2.4
4117	AB010203	Leptospira interrogans gene, 19kb region containing 5S rRNA gene	1.4
4118	XM_007094	Homo sapiens collagen, type IV, alpha 1 (COL4A1), mRNA	1.9
4120	AF124049	Fugu rubripes double stranded RNA adenosine deaminase RED1B gene, complete cds	0.066
4121	AY007236	Pneumocystis carinii pheromone receptor a mRNA, complete cds	0.53
4122	AF307966	Aptostichus simus clone PD1 16S ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	2
4123	AJ001022	Marmata monax mRNA for tumor suppressor, p53	1.3
4124	AF239469	Polycycnis gratiosa maturase (matK) gene, partial cds; chloroplast gene for chloroplast product	0.65
4125	X75675	C.parapsilosis mitochondrial ND6 and ND1 genes	0.00001
4126	AF335589	Glycine max chitinase class I (Chia1) and hypothetical protein genes, complete cds	0.0003
4127	U33175	Oryza sativa sucrose phosphate synthase gene, complete cds	6.4
4128	AB028198	Arabidopsis thaliana ZF14 mRNA, complete cds	0.008
4129	AF372653	Heteropneustes fossilis prolactin hormone (PRL) mRNA, complete cds	1.3
4130	M63955	S.oedipus MHC class I SO-NI gene	0.6
4131	BC003238	Mus musculus, protein kinase, cAMP dependent, catalytic, alpha, clone MGC:6169 IMAGE:3497908, mRNA, complete cds	0.22
4132	AJ001688	Homo sapiens NKG2D gene, exons 6-9	0.67
4133	D10872	Humam h NAT allele 3-2 gene for arylamine N-acetyltransferase	0.016

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
4134	AF049877	Cotesia congregata EP1 locus with complete integrated Cotesia congregata virus EP1 circle and partial integrated A circle	0.19
4135	Y15783	Rickettsia prowazekii groESL gene	0.3
4136	Y00354	Xenopus laevis gene encoding vitellogenin A2	0.077
4137	NC_001950	Scyliorhinus canicula mitochondrion, complete genome	0.019
4138	AF266048	Macromia splendens small subunit ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	0.42
4139	AL035426	Human DNA sequence from clone 370N13 on chromosome Xq25-26.3. Contains an exon of the GRIA3 gene for glutamate receptor, ionotrophic, AMPA 3. Contains ESTs, complete sequence [Homo sapiens]	0.0006
4140	AF018434	Mus musculus long-chain acyl-CoA dehydrogenase (Acadl) gene, intron 1	6.4
4141	AF309654	Mus musculus U2AF small subunit-related protein (U2af1-rs1) gene, complete cds	0.64
4142	AJ009913	Bos taurus plp gene	2.1
4143	XM_028213	Homo sapiens up-regulated by BCG-CWS (LOC64116), mRNA	0.078
4144	U67550	Methanococcus jannaschii section 92 of 150 of the complete genome	0.081
4145	AB037771	Homo sapiens mRNA for KIAA1350 protein, partial cds	0
4146	AP001438	Homo sapiens genomic DNA, chromosome 21q22.2, clone:T695, LB7T-ERG region, complete sequence	0.009
4147	U88995	Callithrix geoffroyi clone CGE85 mitochondrial D-loop, partial sequence	0.57
4148	AE007343	Streptococcus pneumoniae section 26 of 194 of the complete genome	1.9
4149	Z83832	Avena sativa mRNA for UDP-glucose:sterol glucosyltransferase	0.072
4150	BC007664	Homo sapiens, hepatocellular carcinoma-associated antigen 59, clone MGC:866 IMAGE:3140172, mRNA, complete cds	0
4151	NM_002577	Homo sapiens p21 (CDKN1A)-activated kinase 2 (PAK2), mRNA	5E-39
4152	XM_040120	Homo sapiens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), mRNA	2.1
4153	NM_031511	Rattus norvegicus Insulin-like growth factor II (somatomedin A) (Igf2), mRNA	0.024
4154	XM_049817	Homo sapiens Sec23-interacting protein p125 (P125), mRNA	1.8
4155	BC010892	Homo sapiens, clone MGC:13350 IMAGE:4333615, mRNA, complete cds	0.000004
4156	AJ222787	Hordeum vulgare mRNA for alpha-keto acid dehydrogenase-like protein, clone RG136	0.075
4157	AL021306	Human DNA sequence from clone CTB-1109B5 on chromosome 22 Contains a GSS, complete sequence [Homo sapiens]	0.000001
4158	AF315813	Norwalk virus (Hu/NLV/OC96065/1996/JP) polymerase gene, partial cds	0.71

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
4159	AE001407	Plasmodium falciparum chromosome 2, section 44 of 73 of the complete sequence	0.0008
4160	U32706	Haemophilus influenzae Rd section 21 of 163 of the complete genome	0.6
4161	AF293663	Anopheles culicifacies 12S ribosomal RNA gene, partial sequence; mitochondrial control region, complete sequence; and tRNA-Ile gene, partial sequence; mitochondrial genes for mitochondrial products	0.066
4162	XM_037617	Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA	3E-35
4163	AF305712	Bos taurus insulin-like growth factor binding protein-3 (IGFBP3) gene, complete cds	0.23
4164	AK018618	Mus musculus adult male cecum cDNA, RIKEN full-length enriched library, clone:9130014E20, full insert sequence	0.68
4165	Y00354	Xenopus laevis gene encoding vitellogenin A2	0.079
4166	M61827	Human leukosialin (CD43) gene, complete cds	2.2
4167	M64861	D.discoideum TFIID mRNA, complete cds	0.066
4169	AB028894	Mus musculus Rps11, U35 genes for ribosomal protein S11 and U35 snoRNA, complete cds and sequence	0.6
4170	XM_003974	Homo sapiens hypothetical protein FLJ11159 (FLJ11159), mRNA	0.68
4171	AF100658	Caenorhabditis elegans cosmid H08G01	0.75
4172	AF115645	Sedum multiceps maturase K (matK) gene, partial cds; chloroplast gene for chloroplast product	0.0001
4173	AF064029	Helianthus tuberosus lectin 1 mRNA, complete cds	0.11
4175	AF093754	Arabidopsis thaliana trans-membrane nitrate transporter protein AtNRT2:1 mRNA, complete cds	0.22
4176	M14292	Human L1Heg repetitive element from the intergenic region of the epsilon and G-gamma globin genes	2E-08
4177	NM_013564	Mus musculus insulin-like 3 (Insl3), mRNA	0.067
4178	AF218815	Coturnix japonica early response to neural induction ERNI (ERNI) mRNA, partial cds	0.21
4179	U67616	Human 28S ribosomal RNA pseudogenes and alu repeat region sequence	6E-20
4180	AJ297945	Frankia sp. Arl3 cryptic plasmid pFQ31 ORF AF, korSAF gene, ORF CrF, ORF DrF, repF gene, ORF FrF, ORF GF, ORF HF, ORF JF, ORF KrF, ORF LrF, ORF MF, ORF NrF, ORF OF, ORF PrF, parAF gene and ORF SrF	0.68
4181	AB035429	Homo sapiens AGL gene for glycogen-debranching enzyme, exon 14	0.62
4182	AE006774	Sulfolobus solfataricus section 133 of 272 of the complete genome	0.063
4183	U38803	Dictyostelium discoideum vacuolar proton ATPase 100-kDa subunit (vatM) mRNA, complete cds	0.025
4184	U78096	Human macrophage colony stimulating factor receptor (c-fms) gene, exon 1A, 2 and partial cds	0.0001

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
4185	X57037	T.thermophila G8-scRNA DNA	5.7
4186	AJ001005	Picea abies chloroplast DNA for rbcL pseudogene	0.67
4187	XM_048652	Homo sapiens Apobec-1 complementation factor; APOBEC-1 stimulating protein (ACF), mRNA	4E-12
4188	Y07654	P.crispum pal1 gene	0.24
4189	Z78708	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA14H12	1E-28
4190	AE002143	Ureaplasma urealyticum section 44 of 59 of the complete genome	2.1
4191	AF247729	Oncorhynchus mykiss glucose transporter 1B mRNA, partial cds	1.8
4192	Z72929	S.cerevisiae chromosome VII reading frame ORF YGR144w	0.003
4193	M87754	Human simple repeat polymorphism	0.081
4194	AL021809	S.pombe chromosome I cosmid c25A8	0.026
4195	D12820	Rat mRNA for GUST27 protein, complete cds	3.7
4196	M60352	Mouse testosterone 16a-hydroxylase type b (16aoh-b), exon 1	4.7
4197	XM_007360	Homo sapiens hepatocyte nuclear factor 3, alpha (HNF3A), mRNA	0.95
4198	Z36064	S.cerevisiae chromosome II reading frame ORF YBR195c	0.52
4199	AK023959	Homo sapiens cDNA FLJ13897 fis, clone THYRO1001706	0.49
4200	U48298	Dictyostelium discoideum rtoA gene, complete cds	0.68
4201	L47461	Heterodontus francisci tcr beta gene	1.6
4202	AB041023	Humulus lupulus DNA, 18S-26S intergenic spacer, complete sequence	0.0008
4203	AF118226	Hordeum vulgare high pI alpha-glucosidase (AGL97) gene, complete cds	1.8
4204	AF158049	Platybrachys decemmacula 16S ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	0.077
4205	U63855	Drosophila virilis decapentaplegic protein (dpp) gene, complete cds, haploinsufficient region	0.2
4206	AF248814	Maoricicada cassiope isolate TB-MI-004 tRNA-Asp gene, complete sequence; ATPase subunit 8 gene, complete cds; and ATPase subunit 6 gene, partial cds; mitochondrial genes for mitochondrial products	0.023
4207	XM_037529	Homo sapiens KIAA0410 gene product (KIAA0410), mRNA	0.78
4208	AF330636	Plant DNA excision vector pX6-GFP, complete sequence	0.76
4209	AL080235	Homo sapiens mRNA; cDNA DKFZp586E1621 (from clone DKFZp586E1621)	0.007
4210	NM_021262	Rattus norvegicus Acid phosphatase 1, soluble (Acp1), mRNA	0.16
4211	M11449	Yeast mitochondrial ori2-ori7 region DNA with putative peptide	0.25
4212	AF211134	Carsonella ruddii natural-host Ctenarytaina longicauda 16S ribosomal RNA gene, partial sequence; 23S ribosomal RNA and 5S ribosomal RNA genes, complete sequence; transaldolase (tal) and alkyl hydroperoxide reductase small subunit (ahpC) genes, complete>	0.074
4213	AF157293	Sporodiniella umbellata translation elongation factor 1-alpha (EF-1alpha) gene, partial cds	0.77

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
4214	AL390767	Human DNA sequence from clone RP1-68P15 on chromosome 11p13-14.2 Contains GSSs and ESTs. Contains part of a novel gene, complete sequence [Homo sapiens]	0.004
4215	XM_004579	Homo sapiens HGC6.1.1 protein (HGC6.1.1), mRNA	4E-08
4216	XM_043964	Homo sapiens similar to KIAA0220 protein (H. sapiens) (LOC92263), mRNA	5E-40
4217	AL390767	Human DNA sequence from clone RP1-68P15 on chromosome 11p13-14.2 Contains GSSs and ESTs. Contains part of a novel gene, complete sequence [Homo sapiens]	0.004
4218	AF147082	Homo sapiens gamma-glutamyl hydrolase gene, exons 3 through 7	0.088
4219	AY023560	Oryza sativa microsatellite MRG5885 containing (TTA)X8, closest to marker R2561, genomic sequence	0.026
4220	XM_050088	Homo sapiens hepatocellular carcinoma-associated antigen 127 (HCA127), mRNA	0.007
4221	AF131999	Plasmodium falciparum putative erythrocyte binding protein EBL-1 (ebl-1) gene, partial cds	0.68
4222	AF008434	Solanum fendleri farnesyl-protein transferase beta subunit gene, intron 10	0.21
4223	AF367267	Arabidopsis thaliana AT3g26020/MPE11_17 mRNA, complete cds	0.53
4224	XM_006706	Homo sapiens primase, polypeptide 1 (49kD) (PRIM1), mRNA	7E-12
4225	AK004675	Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200009I20, full insert sequence	0.017
4226	AB026660	Arabidopsis thaliana genomic DNA, chromosome 5, BAC clone:T20O7	0.23
4227	AF272387	Homo sapiens leucine zipper nuclear factor (BLZF1) gene, exon 6	5E-09
4228	L08897	Mycoplasma gallisepticum (strain A5969) 16S-, 23S-, 5S ribosomal RNA (rrsA, rrlA, rrfA) genes	0.073
4229	Z26314	P.falciparum gene for STARP antigen	0.008
4230	NC_001942	Mycoplasma arthritidis bacteriophage MAV1, complete genome	0.18
4231	Y18277	Gallus gallus mRNA for neurobeachin, partial	3
4232	XM_047009	Homo sapiens pleiomorphic adenoma gene-like 2 (PLAGL2), mRNA	1.8
4233	X84729	S.cereale repeated DNA sequence	0.21
4234	AL513132	Human DNA sequence from clone RP11-460C6 on chromosome 9, complete sequence [Homo sapiens]	0
4235	Z71694	E.herklotsi mitochondrial genes for NADH Dehydroenase subunit 5 and 6	0.6
4236	Z33215	M.capricolum DNA for CONTIG MC294	0.54
4237	X86012	Human DNA sequence from intron 22 of the factor VIII gene, Xq28. Contains the end of a 9.5kb repeated region, int22h-1, involved in many cases of haemophilia	0.0000005
4238	AF174355	Praon barbatum 16S ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	0.026

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
4239	AY039607	Arabidopsis thaliana AT3g52380/F22O6_240 mRNA, complete cds	6.1
4240	AJ223385	Fowlpox virus strain HP-440 DNA, isolate FP9, 14.6 kb fragment	0.000004
4241	AF277282	Daphnia cristata country Lithuania 12S ribosomal RNA gene, partial sequence	1.9
4242	NM_023850	Mus musculus carbohydrate (keratan sulfate Gal-6) sulfotransferase 1 (Chst1), mRNA	0.59
4243	AJ238599	Lepilemur septentrionalis genomic fragment, RAPD with primer operon OPH4, clone A1	0.2
4244	XM_051747	Homo sapiens eukaryotic translation initiation factor 4 gamma, 2 (EIF4G2), mRNA	3E-58
4245	M63376	Human TRPM-2 protein gene, exons 1,2 and 3	0.7
4246	AF367267	Arabidopsis thaliana AT3g26020/MPE11_17 mRNA, complete cds	0.59
4247	AJ294714	Pichia anomala leu2 gene for beta-isopropylmalate dehydrogenase	0.17
4248	AF320616	Mus musculus amnionless precursor protein (Amn) gene, partial cds	0.57
4249	AL049609	S.pombe chromosome III cosmid c297	1.8
4250	AJ252313	Homo sapiens genomic hybrid Rhesus box	3.8
4251	XM_034693	Homo sapiens ectodermal dysplasia 1, anhidrotic (ED1), mRNA	0.2
4252	NC_001463	Caprine arthritis-encephalitis virus, complete genome	1.3
4253	AC018655	Homo sapiens 12q BAC RP11-946G22 (Roswell Park Cancer Institute Human BAC Library) complete sequence	5.9
4254	AF003519	Paraligoneurus sp. 16S ribosomal RNA gene, partial sequence	0.024
4255	AL049434	Homo sapiens mRNA; cDNA DKFZp586M151 (from clone DKFZp586M151)	0.0008
4256	U39321	Triticum aestivum acetyl-CoA carboxylase gene, exons 1-30, complete cds	0.22
4257	AB055106	Oryza sativa V-ATPase B gene for vacuolar ATPase B subunit, complete cds	1.7
4258	AF150091	Rattus norvegicus small zinc finger-like protein (TIM10) mRNA, complete cds	0.24
4259	AF047677	Homo sapiens dystrophin (DMD) gene, deletion breakpoints 1-3 in intron 5	0.025
4260	Z81504	Caenorhabditis elegans cosmid F15H9, complete sequence	0.24
4261	AF226147	HIV-1 isolate 630469c from USA protease (pol) gene, partial cds	2
4262	AF270072	Staphylococcus epidermidis strain SR1 clone step.1047b05 genomic sequence	0.68
4263	U56088	Human periodic tryptophan protein 2 (PWP2) gene, exons 3 to 14	0.076
4264	X83692	Brassica napus (tournefortii) mitochondrial genes for atp6, and ORF263	2.1

	Table 3A Nearest Neighbor (BlastN vs. Genbank)		
SEQ ID NO	ACCESSN	DESCRIP	P VALUE
4265	AF243425	Penicillium oxalicum vacuolar serine protease mRNA, complete cds	0.63
4266	NM_024381	Rattus norvegicus ATP-stimulated glucocorticoid-receptor translocaton promoter (Gyk), mRNA	0.68
4267	AF098919	Gallus gallus alpha-globin gene domain 5' region	2.3
4268	AJ297909	Hypocrea jecorina rho3 gene, exons 1-5	0.23
4269	U67528	Methanococcus jannaschii section 70 of 150 of the complete genome	0.029
4270	AF104920	Arabidopsis thaliana BAC T9E19	0.026
4271	AF137394	Euperipatoides rowelli elongation factor-1 alpha mRNA, partial cds	0.23
4272	AF243087	Homo sapiens intrinsic factor-vitamin B12 receptor (CUBN) gene, exons 11, 12, and 13	0
4273	AF264703	Astyanax mexicanus retinal homeobox protein (Rx1) mRNA, complete cds	2.2
4274	AJ311054	Chironomus pallidivittatus 4L ORF for putative recombinase subtelocentric clone, Cp5.5	0.025
4275	AF267209	Candidatus Carsonella ruddii natural-host Calophya schini ATP synthase alpha subunit (atpA) gene, partial cds; ATP synthase gamma subunit (atpG) gene, complete cds; and ATP synthase beta subunit (atpD) gene, partial cds	0.0008
4276	Z17148	H. sapiens (D11S935) DNA segment containing (CA) repeat; clone AFM254zb9; single read	0.008
4277	AF175434	Gallus gallus T cell receptor delta chain (TCRD) pseudogene, partial sequence	2.3
4278	AK011996	Mus musculus 10 days embryo cDNA, RIKEN full-length enriched library, clone:2610306H15, full insert sequence	0.49
4279	AF269490	Staphylococcus epidermidis strain SR1 clone step.1005h04 genomic sequence	0.087
4280	XM_050118	Homo sapiens hephaestin (HEPH), mRNA	2E-75
4281	AF232828	Mus musculus ventral neuron-specific protein 1 NOVA1 (Nova1) mRNA, partial cds	0.008
4282	XM_029168	Homo sapiens hypothetical gene supported by AK023162 (LOC90120), mRNA	0.53
4283	L31645	Helianthus annuus ribosomal protein S3a mRNA, complete cds	0.67
4284	XM_012756	Homo sapiens transcription factor 4 (TCF4), mRNA	0.22
4285	AK021049	Mus musculus adult male corpus striatum cDNA, RIKEN full-length enriched library, clone:C030006F08, full insert sequence	0.006
4286	AB020763	Ptychodera flava mRNA for Pax19, complete cds	0.26
4287	XM_047401	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA	0.25
4288	AF250952	Osmia satoi 16S ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	0.24
4289	AF267985	Homo sapiens 15 kDa selenoprotein gene, exon 4	0.024
4290	AJ409503	Mus musculus RNA binding site for Dazl protein, clone jd8	0.029
4291	AC009304	Homo sapiens clone NH0111I09, complete sequence	0.026

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
4292	XM_050269	Homo sapiens solute carrier family 1 (glial high affinity glutamate transporter), member 3 (SLC1A3), mRNA	0.21
4293	AK004286	Mus musculus 18 days embryo cDNA, RIKEN full-length enriched library, clone:1110057K12, full insert sequence	2.1
4294	NC_002095	Chlorobium limicola plasmid pCL1, complete sequence	0.24
4295	AC006678	Caenorhabditis elegans cosmid R05G9, complete sequence	2.1
4296	AF217235	Staphylococcus aureus pathogenicity island SaPIbov, complete sequence	0.009
4297	XM_012045	Homo sapiens hypothetical protein FLJ13074 (FLJ13074), mRNA	0.68
4298	NM_022087	Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA	e-158
4299	XM_010678	Homo sapiens similar to zinc finger protein 258 (H. sapiens) (LOC65323), mRNA	7E-63
4300	AJ311847	Nicotiana tabacum chloroplast mRNA for FtsZ-like protein (ftsZ gene), clone FtsZ2-2	0.55
4301	Z24366	H. sapiens (D18S480) DNA segment containing (CA) repeat; clone AFM320yc9; single read	8E-12
4302	AK003805	Mus musculus 18 days embryo cDNA, RIKEN full-length enriched library, clone:1110019B22, full insert sequence	0.009
4303	AB047606	Macaca fascicularis brain cDNA, clone:QnpA-10881	0
4304	AK000493	Homo sapiens cDNA FLJ20486 fis, clone KAT08039	0.24
4305	AF375597	Mus musculus medium and short chain L-3-hydroxyacyl-Coenzyme A dehydrogenase (Mschad) gene, exons 2 through 8, and complete cds; nuclear gene for mitochondrial product	0.75
4306	AP000301	Homo sapiens genomic DNA, chromosome 21q22.1, D21S226-AML region, clone:D16B8, complete sequence	0.081
4307	AK019632	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930455M05, full insert sequence	0.068
4308	X94556	R.cingulata DNA for internal transcribed spacer ITS2 of rDNA unit	0.079
4310	AY027174	Arabidopsis thaliana sequence flanking 3' end of Ds-GeneTrap insertion from line GT2850	0.2
4311	AC092063	Homo sapiens clone RP11-745H7, complete sequence	0.14
4312	AJ297034	Homo sapiens SDS-stable vimentin-bound DNA fragment HEF19VIM18	e-117
4313	Z82088	Caenorhabditis elegans cosmid ZK256, complete sequence	0.015
4314	AC006709	Caenorhabditis elegans cosmid Y119C1A, complete sequence	0.17
4315	AF016620	Mus musculus Rb-8 neural cell adhesion molecule long form (RNCAM) mRNA, partial cds	6.2
4316	AK013121	Mus musculus 10, 11 days embryo cDNA, RIKEN full-length enriched library, clone:2810421E14, full insert sequence	1.9
4317	XM_033379	Homo sapiens KIAA1607 protein (KIAA1607), mRNA	4E-09
4318	AL355864	Human DNA sequence from clone RP4-803A2 on chromosome 1, complete sequence [Homo sapiens]	1.4

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
4319	AE001422	Plasmodium falciparum chromosome 2, section 59 of 73 of the complete sequence	0.028
4320	AL157437	Homo sapiens mRNA; cDNA DKFZp434E1512 (from clone DKFZp434E1512); partial cds	4.9
4321	U31929	Human orphan nuclear receptor (DAX1) gene, complete cds	5.4
4322	AF338875	Hylobates moloch NAN03 cytochrome b gene, partial cds; and tRNA-Thr, tRNA-Pro, and tRNA-Phe genes, complete sequence; mitochondrial genes for mitochondrial products	0.6
4323	X04502	Human SLPI gene for secretory leukocyte protease inhibitor	2
4324	U07018	Human immunodeficiency virus type 1 SH803 (env) gene, partial cds	0.64
4325	AF046143	Homo sapiens chromosome Xp22 958-13	0.023
4326	U17081	Human fatty acid binding protein (FABP3) gene, complete cds	6
4327	AJ249365	Plasmodium falciparum partial mRNA for delta-aminolevulinic acid dehydratase	0.009
4328	AF090936	Homo sapiens clone HQ0582	0.006
4329	X97970	A.thaliana mRNA for RNA helicase	0.079
4330	XM_047794	Homo sapiens KIAA1641 protein (KIAA1641), mRNA	e-156
4331	AF334172	Zea mays clone B7 chromosome 4 centromeric region	3.9
4332	AJ401041	Human immunodeficiency virus type 1 proviral partial gp160 gene for envelope protein, strain J_97DC.KTB147	0.64
4333	XM_038175	Homo sapiens KIAA0872 protein (KIAA0872), mRNA	0.65
4334	Y16473	Chlamydomonas reinhardtii chloroplast DNA for rps18 gene, and orf570	0.028
4335	AF190381	Eucalyptus tetragona photosystem Q(B) protein (psbA) pseudogene and tRNA-His (trnH) gene, partial sequence; chloroplast genes for chloroplast products	0.008
4336	AE006276	Lactococcus lactis subsp. lactis IL1403 section 38 of 218 of the complete genome	0.22
4337	AK020646	Mus musculus adult male urinary bladder cDNA, RIKEN full-length enriched library, clone:9530077A04, full insert sequence	2.3
4338	Z69666	Human DNA sequence from cosmid 24F8 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs, repeat polymorphism and CpG island	0.018
4339	AF017254	West Nile virus nonstructural protein NS5 (NS5) gene, partial cds	0.73
4341	NM_008645	Mus musculus murinoglobulin 1 (Mug1), mRNA	0.00009
4342	AF114927	Saccharomyces pastorianus CBS1538 small subunit ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, complete sequence	0.25
4343	AL451057	Human DNA sequence from clone CTD-2010K20 on chromosome 10, complete sequence [Homo sapiens]	0.17
4344	AK022875	Homo sapiens cDNA FLJ12813 fis, clone NT2RP2002503, weakly similar to ZINC FINGER PROTEIN 45	1.7
4345	D10910	Arabidopsis thaliana Atpk7 gene for serine/threonine protein kinase, complete cds	0.61

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
4346	X53096	S.aureus genes encoding Sau96I DNA methyltransferase and Sau96I restriction endonuclease	0.2
4347	M57855	Human protein S-beta pseudogene, exons 5 and 6	0.2
4348	Z73523	S.cerevisiae chromosome XVI reading frame ORF YPL167c	0.065
4349	U67562	Methanococcus jannaschii section 104 of 150 of the complete genome	0.54
4350	Y09047	M.musculus pxF gene, strain 129VJ	0.002
4351	XM_027332	Homo sapiens ribosomal protein L36 (RPL36), mRNA	0.0001
4352	AF106029	Thomomys mazama clone 12-8 microsatellite sequence	0.25
4353	AL137428	Homo sapiens mRNA; cDNA DKFZp761N1323 (from clone DKFZp761N1323)	0.028
4354	L81915	Homo sapiens (subclone 1_g8 from BAC H76) DNA sequence, complete sequence	0.63
4355	J01291	soybean 7s seed storage protein alpha subunit mrna (b), from gmc-alpha'-alpha 236	3.7
4356	NM_006649	Homo sapiens serologically defined colon cancer antigen 16 (SDCCAG16), mRNA	0.69
4357	AL137635	Homo sapiens mRNA; cDNA DKFZp434E175 (from clone DKFZp434E175)	6.1
4358	Y14422	M.musculus DNA for retinal protein	0.23
4359	D32056	Human gene for 2-oxoglutarate dehydrogenase, exon 1 sequence	6.4
4360	D14337	Yeast pck1+ gene for protein kinase, complete cds	0.085
4361	J02756	Mouse band 3 anion exchange protein gene, complete cds	1.9
4362	XM_048747	Homo sapiens KIAA1223 protein (KIAA1223), mRNA	0.69
4363	M97514	Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds	0.19
4364	D10910	Arabidopsis thaliana Atpk7 gene for serine/threonine protein kinase, complete cds	0.53
4365	AK015420	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930448I18, full insert sequence	0.003
4366	U82487	Branchiostoma floridae engrailed protein (AmphiEn) mRNA, complete cds	0.22
4367	AB052798	Feline foamy virus env gene for envelope protein, complete cds, clone:HFFV	0.08
4368	AY027174	Arabidopsis thaliana sequence flanking 3' end of Ds-GeneTrap insertion from line GT2850	0.25
4369	AJ298684	Phylloxera sp. MBLM2 mitochondrial ATP6 gene for ATP synthase A chain subunit 6	0.67
4370	NM_013696	Mus musculus thyrotropin releasing hormone receptor (Trhr), mRNA	0.000003
4371	AF176830	Dictyostelium discoideum polyphosphate kinase (PPK) gene, complete cds	0.83
4372	AB036665	Bacteriophage WO genes, ISW1 inserted sequence, partial and complete cds	0.17
4373	AJ310187	Prevotella albensis dpp-IV gene for dipeptidyl peptidase IV	1.6
4374	L77040	Homo sapiens (subclone 8_c11 from P1 H22) DNA sequence	0.025

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
4375	AJ277162	Beta vulgaris mRNA for putative Cdc2-related protein kinase CRK2	0.009
4376	K02781	Mouse PND gene encoding atrial natriuretic factor, complete cds	0.24
4377	AL110166	Homo sapiens mRNA; cDNA DKFZp586M1424 (from clone DKFZp586M1424)	0.69
4378	AE006400	Lactococcus lactis subsp. lactis IL1403 section 162 of 218 of the complete genome	6.4
4379	AF310887	Dictyostelium discoideum RacB (racB) gene, partial cds; and unknown gene	0.23
4380	AY023357	Oryza sativa microsatellite MRG5682 containing (TAA)X20, genomic sequence	2.3
4381	AL133038	Homo sapiens mRNA; cDNA DKFZp434D1835 (from clone DKFZp434D1835)	0.00004
4382	M37760	Mouse serine 2 ultra high sulfur protein gene, complete cds	0.083
4383	AF151698	Agrobacterium tumefaciens cryptic plasmid pAtC58 transcriptional repressor, GlnH homolog, GlnP/GlnQ homolog, putative oxidoreductase, and AgaE homolog genes, complete cds	0.25
4384	X59370	X.laevis POMC-A gene for proopiomelanocortin-A	0.007
4385	AF244933	Oryctolagus cuniculus interferon gamma precursor, mRNA, complete cds	0.66
4386	Z69919	Human DNA sequence from cosmid 91K3, Huntington's Disease Region, chromosome 4p16.3 contains CpG island	0.077
4387	AK027136	Homo sapiens cDNA: FLJ23483 fis, clone KAIA04052	1.7
4388	AK027136	Homo sapiens cDNA: FLJ23483 fis, clone KAIA04052	6.6
4389	AL589705	Human DNA sequence from clone RP11-64M7 on chromosome 6, complete sequence [Homo sapiens]	0.63
4390	AF035192	Campylobacter rectus S-layer-RTX protein (csxB) gene, complete cds; tRNA-Arg gene, complete sequence; and putative histidine kinase gene, partial cds	0.34
4391	AK021269	Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length enriched library, clone:C530007A02, full insert sequence	0.69
4392	XM_030404	Homo sapiens acid phosphatase 1, soluble (ACP1), mRNA	0.007
4393	BC006633	Mus musculus, Flt3 interacting zinc finger protein 1, clone MGC:7201 IMAGE:3482191, mRNA, complete cds	2
4394	AK009564	Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310032D21, full insert sequence	1.6
4395	L04802	Silkmoth apoptosis preventing protein (p35) gene sequence	0.21
4396	AB026599	Neogerris parvulus mitochondrial gene for 16S ribosomal RNA, partial sequence	0.027
4397	BC005581	Mus musculus, RIKEN cDNA 2310022K15 gene, clone MGC:11736 IMAGE:3968615, mRNA, complete cds	0.22
4398	XM_033374	Homo sapiens myosin, heavy polypeptide 7, cardiac muscle, beta (MYH7), mRNA	0.23
4399	U31534	Isla Vista virus MC-SB-1 nucleocapsid protein mRNA, complete cds	0.54

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
4400	XM_005318	Homo sapiens hypothetical protein FLJ11125 (FLJ11125), mRNA	0.44
4401	U76670	Arabidopsis thaliana recA-like protein (AtDMC1) gene, complete cds	0.051
4402	AK009448	Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310021K08, full insert sequence	1.6
4403	AY003917	Phytophthora infestans isolate 94-52 NADH dehydrogenase subunit 4 gene, partial cds; mitochondrial gene for mitochondrial product	0.16
4404	AC084160	Caenorhabditis elegans cosmid Y73B3B, complete sequence	0.21
4405	AF330120	Homo sapiens voltage-gated sodium channel type III alpha subunit (SCN3A) gene, exon 4	2.4
4406	AK022135	Homo sapiens cDNA FLJ12073 fis, clone HEMBB1002387	0.49
4407	AF332583	Homo sapiens stratum corneum chymotryptic enzyme (KLK7) gene, complete cds, alternative transcripts	1.7
4408	XM_043049	Homo sapiens hypothetical gene supported by AL080215 (LOC92138), mRNA	0.7
4409	AK017682	Mus musculus 8 days embryo cDNA, RIKEN full-length enriched library, clone:5730465I09, full insert sequence	2.1
4410	AJ409162	Solanum ochranthum LINE retrotransposon within partial ure gene for urease, exons 6-8	0.025
4411	AF183584	Papio hamadryas tyrosinase gene, exon 2	0.24
4412	AK010138	Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310069P03, full insert sequence	0.56
4413	AF112141	Oryzias latipes homeodomain transcription factor (eng2) mRNA, complete cds	0.021
4414	AK022458	Homo sapiens cDNA FLJ12396 fis, clone MAMMA1002758	4.9
4415	AK024159	Homo sapiens cDNA FLJ14097 fis, clone MAMMA1000760	0.00007
4416	AB060834	Macaca fascicularis brain cDNA clone:QtrA-10686, full insert sequence	2.1
4417	AF063864	Schizosaccharomyces pombe essential nuclear protein Mcm3p (mcm3+) gene, complete cds	0.21
4418	AF233288	Drosophila melanogaster WDS (wds) and egghead (egh) genes, complete cds	1.3
4419	AE003106	Drosophila melanogaster genomic scaffold 142000013386018, complete sequence	0.007
4421	AB001919	Oryza sativa DNA for phospholipase D, complete cds	0.23
4422	AF216290	Mus musculus heterochromatin protein 1 alpha mRNA, complete cds	0.66
4423	AF028828	Homo sapiens Tax interaction protein 43 mRNA, partial cds	0.18
4424	AF011446	Mus musculus granzyme K gene, complete cds	1.9
4425	AF200375	Ceratosolen bisulcatus cytochrome oxidase subunit I (COI) gene, partial cds; tRNA-Leu gene, complete sequence; and cytochrome oxidase subunit II (COII) gene gene, partial cds; mitochondrial genes for mitochondrial products	0.68

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
4426	AF328031	Zygoballus rufipes NADH dehydrogenase subunit I (ND1) gene, partial cds; mitochondrial gene for mitochondrial product	1.7
4427	AF289983	Alouatta stramineus cytochrome b gene, partial cds; mitochondrial gene for mitochondrial product	0.72
4428	Z73253	S.cerevisiae chromosome XII reading frame ORF YLR081w	0.19
4429	NM_018706	Homo sapiens hypothetical protein DKFZp762M115 (KIAA1630), mRNA	1E-48
4430	AF298209	Dictyostelium discoideum non-LTR retrotransposon TRE5-B, polyprotein (gag) and group-specific antigen (pol) genes, complete cds	0.74
4431	AJ276991	Mus musculus partial mRNA for ClpX protein	0.079
4432	AB047240	Human endogenous retrovirus HERV-K(II) DNA, complete sequence and flanking region	0.13
4433	L40389	Candida glabrata ERG11 gene, complete cds	0.027
4434	K02592	Mouse Ins DNA; cellular component that mediates integration and excision of polyoma virus DNA	0.38
4435	D31782	Snake (green habu) gTgTBP gene for TATA-box binding protein	1.5
4436	AK019649	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930480I16, full insert sequence	0.25
4437	U36777	Carassius auratus aldolase C mRNA, complete cds	0.094
4438	AF036690	Caenorhabditis elegans cosmid F09C11	0.72
4439	NM_012750	Rattus norvegicus Tyrosine kinase receptor ligand 2 (Retl2), mRNA	0.63
4440	M74000	Brugia malayi myosin heavy chain gene, complete cds	0.073
4441	XM_042656	Homo sapiens LOC87184 (LOC87184), mRNA	0.66
4442	AF335329	Kallichroma tethys isopenicillin N synthase (pcbC) and alpha-aminoadipyl-cysteinyl-valine synthetase (pcbAB) genes, complete cds	6.1
4443	XM_037269	Homo sapiens region containing hypothetical protein FLJ10549; hypothetical protein FLJ10517 (LOC82252), mRNA	0.26
4444	AF130079	Homo sapiens clone FLC0578 PRO2852 mRNA, complete cds	0.24
4445	AF086241	Homo sapiens full length insert cDNA clone ZD29F04	0.51
4446	AF262583	Schedorhinotermes sarawakensis 16S mitochondrial ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	4.6
4447	AF170550	Arabidopsis thaliana germin-like protein 7 (GLP7) gene, complete cds	2
4448	AC084500	Caenorhabditis briggsae cosmid G13G15, complete sequence	0.66
4449	M23360	Trypanosoma brucei cytochrome C mRNA, partial cds	2.1
4450	AF236387	Schizosaccharomyces pombe zinc finger protein Grt1 (grt1) gene, complete cds	0.076
4453	XM_010610	Homo sapiens hypothetical protein (FLJ10287), mRNA	0.027
4454	AY021908	Oryza sativa microsatellite MRG4233 containing (TA)X42, closest to marker C563, genomic sequence	0.025
4455	AK021675	Homo sapiens cDNA FLJ11613 fis, clone HEMBA1004012	0.073

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
4456	NM_030995	Rattus norvegicus Microtubule-associated protein 1a (Map1a), mRNA	1.8
4457	AF015298	Human herpesvirus 6 IE-2 protein (ie2hom) gene, complete cds	0.058
4458	XM_011297	Homo sapiens hypothetical protein FLB3342 (FLB3342), mRNA	0.0000009
4459	AE006714	Sulfolobus solfataricus section 73 of 272 of the complete genome	0.002
4460	AE001434	Plasmodium falciparum chromosome 2, section 71 of 73 of the complete sequence	0.004
4461	AF068270	Rachiplusia ou nuclear polyhedrosis virus protein-tyrosine phosphatase (ptp), late expression factor-2 (lef-2), occlusion matrix protein (polh), capsid-associated protein, and protein kinase (pk1) genes, complete cds; and unknown genes	0.027
4462	AK015582	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930477O15, full insert sequence	0.08
4463	XM_039778	Homo sapiens HSPC047 protein (HSPC047), mRNA	0
4464	S73580	putative polymerase...capsid protein [potato aucuba mosaic potexvirus PAMV, Genomic RNA Complete, 6 genes, 7059 nt]	0.071
4465	XM_016858	Homo sapiens LOC87857 (LOC87857), mRNA	3E-13
4466	AE004427	Vibrio cholerae chromosome II, section 84 of 93 of the complete chromosome	0.69
4467	AK025346	Homo sapiens cDNA: FLJ21693 fis, clone COL09609	4.9
4468	U89926	Drosophila melanogaster cut gene, partial sequence	0.22
4469	X57171	D.caryophyllus CARSR12 gene	2
4470	L36434	Mus Musculus basic domain/leucine zipper transcription factor mRNA, 3' end of cds	2
4471	AF115469	Arabidopsis thaliana cultivar Landsberg erecta Arac2 (Arac2) gene, complete cds	1.9
4472	AB063169	Petunia x hybrida taz1 gene for tapetum-specific zinc finger protein 1, promoter region and partial cds	0.64
4473	L41691	Bos taurus (clones L6, C15, C12, C8, C9, C17, C19, C12, C18, C5, C6, C3, C13, C10, C47) mRNA, 3' end of cds	0.47
4474	U61463	Human myosin VIIa (MYO7A) gene, 5' exon 36	0.0007
4475	NM_008992	Mus musculus ATP-binding cassette, sub-family D (ALD), member 4 (Abcd4), mRNA	1.9
4476	XM_050942	Homo sapiens ribosomal protein L6 (RPL6), mRNA	0.00009
4477	AK005146	Mus musculus adult male cerebellum cDNA, RIKEN full-length enriched library, clone:1500004F14, full insert sequence	0.71
4478	AF345089	Hepatitis C virus isolate SCpreSC2c14 nonfunctional polyprotein gene, partial sequence	0.71
4479	AK008812	Mus musculus adult male stomach cDNA, RIKEN full-length enriched library, clone:2210403E17, full insert sequence	6.4
4480	XM_006983	Homo sapiens A kinase (PRKA) anchor protein 3 (AKAP3), mRNA	1.6
4481	X06438	Soybean leghaemoglobin gene lba promoter region	0.19
4482	AF020051	Blackcurrant reversion virus RNA2 polyprotein mRNA, complete cds	0.71

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
4483	XM_051560	Homo sapiens peroxisome proliferative activated receptor, gamma (PPARG), mRNA	0.6
4484	AB023481	Cyprinus carpio mRNA for mitogen activated protein (MAP) kinase p38, complete cds	6.3
4485	AJ250933	Homo sapiens partial SIP1 gene for survival interacting protein 1, exons 3-4	2.2
4486	XM_039989	Homo sapiens microfibrillar-associated protein 3 (MFAP3), mRNA	0.69
4487	XM_047554	Homo sapiens similar to KIAA1473 protein (H. sapiens) (LOC92830), mRNA	6.7
4488	AB042411	Homo sapiens strg gene for striatum-specific G potein-coupled receptor, complete cds	2
4489	XM_035221	Homo sapiens ancient ubiquitous protein 1 (AUP1), mRNA	0.16
4490	D14061	Schizosaccharomyces pombe mRNA for ORF	0.015
4491	AE001426	Plasmodium falciparum chromosome 2, section 63 of 73 of the complete sequence	0.074
4492	M18349	Rat leukocyte common antigen (L-CA) gene, exons 1 through 5	0.16
4493	AF020726	Tetrahymena thermophila phosphoglucomutase (PGM1) gene, complete cds	0.058
4494	M80241	Caenorhabditis elegans unc-6 gene, complete cds	2.1
4495	U67234	Human clone HS5.29 Alu-Ya5 sequence	0.083
4496	AK000864	Homo sapiens cDNA FLJ10002 fis, clone HEMBA1000046	0.00001
4498	AK024393	Homo sapiens cDNA FLJ14331 fis, clone PLACE4000320	0.064
4499	AF071754	Mus musculus DNA cytosine methyltransferase mRNA	0.21
4500	XM_047325	Homo sapiens hypothetical protein LOC57187 (LOC57187), mRNA	0
4501	XM_043434	Homo sapiens villin-like (VILL), mRNA	1.8
4502	NM_032675	Homo sapiens hypothetical protein MGC10954 (MGC10954), mRNA	0.0008
4503	AL589203	Human DNA sequence from clone RP11-391F23 on chromosome 6, complete sequence [Homo sapiens]	0.0003
4504	M86544	Cow prostaglandin F synthetase II (PGFSII) mRNA, complete cds	0.66
4505	AF339782	Homo sapiens clone IMAGE:1871856, mRNA sequence	0
4506	Z74196	S.cerevisiae chromosome IV reading frame ORF YDL148c	6.2
4507	AF012751	Danio rerio olfactory receptor protein 2.4 mRNA, complete cds	6.8
4508	AF184796	Arabidopsis thaliana inhibitor tagged site ITS29 genomic sequence	1
4509	AE006187	Pasteurella multocida PM70 section 154 of 204 of the complete genome	1.8
4510	AJ272171	Podospora anserina degenerate gypsy-like retrotransposon Yeti	0.074
4511	AK024656	Homo sapiens cDNA: FLJ21003 fis, clone CAE03685	1E-90
4512	NC_002629	Lithobius forficatus mitochondrion, complete genome	0.066
4513	X87205	M.fascicularis mRNA for metalloprotease-like, disintegrin-like protein, IVa	4.9

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
4514	XM_011595	Homo sapiens CDC10 (cell division cycle 10, S. cerevisiae, homolog) (CDC10), mRNA	5E-47
4515	AK021537	Homo sapiens cDNA FLJ11475 fis, clone HEMBA1001734, moderately similar to CADHERIN-11 PRECURSOR	0.068
4516	AB044877	Equus caballus DNA, microsatellite TKY377	0.076
4517	AC079391	Homo sapiens clone CTD-2243M11, complete sequence	0.00001
4518	AK000932	Homo sapiens cDNA FLJ10070 fis, clone HEMBA1001581	0
4519	AE001376	Plasmodium falciparum chromosome 2, section 13 of 73 of the complete sequence	0.24
4520	XM_040095	Homo sapiens hypothetical protein (DKFZP434G0310), mRNA	1.8
4521	AF224317	Gallus gallus Frizzled-7 (cFz-7) mRNA, complete cds	1.5
4522	AE001155	Borrelia burgdorferi (section 41 of 70) of the complete genome	2
4523	AJ313130	Medicago truncatula transposon (CACTA type), clone 65K06	2
4524	AF020187	Amblyomma americanum ecdsyteroid receptor (AamEcRA1) mRNA, complete cds	6.3
4525	AP000249	Homo sapiens genomic DNA, chromosome 21q22.1, D21S226-AML region, clone:B762O15, complete sequence	2E-19
4526	AF218380	Mus musculus CBLN3 (Cbln3) gene, complete cds	0.69
4527	AP000601	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJL14	0.029
4528	AE001140	Borrelia burgdorferi (section 26 of 70) of the complete genome	0.64
4529	AL358852	Human DNA sequence from clone RP1-317N9 on chromosome 6, complete sequence [Homo sapiens]	2.2
4530	NM_024596	Homo sapiens hypothetical protein FLJ12847 (FLJ12847), mRNA	0.82
4531	X12918	Human Na+,K+ ATPase gene part of intron XVI (alpha III isoform)	0.0003
4532	AF298180	Caenorhabditis elegans tropomyosin isoform IV mRNA, complete cds	0.57
4533	M21590	M.mycoides capri Gly-tRNA gene	0.48
4534	AF250227	Homo sapiens adenylyl cyclase type VI gene, partial cds	0.19
4535	Z36061	S.cerevisiae chromosome II reading frame ORF YBR192w	0.071
4536	AF006510	Endogone pisiformis 18S ribosomal RNA gene, partial sequence, internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence, and 26S ribosomal RNA gene, partial sequence	0.08
4537	D88262	Pisum sativum PsCHS5 gene for chalcone synthase, complete cds	0.075
4538	L31504	Neurospora crassa cytoplasmic dynein heavy chain (ro-1) gene, complete cds	2.3
4539	S81605	S100 beta =neural calcium binding protein beta subunit {5' region} [rats, Genomic, 2279 nt]	0.66
4540	X95275	P.falciparum complete gene map of plastid-like DNA (IR-A)	0.23
4541	U18868	Squalus acanthias multifunctional protein CAD mRNA, complete cds	0.024

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
4542	AF184835	Arabidopsis thaliana inhibitor tagged site ITS68 genomic sequence	0.71
4543	AL513350	Human DNA sequence from clone RP11-509D8 on chromosome 9, complete sequence [Homo sapiens]	0.64
4544	Z68107	Caenorhabditis elegans cosmid F48C5, complete sequence	2
4545	AK002184	Homo sapiens cDNA FLJ11322 fis, clone PLACE1010329	0.71
4546	U00025	Caenorhabditis elegans cosmid PAR2, complete sequence	0.46
4547	U39548	Meloidogyne artiellia mtcuticline-1 gene, 5' upstream region	0.64
4548	AK024271	Homo sapiens cDNA FLJ14209 fis, clone NT2RP3003346	0.0003
4549	AF248989	Arabidopsis griffithiana chalcone synthase gene, promoter region and partial cds	0.3
4550	AF081208	Monoclea gottschei subsp. gottschei tRNA-Thr/tRNA-Leu intergenic spacer, partial chloroplast sequence	0.009
4551	XM_002770	Homo sapiens hypothetical protein (FLJ10996), mRNA	5.8
4552	AF035672	Mus musculus MHC class I related protein 1 (MR1) gene, complete cds	1.1
4553	AF374466	Macrobrachium intermedium 16S ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	5.9
4554	S80559	pdm-2=POU domain gene [Drosophila melanogaster, mRNA, 2171 nt]	0.009
4555	AY029489	Homo sapiens aminophospholipid-transporting ATPase (ATP10C) gene, exon 3	1E-89
4556	NM_026255	Mus musculus RIKEN cDNA 4930433D19 gene (4930433D19Rik), mRNA	2.2
4557	AJ276163	Homo sapiens partial GDH gene for uridine diphospho-glucose dehydrogenase, exons 8-11	0.0002
4558	NC_001566	Apis mellifera ligustica mitochondrion, complete genome	0.19
4559	BC003453	Mus musculus, calreticulin, clone MGC:6209 IMAGE:2655918, mRNA, complete cds	2
4560	XM_048784	Homo sapiens mature T-cell proliferation 1 (MTCP1), mRNA	0.62
4561	AF119845	Homo sapiens PRO1304 mRNA, complete cds	0.01
4562	AF251477	Plasmodium berghei glutathione reductase gene, partial cds	0.053
4563	XM_018443	Homo sapiens ATPase, Na+/K+ transporting, beta 3 polypeptide (ATP1B3), mRNA	2
4564	AF145282	Trichomonas vaginalis calcium motive P-type ATPase (CA-2) gene, partial cds	0.11
4565	AF280548	Homo sapiens neuropilin-1 (NRP1) gene, exons 1, 2, and partial cds	2.1
4566	NC_002253	Buchnera sp. APS plasmid pLeu, complete sequence	0.24
4567	AJ238613	Gallus gallus mRNA for teneurin-1	0.61
4568	Y08926	P.falciparum mRNA for AARP1 protein, partial	0.21
4569	Z86105	A.thermophilum celA gene and manA pseudogene	0.69
4570	AL583902	S.pombe chromosome I p1 p32A8	1.1
4571	AL358951	Human DNA sequence from clone RP3-456L16 on chromosome 6, complete sequence [Homo sapiens]	0.072
4572	AJ001164	Drosophila melanogaster additional sex combs cDNA sequence	0.1

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
4573	AF301004	Schistosoma mansoni thioredoxin peroxidase 3 (TPx3) gene, complete cds	0.19
4574	AF276995	Xenopus laevis homeobox protein Six4.2 (Six4.2) gene, partial cds	2
4575	BC007465	Homo sapiens, clone IMAGE:3828547, mRNA	0.00002
4576	AL589824	Human DNA sequence from clone RP11-76G11 on chromosome X, complete sequence [Homo sapiens]	0.17
4577	AF151171	Ornithorhynchus anatinus mannose 6-phosphate/insulin-like growth factor 2 receptor (M6p/Igf2r) gene, exons 2 and 3 and partial cds	0.67
4578	AK000883	Homo sapiens cDNA FLJ10021 fis, clone HEMBA1000568	0
4579	XM_016630	Homo sapiens KIAA1046 protein (KIAA1046), mRNA	1.1
4580	NM_015906	Homo sapiens transcriptional intermediary factor 1 gamma (TIF1GAMMA), transcript variant alpha, mRNA	2
4581	AF274053	Xenopus laevis maxi-K potassium channel alpha subunit Slo mRNA, complete cds	0.19
4582	AB035874	Pseudoregma pendleburyi mitochondrial genes for small subunit rRNA, tRNA-Val, large subunit rRNA, partial and complete sequences	0.003
4583	AF277081	Ajellomyces dermatitidis strain 104 blastomyces yeast phase-specific protein 1 (bys1) gene, complete cds	0.26
4584	AF334561	Homo sapiens chromosome Y landmark: proximal external boundary of P7 VCY inverted repeat	0.69
4585	X55197	P.yoelii YEL6 gene for ATPase	0.23
4586	L32141	Mitochondrion Lymantria dispar ribosomal RNA large subunit	0.008
4587	AF272001	Ebola virus subtype Zaire strain Mayinga complete genome	1.5
4588	AE004405	Vibrio cholerae chromosome II, section 62 of 93 of the complete chromosome	1.9
4589	XM_010966	Homo sapiens debranching enzyme (S. Cerevisiae) homolog 1 (DBR1), mRNA	2
4591	U68246	Dictyostelium discoideum WacA (wacA) gene, complete cds	0.002
4592	XM_047617	Homo sapiens KIAA1349 protein (KIAA1349), mRNA	0.027
4593	AK003428	Mus musculus 18 days embryo cDNA, RIKEN full-length enriched library, clone:1110004J07, full insert sequence	2.2
4594	XM_029072	Homo sapiens LOC89256 (LOC89256), mRNA	0.009
4595	L43549	Buchnera aphidicola aspartyl-tRNA synthetase (aspS), thioredoxin reductase (trxB), seryl-tRNA synthase (serS), phosphoserine aminotransferase (serC), 3-enolpyruvylshikimate-5-phosphate synthetase (aroA), ribosomal protein S1 (rpsA), integration host fa>	0.21
4596	AK023907	Homo sapiens cDNA FLJ13845 fis, clone THYRO1000815	0
4598	AB042649	Watermelon spotted wilt virus nss, np genes for non-structural, nucleocapsid protein, complete cds, isolate:WS-O	0.024
4599	D85547	Bacillus sp. DNA for cytochrome c oxidase subunit I,II and III, complete and partial cds	0.23

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
4600	L29252	Human (clone D13-2) L-iditol-2 dehydrogenase gene, exon 4, exon 5, exon 6 and exon 7	2E-08
4601	AE003872	Xylella fastidiosa 9a5c, section 18 of 229 of the complete genome	1.5
4602	U29924	Human AMP deaminase (AMPD3) gene, exon 12	0.0003
4603	AE000653	Helicobacter pylori 26695 section 131 of 134 of the complete genome	0.75
4605	AP001235	Homo sapiens genomic DNA, chromosome 2p11.2, clone:cos607/7B8	0.024
4606	AF207725	Mustela lutreola isolate D23 mitochondrial D-loop, partial sequence	0.028
4607	AE007377	Streptococcus pneumoniae section 60 of 194 of the complete genome	0.083
4608	XM_018430	Homo sapiens LOC88330 (LOC88330), mRNA	4E-27
4609	AF273674	Plasmodium falciparum DNA-dependent RNA polymerase (TRNAP) gene, complete cds; nuclear gene for probable mitochondrial product	0.002
4610	AY018919	Oryza sativa microsatellite MRG1244 containing (AT)X23, genomic sequence	6.7
4611	AB025642	Arabidopsis thaliana genomic DNA, chromosome 5, BAC clone:T32G24	2.1
4612	X59275	D.melanogaster mRNA for posterior sex combs	0.68
4613	AF052959	Homo sapiens type XV collagen (COL15A1) gene, exon 6	0.71
4614	U32730	Haemophilus influenzae Rd section 45 of 163 of the complete genome	0.025
4615	AF212976	Bolitoglossa mexicana isolate MEX_6C cytochrome b gene, partial cds; mitochondrial gene for mitochondrial product	0.076
4616	AF031493	Cancer magister molt-inhibiting hormone precursor mRNA, complete cds	0.22
4617	AJ245965	Danio rerio mRNA for pbxy homeodomain protein (pbxy gene)	0.068
4618	XM_031524	Homo sapiens AF15q14 protein (AF15Q14), mRNA	0
4619	AL096876	S.pombe chromosome II cosmid c418	0.001
4620	XM_051190	Homo sapiens similar to frizzled (Drosophila) homolog 4 (H. sapiens) (LOC93401), mRNA	6
4621	XM_005411	Homo sapiens interferon, omega 1 (IFNW1), mRNA	0.22
4622	Z50156	D.discoideum gene for 34 kD actin binding protein	0.027
4623	BC006182	Homo sapiens, Similar to calmodulin 2 (phosphorylase kinase, delta), clone MGC:715 IMAGE:3528814, mRNA, complete cds	2
4624	AF106933	Drosophila melanogaster plexin B (plexB) mRNA, complete cds	0.66
4625	U44392	Human Down Syndrome region of chromosome 21, clone A12H1-1G10	0.077
4626	AF145452	Arabidopsis thaliana branched chain alpha-keto acid dehydrogenase E1 beta subunit (din4) mRNA, complete cds; nuclear gene for mitochondrial product	6.3
4627	AE006315	Lactococcus lactis subsp. lactis IL1403 section 77 of 218 of the complete genome	0.62

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
4628	X55978	T. brucei ESAG 8 gene for a leucine-rich repeat family protein	0.24
4629	U41529	Caenorhabditis elegans cosmid EGAP3	0.59
4630	XM_039502	Homo sapiens associated molecule with the SH3 domain of STAM (AMSH), mRNA	5.3
4631	AF141650	Nyctalus noctula microsatellite P223 sequence	1.5
4633	AL096887	Human DNA sequence from clone RP6-152C18 on chromosome Xq26.1-27.3, complete sequence [Homo sapiens]	0.02
4634	AL137458	Homo sapiens mRNA; cDNA DKFZp434E2221 (from clone DKFZp434E2221)	0.074
4635	AE002292	Chlamydia muridarum, section 24 of 85 of the complete genome	5.1
4636	XM_048200	Homo sapiens KIAA0276 protein (KIAA0276), mRNA	5.4
4637	AF017041	Dictyostelium discoideum LTR-retrotransposon Skipper, partial genomic sequence, 5' end	0.16
4638	Z98853	Caenorhabditis elegans cosmid R08A2, complete sequence	5.7
4639	XM_017899	Homo sapiens LOC89635 (LOC89635), mRNA	0
4640	BC006943	Mus musculus, Similar to RIKEN cDNA 3230401N03 gene, clone MGC:6906 IMAGE:2655807, mRNA, complete cds	2
4641	AF275345	Lycopersicon esculentum MADS-box transcription factor jointless gene, complete cds	0.62
4642	AK018612	Mus musculus adult male cecum cDNA, RIKEN full-length enriched library, clone:9130011L11, full insert sequence	1.9
4643	AE006568	Streptococcus pyogenes M1 GAS strain SF370, section 97 of 167 of the complete genome	6.6
4644	AF057019	Dictyostelium discoideum interaptin (abpD) gene, complete cds	0.67
4645	XM_010198	Homo sapiens immune dysregulation, polyendocrinopathy, enteropathy, X-linked (IPEX), mRNA	5E-29
4646	NM_022599	Rattus norvegicus outer membrane protein (Omp25), mRNA	1E-14
4647	U08455	HIV-1 isolate 965 clone 26 from Malawi, envelope glycoprotein (env) gene, partial cds	0.72
4648	AK023304	Homo sapiens cDNA FLJ13242 fis, clone OVARC1000578	6
4649	U20803	Gallus gallus fibrinogen alpha and alpha-E subunit gene, exons 5 and 6, and complete cds for alpha and alpha-E subunits	2
4650	AF189768	Homo sapiens leukocyte immunoglobulin-like receptor 5 (LIR5) gene, complete cds	0.025
4651	AK002614	Mus musculus adult male kidney cDNA, RIKEN full-length enriched library, clone:0610012K15, full insert sequence	2.1
4652	AF010568	Plasmodium falciparum microsatellite TA80 sequence	0.05
4653	AF042283	Schizosaccharomyces pombe sulfide dehydrogenase (hmt2) gene, complete cds	0.63
4654	Y16262	Daucus carota mRNA for neutral invertase	0.22
4655	XM_035796	Homo sapiens hypothetical gene supported by AF001893; AH005586 (LOC91063), mRNA	1.5
4656	AB008565	Homo sapiens gene for deoxylribonuclease II, 5'-upstream region	0.73
4657	Y17275	Lycopersicon esculentum p69a gene, complete CDS	0.51
4658	X03100	Human HLA-SB(DP) alpha gene	0.23

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
4659	AL121822	Human DNA sequence from clone 346P11 on chromosome Xq21.2-21.33, complete sequence [Homo sapiens]	1E-08
4660	AE001813	Thermotoga maritima section 125 of 136 of the complete genome	0.18
4661	AK004553	Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200002O22, full insert sequence	0.61
4662	AJ387942	Fagonia cretica chloroplast tRNA-Leu intron and trnL-trnF intergenic spacer	0.6
4663	AB053560	Carabus venustus subsp. liaoningensis mitochondrial gene for NADH dehydrogenase subunit 5, partial cds, isolate:73-MoVe99LB02	0.027
4664	Z78708	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA14H12	2E-63
4665	AF010563	Plasmodium falciparum microsatellite TA73 sequence	0.16
4666	AB030620	Mus musculus Chetk-alpha gene for choline/ethanolamine kinase-alpha, exon 4, 5, 6, 7, 8	0.73
4667	L77036	Homo sapiens (subclone 5_d9 from P1 H19) DNA sequence	0.007
4668	U23037	Oryctolagus cuniculus eukaryotic initiation factor 2B-epsilon mRNA, complete cds	2.3
4669	AY031967	HIV-1 isolate NC5413-1999 from USA pol polyprotein (pol) gene, partial cds	0.67
4670	AF026069	Homo sapiens phosphomevalonate kinase (HUMPMKI) gene, partial cds	6.1
4671	XM_005151	Homo sapiens RecQ protein-like 4 (RECQL4), mRNA	6.1
4672	M34662	Human chaperonin (HSP60) non-functional pseudogene 2	5.3
4674	AF009255	Homo sapiens putative chloride channel gene (CLCN6), exons 14, 15, 16, and 17	2.1
4675	AF298224	Homo sapiens RPCI-II 289E13 CD21 gene, partial cds	0.00004
4676	NC_002087	Plasmid pRL765, complete sequence	0.7
4677	AF270613	Homo sapiens clone 5qtel_ctg0024_c103t3c80t7_stelrpt sequence	0.078
4678	AP001467	Homo sapiens genomic DNA, chromosome 21q22.3, clone:21B27A14, telomere region, complete sequence	0.000001
4679	AY026945	Rattus norvegicus T:G mismatch thymine glycosylase mRNA, complete cds	2.1
4680	NM_017783	Homo sapiens hypothetical protein FLJ20357 (FLJ20357), mRNA	0.67
4681	Z57523	H.sapiens CpG island DNA genomic Mse1 fragment, clone 182d9, reverse read cpg182d9.rt1b	3E-55
4682	U11761	Cryptosporidium parvum KSU-1 heat shock 70 kDa protein (hsp70) gene, complete cds	0.076
4683	AF142642	Picea abies isolate D nad1 gene, intron b/c; mitochondrial gene for mitochondrial product	0.08
4684	XM_018315	Homo sapiens hypothetical protein FLJ12078 (FLJ12078), mRNA	0.64

	Table 3A Nearest Neighbor (BlastN vs. Genbank)		
SEQ ID NO	ACCESSN	DESCRIP	P VALUE
4685	U60297	Gallus gallus DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, partial cds	0.65
4686	M17837	D.melanogaster (strain Ja-F) alcohol dehydrogenase gene (allele Adh-F), complete cds	0.08
4687	X17265	Human germline kappa-immunoglobulin variable region (V-kappa-II) gene Vcc	0.25
4688	XM_030896	Homo sapiens similar to hypothetical protein MGC5384 (H. sapiens) (LOC90321), mRNA	7E-32
4689	AF083064	Mus musculus paxillin-like protein (Hic5) gene, complete cds	e-103
4690	X57248	L.helveticus galK, galT and galM genes for galactokinase, galactose-1-P uridyl transferase and mutarotase, partial cds	0.003
4692	AF074020	Mus musculus integral membrane protein 2A (Itm2a) gene, complete cds	0.059
4693	D17668	Clostridium septicum gene for alpha-toxin, complete cds	0.08
4694	AF089042	Molothrus badius cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds	0.076
4695	AK004553	Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200002O22, full insert sequence	0.63
4696	AF047579	Bacillus thuringiensis insecticidal crystal protein (NRcryV) gene, complete cds	0.69
4697	AF049489	Canis familiaris factor VIII mRNA, complete cds	6.3
4698	X57599	S.xylosus xylR, xylA, xylB genes for Xyl repressor, xylose isomerase, xylulokinase	0.024
4699	L04873	Mus musculus cystic fibrosis transmembrane regulator (CFTR) gene, exon 1, and upstream region	0.25
4700	XM_041483	Homo sapiens hypothetical protein MGC15827 (MGC15827), mRNA	2.2
4701	U30355	Plocamium cartilagineum complete internal transcribed spacer region including ITS 1, 5.8s rDNA and ITS 2	0.082
4702	AF346599	Gallus gallus myostatin (MSTN) gene, exons 1,2 and 3 and complete cds	1.8
4703	XM_007118	Homo sapiens A kinase (PRKA) anchor protein 11 (AKAP11), mRNA	6.2
4704	XM_042395	Homo sapiens superkiller viralicidic activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA	3.5
4705	Z78791	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA16H6	2E-08
4706	AE006402	Lactococcus lactis subsp. lactis IL1403 section 164 of 218 of the complete genome	0.7
4707	X97876	H.sapiens EP4 prostaglandin receptor pseudogene C17	6.6
4708	AP001438	Homo sapiens genomic DNA, chromosome 21q22.2, clone:T695, LB7T-ERG region, complete sequence	0.0001
4709	XM_049375	Homo sapiens WW domain binding protein 4 (formin binding protein 21) (WBP4), mRNA	3E-16
4710	AB016828	Luehdorfia longicaudata mitochondrial ND5 gene for NADH dehydrogenase subunit 5, partial cds	0.45

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
4711	U23439	Bovine herpesvirus 4 1.1-kb mRNA	0.64
4712	AP001438	Homo sapiens genomic DNA, chromosome 21q22.2, clone:T695, LB7T-ERG region, complete sequence	0.00003
4713	AP000378	Arabidopsis thaliana genomic DNA, chromosome 5, BAC clone:T4M5	0.24
4714	AC064850	Homo sapiens clone RP11-117H9, complete sequence	0.009
4715	Z93943	Human DNA sequence from cosmid U235H3 on chromosome X	0.006
4716	AJ132901	Drosophila guanche mitochondrial A+T-rich region	0.052
4717	AE006291	Lactococcus lactis subsp. lactis IL1403 section 53 of 218 of the complete genome	0.24
4718	AF227741	Rattus norvegicus protein kinase WNK1 (WNK1) mRNA, complete cds	6.1
4720	Z73524	S.cerevisiae chromosome XVI reading frame ORF YPL168w	0.072
4721	AF142484	Sebastes melanops microsatellite Sme2 sequence	0.19
4722	X51938	D. melanogaster DNA for a region 3' to the white gene, corresponding to the FB-NOF insertion site in TE146	2
4723	Z80361	H.sapiens HLA-DRB pseudogene, repeat region;	0.55
4724	AF312620	Plasmodium vivax clone C19b thrombospondin-related adhesive protein gene, partial cds	2.1
4725	XM_017198	Homo sapiens hypothetical protein FLJ12085 (FLJ12085), mRNA	1E-35
4726	AJ408943	Homo sapiens chromosomal breakpoint fragment derivative 11, MLL/AF4 fusion, patient UPN051	0.001
4727	XM_050754	Homo sapiens KIAA1594 protein (KIAA1594), mRNA	0.5
4728	AE002938	Drosophila melanogaster genomic scaffold 142000013385520, complete sequence	0.008
4729	AE001390	Plasmodium falciparum chromosome 2, section 27 of 73 of the complete sequence	0.21
4730	AK000109	Homo sapiens cDNA FLJ20102 fis, clone COL04783	2.1
4731	AF163325	Trichoderma harzianum mitochondrial plasmid pThr1, complete plasmid sequence	0.028
4732	AL137277	Homo sapiens mRNA; cDNA DKFZp434M1114 (from clone DKFZp434M1114)	1.9
4733	U43145	Plasmodium chabaudi repeat organellar protein gene, complete cds	0.64
4734	X71875	H.sapiens gene for protein serine kinase PSK-H1, first coding exon	1.7
4735	AE001479	Helicobacter pylori, strain J99 section 40 of 132 of the complete genome	0.74
4736	M29586	Elops saurus Ig germline H-chain pseudogene V-region, partial cds	0.66
4737	AK020838	Mus musculus adult retina cDNA, RIKEN full-length enriched library, clone:A930009F24, full insert sequence	0.025
4738	AB038343	Melon yellow spot virus NSs and N genes for nonstructural protein and nucleoprotein, complete cds, isolate:Tospo-melo	0.68
4739	AB005130	Candida maltosa gene for EPD1, complete cds	0.25

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
4740	AF361581	Arabidopsis thaliana AT4g35320/F23E12_120 gene, complete cds	1.9
4741	Z75032	S.cerevisiae chromosome XV reading frame ORF YOR124c	0.025
4742	U17681	Human neurofibromatosis 1 (NF1) gene, exons 16, 17, 18 and 19a	0.45
4743	AK025048	Homo sapiens cDNA: FLJ21395 fis, clone COL03557	0.66
4744	AF198444	Homo sapiens 10q21 mRNA sequence	0.008
4745	AE005556	Escherichia coli O157:H7 EDL933 genome, contig 3 of 3, section 175 of 290	0.71
4746	X74784	M.musculus mk2e mRNA	0.17
4747	AB029480	Oryzias latipes gene for Y3 olfactory receptor, complete cds	0.077
4749	AF072932	Medicago sativa cold acclimation responsive protein CAR1 (CAR1) mRNA, complete cds	0.66
4750	AF176056	Capitonus sp. 16S ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	0.009
4751	X03366	Bovine spleen trypsin inhibitor II (SI) gene	0.12
4752	L22951	Human immunodeficiency virus type 1 (UG275) proviral DNA encoding env, tat, vpu, rev, and nef genes	0.23
4753	U95851	Amblyomma darwini 12S ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence	5.4
4754	AE001372	Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence	2.2
4755	AF147813	Protrama radicis elongation factor 1 alpha gene, partial cds	0.24
4756	U77974	Tribolium castaneum transcription factor homolog (Tc-eve) gene, complete cds	0.003
4757	XM_045423	Homo sapiens KIAA0701 protein (KIAA0701), mRNA	6.3
4758	J04357	Red clover necrotic mosaic virus RNA-1, complete sequence	0.96
4759	XM_010136	Homo sapiens O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase) (OGT), mRNA	0.69
4760	XM_030855	Homo sapiens similar to KIAA1361 protein (H. sapiens) (LOC90315), mRNA	0.008
4761	AY031575	HIV-1 isolate NC5000-1999 from USA pol polyprotein (pol) gene, partial cds	6.2
4762	XM_007592	Homo sapiens Homer, neuronal immediate early gene, 2 (HOMER-2B), mRNA	2.2
4763	AC016707	Homo sapiens BAC clone RP11-221K4 from Y, complete sequence	0.75
4764	AF001848	Oxytricha nova phosphoglycerate kinase (PGK) gene, complete cds	5.7
4765	BC006693	Mus musculus, clone MGC:7897 IMAGE:3582679, mRNA, complete cds	1.9
4766	L81574	Homo sapiens (subclone 7_g1 from P1 H11) DNA sequence, complete sequence	0.00003
4767	U67508	Methanococcus jannaschii section 50 of 150 of the complete genome	0.23

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
4768	AY021494	Oryza sativa microsatellite MRG3819 containing (TA)X27, genomic sequence	0.023
4769	L75945	Borrelia burgdorferi flagellar hook protein (flgE), flbD, flagellar motor apparatus (motAB), fliL, fliM, fliZ, flagellar export apparatus (fliPQR, flhB), flhF, flbE genes	0.76
4770	AL590606	S.pombe chromosome II BAC pB7E8	0.068
4771	AF060728	Conospermum mitchelii chloroplast atpB-rbcL intergenic spacer region, partial sequence	0.2
4772	AB056833	Macaca fascicularis brain cDNA clone:QflA-14255, full insert sequence	0.068
4773	AP001416	Homo sapiens genomic DNA, chromosome 21q22.2, clone:D34, LB7T-ERG region, complete sequence	0.0003
4774	XM_007838	Homo sapiens nuclear factor of activated T-cells 5, tonicity-responsive (NFAT5), mRNA	0.59
4775	AC024777	Caenorhabditis elegans cosmid Y42H9AR, complete sequence	0.74
4776	AF333186	Dictyostelium discoideum beta-alanine synthase (pyd3) mRNA, complete cds	0.057
4778	D01021	Anthocidaris crassispina mRNA for dynein beta-heavy chain, complete cds	0.69
4779	U65750	Xenopus laevis fork head related (XFD-1') gene, complete cds	0.079
4780	NM_008176	Mus musculus GRO1 oncogene (Gro1), mRNA	1.8
4781	M88115	Hylobates lar Myc gene, complete cds	0.73
4782	AP000388	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:MRI12	0.022
4783	AE007246	Sinorhizobium meliloti plasmid pSymA section 52 of 121 of the complete plasmid sequence	6.7
4784	XM_043069	Homo sapiens KIAA1464 protein (KIAA1464), mRNA	0.08
4785	U41482	Human Down Syndrome region of chromosome 21 genomic sequence, clone A39D1-1H8	0.001
4786	AL110134	Homo sapiens mRNA; cDNA DKFZp564H072 (from clone DKFZp564H072)	0.058
4787	XM_005044	Homo sapiens KIAA0628 gene product (KIAA0628), mRNA	0.002
4788	XM_052430	Homo sapiens E3 ubiquitin ligase SMURF1 (SMURF1), mRNA	2E-30
4790	NM_031320	Rattus norvegicus cadherin EGF LAG seven-pass G-type receptor 3 (Celsr3), mRNA	1.9
4791	AF184590	Plasmodium falciparum ADA2-like protein gene, partial cds	0.009
4792	AF061434	Vicia faba amino acid transporter a (AAPA) mRNA, partial cds	1.9
4793	AL117594	Homo sapiens mRNA; cDNA DKFZp564C1563 (from clone DKFZp564C1563)	0.074
4794	AJ133025	Megaselia abdita zen gene, exons 1-2	0.02
4795	XM_033087	Homo sapiens hypothetical protein FLJ20359 (FLJ20359), mRNA	0.024
4796	AE001462	Helicobacter pylori, strain J99 section 23 of 132 of the complete genome	1.1
4797	XM_042814	Homo sapiens hypothetical protein FLJ13397 (FLJ13397), mRNA	0.063

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
4798	AL137325	Homo sapiens mRNA; cDNA DKFZp434M0835 (from clone DKFZp434M0835)	2E-14
4799	AB030620	Mus musculus Chetk-alpha gene for choline/ethanolamine kinase-alpha, exon 4, 5, 6, 7, 8	0.64
4800	AB037417	Oryza sativa gene for aspartate carbamoyl transferase, complete cds	0.026
4801	AK024522	Homo sapiens cDNA: FLJ20869 fis, clone ADKA02377	0.21
4802	X62463	H.sapiens 3' flanking region for estrogen receptor (placenta) gene	0.7
4803	AE001127	Borrelia burgdorferi (section 13 of 70) of the complete genome	0.2
4804	Z70751	Caenorhabditis elegans cosmid F11A3, complete sequence	0.22
4805	XM_038231	Homo sapiens KIAA0793 gene product (KIAA0793), mRNA	6E-53
4806	AF223425	Mus musculus MAB21L2 (MAb21l2) gene, complete cds	4.5
4807	XM_039048	Homo sapiens hypothetical protein MGC11303 similar to Zink transporter 2 (MGC11303), mRNA	2
4808	U75604	Tilapia nilotica type I estrogen receptor mRNA, complete cds	0.057
4809	XM_015243	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50), mRNA	1.7
4810	AF247970	Caenorhabditis elegans cell cycle checkpoint protein Rad9 gene, complete cds	0.008
4811	X12574	Parsley PcPR1-2 mRNA for pathogenesis-related protein type A	0.077
4812	AF332562	Simian virus 40 strain 777, complete genome	0.64
4813	XM_005118	Homo sapiens general transcription factor IIE, polypeptide 2 (beta subunit, 34kD) (GTF2E2), mRNA	1
4814	BC006700	Mus musculus, Similar to RIKEN cDNA 2310035M22 gene, clone MGC:6680 IMAGE:3501285, mRNA, complete cds	0.21
4815	AB025319	Yaba monkey tumor virus DNA, BamH1 restriction fragment E, M and partial C, partial and complete cds	0.18
4816	XM_048433	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump), subunit 1 (ATP6S1), mRNA	0.55
4817	Y11095	Rice stripe virus RNA 3	5.9
4818	AL589991	Human DNA sequence from clone RP11-241J5 on chromosome 6, complete sequence [Homo sapiens]	3E-78
4819	XM_043498	Homo sapiens G protein-coupled receptor 44 (GPR44), mRNA	0.0002
4820	XM_047477	Homo sapiens KIAA1638 protein (KIAA1638), mRNA	0.077
4821	AJ242480	Streptococcus thermophilus ORF1, ORF2, ORF3, ORF4, ORF5 and ORF6 DNA, strain St0	0.18
4822	XM_016395	Homo sapiens region containing hypothetical protein; mutL (E. coli) homolog 3 (LOC82389), mRNA	6E-74
4823	XM_043492	Homo sapiens 42259 (KIAA1728), mRNA	0.0000006
4824	L43603	Gallus gallus Na+/K+-ATPase alpha-1 subunit gene, promoter region	0.41
4825	AF257746	Rattus norvegicus multidrug resistance protein 1a (Pgy1) mRNA, complete cds	0.5
4826	X68794	D.melanogaster "ten-a" mRNA for secreted protein	1.2

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
4827	AF330118	Homo sapiens voltage-gated sodium channel type III alpha subunit (SCN3A) gene, exon 2	0.12
4828	XM_011230	Homo sapiens ALL1 fused gene from 5q31 (AF5Q31), mRNA	5.8
4829	XM_030669	Homo sapiens hypothetical gene supported by AL133011 (LOC90288), mRNA	1.9
4830	U36927	Plasmodium yoelii rhoptry protein gene, complete cds	0.21
4831	AF201353	Columba livia glutamate receptor C gene, partial cds	5
4832	AF331435	HIV-1 D2 from Australia envelope protein (env) gene, partial cds	0.07
4833	AF362391	Candida albicans heat shock protein Hsp104 (HSP104) gene, HSP104-b allele, complete cds	1.1
4834	XM_027927	Homo sapiens hypothetical gene supported by Z97017 (LOC89989), mRNA	0.48
4835	AE001127	Borrelia burgdorferi (section 13 of 70) of the complete genome	0.72
4836	AL390126	S. pombe chromosome III cosmid c233	0.023
4837	AF110213	Rattus norvegicus insulin receptor precursor, exon 14	0.56
4838	M38534	Paramecium aurelia immobilization antigen (51C) gene, exon 5 and complete cds	0.015
4839	AE001430	Plasmodium falciparum chromosome 2, section 67 of 73 of the complete sequence	0.052
4840	AF181475	Mus musculus synaptonemal complex protein 3 (Sycp3) gene, exon 5	0.19
4841	AF177242	Bodo saltans clone pBME40 mitocondrial minicircle DNA	0.024
4842	XM_004347	Homo sapiens elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2 (ELOVL2), mRNA	0.66
4843	AF083494	Mus musculus phospholipase D1 (PLD1) gene, exons 23 and 24, complete sequence	0.53
4844	U89684	Lycopersicon esculentum protein kinase (LePK7) gene, partial cds	0.22
4845	AB025716	Staphylococcus aureus gene for FmtB, complete cds	0.57
4846	AF017180	Schizosaccharomyces pombe hexose transporter (Ght2) mRNA, complete cds	0.87
4847	Z26314	P.falciparum gene for STARP antigen	0.007
4848	XM_045160	Homo sapiens KIAA0275 gene product (KIAA0275), mRNA	1
4849	AK016495	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4931431C02, full insert sequence	0.62
4850	BC004496	Homo sapiens, Similar to hypothetical protein FLJ14058, clone IMAGE:3831313, mRNA	1.7
4851	XM_005684	Homo sapiens tolloid-like 2 (TLL2), mRNA	1.6
4852	AF249077	Sphaerotheca pluvialis cytochrome b (cytb) gene, partial cds; mitochondrial gene for mitochondrial product	0.047
4853	XM_016934	Homo sapiens hypothetical protein FLJ12891 (FLJ12891), mRNA	5.4
4854	X65747	R.norvegivus gnat-3 mRNA for gustducin	0.2
4855	XM_011705	Homo sapiens paraneoplastic antigen MA2 (PNMA2), mRNA	0.2

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
4856	L10692	Arabidopsis thaliana cytosine-5 methyltransferase mRNA, complete cds	2.1
4857	AB052250	Arabidopsis thaliana gene for MYB transcription factor Atmyb2, complete cds, strain:Yo-0	0.36
4859	XM_033535	Homo sapiens region containing tryptase beta 2; tryptase beta 1 (LOC82314), mRNA	1.3
4860	U49846	Rattus norvegicus stem cell factor gene, 5' flanking region and exon 1, partial sequence	0.18
4861	AJ244021	Tetrahymena thermophila kin2 gene for kinesin-II homologue, exons 1-4	0.063
4862	AF201021	Stachyarrhena sp. Jansen-Jacobs 4707 ribosomal protein S16 (rps16) gene, partial intron sequence; chloroplast gene for chloroplast product	0.057
4863	AJ245636	Mus musculus P2Y1 gene for P2Y1 receptor	0.2
4864	AK023175	Homo sapiens cDNA FLJ13113 fis, clone NT2RP3002590	0.2
4865	XM_034638	Homo sapiens hypothetical gene supported by AK024355 (LOC90867), mRNA	1E-08
4866	AB011006	Rattus norvegicus gene for leptin receptor, partial cds	5.5
4867	XM_031128	Homo sapiens hypothetical protein DKFZp761I172 (DKFZP761I172), mRNA	0.22
4868	AK001442	Homo sapiens cDNA FLJ10580 fis, clone NT2RP2003533	2E-12
4870	AF307954	Saccharomyces servazzii 46.1 kDa protein, KAR4-like protein, and SPB1-like protein genes, complete cds	0.19
4871	AF055079	Panulirus argus inositol 1,4,5-trisphosphate receptor (IP3R) mRNA, complete cds	6
4872	X88849	C.coli ceuB, ceuC, ceuD, ceuE, OrfA, OrfB genes	0.0008
4873	XM_039699	Homo sapiens hypothetical protein FLJ23309 (FLJ23309), mRNA	3E-42
4874	AF212847	Lactococcus lactis bacteriophage ul36.2 ORF111b (ORF111b), ORF78b (ORF78b), ORF61b (ORF61b), ORF245 (ORF245), ORF364 (ORF364), and putative replisome organizer (ORF255) genes, complete cds; and ORF241 (ORF241) gene, partial cds	1.9
4875	XM_052223	Homo sapiens DKFZP564G092 protein (DKFZP564G092), mRNA	0.69
4876	AK024606	Homo sapiens cDNA: FLJ20953 fis, clone ADSE01979	3E-89
4877	U96097	Clavibacter michiganensis subsp. sepedonicus species-specific DNA clone Cms85	0.47
4878	Z48599	L.mexicana lmcpc gene cathepsin B-like cysteine proteinase	0.063
4879	NM_014160	Homo sapiens HSPC070 protein (HSPC070), mRNA	5
4880	XM_031388	Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5 (13kD, B13) (NDUFA5), mRNA	0.55
4881	AF059531	Homo sapiens protein arginine N-methyltransferase 3 (PRMT3) mRNA, partial cds	0.18
4882	AF240700	Gymnocrotaphus curvidens cytochrome b (cytb) gene, partial cds; mitochondrial gene for mitochondrial product	0.65

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
4883	AE005988	Caulobacter crescentus section 314 of 359 of the complete genome	2
4884	AF332785	Neocalanus plumchrus cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial gene for mitochondrial product	0.65
4885	AJ278986	Pichia etchellsii plasmid pPE1B	0.051
4886	AL512660	Human DNA sequence from clone RP11-353M9 on chromosome 10, complete sequence [Homo sapiens]	6.3
4887	AF147082	Homo sapiens gamma-glutamyl hydrolase gene, exons 3 through 7	2
4888	AL389874	Human DNA sequence from clone RP11-563A22 on chromosome 20 Contains the 5' end of a novel gene weakly similar to Xenopus laevis putative Zic3 binding protein, complete sequence [Homo sapiens]	0.008
4889	AC084157	Caenorhabditis elegans cosmid Y46E12BR, complete sequence	0.084
4891	AE001183	Borrelia burgdorferi (section 69 of 70) of the complete genome	0.66
4892	AE002137	Ureaplasma urealyticum section 38 of 59 of the complete genome	0.52
4893	XM_028606	Homo sapiens Sp1 transcription factor (SP1), mRNA	5
4894	NC_001453	Strongylocentrotus purpuratus mitochondrion, complete genome	6
4895	AK023104	Homo sapiens cDNA FLJ13042 fis, clone NT2RP3001318	0.064
4896	XM_015243	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50), mRNA	1.7
4897	XM_043823	Homo sapiens hypothetical protein FLJ20958 (FLJ20958), mRNA	0.000004
4898	AB049900	Macaca fascicularis brain cDNA, clone:QnpA-19713	6.1
4899	AE001390	Plasmodium falciparum chromosome 2, section 27 of 73 of the complete sequence	0.23
4900	AE007346	Streptococcus pneumoniae section 29 of 194 of the complete genome	0.73
4901	X17339	Dengue-2 virus NS1 gene for nonstructural protein (patient M2)	0.24
4902	AK000864	Homo sapiens cDNA FLJ10002 fis, clone HEMBA1000046	0.00001
4903	AF180076	Panorpa helena cytochrome oxidase I (COI) gene, partial cds; mitochondrial gene for mitochondrial product	0.6
4904	AC008855	Homo sapiens chromosome 5 clone CTD-2178M23, complete sequence	3E-12
4905	K02990	Human hepatitis A virus, complete genome	0.23
4906	AE005310	Escherichia coli O157:H7 EDL933 genome, contig 1 of 3, section 134 of 155	0.078
4907	NM_032717	Homo sapiens hypothetical protein MGC11324 (MGC11324), mRNA	0.68
4908	BC004118	Homo sapiens, clone MGC:11170 IMAGE:3843148, mRNA, complete cds	1.5
4909	L29252	Human (clone D13-2) L-iditol-2 dehydrogenase gene, exon 4, exon 5, exon 6 and exon 7	0.0000001
4910	S68117	rPLP-A=prolactin-like protein A {5' region, exon 1, intron 1} [rats, Genomic, 1187 nt]	0.11

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
4911	NM_016701	Mus musculus nestin (Nes), mRNA	0.21
4912	AE006418	Lactococcus lactis subsp. lactis IL1403 section 180 of 218 of the complete genome	0.009
4913	XM_041162	Homo sapiens hypothetical protein KIAA1165 (KIAA1165), mRNA	4E-50
4914	AF147358	Homo sapiens full length insert cDNA clone YB61E03	0.00003
4915	AE000642	Helicobacter pylori 26695 section 120 of 134 of the complete genome	1.9
4916	XM_040436	Homo sapiens nebulin (NEB), mRNA	2
4917	AB026296	Pisum sativum mRNA for hsr203J homolog, complete cds	0.024
4918	AF159148	Danio rerio Noggin 2 mRNA, complete cds	0.23
4919	AF234184	Lucilia cuprina sex-lethal protein SXL2 mRNA, complete cds, alternatively spliced	0.026
4920	AK007229	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:1700121L03, full insert sequence	0.21
4921	AJ404228	Saccharomyces douglasii mitochondrial tRNA gene cluster	0.021
4922	X71604	H.sapiens son-pseudogene	0.53
4923	AF169122	Homo sapiens DNA (cytosine-5) methyltransferase gene, intron 4, partial sequence	0.059
4924	XM_040202	Homo sapiens protein phosphatase, EF hand calcium-binding domain 1 (PPEF1), mRNA	6E-09
4925	AY027893	Homo sapiens voltage-dependent calcium channel beta 2 subunit (CACNB2) gene, exon 1	3.3
4926	AF136008	Desulfobacterium sp. BSv41 16S ribosomal RNA gene, partial sequence	5.6
4927	NM_007439	Mus musculus anaplastic lymphoma kinase (Alk), mRNA	0.071
4928	XM_006758	Homo sapiens frizzled (Drosophila) homolog 10 (FZD10), mRNA	2
4929	AL139329	Human DNA sequence from clone RP11-228P1 on chromosome 6, complete sequence [Homo sapiens]	4E-38
4930	L03188	Saccharomyces cerevisiae integrin analogue gene, complete cds	0.23
4931	AB039881	Canis familiaris mRNA for cytochrome P450c21, complete cds	0.55
4932	AK004783	Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200015E14, full insert sequence	6.2
4933	U41343	Human prolargin (PRELP) gene, exon 2	0.0000004
4934	AF157369	Homo sapiens Niemann-Pick C1 protein (NPC1) gene, exon 5	0.58
4935	XM_016505	Homo sapiens KIAA0999 protein (KIAA0999), mRNA	9E-26
4936	U07807	Human metallothionein IV (MTIV) gene, complete cds	0.008
4937	NM_018818	Mus musculus choroidermia (Chm), mRNA	1.7
4938	BC009075	Mus musculus, beta-1,3-N-acetylglucosaminyltransferase 1, clone MGC:6892 IMAGE:2654354, mRNA, complete cds	1.2
4939	AF304354	Homo sapiens proteoglycan 3 (PRG3) gene, complete cds	0.24
4940	AK000864	Homo sapiens cDNA FLJ10002 fis, clone HEMBA1000046	0.00001
4941	AF076601	Dictyostelium discoideum developmental protein (DG1105) gene, partial cds	0.95

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
4942	AF025542	Bombyx mori insulin receptor-like protein precursor (BIR) mRNA, complete cds	0.64
4943	XM_038714	Homo sapiens hypothetical protein dJ37E16.5 (DJ37E16.5), mRNA	6.3
4944	AC016707	Homo sapiens BAC clone RP11-221K4 from Y, complete sequence	0.054
4945	XM_005684	Homo sapiens tolloid-like 2 (TLL2), mRNA	1.1
4946	AJ276170	Rattus norvegicus partial Vps54l processed pseudogene, 3' end	0.041
4947	AJ132986	Vibrio sp. partial 16S ribosomal RNA, isolate A515	5.9
4948	XM_009513	Homo sapiens hypothetical protein (HSPC207), mRNA	0.21
4949	AF181668	Homo sapiens clone 173p17 polymorphic microsatellite sequence	0.17
4950	AF045453	Dictyostelium discoideum protein kinase YakA (yakA) mRNA, complete cds	0.007
4951	AF279135	Dictyostelium discoideum spore coat structural protein SP65 (cotE) gene, complete cds	0.003
4952	AK012631	Mus musculus 10, 11 days embryo cDNA, RIKEN full-length enriched library, clone:2810001G20, full insert sequence	0.071
4953	AB047630	Macaca fascicularis brain cDNA, clone:QnpA-13555	0.69
4954	AJ011848	Hordeum vulgare chloroplast rps15 (partial), ndhH, ndhI, ndhG, ndhE, psaC, ndhD and ndhA genes	0.054
4955	U34363	Plasmodium falciparum CTRP gene, complete cds	0.18
4956	AF220175	Homo sapiens acid ceramidase (ASAH) gene, exons 5 through 14, and complete cds	0.0009
4958	D26442	Yeast gene for PES4 PAB-like protein, complete cds	0.003
4959	NC_002184	Penaeus monodon mitochondrion, complete genome	1.9
4960	XM_039251	Homo sapiens 37381 (KIAA1660), mRNA	5
4961	XM_004462	Homo sapiens signal sequence receptor, alpha (translocon-associated protein alpha) (SSR1), mRNA	0.72
4962	AF252420	Bos taurus clone MNB-5 microsatellite sequence	0.08
4963	XM_035186	Homo sapiens RCE1 (S. Cerevisiae) homolog, prenyl protein protease (RCE1), mRNA	2
4964	AL110134	Homo sapiens mRNA; cDNA DKFZp564H072 (from clone DKFZp564H072)	0.058
4965	AL049452	Homo sapiens mRNA; cDNA DKFZp586C1322 (from clone DKFZp586C1322)	0.67
4966	AB047614	Macaca fascicularis brain cDNA, clone:QnpA-12025	0.077
4967	XM_043315	Homo sapiens KIAA0229 protein (KIAA0229), mRNA	6.2
4968	AK017495	Mus musculus 8 days embryo cDNA, RIKEN full-length enriched library, clone:5730405K23, full insert sequence	0.025
4969	AB012141	Candida glabrata TEF3 gene for translation elongation factor3, complete cds	0.003
4970	AK022914	Homo sapiens cDNA FLJ12852 fis, clone NT2RP2003445	0.0003
4971	AF133211	Homo sapiens COT kinase proto-oncogene, partial cds, alternatively spliced	0.008

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
4972	AF349681	Simian immunodeficiency virus strain SIVrcmNg409 from Nigeria 5' long terminal repeat, partial sequence; gag protein (gag) gene, complete cds; pol protein (pol) gene, partial cds; and vif gene, complete sequence	0.68
4973	AF350254	Homo sapiens fibrinogen gamma chain precursor (FGG) gene, complete cds, alternatively spliced	0.21
4974	AF314052	Rhizobium sp. CIAT613 nifHc gene, partial sequence	1.9
4975	XM_036277	Homo sapiens inhibitor of DNA binding 4, dominant negative helix-loop-helix protein (ID4), mRNA	0.076
4976	AF057740	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exon 24 and complete cds	0.00003
4977	XM_051777	Homo sapiens similar to NAD(P) dependent steroid dehydrogenase-like (M. musculus) (LOC93517), mRNA	4E-11
4978	AF314052	Rhizobium sp. CIAT613 nifHc gene, partial sequence	2
4979	BC010911	Homo sapiens, Similar to adaptor protein containing pH domain, PTB domain and leucine zipper motif, clone IMAGE:4295177, mRNA	0.076
4980	AF214529	Homo sapiens dystrophin (DMD) gene, intron 51, partial sequence	0.001
4981	AK024235	Homo sapiens cDNA FLJ14173 fis, clone NT2RP2002755	e-104
4982	AB035089	Homo sapiens SCCA2 gene for squamous cell carcinoma antigen 2, complete cds	0.23
4983	M97555	Schistosoma mansoni tropomyosin mRNA, complete cds	0.22
4984	AE002745	Drosophila melanogaster genomic scaffold 142000013385404, complete sequence	0.003
4985	X99288	B.calamita repeat region, clone-lib micro-8	0.23
4987	AJ308840	Coffea arabica microsatellite DNA, clone 16-6CTG	0.025
4988	AB049134	Cucurbita moschata CmATS1;1 gene for acyl-(acyl-carrier-protein): glycerol-3-phosphate acyltransferase, complete cds	0.53
4989	X03991	Human glucagon gene	0.074
4990	AY042871	Arabidopsis thaliana zinc finger-like protein (F3C22_200) mRNA, complete cds	0.077
4991	AF214529	Homo sapiens dystrophin (DMD) gene, intron 51, partial sequence	0.001
4992	AF269319	Staphylococcus epidermidis strain SR1 clone step.1002a02 genomic sequence	2
4993	AB009801	Homo sapiens gene for osteonidogen, intron 2	0.69
4994	M69146	Torulopsis glabrata metal-activated transcription factor (amt1) gene, complete cds	0.65
4995	AL121822	Human DNA sequence from clone 346P11 on chromosome Xq21.2-21.33, complete sequence [Homo sapiens]	5E-09
4996	AF072273	Lactuca sativa resistance protein candidate RGC2N (RGC2N) pseudogene, complete sequence	0.22
4997	AL358273	S.pombe chromosome II cosmid c29C10	0.22
4998	BC010011	Homo sapiens, Similar to RIKEN cDNA 4931428D14 gene, clone MGC:15407 IMAGE:4309613, mRNA, complete cds	0.22

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
4999	AF090889	Homo sapiens clone HQ0092	0.71
5000	M93140	Glycine max cv Prize protein kinase mRNA	2.1
5001	AE005266	Escherichia coli O157:H7 EDL933 genome, contig 1 of 3, section 90 of 155	1.8
5002	AE007350	Streptococcus pneumoniae section 33 of 194 of the complete genome	0.23
5003	BC008973	Homo sapiens, transmembrane protein with EGF-like and two follistatin-like domains 2, clone MGC:17007 IMAGE:4180709, mRNA, complete cds	0.023
5004	X13439	Cochliobolus heterostrophus mitochondrial gene for ATPase subunit 6	0.19
5005	AF138069	HIV-1 p5c028-h from USA envelope glycoprotein (env) gene, partial cds	2.1
5006	NM_002847	Homo sapiens protein tyrosine phosphatase, receptor type, N polypeptide 2 (PTPRN2), mRNA	6
5007	XM_036827	Homo sapiens hypothetical gene supported by X04201; X04588; AK026559; AY004867; BC000771; BC008407; BC008425 (LOC91191), mRNA	1
5008	NM_031389	Mus musculus ribonuclease/angiogenin inhibitor 2 (Rnh2), mRNA	1.7
5009	BC010355	Homo sapiens, Similar to nuclear protein, clone IMAGE:4248516, mRNA	5.4
5010	AE003909	Xylella fastidiosa 9a5c, section 55 of 229 of the complete genome	5.1
5011	NM_031389	Mus musculus ribonuclease/angiogenin inhibitor 2 (Rnh2), mRNA	1.7
5012	XM_016747	Homo sapiens latent transforming growth factor beta binding protein 1 (LTBP1), mRNA	2E-10
5013	M85304	Schistosoma mansoni homeodomain protein (smox-5) mRNA, complete cds	0.009
5014	NC_001398	Saccharomyces cerevisiae 2 micron circle plasmid, complete sequence	0.65
5015	AF267746	Drosophila melanogaster rad21 mitotic cohesin (drad21) gene, exons 3 through 8 and complete cds	0.003
5016	XM_052430	Homo sapiens E3 ubiquitin ligase SMURF1 (SMURF1), mRNA	2E-30
5017	X67813	C.familiaris SRP72 mRNA for signal recognition particle	0.16
5018	AF031848	Dermacentor marginatus 12S ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence	0.061
5019	XM_003317	Homo sapiens PDZ domain containing guanine nucleotide exchange factor(GEF)1 (PDZ-GEF1), mRNA	0.67
5020	XM_030673	Homo sapiens methyl-CpG binding domain protein 4 (MBD4), mRNA	0.6
5021	L38957	Saccharomyces cerevisiae nuclear-encoded mitochondrial isoleucyl-tRNA synthetase (ISM1) gene, complete cds	2.1
5022	AF345089	Hepatitis C virus isolate SCpreSC2c14 nonfunctional polyprotein gene, partial sequence	0.59

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
5023	AC091124	Caenorhabditis elegans cosmid Y47A7, complete sequence	1.7
5024	X66451	E.octocarinatus RPA2 gene for RNA polymerase I second largest subunit	0.066
5025	XM_010563	Homo sapiens hypothetical gene supported by AB033071; AB051480; AK000726; NM_015383 (LOC92396), mRNA	1E-15
5026	AF256722	Salmo salar clone BHMS458 microsatellite sequence	0.5
5027	AF385609	Homo sapiens minisatellite sequence	5.3
5028	AF355103	Pleurotus ostreatus linear mitochondrial plasmid mlp2, partial sequence	0.18
5029	XM_034863	Homo sapiens similar to hypothetical protein FLJ22294 (H. sapiens) (LOC90918), mRNA	1.8
5030	AF374005	Rattus norvegicus bradykinin B2 receptor gene, promoter sequence	8.3
5031	AK014447	Mus musculus 18 days pregnant adult female placenta and extra embryonic tissue cDNA, RIKEN full-length enriched library, clone:3830421F13, full insert sequence	0.18
5032	AL355577	Human DNA sequence from clone RP11-299G2 on chromosome 6 Contains a GSS, complete sequence [Homo sapiens]	0.0003
5033	AB030616	Mus musculus Chetk-alpha gene for choline/ethanolamine kinase-alpha, exon 1 and 5'-flanking region	6.1
5034	S66671	pol [simian Mason-Pfizer D-type retrovirus SM-PDT, systemic lupus erythematosus patient TFA 68, Genomic RNA, 113 nt]	0.008
5035	AB038481	Codium lucasii chloroplast rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial cds	0.22
5036	U05013	Rattus norvegicus Sprague-Dawley heme oxygenase-2 non-reducing isoform gene, complete cds	1.9
5037	L81904	Homo sapiens (subclone 1_h7 from P1 H69) DNA sequence, complete sequence	1.7
5038	AF242384	Homo sapiens phytanoyl-CoA hydroxylase (PHYH) gene, exon 7	1.9
5039	X52863	G.max Gy4 gene for glycinin	5.9
5040	XM_002625	Homo sapiens ankyrin repeat and SOCS box-containing 3 (ASB3), mRNA	6
5041	U00789	Mus musculus Dp71 (DMD) gene, partial cds	0.068
5042	AB017429	Oryza sativa gene for mitochondrial ribosomal portein S14, succinate dehydrogenase iron-protein subunit (SDHB)	2
5043	U67518	Methanococcus jannaschii section 60 of 150 of the complete genome	0.002
5044	XM_048782	Homo sapiens c6.1A (C6.1A), mRNA	0.2
5045	AB055263	Macaca fascicularis brain cDNA, clone:QflA-10674	0.003
5046	S65281	drebrin {clone eDcg5} [chickens, Genomic, 160 nt, segment 3 of 10]	0.61
5047	AF296203	Uncultured bacterium SY6-54 16S ribosomal RNA gene, partial sequence	0.25
5048	X06266	Anthirrhinum majus DNA for transposon tam2	0.007

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
5049	AF272387	Homo sapiens leucine zipper nuclear factor (BLZF1) gene, exon 6	7E-22
5050	NC_001587	Human papillomavirus type 34, complete genome	0.25
5051	NM_017078	Rattus norvegicus Acetylcholine receptor alpha 5 (Chrna5), mRNA	0.64
5052	XM_030510	Homo sapiens microfibrillar-associated protein 2 (MFAP2), mRNA	2
5053	Z48433	L.odomensis vicilin pseudogene	0.047
5054	M21084	P.hybrida 5-enolpyruvylshikimate 3-phosphate synthase mRNA, complete cds	0.2
5055	U67518	Methanococcus jannaschii section 60 of 150 of the complete genome	0.002
5056	AF215555	Blakea trinervia NADH dehydrogenase subunit F (ndhF) gene, partial cds; chloroplast gene for chloroplast product	0.63
5057	AE001379	Plasmodium falciparum chromosome 2, section 16 of 73 of the complete sequence	5.4
5059	AF362391	Candida albicans heat shock protein Hsp104 (HSP104) gene, HSP104-b allele, complete cds	4.4
5060	AJ000056	Homo sapiens tyrosine aminotransferase gene, 5' flanking region	0.57
5061	AF112541	HIV-1 isolate 08108v3 from USA, envelope glycoprotein (env) gene, partial cds	0.007
5062	AF300534	Diadasia consociata cytochrome oxidase subunit I gene, partial cds; tRNA-Leu gene, complete sequence; and cytochrome oxidase subunit II gene, partial cds; mitochondrial genes for mitochondrial products	0.22
5063	J00571	Mouse Ig kappa unproductively rearranged V-T2; V-J region	0.001
5064	X95275	P.falciparum complete gene map of plastid-like DNA (IR-A)	0.062
5065	Y09746	H.oligactis mRNA for heat shock protein 70	0.46
5066	X95536	H.sapiens ear1 gene	2E-64
5067	D10997	C.ellipsoidea rbcL, rps14, trnM, trnG, trnD, trnS, rps4, atpE, atpB genes, complete cds	1.8
5068	Z73968	Caenorhabditis elegans cosmid C05A2, complete sequence	0.67
5069	XM_012733	Homo sapiens KIAA1012 protein (KIAA1012), mRNA	0.24
5070	AE000745	Aquifex aeolicus section 77 of 109 of the complete genome	0.21
5071	AF208521	Diploptera punctata high-affinity Na+-dependent glutamate transporter (EAAT1) mRNA, complete cds	0.08
5072	XM_032656	Homo sapiens mannosidase, alpha, class 2B, member 1 (MAN2B1), mRNA	1.8
5073	Z28063	S.cerevisiae chromosome XI reading frame ORF YKL063c	6.2
5074	XM_050445	Homo sapiens KIAA0164 gene product (KIAA0164), mRNA	0.66
5075	AF265211	Pectobacterium chrysanthemi ArgG (argG) gene, partial cds; regulatory protein PecS (pecS), regulatory protein PecM (pecM), indigoidine systhesis protein IdgA (idgA), and indigoidine systhesis protein IdgB (idgB) genes, complete cds; and indigoidine sys>	0.72

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
5076	X87201	Borrelia burgdorferi plasmid, orfA, B, C, D, F, bdrV genes, clone pOMB14 and pOMB17	0.076
5077	AF120475	Mus musculus myelin-associated oligodendrocytic basic proteins MOBP170 and MOBP69 (Mobp) gene, exons 3 through 5 and complete cds, alternatively spliced	0.0009
5078	AF270407	Staphylococcus epidermidis strain SR1 clone step.4050g06 genomic sequence	0.67
5079	U47138	Inkoo virus SW AR 83-161 nucleocapsid protein and non-structural protein genes, complete cds	0.16
5080	AB049420	Mus musculus DNA, clone:7-1, derived from 4x chromosome of T(X;4)37H translocation	6.5
5081	AF009415	Staphylococcus xylosus choline transporter (cudT), putative regulatory protein (cudC), glycine betaine aldehyde dehydrogenase (cudA), and choline dehydrogenase (cudB) genes, complete cds	0.075
5082	AE001395	Plasmodium falciparum chromosome 2, section 32 of 73 of the complete sequence	0.24
5083	U62542	Drosophila melanogaster dead ringer (dead ringer) mRNA, complete cds	0.12
5084	AL445527	Human DNA sequence from clone RP11-115C2 on chromosome 1, complete sequence [Homo sapiens]	5.5
5085	XM_016052	Homo sapiens LOC86766 (LOC86766), mRNA	0.24
5086	XM_037781	Homo sapiens hypothetical gene supported by J04178 (LOC91343), mRNA	6.4
5087	X96932	N.tabacum gene encoding ascorbate oxidase-related protein	1.6
5088	AJ006986	Streptococcus pneumoniae type 33F DNA, capsular gene cluster	0.019
5089	M60858	Human nucleolin gene, complete cds	0.66
5090	AK026299	Homo sapiens cDNA: FLJ22646 fis, clone HSI07178	0.21
5091	AC006025	Homo sapiens PAC clone RP5-1188N21 from 7q11.23-q21.1, complete sequence	0.67
5092	X03100	Human HLA-SB(DP) alpha gene	1.8
5093	AF181671	Homo sapiens clone 77j13 polymorphic microsatellite sequence	0.055
5094	AF356600	Dictyostelium discoideum filament-interacting protein (fip) mRNA, complete cds	0.19
5095	U36619	Human Y-chromosome RNA recognition motif protein (YRRM) gene, exon 5, partial cds, subclone 7S2	0.023
5096	AF243117	Homo sapiens intrinsic factor-vitamin B12 receptor (CUBN) gene, exons 52 and 53	2
5097	XM_050127	Homo sapiens oligophrenin 1 (OPHN1), mRNA	0.5
5098	AJ251892	Drosophila melanogaster mRNA for LIM domain protein (espinas gene)	0.072
5099	AF036696	Caenorhabditis elegans cosmid F15B10	0.2
5100	AF052294	Mus musculus phospholipase D2 gene, exons 13 through 25 and complete cds	5.7
5101	AK026741	Homo sapiens cDNA: FLJ23088 fis, clone LNG07026	0.003
5102	K02212	Human alpha-1-antitrypsin gene (S variant), complete cds	1.7

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
5103	AB055370	Macaca fascicularis brain cDNA, clone:QflA-12708	0.079
5104	AK008762	Mus musculus adult male stomach cDNA, RIKEN full-length enriched library, clone:2210021I22, full insert sequence	2.1
5105	M71245	Rat prostatein C3 subunit gene, complete cds	0.69
5106	AY007089	Homo sapiens clone TCCCIA00110 mRNA sequence	0.000009
5107	AF113007	Homo sapiens PRO0066 mRNA, complete cds	0.0007
5108	AF125461	Caenorhabditis elegans cosmid Y8A9A, complete sequence	0.69
5109	AF016179	Rattus norvegicus putative pheromone receptor (Go-VN2) mRNA, complete cds	0.071
5110	AK021604	Homo sapiens cDNA FLJ11542 fis, clone HEMBA1002801	0.026
5111	Z73968	Caenorhabditis elegans cosmid C05A2, complete sequence	0.54
5112	U40995	Danio rerio Hox-a1 gene, complete cds	0.009
5113	NC_001728	Odontoglossum ringspot virus, complete genome	0.027
5114	2056.P10.gz43_268157	8778469	gi|8778469|gb|AAF79477.1|AC022492_21 (AC022492) F1L3.30 [Arabidopsis thaliana]
5115	AF234932	Chtenopteryx sicula clone 9 actin gene, partial cds	0.24
5116	M60858	Human nucleolin gene, complete cds	0.66
5117	XM_003100	Homo sapiens hypothetical protein FLJ11142 (FLJ11142), mRNA	0.23
5118	AF129278	Buchnera aphidicola natural-host Diuraphis noxia gluconate-6-phosphate dehydrogenase (gnd) gene, partial cds	6.4
5119	AF283665	Heterodera glycines guanylyl cyclase mRNA, complete cds	5.4
5120	AJ005205	Homo sapiens 5HT3 gene for serotonin 3 receptor	0.24
5121	AF135472	Clostridium beijerinckii Rep protein gene, complete cds	0.23
5122	XM_036007	Homo sapiens transmembrane protein 1 (TMEM1), mRNA	2.1
5123	AL031426	Human DNA sequence from clone CTA-191D12 on chromosome 22q13.1 Contains two exons of the APOL2 gene for apolipoprotein L 2, ESTs and GSSs, complete sequence [Homo sapiens]	0.000001
5124	XM_049821	Homo sapiens hypothetical protein MGC14832 (MGC14832), mRNA	5.4
5125	XM_028344	Homo sapiens ribosomal protein L5 (RPL5), mRNA	0.16
5126	AF016653	Caenorhabditis elegans cosmid C41D7, complete sequence	0.7
5127	Z96752	H.sapiens telomeric DNA sequence, clone 8QTEL025, read 8QTELOO025.seq	0.006
5128	M61883	Sus scrofa (pig) apomucin mRNA, 3' end	0.026

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
5129	AY005107	Pentachondra pumila specimen-voucher Cherry 96/1 maturase (matK) gene, partial cds; chloroplast gene for chloroplast product	2.2
5130	AF195044	Homo sapiens beaded filament component protein (CP49) gene, partial cds	0.57
5131	AK021963	Homo sapiens cDNA FLJ11901 fis, clone HEMBA1007347	0.0005
5132	AF034085	Caenorhabditis elegans UNC-45 (unc-45) gene, complete cds	0.0001
5133	U91929	Mus musculus L1 neural cell adhesion protein gene, 5' sequence and exon 1	2.1
5134	NM_010781	Mus musculus mast cell protease 6 (Mcpt6), mRNA	0.68
5135	AB017918	Mus musculus gene for gross cystic disease fluid protein 15, complete cds	0.001
5136	U55243	Dictyostelium discoideum glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, partial cds	0.24
5137	AF061296	Homo sapiens sulfonylurea receptor (SUR2) gene, exon 9	9E-45
5138	AL050314	Human DNA sequence from clone 100G10 on chromosome 22q13.31-13.33. Contains GSSs, complete sequence [Homo sapiens]	6.4
5139	XM_036394	Homo sapiens calcium/calmodulin-dependent protein kinase IV (CAMK4), mRNA	0.003
5140	XM_047419	Homo sapiens LOC87974 (LOC87974), mRNA	0.21
5141	AJ404314	Amphisorus hemprichii 18S rRNA gene, isolate 720	0.71
5142	AF324889	Homo sapiens myosin phosphatase target subunit 2 (MYPT2) gene, exon 1	0.23
5143	J04434	Bacteriophage PBS2 (from B.subtilis) uracil-DNA glycosylase inhibitor gene, complete cds	0.61
5144	XM_041213	Homo sapiens inter-alpha (globulin) inhibitor, H1 polypeptide (ITIH1), mRNA	5.5
5145	AF187881	Homo sapiens leukointegrin alpha d gene, promoter and partial cds	0.026
5146	Z70180	P.quinquangularis chloroplast matK gene	2
5147	AK025364	Homo sapiens cDNA: FLJ21711 fis, clone COL10156	0
5148	XM_045594	Homo sapiens hypothetical protein MGC4816 (MGC4816), mRNA	5E-82
5150	AB029068	Mus musculus gene for Ser/Thr kinase KKIAMRE, exon 1, 2, 3, 4, 5	0.63
5151	AF215555	Blakea trinervia NADH dehydrogenase subunit F (ndhF) gene, partial cds; chloroplast gene for chloroplast product	0.71
5152	XM_026967	Homo sapiens hypothetical protein MGC2668 (MGC2668), mRNA	1.9
5153	M32328	C.pipiens esterase B1 gene, complete cds	0.008
5154	U58744	Caenorhabditis elegans cosmid F55F1	0.43
5155	AF228498	Escherichia coli AgaR (agaR), KbaZ (kbaZ), AgaV (agaV), AgaW (agaW), AgaE (agaE), AgaF (agaF), AgaA (agaA), AgaS (agaS), KbaY (kbaY), AgaB (agaB), AgaC (agaC), AgaD (agaD), and AgaI (agaI) genes, complete cds	0.72

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
5156	L36898	Saccharomyces cerevisiae mitochondrion transfer RNA-Glu (tRNA-Glu) gene	0.69
5158	D88262	Pisum sativum PsCHS5 gene for chalcone synthase, complete cds	0.7
5159	AK018080	Mus musculus 11 days embryo head cDNA, RIKEN full-length enriched library, clone:6230403H02, full insert sequence	6.4
5160	X95275	P.falciparum complete gene map of plastid-like DNA (IR-A)	0.022
5161	D16417	Dictyostelium discoideum mRNA	0.009
5162	AF267204	Candidatus Carsonella ruddii natural-host Cacopsylla brunneipennis ATP synthase alpha subunit (atpA) gene, partial cds; ATP synthase gamma subunit (atpG) gene, complete cds; and ATP synthase beta subunit (atpD) gene, partial cds	0.026
5163	AF264650	Asterella tenella trnL gene, intron sequence; chloroplast gene for chloroplast product	6.4
5164	AF003143	Caenorhabditis elegans cosmid C53H9, complete sequence	0.23
5165	M19459	Plasmodium falciparum interspersed repetitive DNA and an open reading frame	0.008
5166	AK001362	Homo sapiens cDNA FLJ10500 fis, clone NT2RP2000369	0.23
5167	AF170023	Anopheles gambiae clone I38 genomic sequence	0.57
5168	AJ012333	Buchnera aphidicola plasmid pBTc2, trpE and trpG genes	0.006
5169	AF158077	Pisacha naga 16S ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	0.019
5170	U68721	Botryotinia fuckeliana endopolygalacturonase 5 (BcPGA5) gene, complete cds	0.21
5171	AK026372	Homo sapiens cDNA: FLJ22719 fis, clone HSI14307	e-116
5172	NM_031130	Rattus norvegicus nuclear receptor subfamily 2, group F, member 1 (Nr2f1), mRNA	3
5173	AY034470	Homo sapiens clone BGL2 mRNA sequence	0.064
5174	AF108841	Homo sapiens human endogenous retrovirus HERV-H10 pol protein (pol) gene, partial cds; env pseudogene and 3' LTR, complete sequence	0.009
5175	AJ251957	Ciona intestinalis mRNA for nuclear lamin (lamin L2 gene)	1.9
5176	XM_045437	Homo sapiens a disintegrin and metalloproteinase domain 33 (ADAM33), mRNA	0.71
5177	AF177983	Homo sapiens NAD+-dependent 15-hydroxyprostaglandin dehydrogenase (PGDH) gene, promoter, exons 1 and 2 and partial cds	9.9
5178	AF181632	Drosophila melanogaster BcDNA.GH05095 (BcDNA.GH05095) mRNA, complete cds	0.23
5179	AK018339	Mus musculus 10 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:6530414F19, full insert sequence	2.1
5180	XM_050838	Homo sapiens wingless-type MMTV integration site family, member 10A (WNT10A), mRNA	0.22
5181	AJ308588	Medicago truncatula partial mRNA for nodulin 25 (nod25 gene), clone 3	4.3

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
5182	AF229797	Homo sapiens cis-golgi SNARE (GOSR1) gene, exon 9 and partial cds	0
5185	Z68107	Caenorhabditis elegans cosmid F48C5, complete sequence	2.1
5186	AY026045	Mus musculus germ cell-specific unknown protein mRNA, complete cds	0.079
5187	AF309515	Staphylococcus aureus serine protease operon, complete sequence	1
5188	AF355103	Pleurotus ostreatus linear mitochondrial plasmid mlp2, partial sequence	0.069
5189	AF055079	Panulirus argus inositol 1,4,5-trisphosphate receptor (IP3R) mRNA, complete cds	5.2
5190	AC007184	Arabidopsis thaliana chromosome II section 163 of 255 of the complete sequence. Sequence from clones T11P11	6.1
5191	AB044348	Arabidopsis thaliana AtSUG1 mRNA, complete cds	1.2
5192	XM_003320	Homo sapiens hypothetical protein FLJ11155 (FLJ11155), mRNA	5.3
5193	AF148987	Legionella fallonii macrophage infectivity potentiator (mip) gene, partial cds	0.067
5194	X54200	Chicken mRNA for GARS-AIRS-GART	0.019
5195	AE005885	Caulobacter crescentus section 211 of 359 of the complete genome	0.62
5196	AF228498	Escherichia coli AgaR (agaR), KbaZ (kbaZ), AgaV (agaV), AgaW (agaW), AgaE (agaE), AgaF (agaF), AgaA (agaA), AgaS (agaS), KbaY (kbaY), AgaB (agaB), AgaC (agaC), AgaD (agaD), and AgaI (agaI) genes, complete cds	0.63
5197	U09859	Bos taurus enterokinase mRNA, complete cds	6.2
5198	AF057708	Populus balsamifera subsp. trichocarpa PTD protein (PTD) gene, complete cds	0.68
5199	AF238381	Homo sapiens PTOV1 (PTOV1) gene, complete cds	0.18
5200	AF119554	Plasmodium falciparum para-aminobenzoic acid synthetase gene, complete cds	0.13
5201	X82675	B.taurus BoLA-A11 gene (exon 6-8)	0.71
5202	AF303087	Tilapia mossambica glycoprotein alpha subunit mRNA, partial cds	0.64
5203	NM_006649	Homo sapiens serologically defined colon cancer antigen 16 (SDCCAG16), mRNA	1.7
5204	AF240597	Homo sapiens clone 7ptelc11t7 sequence	e-112
5205	BC006702	Mus musculus, RIKEN cDNA 4930529O08 gene, clone MGC:7935 IMAGE:3583936, mRNA, complete cds	6.3
5206	AF295769	Mus musculus SMAD1 gene, intron 1, partial sequence	0.007
5207	AF118099	Toxoplasma gondii PITSLRE-like protein kinase (tpk1) gene, partial cds	1.9
5208	AF143952	Homo sapiens PELOTA (PELOTA) gene, complete cds	0.44
5209	AF028710	Influenza A virus (A/HongKong/156/97(H5N1)) nucleoprotein mRNA, complete cds	1.7
5210	XM_017097	Homo sapiens active BCR-related gene (ABR), mRNA	0.7

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
5211	M33312	Rat hepatic steroid hydroxylase IIA1 (CYP2A1) gene, complete cds	0.54
5212	L05616	Dictyostelium purpureum (Dpp4) DNA sequence, repeat region	0.061
5213	AE001425	Plasmodium falciparum chromosome 2, section 62 of 73 of the complete sequence	0.001
5214	XM_006574	Homo sapiens similar to plakophilin 2 (H. sapiens) (LOC93271), mRNA	0.009
5215	XM_011195	Homo sapiens centromere protein E (312kD) (CENPE), mRNA	0.002
5216	AF181881	Helicobacter pylori TolB (tolB) and PAL (excC) genes, complete cds	0.65
5217	U33208	Human B-lymphocyte activation antigen (B7.1) gene, enhancer region and 5' UTR	0.0003
5218	AB052187	Macaca fascicularis brain cDNA, clone:QnpA-12170	0.7
5219	AY032741	Drosophila melanogaster H.M.S. Beagle transposon long terminal repeat, complete sequence; and heat shock protein Hsp70Ab gene, promoter and partial cds	0.63
5220	AJ276592	Pisum sativum lip1 mutant cop1 gene for constitutively photomorphogenic 1 protein, exons 1-19	5.7
5221	XM_045136	Homo sapiens similar to cadherin related 23 (H. sapiens) (LOC92444), mRNA	2E-52
5222	AK014534	Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched library, clone:4631424J17, full insert sequence	2E-55
5223	U67572	Methanococcus jannaschii section 114 of 150 of the complete genome	0.65
5224	AK026607	Homo sapiens cDNA: FLJ22954 fis, clone KAT09813, highly similar to AF010315 Homo sapiens Pig11 (PIG11) mRNA	0.21
5225	Y08580	F.rubripes hsp70-3 gene, 3'UTR	1.8
5226	AL359819	Human DNA sequence from clone RP11-109B17 on chromosome 1, complete sequence [Homo sapiens]	0.76
5227	AF118099	Toxoplasma gondii PITSLRE-like protein kinase (tpk1) gene, partial cds	1.9
5228	U48937	Homo sapiens amiloride-sensitive epithelial sodium channel gamma subunit gene, promoter region and exon 1	5.1
5229	AK017057	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4933434I20, full insert sequence	1.8
5230	AF044770	Phaeoprogne tapera microsatellite HrU6 allele 2 repeat region	4.6
5231	XM_012268	Homo sapiens amino acid transporter 2 (KIAA1382), mRNA	0.009
5232	BC008544	Mus musculus, Similar to hypothetical protein, clone MGC:7703 IMAGE:3497634, mRNA, complete cds	7E-22
5233	AB046353	Sapporo-like virus Yak2-2000-jp pol gene for RNA-dependent RNA polymerase, partial cds	6.2
5234	L07305	Histoplasma capsulatum (clone pMS3) H-ATPase gene, complete cds	0.65
5235	NM_012828	Rattus norvegicus Calcium channel subunit beta 3 (Cacnb3), mRNA	2
5236	AF277959	Helicobacter pylori strain 96-74 BabB (babB) gene, partial cds	0.71

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
5237	Z16681	H. sapiens (D8S266) DNA segment containing (CA) repeat; clone AFM151ye3; single read	0.003
5238	AB049452	Staphylococcus epidermidis composite transposon DNA, complete sequence	0.077
5239	X83673	X.laevis SSB1 gene	1.5
5240	XM_045182	Homo sapiens serine (or cysteine) proteinase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 2 (SERPINF2), mRNA	6.2
5241	AF263074	Cobitis paludica cytochrome b gene, partial cds; mitochondrial gene for mitochondrial product	0.15
5242	XM_029785	Homo sapiens Kell blood group (KEL), mRNA	2.1
5243	AE006148	Pasteurella multocida PM70 section 115 of 204 of the complete genome	5.5
5244	X81975	B.vulgaris mRNA for sucrose 6-phosphate synthase	1.3
5245	NM_033105	Homo sapiens beta cysteine string protein (LOC85479), mRNA	0.000006
5246	AC006164	Homo sapiens clone UWGC:y28gap from 6p21, complete sequence	0.47
5247	AJ279971	Canis familiaris microsatellite DNA, clone DTRcn.20	0.022
5248	AE005618	Escherichia coli O157:H7 EDL933 genome, contig 3 of 3, section 237 of 290	0.56
5249	AJ012338	Listeria monocytogenes NotI restriction site number two and flanking sequences	1.6
5251	D14027	Mouse DNA for TL antigen, complete cds	5
5252	Y12285	H.armigera mRNA for putative serine protease, clone SR106	0.009
5253	AF281912	Homo sapiens clone 16qtel_c89bt7 sequence	1E-68
5254	NC_001790	Ovine papillomavirus 2, complete genome	0.61
5255	XM_031110	Homo sapiens kallikrein 10 (KLK10), mRNA	0.041
5256	XM_042732	Homo sapiens guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3 (GNAI3), mRNA	0.42
5257	XM_033541	Homo sapiens KIAA0704 protein (ORP3), mRNA	0.022
5258	AL512432	Human DNA sequence from clone RP11-245H22 on chromosome 6 Contains GSSs, complete sequence [Homo sapiens]	0.0001
5259	S82508	Human adenovirus type 9 E4 protein (E4), Orf2, Orf3, Orf4, and Orf6 genes, complete cds; and Orf7 gene, partial cds	1.6
5260	XM_015579	Homo sapiens hypothetical protein FLJ13105 (FLJ13105), mRNA	1.2
5261	AF009177	Helicobacter pylori pfs protein homolog (pfs) and sigma 80 (rpoD) genes, complete cds	0.6
5262	AB015470	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K1B16	5.2
5264	L08970	Nematode choline acetyltransferase (cha-1) gene, exons 1-11 and complete cds	0.29
5265	D88193	Brassica rapa DNA for S-receptor kinase, complete cds	0.69
5266	XM_046294	Homo sapiens testis expressed sequence 15 (TEX15), mRNA	0.21
5267	XM_027078	Homo sapiens ATPase, Class V, type 10D (ATP10D), mRNA	0.22

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
5268	AK019309	Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched library, clone:2900009I19, full insert sequence	2E-13
5269	NM_016985	Mus musculus myotubularin related protein 1 (Mtmr1), mRNA	0.0004
5270	AK020049	Mus musculus 13 days embryo male testis cDNA, RIKEN full-length enriched library, clone:6030408K18, full insert sequence	1.8
5271	AF323989	Danio rerio transcriptional intermediary factor 2 mRNA, complete cds	6.3
5272	AF175275	Pisum sativum trans-cinnamic acid hydroxylase (CYP73A9) gene, CYP73A9-v1 allele, partial cds	0.073
5274	AF327749	Mus musculus smoothelin gene, promoter and partial sequence	6E-11
5275	AJ276633	Glomus mosseae partial TOR2 gene, exons 1-9	6
5276	AF110612	Boophilus microplus cytochrome b apoenzyme (Cytb) gene, partial cds; tRNA-Ser, tRNA-Leu, tRNA-Cys, and tRNA-Met genes, complete sequence; and NADH dehydrogenase subunit 2 (ND2) gene, partial cds, mitochondrial genes for mitochondrial products	0.072
5278	XM_043395	Homo sapiens fatty acid desaturase 2 (FADS2), mRNA	3E-36
5279	XM_046528	Homo sapiens zinc finger protein 133 (clone pHZ-13) (ZNF133), mRNA	2
5280	U20807	Bos taurus protein tyrosine phosphatase BA14 mRNA, complete cds	0.19
5281	XM_036368	Homo sapiens hypothetical gene supported by AK026802 (LOC91132), mRNA	0.026
5282	XM_007023	Homo sapiens G protein-coupled receptor kinase-interactor 2 (GIT2), mRNA	7E-44
5283	U86362	Saccharomyces cerevisiae MAL gene divergent promoter region, and hypothetical protein, complete cds	0.24
5284	Y11740	H.sapiens whn gene, exon 1a and 1b	0.22
5285	S78915	{Mu1 element insertion site, clone 11} [maize, Transposon, 300 nt]	0.002
5286	AF310896	Dictyostelium discoideum RacJ (racJ) gene, complete cds; LagC-like protein (lagC3) gene, partial cds; and unknown genes	0.23
5287	AJ012333	Buchnera aphidicola plasmid pBTc2, trpE and trpG genes	0.027
5288	AF282046	Homo sapiens clone 15qtel_c321bt7 sequence	4E-30
5289	L25128	Lycopersicon esculentum auxin-induced proteinase inhibitor (ARPI) gene, complete cds	0.51
5290	XM_049605	Homo sapiens KIAA1467 protein (KIAA1467), mRNA	2E-46
5291	AE002114	Ureaplasma urealyticum section 15 of 59 of the complete genome	0.054
5292	AF208678	Aedes aegypti clone p502, Pony-Aa-B6 MITE repeat region	3.9
5293	AK024656	Homo sapiens cDNA: FLJ21003 fis, clone CAE03685	5E-55
5294	NC_002355	Bombyx mori mitochondrion, complete genome	2.1
5295	AK023898	Homo sapiens cDNA FLJ13836 fis, clone THYRO1000734	0.008
5296	AE002342	Chlamydia muridarum, section 70 of 85 of the complete genome	1.9

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
5297	XM_032347	Homo sapiens region containing TLS-associated serine-arginine protein 1; TLS-associated serine-arginine protein 2; TLS-associated serine-arginine protein 2; TLS-associated serine-arginine protein 2; TLS-associated serine-arginine protein 1; TLS-associa>	0
5298	Z63116	H.sapiens CpG island DNA genomic Mse1 fragment, clone 78e4, reverse read cpg78e4.rt1a	0.24
5299	AE006833	Sulfolobus solfataricus section 192 of 272 of the complete genome	6.4
5300	XM_032811	Homo sapiens similar to ZINC FINGER PROTEIN 20 (ZINC FINGER PROTEIN KOX13) (DKFZP572P0920) (H. sapiens) (LOC90591), mRNA	0.21
5301	AF202552	Homo sapiens DNA methyltransferase (DNMT1) gene, exons 2, 3, and 4	0.23
5302	U92963	Pygathrix roxellana NADH dehydrogenase subunit 3 (ND3) gene, partial cds, tRNA-Arg gene, complete sequence, NADH dehydrogenase subunit 4L (ND4L) and NADH dehydrogenase subunit 4 (ND4) genes, complete cds, and tRNA-His, tRNA-Ser and tRNA-Leu genes, comp>	0.17
5303	Z99833	Euglena deses chloroplast psbC gene: complete group III twintron, complete internal mat1 gene, partial 5' and 3' psbC exons	4.7
5304	AB047962	Macaca fascicularis brain cDNA, clone:QnpA-13041	e-125
5305	AF159913	Euplotes crassus transposon Tec1 clone Tec1-2 orf 2 and orf 3 pseudogenes, complete sequence	0.5
5306	Y15435	Kluyveromyces lactis PDC1 gene, promoter region	0.087
5307	U67506	Methanococcus jannaschii section 48 of 150 of the complete genome	1.4
5308	U73943	Bacillus subtilis phosphofructokinase I (pfkI) gene, partial cds; and pyruvate kinase I gene, complete cds	2.2
5309	U72027	Bos taurus photoreceptor disk rim specific protein rom-1 (ROM1) mRNA, partial cds	0.06
5310	X16509	Rice alpha-amylase gene	2.1
5312	AB049900	Macaca fascicularis brain cDNA, clone:QnpA-19713	0.01
5313	Z24756	S.pombe rhp51 and rpa1 genes, complete CDS's	0.003
5314	XM_002989	Homo sapiens similar to hypothetical protein FLJ10546 (H. sapiens) (LOC93548), mRNA	5E-62
5316	AL358272	S.pombe chromosome I cosmid c458	0.61
5317	XM_044123	Homo sapiens cadherin 20, type 2 (CDH20), mRNA	4E-48
5318	AF038866	Bacteroides fragilis transposon Tn5520 transposase (bipH) and mobilization protein BmpH (bmpH) genes, complete cds	0.73
5319	AF332577	Homo sapiens prosomal P27K protein (PSMA6) gene, partial cds	2E-51
5320	X68650	O.cuniculus mRNA for ryanodine receptor	0.55
5321	XM_038450	Homo sapiens hypothetical protein FLJ20694 (FLJ20694), mRNA	0

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
5322	Z65960	H.sapiens CpG island DNA genomic Mse1 fragment, clone 69d2, reverse read cpg69d2.rt1b	1.7
5323	AF317661	Candida albicans 60S acidic ribosomal protein type P2-A (p2A) gene, complete cds	5.8
5324	AE001776	Thermotoga maritima section 88 of 136 of the complete genome	0.64
5325	NM_031987	Rattus norvegicus carnitine octanoyltransferase (COT), mRNA	0.62
5326	AB035500	Rana rugosa gene for FTZ-F1, exon 1	0.009
5327	U67490	Methanococcus jannaschii section 32 of 150 of the complete genome	0.2
5328	AB060000	Glycine max mRNA for hypothetical protein, complete cds, clone:SSC2	0.22
5329	U50840	Borrelia garinii 70 kbp plasmid D6 protein gene, complete cds	0.072
5330	U67535	Methanococcus jannaschii section 77 of 150 of the complete genome	2.1
5331	AK001125	Homo sapiens cDNA FLJ10263 fis, clone HEMBB1000991	3E-43
5333	AF029114	Ascogaster sp. 16S ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence	0.068
5334	AF320594	Homo sapiens PKD1P4 pseudogene, exons 2 through 15	6.3
5335	AY021494	Oryza sativa microsatellite MRG3819 containing (TA)X27, genomic sequence	0.024
5336	AF146651	Homo sapiens glyoxalase-I gene, complete cds	0.056
5337	AB054516	Globicephala melas DNA, SINE flanking sequence Mago22 locus	0.024
5338	AC001052	Homo sapiens (subclone 1_f6 from P1 H56) DNA sequence, complete sequence	0.003
5339	U00951	Human clone A9A2BR11 (CAC)n/(GTG)n repeat-containing mRNA	0.65
5340	AF298180	Caenorhabditis elegans tropomyosin isoform IV mRNA, complete cds	0.64
5341	XM_042336	Homo sapiens hypothetical gene supported by AK025398 (LOC92036), mRNA	2.1
5342	L44121	Homo sapiens (clone pHK2.1D) CMT1A gene, repeat unit	0.0003
5343	AE005556	Escherichia coli O157:H7 EDL933 genome, contig 3 of 3, section 175 of 290	0.23
5344	AB035185	Homo sapiens RHD gene, intron 9, complete sequence	0.63
5345	AC013455	Homo sapiens BAC clone CTD-2347O14 from 7p12-p14, complete sequence	0.23
5346	AJ234722	Hordeum vulgare genomic DNA fragment; clone MWG2031.rev	0.24
5347	X79699	H.sapiens ALU repeat, 230bp	0.0003
5348	XM_050246	Homo sapiens secretory protein SEC8; KIAA1699 protein (SEC8), mRNA	0
5349	AB063075	Macaca fascicularis brain cDNA clone:QtrA-11888, full insert sequence	2E-19
5350	Z56909	H.sapiens CpG island DNA genomic Mse1 fragment, clone 152h9, reverse read cpg152h9.rt1a	0.69
5351	L44121	Homo sapiens (clone pHK2.1D) CMT1A gene, repeat unit	0.069

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
5352	AE002722	Drosophila melanogaster genomic scaffold 142000013385665, complete sequence	1.5
5353	AF201021	Stachyarrhena sp. Jansen-Jacobs 4707 ribosomal protein S16 (rps16) gene, partial intron sequence; chloroplast gene for chloroplast product	0.072
5354	Y17506	Euplotes octocarinatus tRNA-Cys gene	0.024
5356	XM_040513	Homo sapiens hypothetical protein FLJ14454 (FLJ14454), mRNA	0.7
5357	AF287736	Mus musculus DREAM/calsenilin/KChIP3 gene, complete cds and exons 3, 4 and 5, alternatively spliced	2
5358	AF230807	Danio rerio PITP-less RdgB-like protein (plrdgB) mRNA, complete cds	6.1
5359	U67563	Methanococcus jannaschii section 105 of 150 of the complete genome	0.24
5360	AE000935	Methanobacterium thermoautotrophicum from bases 1655364 to 1666496 (section 141 of 148) of the complete genome	0.21
5361	NM_031819	Rattus norvegicus FAT tumor suppressor (Drosophila) homolog (Fat), mRNA	5.2
5362	XM_005889	Homo sapiens kinesin-like 1 (KNSL1), mRNA	3.6
5363	AF339829	Homo sapiens clone IMAGE:609847, mRNA sequence	0.022
5364	NM_007715	Mus musculus circadian locomoter output cycles kaput (Clock), mRNA	e-116
5365	XM_016117	Homo sapiens hypothetical protein DKFZp586F1122 similar to axotrophin (DKFZP586F1122), mRNA	0
5366	XM_005554	Homo sapiens regulator of differentiation (in S. pombe) 1 (ROD1), mRNA	6.3
5368	X76311	H.sapiens endothelial nitric oxidase synthase gene, exons 15 and 16	0.7
5369	XM_001738	Homo sapiens proteoglycan 4, (megakaryocyte stimulating factor, articular superficial zone protein) (PRG4), mRNA	0.63
5370	AE000935	Methanobacterium thermoautotrophicum from bases 1655364 to 1666496 (section 141 of 148) of the complete genome	0.23
5371	Y18011	Phaedon cochleariae mRNA for chitinase	0.021
5372	Z99768	Flaveria trinervia gdcsP pseudogene	4.5
5373	AF342852	Fusobacterium ulcerans strain NCTC 12112 16S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, complete sequence; and 23S ribosomal RNA gene, partial sequence	0.18
5374	BC003397	Homo sapiens, hypothetical protein FLJ20505, clone MGC:4960 IMAGE:3448518, mRNA, complete cds	1E-69
5375	AF385088	Homo sapiens NOD2 (NOD2) gene, NOD2-2722G>C allele, exon 8 and partial cds	0.58
5376	NC_000863	Papio cynocephalus provirus, complete genome	0.22
5377	AF121217	Rattus norvegicus pro-alpha-2(I) collagen (col1a2) mRNA, complete cds	5.5
5378	BC009075	Mus musculus, beta-1,3-N-acetylglucosaminyltransferase 1, clone MGC:6892 IMAGE:2654354, mRNA, complete cds	1.8

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
5379	XM_001341	Homo sapiens DKFZP547E1010 protein (DKFZP547E1010), mRNA	3E-15
5380	XM_046408	Homo sapiens KIAA1041 protein (KIAA1041), mRNA	0.52
5381	AK020701	Mus musculus 6 days neonate skin cDNA, RIKEN full-length enriched library, clone:A030009B12, full insert sequence	0.000001
5383	U32711	Haemophilus influenzae Rd section 26 of 163 of the complete genome	0.021
5384	XM_046598	Homo sapiens DKFZP434K156 protein (DKFZP434K156), mRNA	0.58
5385	L43551	Buchnera aphidicola anthranilate synthase large subunit (trpE) gene and anthranilate synthase small subunit (trpG) gene, complete cds	0.65
5386	XM_012233	Homo sapiens MDS023 protein (MDS023), mRNA	0.6
5387	AF139358	Homo sapiens BUB1 protein gene, exon 17	0.008
5388	AK020916	Mus musculus adult retina cDNA, RIKEN full-length enriched library, clone:A930031L14, full insert sequence	1.5
5389	AL390170	Homo sapiens mRNA; cDNA DKFZp547E184 (from clone DKFZp547E184)	1.8
5390	AK021659	Homo sapiens cDNA FLJ11597 fis, clone HEMBA1003856	0.21
5391	AK024200	Homo sapiens cDNA FLJ14138 fis, clone MAMMA1002765	0.00003
5392	AJ011727	Homo sapiens partial TOP2 beta gene, sequence G	0.00003
5393	AF018079	Homo sapiens leukemia inhibitory factor receptor (LIFG) gene, alternative promoter which is functional in non-placental tissues	6.2
5394	AB063085	Macaca fascicularis brain cDNA clone:QtrA-14876, full insert sequence	0.026
5395	AF154673	Homo sapiens olfactory receptor HPFH1OR (HPFH1OR) gene, complete cds	0.23
5396	AE007505	Streptococcus pneumoniae section 188 of 194 of the complete genome	6.6
5397	Z75199	S.cerevisiae chromosome XV reading frame ORF YOR291w	0.081
5398	AB042120	Bombyx mori Pao-like retrotransposon Kamikaze DNA, similar to polyprotein coding region	0.24
5399	AF379854	Cloning vector pVLH/hsp, complete sequence	0.0003
5400	XM_009648	Homo sapiens HSPC072 protein (HSPC072), mRNA	0.022
5401	AB056333	Macaca fascicularis brain cDNA, clone:QflA-13486	9E-14
5402	AK021824	Homo sapiens cDNA FLJ11762 fis, clone HEMBA1005670	3E-46
5403	AL513010	Human DNA sequence from clone RP11-30M17 on chromosome 6, complete sequence [Homo sapiens]	0.026
5404	AK023753	Homo sapiens cDNA FLJ13691 fis, clone PLACE2000100	0.077
5406	AK014452	Mus musculus 18 days pregnant adult female placenta and extra embryonic tissue cDNA, RIKEN full-length enriched library, clone:3830422K02, full insert sequence	0.17
5407	XM_003220	Homo sapiens polybromo 1 (PB1), mRNA	1E-35
5408	Z78918	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA19C6	1.5

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
5409	L13289	Mycoplasma pirum purine phosphorylase gene, 3' end, deoxyriboaldolase, thymidine phosphorylase, cytidine deaminase, phosphomannomutase genes, complete cds, and triose phosphate isomerase gene, 5' end	0.06
5410	AC024203	Caenorhabditis elegans cosmid Y72A2A, complete sequence	6.3
5411	AF373586	Homo sapiens translocation breakpoint MLLT1/MLL fusion gene, partial sequence	0.54
5412	Z46774	A.pleuropneumoniae tfbA gene for transferrin-binding protein (1949 bp)	0.025
5413	AF319044	Methanosarcina acetivorans strain C2A MtaF (mtaF) and MtaG (mtaG) genes, complete cds	0.44
5414	AE001933	Deinococcus radiodurans R1 section 70 of 229 of the complete chromosome 1	6.3
5415	M22734	Human platelet-derived growth factor A type receptor mRNA, complete cds	0.59
5416	AF264650	Asterella tenella trnL gene, intron sequence; chloroplast gene for chloroplast product	6.4
5417	AF378571	Sambucus nigra clone VBL85 thaumatin-like protein (TLPl) mRNA, complete cds	1.6
5418	U53183	Rattus norvegicus 250 kDa estrous-specific protein mRNA, partial cds	0.7
5419	AK026673	Homo sapiens cDNA: FLJ23020 fis, clone LNG00943	0.24
5420	XM_041367	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4 (15kD, B15) (NDUFB4), mRNA	2E-10
5421	AY039939	Arabidopsis thaliana unknown protein (F11F12.23) mRNA, complete cds	5.5
5422	AF250135	Mus musculus splicing factor Sc35 (Pr264) mRNA, partial cds, alternatively spliced	2.1
5423	M32328	C.pipiens esterase B1 gene, complete cds	0.003
5424	U95369	Bos taurus inward rectifier potassium channel BIK mRNA, complete cds	0.009
5425	AE002157	Ureaplasma urealyticum section 58 of 59 of the complete genome	5.7
5426	AF270633	Homo sapiens clone 5qtel_c25t3 sequence	9E-56
5427	Z28252	S.cerevisiae chromosome XI reading frame ORF YKR027w	0.18
5428	AE002601	Drosophila melanogaster genomic scaffold 142000013385253, complete sequence	0.2
5429	AJ403990	Hyla arborea microsatellite DNA, clone WHA1-61	3.8
5430	NM_019253	Rattus norvegicus protein tyrosine phosphatase, non-receptor type 5 (Ptpn5), mRNA	0.73
5431	AE006543	Streptococcus pyogenes M1 GAS strain SF370, section 72 of 167 of the complete genome	0.61
5432	AF146363	Homo sapiens islet cell autoantigen ICA69 (ICA1) gene, exon 1 and partial cds	0.073
5433	M96943	Human profilaggrin gene exons 1-3, 5' end	0.066
5434	AK025246	Homo sapiens cDNA: FLJ21593 fis, clone COL07050	0.18

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
5435	XM_027835	Homo sapiens general transcription factor IIIC, polypeptide 4 (90kD) (GTF3C4), mRNA	5.9
5437	AJ223441	Branchiostoma floridae Pax6 gene (AmphiPax6), clone J2	0.24
5438	AB048345	Equus caballus DNA, chromosome Xp21, microsatellite TKY39	0.73
5439	AB049844	Macaca fascicularis brain cDNA, clone:QnpA-18434	2.2
5440	XM_036740	Homo sapiens similar to nuclear pore membrane glycoprotein 210 (M. musculus) (LOC91181), mRNA	0.19
5441	AK019537	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4921505C17, full insert sequence	0.081
5442	AE003964	Xylella fastidiosa 9a5c, section 110 of 229 of the complete genome	6
5443	X95276	P.falciparum complete gene map of plastid-like DNA (IR-B)	0.008
5444	AF310264	Ovis aries leptin mRNA, partial 3' UTR	2.2
5445	XM_048688	Homo sapiens hypothetical protein FLJ10420 (FLJ10420), mRNA	2.2
5446	AC007133	Arabidopsis thaliana chromosome II section 209 of 255 of the complete sequence. Sequence from clones T6A23, F13I13	2
5447	AJ011727	Homo sapiens partial TOP2 beta gene, sequence G	0.00003
5448	AF214665	Homo sapiens cAMP responsive element modulator (CREM) gene, exon H	0.52
5449	AF269319	Staphylococcus epidermidis strain SR1 clone step.1002a02 genomic sequence	1.9
5450	AE001393	Plasmodium falciparum chromosome 2, section 30 of 73 of the complete sequence	0.72
5451	XM_002437	Homo sapiens cAMP-regulated guanine nucleotide exchange factor II (CAMP-GEFII), mRNA	7E-32
5452	AF298224	Homo sapiens RPCI-II 289E13 CD21 gene, partial cds	0.007
5453	AF254641	Homo sapiens oxytocin/vasopressin intergenic region	0.01
5454	XM_010303	Homo sapiens phosphate cytidylyltransferase 1, choline, beta isoform (PCYT1B), mRNA	2
5455	AK014447	Mus musculus 18 days pregnant adult female placenta and extra embryonic tissue cDNA, RIKEN full-length enriched library, clone:3830421F13, full insert sequence	0.22
5456	M21084	P.hybrida 5-enolpyruvylshikimate 3-phosphate synthase mRNA, complete cds	0.24
5457	XM_006648	Homo sapiens Microfibril-associated glycoprotein-2 (MAGP2), mRNA	1.4
5458	AF175434	Gallus gallus T cell receptor delta chain (TCRD) pseudogene, partial sequence	0.76
5459	AE000775	Aquifex aeolicus section 107 of 109 of the complete genome	0.0008
5460	XM_031261	Homo sapiens similar to KIAA0377 gene product (H. sapiens) (LOC90371), mRNA	1.6
5461	BC008389	Homo sapiens, Similar to hypothetical protein LOC57821, clone IMAGE:4076369, mRNA	0.24

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
5462	AF327739	Streptococcus thermophilus Peb1 (peb1), GlnQ (glnQ), response regulator Rr1 (rr1), Hpk2 (hpk2), YycJ-like protein (yycJ), and MurM (murM) genes, complete cds	0.63
5463	AY030939	HIV-1 isolate NC3940-1998 from USA pol polyprotein (pol) gene, partial cds	0.026
5464	XM_049237	Homo sapiens KIAA0841 protein (KIAA0841), mRNA	0.053
5465	AY017147	Paracheilognathus imberbis mitochondrial control region, partial sequence	0.25
5466	X81451	N.frontalis enolase gene, promotor region	0.009
5467	AF271036	Mus musculus clone rF12m odorant receptor gene, partial cds	2E-08
5468	J05637	Yeast (S.cerevisiae) 70 kDa heat shock protein (SSA4) gene, complete cds	0.22
5469	X75420	P.falciparum (FCR3) cpn60 gene	0.025
5470	AF213017	Acinetobacter calcoaceticus KHP18 partial pKLH2 plasmid including aberrant mercury resistance transposon TnPKLH2, truncated insertion sequence IS1011.D1, and determinants for CinH resolution system	1.9
5471	AC024806	Caenorhabditis elegans cosmid Y52E8A, complete sequence	0.026
5472	AF183178	Drosophila melanogaster filamin isoforms A and B (Filamin) gene, exons 1 and 2	0.043
5473	AF209925	Plasmodium falciparum STARP antigen (STARP) gene, complete cds	2.1
5474	AJ410864	Ectomycorrhizal isolate ECM 133 internal partial internal transcribed spacer 1 (ITS1), 5.8S ribosomal RNA gene, and partial internal transcribed spacer 2 (ITS2); isolate ECM 133	2
5475	NC_001889	Dictyostelium discoideum plasmid Ddp5, complete sequence	2.1
5476	AY009594	Boophilus microplus clone PNC 189 isolate Kilkivan2 microsatellite sequence	0.19
5477	U55723	Human ataxia-telangiectasia (ATM) gene, exon 25	0.69
5478	AF197229	Saguinus oedipus MHC class II antigen (Saoe-DRB1) gene, Saoe-DRB1*0303 allele, partial sequence	0.00004
5479	AE001290	Chlamydia trachomatis section 17 of 87 of the complete genome	0.2
5480	XM_016611	Homo sapiens similar to 8-oxoguanine DNA glycosylase (H. sapiens) (LOC93577), mRNA	0.069
5481	AJ224148	Saccharomyces cerevisiae mitochondrial Tyr-tRNA, Asn-tRNA and Met-tRNA genes	0.026
5482	AK022243	Homo sapiens cDNA FLJ12181 fis, clone MAMMA1000746	0.17
5483	U07354	Legionella pneumophila Philadelphia-1 intracellular multiplication region (icmV, icmW, icmX, lphB) genes, complete cds	0.33
5484	AE001366	Plasmodium falciparum chromosome 2, section 3 of 73 of the complete sequence	0.14
5485	AE001385	Plasmodium falciparum chromosome 2, section 22 of 73 of the complete sequence	1.5
5486	L81686	Homo sapiens (subclone 1_a3 from P1 H54) DNA sequence, complete sequence	0.62
5487	XM_017648	Homo sapiens leucine-rich repeat-containing 2 (LRRC2), mRNA	0.0006

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
5488	AE001372	Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence	1.9
5489	Z46943	H.sapiens lipoprotein lipase (LPL) gene (intron 9)	0.58
5490	U68246	Dictyostelium discoideum WacA (wacA) gene, complete cds	0.003
5491	AK009952	Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310057C01, full insert sequence	0.08
5492	AF190794	Arabidopsis thaliana subtilisin-type serine endopeptidase XSP1 mRNA, complete cds	1.9
5493	AF336796	Plasmodium falciparum dynamin-like protein (dyn) mRNA, complete cds	9.6
5494	AB035844	Coturnix coturnix japonica DNA, microsatellite GUJ0034 sequence	0.026
5495	AF127240	Nicotiana tabacum cultivar Xanthi arginine decarboxylase 1 (ADC1) gene, complete cds	0.42
5496	AY019789	Oryza sativa microsatellite MRG2114 containing (AT)X78, genomic sequence	0.003
5497	AF106953	Homo sapiens SOS1 (SOS1) gene, partial cds	0.43
5498	XM_007172	Homo sapiens mab-21 (C. elegans)-like 1 (MAB21L1), mRNA	0.014
5499	NM_006915	Homo sapiens retinitis pigmentosa 2 (X-linked recessive) (RP2), mRNA	0.003
5500	X95961	A.thaliana CER3-like gene	0.071
5501	XM_041428	Homo sapiens inositol 1,4,5-triphosphate receptor, type 1 (ITPR1), mRNA	0.18
5502	S50200	dopamine beta-hydroxylase [mice, Genomic/mRNA, 2274 nt]	2.1
5503	AE001178	Borrelia burgdorferi (section 64 of 70) of the complete genome	0.026
5504	Z74797	S.cerevisiae chromosome XV reading frame ORF YOL055c	2.1
5505	X15979	Plasmodium falciparum alpha-tubulin I gene	0.0008
5506	AF221538	Cryptosporidium felis heat shock protein 70 (HSP70) gene, partial cds	1.8
5507	AF083226	Caenorhabditis elegans nuclear receptor NHR-8 (nhr-8) mRNA, complete cds	0.69
5508	AF262729	Ornithorhynchus anatinus olfactory receptor pla32 gene, partial cds	6E-10
5509	AF263057	Cobitis arachthosensis ATP synthase 8 (ATP 8) and ATP synthase 6 (ATP 6) genes, complete cds; mitochondrial genes for mitochondrial products	2
5510	AF061244	Agrocybe aegerita B type DNA polymerase (Mtpol) gene, complete cds; tRNA-Asn gene, complete sequence; and unknown genes, mitochondrial genes for mitochondrial products	0.003
5511	X64612	H.sapiens dystrophin-gene (introns 13/42)	0.69
5512	AF269472	Staphylococcus epidermidis strain SR1 clone step.1005a12 genomic sequence	0.21
5514	AF297021	Homo sapiens GE36 gene, exon 8	0.12
5515	AL391744	S.pombe chromosome I cosmid c17D4	0.42
5516	XM_034682	Homo sapiens similar to general transcription factor II, i (H. sapiens) (LOC90875), mRNA	7E-22

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
5517	AF361817	Arabidopsis thaliana At1g06730/F4H5_22 gene, complete cds	0.69
5518	Z48243	A.thaliana PARP mRNA for PARP protein	0.69
5519	AL390169	Homo sapiens mRNA; cDNA DKFZp547D064 (from clone DKFZp547D064)	e-180
5520	NM_032141	Homo sapiens hypothetical protein DKFZp434K1421 (DKFZP434K1421), mRNA	e-169
5521	XM_037214	Homo sapiens laminin, alpha 5 (LAMA5), mRNA	0.62
5522	AL110675	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation	0.008
5523	AF124216	Dasyurus viverrinus/maculatus mixed DNA library microsatellite Q4.4.10 sequence	1.9
5524	AL583762	Human chromosome 14 DNA sequence Partial sequence from BAC R-1109N18_PCR1 of library RPCI-11 from chromosome 14 of Homo sapiens (Human), complete sequence	6E-42
5525	AC024758	Caenorhabditis elegans cosmid Y37E11AM, complete sequence	1.4
5526	AF260528	Homo sapiens MER receptor tyrosine kinase (MERTK) gene, exons 17 and 18	3E-35
5527	AF246997	Plasmodium falciparum malaria exported protein-1 (EXP-1) gene, complete cds	0.019
5528	XM_011810	Homo sapiens sigma receptor (SR31747 binding protein 1) (SR-BP1), mRNA	3.9
5529	XM_011100	Homo sapiens complement component 7 (C7), mRNA	5.9
5530	X64315	S.scrofa mRNA for Na/D-glucose cotransporter regulatory-subunit	0.0007
5531	XM_048945	Homo sapiens bromodomain adjacent to zinc finger domain, 2A (BAZ2A), mRNA	3.4
5532	XM_046506	Homo sapiens DKFZP566I1024 protein (DKFZP566I1024), mRNA	1E-10
5533	XM_002977	Homo sapiens ring finger protein 13 (RNF13), mRNA	2.8
5534	AJ300359	Homo sapiens partial RYR2 gene for ryanodine receptor 2, exon 20	1E-36
5535	BC008590	Homo sapiens, hypothetical protein FLJ21313, clone MGC:16820 IMAGE:4148772, mRNA, complete cds	e-154
5536	XM_050246	Homo sapiens secretory protein SEC8; KIAA1699 protein (SEC8), mRNA	0
5537	AL442094	Homo sapiens mRNA; cDNA DKFZp547E024 (from clone DKFZp547E024)	2
5538	AF225975	Tribolium castaneum Tc-tailless gene, upstream regulatory region and partial cds; tRNA-Tyr gene, complete sequence; and unknown gene	0.24
5539	AJ304934	Sidalcea malviflora x Sidalcea oregana 5.8S rRNA gene, internal transcribed spacer 1 (ITS1) and internal transcribed spacer 2 (ITS2)	2.1
5540	AE001528	Helicobacter pylori, strain J99 section 89 of 132 of the complete genome	0.009

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
5541	XM_046698	Homo sapiens putative DNA/chromatin binding motif (PLU-1), mRNA	2.5
5542	AF101309	Caenorhabditis elegans cosmid H24G06, complete sequence	2.1
5543	AL023839	Caenorhabditis elegans cosmid Y39A1C, complete sequence	1.4
5544	XM_017673	Homo sapiens hypothetical protein FLJ21934 (FLJ21934), mRNA	0
5545	U27317	Homo sapiens 11 beta-hydroxysteroid dehydrogenase 2 (HSD11B2) gene, complete cds	2E-92
5546	XM_045095	Homo sapiens KIAA1320 protein (KIAA1320), mRNA	0.6
5547	AF143066	Lepidopilum scabrisetum ribosomal protein system 4 (rps4) gene, partial cds	0.25
5548	BC010880	Homo sapiens, Similar to dihydropyrimidinase-like 2, clone MGC:1757 IMAGE:3542012, mRNA, complete cds	5.2
5549	L25128	Lycopersicon esculentum auxin-induced proteinase inhibitor (ARPI) gene, complete cds	0.55
5550	NM_030665	Homo sapiens retinoic acid induced 1 (RAI1), mRNA	9E-57
5552	AF127699	Erythroxylum argentinum chloroplast atpB-rbcL spacer	5.5
5553	U97192	Caenorhabditis elegans cosmid C01F4, complete sequence	2.7
5554	AF145302	Arabidopsis thaliana 14-3-3 protein GF14 epsilon (GRF10) gene, complete cds	8.9
5555	AF169241	Citrus sinensis capsanthin/capsorubin synthase (CCS) gene, complete cds	0.21
5556	AF153268	Tetrahymena thermophila dynein heavy chain (DYH6) gene, partial cds	1E-15
5557	L13966	Mouse delta/YY1/NF-E1/UCRBP transcription factor, exon 3	0.65
5558	AF172730	Streptococcus gordonii Sagp-like protein gene, complete cds; and Oct-like protein gene, partial cds	1.9
5559	AL591422	Human DNA sequence from clone RP11-124P3 on chromosome X, complete sequence [Homo sapiens]	1.8
5560	AF328433	Homo sapiens clone 2qtel_c275_24t3 sequence	4.8
5561	AF052640	Podarcis pityusensis cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds	2.3
5562	AF133000	Cicindela marutha 16S large subunit ribosomal RNA, mitochondrial gene for mitochondrial product, complete sequence	0.024
5563	AJ239057	Antirrhinum majus far gene for farinelli protein	5.1
5564	AL032651	Caenorhabditis elegans cosmid Y6D1A, complete sequence	2
5565	AJ278974	Homo sapiens partial SNAP-23 gene for synaptosome associated protein-23, exons 6-8	1.8
5566	M33379	Guinea pig lipoprotein lipase (gplpl) gene, exon 3-7	0.46
5567	AF303443	Rheum reticulatum tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast gene for chloroplast product	0.018
5568	L81826	Homo sapiens (subclone 1_g10 from P1 H39) DNA sequence, complete sequence	4E-16
5569	NM_005958	Homo sapiens melatonin receptor 1A (MTNR1A), mRNA	2
5570	AJ133356	Homo sapiens MSMB gene (partial), exons 2-3	0.66

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
5571	D86577	Human herpesvirus type 7 U38 gene, U39 gene for glycoprotein B and U40 gene for DNA polymerase, complete and partial cds	0.5
5572	AE006578	Streptococcus pyogenes M1 GAS strain SF370, section 107 of 167 of the complete genome	0.008
5573	U31170	Streptococcus mutans ATPase operon, complete sequence	0.041
5575	AF301004	Schistosoma mansoni thioredoxin peroxidase 3 (TPx3) gene, complete cds	0.23
5576	AF269295	Staphylococcus epidermidis strain SR1 clone step.1000d09 genomic sequence	2
5577	AF114934	Saccharomyces sp. S6U ATP synthase subunit 8 (ATP8) gene, mitochondrial gene encoding mitochondrial protein, complete cds	0.008
5578	AF261143	Homo sapiens chromosome 9 lung cancer-associated mRNA	2
5579	X95276	P.falciparum complete gene map of plastid-like DNA (IR-B)	0.00003
5580	NM_030844	Rattus norvegicus islet cell autoantigen 1, 69 kDa (Ica1), mRNA	0.63
5581	XM_001738	Homo sapiens proteoglycan 4, (megakaryocyte stimulating factor, articular superficial zone protein) (PRG4), mRNA	0.21
5582	AB060860	Macaca fascicularis brain cDNA clone:QtrA-11624, full insert sequence	5.1
5583	NC_001566	Apis mellifera ligustica mitochondrion, complete genome	0.15
5584	AF239566	Polycycnis ornata tRNA-Leu (trnL) gene, partial sequence; and trnL-F intergenic spacer region, complete sequence; chloroplast gene for chloroplast product	0.008
5585	X92893	C.roseus GGPP synthase gene	1.6
5586	XM_002601	Homo sapiens desmin (DES), mRNA	5.7
5587	NM_012745	Rattus norvegicus CD94 antigen (located within the rat natural killer gene complex) (Klrd1), mRNA	1.4
5588	AK022035	Homo sapiens cDNA FLJ11973 fis, clone HEMBB1001221	0.023
5589	AB020595	Plasmodium falciparum 1-CysPxn mRNA for 1-cys peroxidoxin, complete cds	1.4
5590	AL121778	Human DNA sequence from clone RP5-839B11 on chromosome 20. Contains the first coding exon of the gene for a novel protein with a Kunitz/Bovine pancreatic trypsin inhibitor domain and WAP-type (Whey Acidic Protein) 'four-disulfide core' domains and an e>	0.07
5591	AF222338	Rattus norvegicus voltage gated N-type calcium channel alpha1B gene, partial cds, alternatively spliced	5.8
5592	AF247193	Mus musculus endobrevin (Vamp8) gene, exon 1	0.18
5593	AC026061	Homo sapiens BAC clone RP11-223K9 from Y, complete sequence	e-163
5594	XM_030132	Homo sapiens ubiquitin specific protease 9, X chromosome (Drosophila fat facets related) (USP9X), mRNA	0.21
5595	AK015052	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930402K13, full insert sequence	0.22
5596	AK023333	Homo sapiens cDNA FLJ13271 fis, clone OVARC1001000	0.002
5597	AB058702	Homo sapiens mRNA for KIAA1799 protein, partial cds	0.007
5598	Z36800	H.sapiens (xs149) mRNA, 250bp	0.0003

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
5599	XM_044123	Homo sapiens cadherin 20, type 2 (CDH20), mRNA	4E-48
5600	XM_030272	Homo sapiens LOC88835 (LOC88835), mRNA	0.3
5601	AF030944	Brugia malayi microfilarial sheath protein SHP3a (Bmshp3a) and microfilarial sheath protein SHP3 precursor (Bmshp3) genes, complete cds	0.089
5602	U59882	Mus musculus MLH1 gene, exon 2	5.2
5603	AL591498	Human DNA sequence from clone RP11-113L12 on chromosome 13, complete sequence [Homo sapiens]	1.8
5604	AB002169	Rattus norvegicus RT1.P1 pseudogene for TL antigen	2
5605	AB009907	Luciola kuroiwae mitochondrial DNA for 16S rRNA, partial sequence	0.003
5606	AF336829	Rattus norvegicus NEDD8-activating enzyme mRNA, complete cds	0.58
5607	AJ310344	Scyliorhinus canicula partial mRNA for follicle stimulating hormone beta subunit (fsh beta gene)	0.22
5608	D00653	Homo sapiens gene for enteric smooth muscle gamma-actin, exon 8	2
5609	AF203972	Shuttle vector pBA complete sequence	2
5610	AK004804	Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200016B11, full insert sequence	5.3
5611	AF270009	Staphylococcus epidermidis strain SR1 clone step.1040e03 genomic sequence	0.037
5612	BC006448	Homo sapiens, clone IMAGE:3637085, mRNA	1.9
5613	AF298202	Dictyostelium discoideum putative transposon DDT-B, complete sequence	0.019
5614	AF272001	Ebola virus subtype Zaire strain Mayinga complete genome	0.002
5615	M86544	Cow prostaglandin F synthetase II (PGFSII) mRNA, complete cds	0.075
5616	XM_039684	Homo sapiens putative G-protein coupled receptor (SH120), mRNA	0.16
5617	AJ299399	Medicago truncatula mRNA for putative AUX1-like permease (lax3 gene)	6.4
5618	L39214	Ovis aries glucose transporter type 3 (GLUT-3) mRNA, complete cds	0.23
5619	XM_010126	Homo sapiens stromal antigen 2 (STAG2), mRNA	e-127
5620	Z23801	H. sapiens (D17S931) DNA segment containing (CA) repeat; clone AFM248tg5; single read	5E-19
5621	AF210842	Homo sapiens HARP (HARP) gene, exon 17 and complete cds	0.65
5622	AB047239	Staphylococcus aureus DNA, complete structure of cassette chromosome(SCC)-like element, strain:ATCC25923	0.25
5623	AB035193	Homo sapiens RHCE gene, intron 7, complete sequence	2.1
5624	XM_045035	Homo sapiens hypothetical protein FLJ21343 (FLJ21343), mRNA	2.4
5625	XM_052223	Homo sapiens DKFZP564G092 protein (DKFZP564G092), mRNA	0.67
5626	Z28007	S.cerevisiae chromosome XI reading frame ORF YKL007w	0.23

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
5627	M14080	Herpesvirus saimiri thymidylate synthase gene, complete cds	0.025
5628	AF067218	Caenorhabditis elegans cosmid K10E9	0.071
5629	AK017102	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4933437K13, full insert sequence	0.76
5630	XM_038524	Homo sapiens hypothetical protein FLJ23059 (FLJ23059), mRNA	e-118
5631	AB052773	Bombyx mori Bmdsx gene, exon 1, 2, 3, 4, female-specific splicing product complete cds	0.24
5632	AF233069	Galdieria sulphuraria maturase (matK) gene, partial cds; 50S ribosomal protein, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL), ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit (rbcS), acetohydroxy-acid synthase small>	0.55
5633	AK027218	Homo sapiens cDNA: FLJ23565 fis, clone LNG10846	0.24
5634	AF198462	HIV-1 isolate WM710-5 from Australia envelope glycoprotein (env) gene, partial cds	0.61
5636	AF213717	Euhadra quaesita haplotype Mana-B 16S ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	0.21
5637	AE002730	Drosophila melanogaster genomic scaffold 142000013385730, complete sequence	1.4
5638	AF110027	Candida albicans ATP-dependent transporter (YCF) gene, complete cds	0.069
5639	Z73978	Caenorhabditis elegans cosmid ZC302, complete sequence	0.21
5640	AF379877	Aclista sp. M226 16S ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	0.52
5641	AF364544	Larix lyallii microsatellite LLY13 sequence	2.2
5642	AF346905	Dermatophagoides farinae allergen Def f II precursor, mRNA, partial cds	0.008
5643	AE001426	Plasmodium falciparum chromosome 2, section 63 of 73 of the complete sequence	0.001
5644	XM_002850	Homo sapiens TU3A protein (TU3A), mRNA	0.078
5645	AB032899	Rattus norvegicus PIPK2 alpha mRNA for phosphatidylinositol 5-phosphate 4-kinase alpha, complete cds	4.4
5646	AK017370	Mus musculus 6 days neonate head cDNA, RIKEN full-length enriched library, clone:5430431E21, full insert sequence	6E-64
5647	XM_042126	Homo sapiens similar to GTP-RHO BINDING PROTEIN 1 (RHOPHILIN) (M. musculus) (LOC91997), mRNA	3E-47
5648	XM_048666	Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), mRNA	6.3
5649	AJ000259	Caenorhabditis elegans osm-6 mRNA	0.6
5650	AK017713	Mus musculus 8 days embryo cDNA, RIKEN full-length enriched library, clone:5730488L07, full insert sequence	0.087
5651	XM_010294	Homo sapiens arylsulfatase E (chondrodysplasia punctata 1) (ARSE), mRNA	8E-36
5652	XM_039942	Homo sapiens Meis (mouse) homolog 3 (MEIS3), mRNA	0.53

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
5653	AK019524	Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched library, clone:4833439O17, full insert sequence	1.7
5654	XM_045122	Homo sapiens KIAA1451 protein (KIAA1451), mRNA	5E-38
5656	AK009345	Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310014M14, full insert sequence	3E-35
5657	AF192496	Homo sapiens PDX-1 gene, 5' flanking region	1.5
5658	XM_052620	Homo sapiens KIAA0935 protein (KIAA0935), mRNA	0.0003
5659	XM_049514	Homo sapiens hypothetical protein FLJ13153 (FLJ13153), mRNA	5.6
5660	AJ400965	Proteus mirabilis ORF1 DNA, katA gene and menE gene, strain PR	6.5
5661	NM_031809	Rattus norvegicus cyclic nucleotide-gated channel beta subunit 1 (Cngb1), mRNA	0.63
5662	AF230741	Notothenia coriiceps alphaNCP1 (alphaNCPI), betaNCP1 (betaNCPI), alphaNCP2 (alphaNCPII), and betaNCP2 (betaNCPII) genes, complete cds	1.6
5663	AC079878	Homo sapiens BAC clone RP11-343P21 from 7, complete sequence	0.086
5664	XM_029904	Homo sapiens hypothetical gene supported by AK023961 (LOC90205), mRNA	1.9
5665	AY042792	Arabidopsis thaliana translin-like protein (At2g37020; T1J8.20) mRNA, complete cds	4.6
5666	AB018347	Homo sapiens mRNA for KIAA0804 protein, partial cds	0.068
5667	AY018017	Oryza sativa microsatellite MRG0342 containing (AG)X22, closest to marker G1185, genomic sequence	0.059
5668	AE005310	Escherichia coli O157:H7 EDL933 genome, contig 1 of 3, section 134 of 155	0.49
5669	XM_034498	Homo sapiens farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltranstransferase, geranyltranstransferase) (FDPS), mRNA	5.3
5670	AK027123	Homo sapiens cDNA: FLJ23470 fis, clone HSI11950	0.17
5671	NM_013696	Mus musculus thyrotropin releasing hormone receptor (Trhr), mRNA	0.23
5673	L23758	Bos taurus lysozyme 7A mRNA	0.8
5674	AY034963	Arabidopsis thaliana putative polypeptide chain release factor (F13K23.17) mRNA, complete cds	1.4
5675	XM_028009	Homo sapiens KIAA1563 protein (KIAA1563), mRNA	2E-71
5676	XM_046473	Homo sapiens Rho GDP dissociation inhibitor (GDI) alpha (ARHGDIA), mRNA	0.59
5677	NM_000148	Homo sapiens fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included) (FUT1), mRNA	0.0000001
5678	AF203477	Drosophila melanogaster Sticky ch1 (stich1) mRNA, partial cds	2.1
5679	AF269242	Plasmodium falciparum transmission-blocking target antigen Pfs230 (s230) gene, complete cds	0.23

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
5680	AE006954	Mycobacterium tuberculosis CDC1551, section 40 of 280 of the complete genome	2.1
5681	Z93386	Caenorhabditis elegans cosmid R11H6, complete sequence	0.023
5682	XM_012723	Homo sapiens chromosome 18 open reading frame 1 (C18orf1), mRNA	5.8
5683	AF171785	Drosophila melanogaster clone 69 mRNA sequence	0.73
5684	AF159105	Homo sapiens intestinal trefoil factor gene, 5' flanking region	0.02
5685	NM_011889	Mus musculus septin 3 (Sept3), mRNA	4.6
5688	NM_008541	Mus musculus MAD homolog 5 (Drosophila) (Madh5), mRNA	0.0000002
5689	XM_043345	Homo sapiens similar to inner centromere protein antigens (135kD, 155kD) (H. sapiens) (LOC92175), mRNA	0.075
5690	AL590109	Human DNA sequence from clone RP11-405J10 on chromosome 10, complete sequence [Homo sapiens]	0.003
5691	XM_051593	Homo sapiens hypothetical gene supported by AF055004 (LOC93477), mRNA	0.55
5692	U22345	Human chromosome 20q12 locus-specific repeat	0.008
5693	X63385	B.thuringiensis IS231F DNA	0.72
5694	AF288224	Brachyspira hyodysenteriae DNA Gyrase B subunit gene, complete cds	0.006
5695	AF279456	Lycopersicon hirsutum sesquiterpene synthase 2 (SSTLH2) mRNA, complete cds	0.06
5696	AF055992	Homo sapiens Duffy antigen/chemokine receptor (FY) gene, FY*X allele, complete cds	1.5
5697	AF167306	Homo sapiens synuclein alpha interacting protein (SNCAIP) gene, exon 10 and complete cds	0.99
5698	AJ277985	Nicotiana tabacum drepp1 gene, exons 1-4	0.22
5699	NM_030238	Mus musculus dynein, cytoplasmic, heavy chain 1 (Dnchc1), mRNA	4E-25
5701	X95343	N.tabacum mRNA for HSR201 protein	5.9
5702	AE002116	Ureaplasma urealyticum section 17 of 59 of the complete genome	0.68
5704	XM_029907	Homo sapiens anillin (Drosophila Scraps homolog), actin binding protein (ANLN), mRNA	0.72
5705	AJ304804	Homo sapiens ANKRD2 gene for skeletal muscle ankyrin repeat, exons 1-9	0.22
5706	AF371373	Cricetulus griseus hypothetical protein A1-3 mRNA, complete cds	0.72
5707	AE007446	Streptococcus pneumoniae section 129 of 194 of the complete genome	0.18
5708	L44121	Homo sapiens (clone pHK2.1D) CMT1A gene, repeat unit	6.6
5709	X90848	S.scrofa ppk98 gene	0.23
5710	AF397903	Pisum sativum AAA-metalloprotease FtsH (FTSH) mRNA, complete cds; nuclear gene for mitochondrial product	3.8
5711	XM_027365	Homo sapiens ADP-ribosylation factor-like 6 interacting protein (ARL6IP), mRNA	1E-30

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
5712	L01574	Homo sapiens P-selectin CD62 (GRMP) gene, 5' end and promoter region	0.00001
5713	AY023618	Oryza sativa microsatellite MRG5943 containing (TTA)X55, closest to marker RG908, genomic sequence	0.00009
5714	AE004377	Vibrio cholerae chromosome II, section 34 of 93 of the complete chromosome	0.58
5715	AL115472	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation	0.2
5716	XM_042855	Homo sapiens hypothetical gene supported by BC006369; BC008013 (LOC92105), mRNA	8E-23
5717	XM_015203	Homo sapiens region containing deleted in azoospermia 2; deleted in azoospermia (LOC90902), mRNA	1E-19
5718	AY019789	Oryza sativa microsatellite MRG2114 containing (AT)X78, genomic sequence	0.0000003
5719	AB010300	Garlic virus A genomic RNA, complete sequence	0.001
5720	AF171785	Drosophila melanogaster clone 69 mRNA sequence	0.73
5721	AF325188	Phaseolus coccineus suspensor-specific protein (C541-like) gene, complete cds	0.24
5722	XM_048692	Homo sapiens similar to hypothetical protein (H. sapiens) (LOC92998), mRNA	1E-16
5723	AE006878	Sulfolobus solfataricus section 237 of 272 of the complete genome	2.2
5724	AF038919	Dictyostelium discoideum PslA (pslA) gene, complete cds	0.026
5725	AF368257	Bacillus thuringiensis plasmid encoded Cry1Ba (cry1Ba) gene, complete cds	2.1
5726	AF148319	Homo sapiens imprinting center, AS-SRO region	1.8
5727	D49412	Human gene for interleukin 3 receptor alpha subunit, exon 11	0.23
5728	AJ012488	Mus musculus gene encoding serotonin receptor 5-HT2B, exons 1-3	0.25
5729	AL445224	Human DNA sequence from clone RP11-259P20 on chromosome 6, complete sequence [Homo sapiens]	2
5730	AK025021	Homo sapiens cDNA: FLJ21368 fis, clone COL03056, highly similar to AF158555 Homo sapiens glutaminase C mRNA	e-171
5731	D38252	Raphanus sativus dark-inducible and senescence-associated gene, exon 1 to 5	0.62
5732	XM_051880	Homo sapiens hypothetical gene supported by AK026792 (LOC93533), mRNA	5.6
5733	K00769	yeast (s.pombe) 5s rrna gene and flanks, clone pspr11	0.023
5734	AL031254	Caenorhabditis elegans cosmid 4R79, complete sequence	0.082
5735	AK001945	Homo sapiens cDNA FLJ11083 fis, clone PLACE1005232	2.1
5736	XM_012452	Homo sapiens ryanodine receptor 3 (RYR3), mRNA	0.008
5737	XM_046442	Homo sapiens hypothetical protein FLJ23045 (FLJ23045), mRNA	6E-33
5738	AF072513	Illex argentinus microsatellite Ia203	0.69
5739	XM_050747	Homo sapiens TC10-like Rho GTPase (TCL), mRNA	5E-20
5740	AC079757	Homo sapiens clone RP11-109N2, complete sequence	0.62

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
5741	XM_042128	Homo sapiens KIAA1691 protein (KIAA1691), mRNA	4.4
5742	NM_004342	Homo sapiens caldesmon 1 (CALD1), mRNA	4E-67
5743	BC002303	Mus musculus, clone IMAGE:3591199, mRNA	0.69
5744	AF273045	Homo sapiens CTCL tumor antigen se14-3 mRNA, complete cds	5E-28
5745	AE001798	Thermotoga maritima section 110 of 136 of the complete genome	0.71
5746	AF273225	Homo sapiens Fanconi anemia complementation group D2 protein (FANCD2) gene, exon 7	0.009
5747	AL589920	Human DNA sequence from clone RP11-117A20 on chromosome 6, complete sequence [Homo sapiens]	0.026
5748	AF101092	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 29	0.019
5749	S80521	dMax=basic helix-loop-helix/leucine zipper protein {alternatively spliced} [mice, WEHI 231 B-lymphoma cells, mRNA Partial, 752 nt]	0.003
5750	AF291825	Gorilla gorilla von Hippel-Lindau tumor suppressor (VHL) gene, promoter region	0.078
5751	AF120716	Kluyveromyces lactis cytochrome c oxidase subunit III (COX3) gene, mitochondrial gene encoding mitochondrial protein, complete cds	0.027
5752	NM_001423	Homo sapiens epithelial membrane protein 1 (EMP1), mRNA	5E-31
5753	AB045575	Danio rerio DNA, fkk-7c locus, insertion site of the medaka fish Tol2 element	1.7
5754	AL050120	Homo sapiens mRNA; cDNA DKFZp586D211 (from clone DKFZp586D211); partial cds	2
5755	AP000468	Homo sapiens genomic DNA, chromosome 21q22.3, clone:f60A9, complete sequence	0.009
5756	AK001649	Homo sapiens cDNA FLJ10787 fis, clone NT2RP4000481, weakly similar to ATP-DEPENDENT RNA HELICASE DOB1	0
5757	NM_031511	Rattus norvegicus Insulin-like growth factor II (somatomedin A) (Igf2), mRNA	0.025
5758	AL162036	Homo sapiens mRNA; cDNA DKFZp434B249 (from clone DKFZp434B249)	0.71
5760	AF317787	Rattus norvegicus Cd36 gene, promoter region	2.1
5761	XM_032021	Homo sapiens calreticulin (CALR), mRNA	6E-41
5762	XM_037847	Homo sapiens neurexophilin 3 (NXPH3), mRNA	4.2
5763	AF288818	Rattus norvegicus cytochrome P450 4F5 gene, complete cds	0.026
5764	AF269237	Cloning vector pTX-GFP, complete sequence	0.71
5765	AK021493	Homo sapiens cDNA FLJ11431 fis, clone HEMBA1001094	8E-76
5766	AF034077	Equus caballus alpha-1-antitrypsin (Spi2) gene, complete cds	0.0003
5767	XM_030851	Homo sapiens G protein-coupled receptor kinase-interactor 1 (GIT1), mRNA	5.4
5768	AY039919	Arabidopsis thaliana unknown protein (AT4g09340) mRNA, complete cds	4.8

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
5769	AK018211	Mus musculus adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:6330510M09, full insert sequence	6.4
5770	XM_006622	Homo sapiens PTPRF interacting protein, binding protein 1 (liprin beta 1) (PPFIBP1), mRNA	0.079
5771	U72335	Human platelet activating factor acetylhydrolase, brain isoform, 45 kDa subunit (LIS1) gene, exons 3 and 4	0.2
5772	XM_048810	Homo sapiens hypothetical protein FLJ22116 (FLJ22116), mRNA	0
5773	AF218257	Arabidopsis thaliana 12-oxo-phytodienoate reductase gene, complete cds	0.23
5774	AK014450	Mus musculus 18 days pregnant adult female placenta and extra embryonic tissue cDNA, RIKEN full-length enriched library, clone:3830422A13, full insert sequence	0.083
5775	AK005342	Mus musculus adult male cerebellum cDNA, RIKEN full-length enriched library, clone:1500032H18, full insert sequence	1.6
5776	M99412	Human interleukin-8 receptor (IL8RB) gene, complete cds	0.063
5777	NC_001619	Canine oral papillomavirus, complete genome	1.8
5778	NM_030238	Mus musculus dynein, cytoplasmic, heavy chain 1 (Dnchc1), mRNA	0
5779	AL031254	Caenorhabditis elegans cosmid 4R79, complete sequence	0.084
5781	Z74797	S.cerevisiae chromosome XV reading frame ORF YOL055c	2.2
5782	XM_040841	Homo sapiens cullin 5 (CUL5), mRNA	0.23
5783	U20807	Bos taurus protein tyrosine phosphatase BA14 mRNA, complete cds	0.22
5784	AE006648	Sulfolobus solfataricus section 7 of 272 of the complete genome	0.007
5785	AY018666	Oryza sativa microsatellite MRG0991 containing (AT)X19, closest to marker R1713, genomic sequence	0.008
5786	AK026299	Homo sapiens cDNA: FLJ22646 fis, clone HSI07178	0.23
5787	X91787	L.luteus mRNA for tRNA-glutamine synthetase	0.17
5788	XM_017281	Homo sapiens endosulfine alpha (ENSA), mRNA	1.9
5789	XM_017281	Homo sapiens endosulfine alpha (ENSA), mRNA	1.9
5790	AF229090	Homo sapiens myosin VI (MYO6) gene, exon 11	0.69
5791	AK001945	Homo sapiens cDNA FLJ11083 fis, clone PLACE1005232	2.1
5792	AF189157	Foot-and-mouth disease virus (strain O1) polyprotein gene, complete cds	6.5
5793	AK013313	Mus musculus 10, 11 days embryo cDNA, RIKEN full-length enriched library, clone:2810449G22, full insert sequence	6.1
5794	AJ005205	Homo sapiens 5HT3 gene for serotonin 3 receptor	0.69
5795	NM_019083	Homo sapiens hypothetical protein (FLJ10287), mRNA	6E-63
5796	AK021451	Homo sapiens cDNA FLJ11389 fis, clone HEMBA1000557	2E-54
5797	Z34885	T.pyriformis (CGL) gene for TCP1gamma protein	0.6
5798	AF288408	Rattus norvegicus transient receptor potential Trp4beta mRNA, complete cds	0.081
5799	XM_015806	Homo sapiens hypothetical protein FLJ22621 (FLJ22621), mRNA	0

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
5800	AF332918	Plasmodium falciparum Indochina III/CDC erythrocyte binding protein BAEBL (baebl) gene, complete cds	3.9
5801	XM_052063	Homo sapiens hypothetical protein DKFZp547A023 (DKFZp547A023), mRNA	0
5802	AB013796	Ceratopteris richardii mRNA for CRHB6, complete cds	0.024
5803	AF288408	Rattus norvegicus transient receptor potential Trp4beta mRNA, complete cds	0.082
5804	AF174213	Terebra subulata 16S ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	2.8
5805	AF308286	Homo sapiens serologically defined breast cancer antigen NY-BR-18 mRNA, partial cds	0.59
5806	AF030199	Mus musculus type 1 sigma receptor gene, complete cds	0.49
5807	M99412	Human interleukin-8 receptor (IL8RB) gene, complete cds	0.51
5808	Z34885	T.pyriformis (CGL) gene for TCP1gamma protein	0.58
5809	AF305539	Mus musculus B lymphocyte induced maturation protein 1 (Prdm1) gene, exon 8 and complete cds	1E-67
5810	AF288408	Rattus norvegicus transient receptor potential Trp4beta mRNA, complete cds	0.087
5811	AE001181	Borrelia burgdorferi (section 67 of 70) of the complete genome	0.001
5812	AY027894	Homo sapiens voltage-dependent calcium channel beta 2 subunit (CACNB2) gene, exon 2	0.00008
5813	XM_029481	Homo sapiens similar to KIAA0732 protein (H. sapiens) (LOC90154), mRNA	0.68
5814	AK021659	Homo sapiens cDNA FLJ11597 fis, clone HEMBA1003856	2.1
5815	U39721	Mycoplasma genitalium section 43 of 51 of the complete genome	0.19
5816	Z73267	S.cerevisiae chromosome XII reading frame ORF YLR095c	0.009
5817	XM_029453	Homo sapiens oculocerebrorenal syndrome of Lowe (OCRL), mRNA	0.26
5818	AF027728	Xenopus laevis kinesin-related protein (XCENP-E) mRNA, complete cds	0.052
5819	AE001407	Plasmodium falciparum chromosome 2, section 44 of 73 of the complete sequence	0.18
5820	AL157491	Homo sapiens mRNA; cDNA DKFZp434K1111 (from clone DKFZp434K1111)	9E-50
5821	XM_002437	Homo sapiens cAMP-regulated guanine nucleotide exchange factor II (CAMP-GEFII), mRNA	4E-37
5822	XM_050146	Homo sapiens KIAA0472 protein (KIAA0472), mRNA	8E-20
5823	AY032600	Carica papaya xyloglucan endo-transglycosylase mRNA, complete cds	0.19
5824	Z36061	S.cerevisiae chromosome II reading frame ORF YBR192w	3
5825	AK021459	Homo sapiens cDNA FLJ11397 fis, clone HEMBA1000622	0.046
5826	AF261017	Nicotiana tabacum putative chloroplast RNA helicase VDL (VDL) gene, exons 1 through 5 and complete CDS, alternatively spliced; nuclear gene for chloroplast products	2.1
5827	AJ277162	Beta vulgaris mRNA for putative Cdc2-related protein kinase CRK2	0.009

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
5828	AL390874	Human DNA sequence from clone RP11-238K16 on chromosome 9, complete sequence [Homo sapiens]	0.026
5829	S84872	Solanum tuberosum type A phytochrome (c-phyA) mRNA, complete cds	0.43
5830	AF271370	Homo sapiens interphotoreceptor matrix proteoglycan 200 (IMPG2) gene, exon 10	0.078
5831	XM_051183	Homo sapiens embryonic ectoderm development (EED), mRNA	0.00002
5832	BC006523	Homo sapiens, serum/glucocorticoid regulated kinase 2, clone IMAGE:2988475, mRNA	3E-34
5833	AF100658	Caenorhabditis elegans cosmid H08G01	0.44
5834	XM_003725	Homo sapiens putative ribonuclease III (RNASE3L), mRNA	0.008
5835	M58029	Amoeba proteus symbiotic bacterium 29kDa protein (s29x) gene, complete cds	0.71
5836	U46541	Staphylococcus aureus sarA gene, complete cds	0.003
5837	AJ225333	Acidianus ambivalens plasmid pDL10	0.17
5838	X15702	Fruitfly LA9 mRNA for DNA binding protein	0.077
5839	AL031590	Human DNA sequence from clone CTA-232D4 on chromosome 22q13.1 Contains a GSS, complete sequence [Homo sapiens]	0.16
5840	X07946	Yeast plasmid DNA coding for RNA polymerase subunit	0.082
5841	AL590324	Human DNA sequence from clone RP11-479D11 on chromosome 10, complete sequence [Homo sapiens]	0.082
5842	XM_004947	Homo sapiens paraoxonase 2 (PON2), mRNA	1.6
5843	AF262582	Dolichorhinotermes sp. 'Manaus' 16S mitochondrial ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product	0.067
5844	L81839	Homo sapiens (subclone 2_h3 from P1 H43) DNA sequence, complete sequence	0.00006
5845	U67550	Methanococcus jannaschii section 92 of 150 of the complete genome	0.087
5846	XM_044987	Homo sapiens hypothetical gene supported by U00951 (LOC92415), mRNA	6.1
5847	AE001420	Plasmodium falciparum chromosome 2, section 57 of 73 of the complete sequence	0.71
5848	AF315823	Stylonychia mytilus DNA-dependent RNA polymerase II largest subunit RPB1 (RPB1) gene, partial cds	0.51
5849	AB066207	Physcomitrella patens chloroplast genes for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, tRNA-Arg and acetyl-CoA carboxylase beta subunit, complete cds	0.65
5850	AF286898	Plasmodium chabaudi adami carbamoyl phosphate synthetase II gene, partial cds	0.002
5851	AL583888	Human DNA sequence from clone RP11-132E18 on chromosome 10, complete sequence [Homo sapiens]	0.028
5852	AB011811	Chromatium vinosum genes for light-harvesting and reaction center proteins, partial and complete cds	6.4
5853	AF153448	Zea mays nitrate reductase (NR1) gene, complete cds	0.067

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
5854	XM_012762	Homo sapiens hypothetical protein FLJ10891 (FLJ10891), mRNA	0
5855	AF248814	Maoricicada cassiope isolate TB-MI-004 tRNA-Asp gene, complete sequence; ATPase subunit 8 gene, complete cds; and ATPase subunit 6 gene, partial cds; mitochondrial genes for mitochondrial products	0.029
5856	D01021	Anthocidaris crassispina mRNA for dynein beta-heavy chain, complete cds	2E-22
5857	AE001401	Plasmodium falciparum chromosome 2, section 38 of 73 of the complete sequence	0.54
5858	BC007548	Homo sapiens, clone IMAGE:2959994, mRNA	1.9
5859	AB063065	Macaca fascicularis brain cDNA clone:QmoA-12555, full insert sequence	0.18
5860	NM_008538	Mus musculus myristoylated alanine rich protein kinase C substrate (Macs), mRNA	1.5
5861	XM_029266	Homo sapiens sarcoglycan, epsilon (SGCE), mRNA	0.66
5862	AE006685	Sulfolobus solfataricus section 44 of 272 of the complete genome	0.37
5863	BC008007	Homo sapiens, clone IMAGE:3510538, mRNA	6E-34
5864	AB024511	Nicotiana tabacum mRNA for TMV response-related gene product, complete cds	2.1
5865	U25027	Glycine max phosphatidylinositol-specific phospholipase C mRNA, complete cds	0.077
5866	U50715	Mus musculus alpha-galactosidase A gene, complete cds	0.024
5867	U64465	Stylophora pistillata L-type calcium channel alpha-1 subunit (STPCACHL) mRNA, complete cds	0.072
5868	XM_040043	Homo sapiens similar to hypothetical protein DKFZp566D1346 (H. sapiens) (LOC91690), mRNA	0.023
5869	U60135	Arabidopsis thaliana serine/threonine protein phosphatase 2A-3 catalytic subunit gene, complete cds	0.027
5870	AF275745	Lycopersicon esculentum plasma membrane H+-ATPase (LHA2) mRNA, complete cds	1.5
5871	Z29521	C.crispus Chloroplast gene encoding 16S rRNA, tRNA-Ile, tRNA-Ala, and 23S rRNA (partial)	0.003
5872	AJ132557	Oryctolagus cuniculus CYP19 gene, ovarian promoter region	0.24
5873	AF124524	Arabidopsis thaliana gamma-adaptin 1 gene, complete cds	0.24
5874	AK013131	Mus musculus 10, 11 days embryo cDNA, RIKEN full-length enriched library, clone:2810422B04, full insert sequence	0.72
5875	AB044413	Sus scrofa MMP-3 mRNA for matrix metalloproteinase-3, partial cds	0.23
5876	AF247039	Porcine adenovirus 3 171R (E1A), 202R (E1B-1), 474R (E1B-2), 288R (288R), 198R (pIX), 163R* (163R*), 162R (162R), 97R (97R) and 184R (184R) genes, complete cds; and IVa2 (IVa2) gene, partial cds	5.2
5877	AF060579	Gossypium barbadense clone pXP020 repetitive DNA sequence	0.055
5878	AE006499	Streptococcus pyogenes M1 GAS strain SF370, section 28 of 167 of the complete genome	2.1

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
5879	AL591498	Human DNA sequence from clone RP11-113L12 on chromosome 13, complete sequence [Homo sapiens]	0.003
5880	NM_017066	Rattus norvegicus Pleiotrophin (Heparine binding factor, Hbnf, in the mouse) (Ptn), mRNA	0.21
5881	XM_047505	Homo sapiens hypothetical gene supported by AK022483 (LOC92818), mRNA	0.7
5882	J00912	chicken brain tubulin, alpha chain mrna	0.24
5883	M15840	Human interleukin 1-beta (IL1B) gene, complete cds	0.08
5884	X92683	H.sapiens DNase I hypersensitive site (HSS-1)	2.1
5885	AL390767	Human DNA sequence from clone RP1-68P15 on chromosome 11p13-14.2 Contains GSSs and ESTs. Contains part of a novel gene, complete sequence [Homo sapiens]	1.8
5886	XM_012386	Homo sapiens KIAA0377 gene product (KIAA0377), mRNA	1E-48
5887	AL137466	Homo sapiens mRNA; cDNA DKFZp434H1322 (from clone DKFZp434H1322)	0.00001
5888	X62745	Z.mays OBF1 mRNA for ocs-element binding factor 1	0.23
5890	AB048902	Macaca fascicularis brain cDNA, clone:QnpA-17448	0.24
5892	AF221070	Ophiostoma piliferum strain CBS129.32 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence	0.003
5893	AE006530	Streptococcus pyogenes M1 GAS strain SF370, section 59 of 167 of the complete genome	0.22
5894	AB018698	Broad bean wilt virus 2 gene for precursor polyprotein, complete cds, isolate: IP	0.025
5895	U67537	Methanococcus jannaschii section 79 of 150 of the complete genome	0.026
5896	AJ000742	Homo Sapiens hisH1 gene, 5' UTR	0.008
5897	AF247039	Porcine adenovirus 3 171R (E1A), 202R (E1B-1), 474R (E1B-2), 288R (288R), 198R (pIX), 163R* (163R*), 162R (162R), 97R (97R) and 184R (184R) genes, complete cds; and IVa2 (IVa2) gene, partial cds	5.2
5898	AJ290290	Asphodeline lutea chloroplast trnL-trnF intergenic spacer	0.23
5899	XM_042440	Homo sapiens UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 3 (B4GALT3), mRNA	6.4
5900	U78090	Rattus norvegicus potassium channel regulator 1 mRNA, complete cds	2.1
5901	NM_017053	Rattus norvegicus Neuromedin K receptor (Neurokinin B/Tachikin 3) (Tac3r), mRNA	1.9
5902	AF208658	Tapesia yallundae eburicol 14 alpha-demethylase (CYP51) gene, complete cds	6.2
5903	AF281786	HIV-1 isolate DK-g3 from USA gag polyprotein (gag) gene, partial cds	0.63
5904	AJ011019	Capra hircus csn2 gene, exons 1 to 9, allele 0(null)	2
5905	AJ311054	Chironomus pallidivittatus 4L ORF for putative recombinase subtelocentric clone, Cp5.5	0.023

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
5906	Y17466	Fugu rubripes SIAT3C gene, last three exons	0.65
5907	AK022127	Homo sapiens cDNA FLJ12065 fis, clone HEMBB1002249	0.001
5908	X79100	C.vicina (B11) mRNA for arylphorin receptor	0.6
5909	AK023079	Homo sapiens cDNA FLJ13017 fis, clone NT2RP3000628	0.23
5910	AK014448	Mus musculus 18 days pregnant adult female placenta and extra embryonic tissue cDNA, RIKEN full-length enriched library, clone:3830421J05, full insert sequence	1.4
5911	AK020293	Mus musculus adult male cecum cDNA, RIKEN full-length enriched library, clone:9130404H11, full insert sequence	0.23
5912	AE006285	Lactococcus lactis subsp. lactis IL1403 section 47 of 218 of the complete genome	0.25
5913	U41292	Human prolargin (PRELP) gene, 5' flanking sequence and exon 1	0.001
5914	AL109707	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 295344	0.00004
5915	NM_024154	Rattus norvegicus proton gated cation channel ASIC1 (Accn2), mRNA	6.2
5916	U79732	Plasmodium berghei extrachromosomal plastid PB-2, tRNA-Pro, tRNA-Glu, tRNA-Lys, tRNA-Asp, tRNA-Ser, tRNA-Tyr, tRNA-Met, tRNA-Leu, tRNA-Cys, and tRNA-His genes, complete sequence, rps4 gene, complete cds, tRNA-Thr gene, complete sequence, and large subu>	0.023
5917	AF098715	Coniglobus mercatorius 16S ribosomal RNA gene, mitochondrial gene encoding mitochondrial product, partial sequence	0.095
5918	AF095904	Toxoplasma gondii ycf24 protein (ycf24) gene, partial cds; DNA dependent RNA polymerase beta subunit (rpoB) gene, complete cds; and DNA dependent RNA polymerase beta' subunit (rpoC1) gene, plastid genes encoding plastid proteins, partial cds	0.026
5919	XM_027416	Homo sapiens mesothelin (MSLN), mRNA	0.7
5920	BC004772	Mus musculus, Similar to inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta, clone IMAGE:3256890, mRNA	1.6
5921	AK000935	Homo sapiens cDNA FLJ10073 fis, clone HEMBA1001731	0.18
5922	BC009942	Homo sapiens, clone MGC:12595 IMAGE:4303422, mRNA, complete cds	0.001
5923	J05008	Homo sapiens endothelin-1 (EDN1) gene, complete cds	0.5
5924	AE002174	Chlamydophila pneumoniae AR39, section 10 of 94 of the complete genome	0.69
5925	AJ223616	Caehorhabditis elegans mRNA for calcium ATPase	0.7
5926	AF310894	Dictyostelium discoideum prespore-specific protein (pspC) gene, partial cds; RacH (racH) gene, complete cds; and BOP (bopA) gene, partial cds	0.027
5927	AE003910	Xylella fastidiosa 9a5c, section 56 of 229 of the complete genome	0.73
5928	AF335424	Homo sapiens sperm protein Sp17-2 pseudogene, complete sequence	1.8

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
5929	XM_016924	Homo sapiens hypothetical protein MGC4054 (MGC4054), mRNA	4.3
5930	U62057	Mycoplasma capricolum NADH oxidase (naox) gene, partial cds, and lipoate-protein ligase (lpla), pyruvate dehydrogenase EI alpha subunit (odpa), pyruvate dehydrogenase EI beta subunit (odpb), pyruvate dehydrogenase EII (odp2), dihydrolipoamide dehydroge>	0.72
5931	AF202552	Homo sapiens DNA methyltransferase (DNMT1) gene, exons 2, 3, and 4	2.2
5932	AF010604	Homo sapiens SMAD5 (Smad5) gene, exon 3	0.0001
5933	AC084157	Caenorhabditis elegans cosmid Y46E12BR, complete sequence	0.71
5934	XM_027907	Homo sapiens hypothetical protein DKFZp564D172 (DKFZP564D172), mRNA	0.18
5935	AF360191	Arabidopsis thaliana unknown protein (T9C5.150/AT3g49560) mRNA, complete cds	6.3
5938	AF282728	Culex pipiens Twin-Cp5 SINE retroposon, genomic sequence and v-SNARE-like gene, partial sequence	0.066
5939	M81702	Candida boidinii methanol oxidase (AOD1) gene, complete cds	0.008
5940	AF057740	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exon 24 and complete cds	0.21
5941	XM_031463	Homo sapiens exonuclease NEF-sp (LOC81691), mRNA	0.072
5942	AB022048	Mus musculus gene for prolyl oligopeptidase, exon 3, 4, 5, 6	2.1
5943	Z48165	R.violacea chloroplast genes for alpha and beta subunit of phycocyanin	2.1
5944	AF181251	Rattus norvegicus lung Kruppel-like factor (Lklf) gene, complete cds	5.9
5945	AP001057	Homo sapiens genomic DNA, chromosome 21, clone:D40G11, MX1-D21S171 region, complete sequence	0.00001
5946	AK016374	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930589L23, full insert sequence	5.9
5947	M27697	Pig urate oxidase mRNA, complete cds	2.1
5948	XM_032603	Homo sapiens similar to DESTRIN (ACTIN DEPOLYMERIZING FACTOR) (ADF) (H. sapiens) (LOC90563), mRNA	0.69
5949	U39688	Mycoplasma genitalium section 10 of 51 of the complete genome	0.077
5950	AF320250	Lactobacillus delbrueckii YmdA (ymdA) gene, partial cds; and putative undecaprenyl-phosphate N-acetyl-glucosaminyl transferase (rgpG), YvyE (yvyE), putative ComF1 protein (comF1), putative ComF3 protein (comF3), YvyD (yvyD), putative preprotein translo>	0.69
5951	Y09852	H.sapiens FGFR3 gene, partial	2E-10
5952	Z79103	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA22F11	0.00002
5953	AP000321	Homo sapiens genomic DNA, chromosome 21q22.1, D21S226-AML region, clone:Q82F5, complete sequence	0.00004
5954	AK025042	Homo sapiens cDNA: FLJ21389 fis, clone COL03455	2E-66

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
5955	U14576	Dictyostelium discoideum filopodin (talA) gene, complete cds	0.21
5956	AE001405	Plasmodium falciparum chromosome 2, section 42 of 73 of the complete sequence	0.052
5957	M64861	D.discoideum TFIID mRNA, complete cds	0.002
5958	AJ245435	Plasmodium falciparum gc-alpha gene for guanylyl cyclase alpha	0.0001
5959	XM_031443	Homo sapiens phosphodiesterase 8A (PDE8A), mRNA	8E-13
5960	AC079875	Homo sapiens clone CTD-2333B13, complete sequence	0.00003
5961	AF275272	Schizophyllum commune unknown gene; mitochondrial gene for mitochondrial product	0.44
5962	Z60119	H.sapiens CpG island DNA genomic Mse1 fragment, clone 18e1, reverse read cpg18e1.rt1b	0.008
5963	AF100654	Caenorhabditis elegans cosmid C24E9	0.026
5964	AE001399	Plasmodium falciparum chromosome 2, section 36 of 73 of the complete sequence	0.001
5965	U89019	Hepatitis C virus polyprotein gene, complete cds	0.2
5966	XM_052512	Homo sapiens ARP3 (actin-related protein 3, yeast) homolog (ACTR3), mRNA	2E-32
5967	U17634	Human chromosome 21, Down syndrome critical region transcript, SP6 end of clone 3-3-f8	0.7
5968	AF197477	Homo sapiens TRBP pseudogene, partial sequence	0.22
5969	U78599	Streptococcus mutans putative D,D-carboxypeptidase and putative N-acetyl-muramidase genes, partial cds	2.1
5970	AP001414	Homo sapiens genomic DNA, chromosome 21q22.2, clone:D30, LB7T-ERG region, complete sequence	2.1
5971	AJ277067	Homo sapiens partial SSH3BP1/e3B1 gene for spectrin SH3 binding protein, exon 3-5	5.7
5972	X13294	Human mRNA for myb-related gene A-myb 5'-region	6E-74
5973	NC_001796	Human parainfluenza virus 3, complete genome	0.053
5974	AJ222787	Hordeum vulgare mRNA for alpha-keto acid dehydrogenase-like protein, clone RG136	0.073
5975	AF284034	Melanogrammus aeglefinus vitellogenin B (VtgB) mRNA, complete cds	2.1
5976	AF127565	Arabidopsis thaliana ubiquitin-protein ligase 2 (UPL2) gene, complete cds	4.3
5977	AP001419	Homo sapiens genomic DNA, chromosome 21q22.2, clone:PAC24K9, LB7T-ERG region, complete sequence	0.0002
5978	AL590384	Human DNA sequence from clone RP11-349A16 on chromosome Xq22.3-24, complete sequence [Homo sapiens]	0.02
5979	AB014460	Homo sapiens TSC2, NTHL1/NTH1 and SLC9A3R2/E3KARP genes, partial and complete cds	0.69
5980	XM_018334	Homo sapiens hypothetical protein FLJ22418 (FLJ22418), mRNA	0.026
5981	AF229850	Arabidopsis thaliana ferritin (Fer1) gene, complete cds	0.69
5982	AK017445	Mus musculus 10 days neonate head cDNA, RIKEN full-length enriched library, clone:5530402H04, full insert sequence	2.1
5983	AF197159	Mus musculus cubilin mRNA, partial cds	0.7

Table 3A Nearest Neighbor (BlastN vs. Genbank)

SEQ ID NO	ACCESSN	DESCRIP	P VALUE
5984	XM_029346	Homo sapiens hypothetical gene supported by U79302; AK026607 (LOC90138), mRNA	0.026
5985	AK021517	Homo sapiens cDNA FLJ11455 fis, clone HEMBA1001497	0.05
5986	Z74823	S.cerevisiae chromosome XV reading frame ORF YOL081w	0.23
5987	XM_003091	Homo sapiens KIAA0001 gene product; putative G-protein-coupled receptor; G protein coupled receptor for UDP-glucose (KIAA0001), mRNA	1.9
5988	XM_039450	Homo sapiens similar to NONHISTONE CHROMOSOMAL PROTEIN HMG-14 (H. sapiens) (LOC91606), mRNA	4E-47
5989	XM_045103	Homo sapiens G protein coupled receptor interacting protein, complement-c1q tumor necrosis factor-related (ZSIG37), mRNA	0.23
5990	AK026086	Homo sapiens cDNA: FLJ22433 fis, clone HRC09172	0.078
5991	Z22800	H.sapiens microsatellite repeat	3E-45
5992	AF165136	Mycoplasma mycoides mycoides LC hypothetical surface located membrane protein and lipoprotein B precursor (lppB) genes, partial cds	0.23
5993	AF269465	Staphylococcus epidermidis strain SR1 clone step.1004h05 genomic sequence	0.23
5994	XM_049474	Homo sapiens KIAA1538 protein (KIAA1538), mRNA	0.23
5995	AC001478	Homo sapiens (subclone 1_h7 from BAC H112) DNA sequence, complete sequence	0.63
5996	AF380163	Influenza A virus (A/Goose/Guangdong/3/97(H5N1)) segment 3 polymerase (PA) gene, complete cds	0.077
5997	Z74263	S.cerevisiae chromosome IV reading frame ORF YDL215c	0.36
5998	AF282059	Homo sapiens clone 2qtel_edc17fR sequence	7.9
5999	AF233898	Escherichia coli strain KI1218 BfpA (bfpA) gene, partial cds	0.073
6000	M92086	Wasp venom protein mRNA sequence	1.7
6001	XM_006601	Homo sapiens hypothetical protein FLJ10659 (FLJ10659), mRNA	0
6002	D14074	Bovine mRNA for cyclophilin, complete cds	0.23
6003	AC079391	Homo sapiens clone CTD-2243M11, complete sequence	4
6004	AE006055	Pasteurella multocida PM70 section 22 of 204 of the complete genome	0.077
6005	Y09000	R.norvegicus mRNA for dendrin	0.18
6006	AK006991	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:1700084F23, full insert sequence	2.1
6007	AF319636	Pelargonium peltatum cultivar Guenievre microsatellite Pp3a sequence	0.001
6008	D17668	Clostridium septicum gene for alpha-toxin, complete cds	0.077
6009	AK025193	Homo sapiens cDNA: FLJ21540 fis, clone COL06156	0.025
6010	X17191	E.gracilis chloroplast RNA polymerase rpoB-rpoC1-rpoC2 operon	0.22

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
4	12721131	gi|12721131|gb|AAK02908.1| (AE006121) unknown [Pasteurella multocida]	0.14
6	1504016	gi|1504016|dbj|BAA13207.1| (D86971) no similarities to reported gene products [Homo sapiens]	0.0003
7	12838708	gi|12838708|dbj|BAB24303.1| (AK005889) putative [Mus musculus]	5E-74
8	12854246	gi|12854246|dbj|BAB29972.1| (AK015778) putative [Mus musculus]	2.2
9	14715574	gi|14715574|dbj|BAB62041.1| (AB065434) PRPK mutant1 [Homo sapiens]	4E-80
10	6678964	gi|6678964|ref|NP_032671.1| murinoglobulin 1 [Mus musculus] sp|P28665|A2M1_MOUSE MURINOGLOBULIN 1 PRECURSOR (MUG1) gb|AAA73048.1| (M65736) [Mouse murinoglobulin mRNA, complete cds.], gene product [Mus musculus]	4.2
14	11351090	gi|11351090|pir||E82999 probable beta-ketoacyl synthase PA5174 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG08559.1|AE004930_5 (AE004930) probable beta-ketoacyl synthase [Pseudomonas aeruginosa]	9.1
15	9506761	gi|9506761|ref|NP_062298.1| glucosamine-phosphate N-acetyltransferase; glucosamine-6-phosphate acetyltransferase [Mus musculus] emb|CAA04463.1| (AJ001006) EMeg32 protein [Mus musculus] dbj|BAB22120.1| (AK002466) putative [Mus musculus] dbj|BAB25161.1| (AK007647) putative [Mus musculus] dbj|BAB25212.1| (AK007722) putative [Mus musculus] dbj|BAB25240.1| (AK007764) putative [Mus musculus] dbj|BAB25749.1| (AK008566) putative [Mus musculus] dbj|BAB27395.1| (AK011098) putative [Mus musculus] dbj|BAB31241.1| (AK018499) putative [Mus musculus]	1E-84
20	9369403	gi|9369403|gb|AAF87151.1|AC002423_16 (AC002423) T23E23.19 [Arabidopsis thaliana]	7.4
24	12862430	gi|12862430|dbj|BAB32466.1| (AB047280) Gag-like protein [Tricholoma matsutake]	2.6

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
25	7434102	gi|7434102|pir||H71620 aspartate transaminase (EC 2.6.1.1) PFB0200c [similarity] - malaria parasite (Plasmodium falciparum) gb|AAC71829.1| (AE001380) aspartate aminotransferase [Plasmodium falciparum]	0.73
26	14721245	gi|14721245|ref|XP_044013.1| kinesin-like protein 2 [Homo sapiens]	8E-91
27	9506713	gi|9506713|ref|NP_061856.1| nucleolar protein family A, member 1; H/ACA small nucleolar RNPs protein 1 [Homo sapiens] ref|XP_003601.1| nucleolar protein family A, member 1 (H/ACA small nucleolar RNPs) [Homo sapiens] ref|XP_039016.1| nucleolar protein family A, member 1 (H/ACA small nucleolar RNPs) [Homo sapiens] ref|NP_127460.1| nucleolar protein family A, member 1; H/ACA small nucleolar RNPs protein 1 [Homo sapiens] emb|CAB76563.1| (AJ276003) GAR1 protein [Homo sapiens] gb|AAH03413.1|AAH03413 (BC003413) nucleolar protein family A, member 1 (H/ACA small nucleolar RNPs) [Homo sapiens]	4
28	14150082	gi|14150082|ref|NP_115691.1| hypothetical protein MGC4399 [Homo sapiens] gb|AAH04991.1|AAH04991 (BC004991) Similar to RIKEN cDNA 5730438N18 gene [Homo sapiens]	0.001
29	12861366	gi|12861366|dbj|BAB32182.1| (AK020701) putative [Mus musculus]	5E-42
32	14739173	gi|14739173|ref|XP_037531.1| 59395 [Homo sapiens]	3E-23
36	7513572	gi|7513572|pir||S72438 phosphatidylserine decarboxylase (EC 4.1.1.65) precursor, mitochondrial - Chinese hamster	e-112
37	7488381	gi|7488381|pir||T08408 transcription factor homolog F18B3.150 - Arabidopsis thaliana emb|CAB42916.1| (AL049862) transcription factor-like protein [Arabidopsis thaliana]	8.1
38	12849752	gi|12849752|dbj|BAB28466.1| (AK012782) putative [Mus musculus]	5E-89
39	14715574	gi|14715574|dbj|BAB62041.1| (AB065434) PRPK mutant1 [Homo sapiens]	1E-88
40	12832845	gi|12832845|dbj|BAB22281.1| (AK002682) putative [Mus musculus]	4E-51

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
43	12832845	gi|12832845|dbj|BAB22281.1| (AK002682) putative [Mus musculus]	6E-45
47	11558040	gi|11558040|emb|CAC17800.1| (AJ245890) hypothetical protein [Polymyxa betae]	7.6
48	8052306	gi|8052306|emb|CAB92239.1| (AJ242721) AIP37 protein [Mus musculus]	1.3
49	13812380	gi|13812380|ref|NP_113498.1| N-myristoyltransferase [Guillardia theta] emb|CAC27067.1| (AJ010592) N-myristoyltransferase [Guillardia theta]	7
51	8885549	gi|8885549|dbj|BAA97479.1| (AB025604) telomere repeat-binding protein [Arabidopsis thaliana]	1.5
52	14727244	gi|14727244|ref|XP_035596.1| hypothetical protein AF140225 [Homo sapiens] ref|XP_035597.1| 49482 [Homo sapiens] gb|AAH07829.1|AAH07829 (BC007829) Similar to hypothetical protein AF140225 [Homo sapiens]	6E-58
57	14737646	gi|14737646|ref|XP_038048.1| similar to APICAL ENDOSOMAL GLYCOPROTEIN PRECURSOR (R. norvegicus) [Homo sapiens]	0.003
58	13811699	gi|13811699|ref|NP_109668.1| zinc finger protein 313; zinc finger protein 228 [Mus musculus] gb|AAG01141.1|AF282919_1 (AF282919) Zfp228 [Mus musculus]	0.00002
59	14042394	gi|14042394|dbj|BAB55226.1| (AK027604) unnamed protein product [Homo sapiens]	e-112
60	14769036	gi|14769036|ref|XP_036091.1| 19140 [Homo sapiens]	9E-97
61	13648339	gi|13648339|ref|XP_003184.2| zinc finger protein ANC_2H01 [Homo sapiens]	0.0006
64	13638702	gi|13638702|ref|XP_015971.1| hypothetical protein FLJ23384 [Homo sapiens] ref|XP_048858.1| hypothetical protein FLJ23384 [Homo sapiens]	2E-86
65	14150082	gi|14150082|ref|NP_115691.1| hypothetical protein MGC4399 [Homo sapiens] gb|AAH04991.1|AAH04991 (BC004991) Similar to RIKEN cDNA 5730438N18 gene [Homo sapiens]	0.00003
67	14727244	gi|14727244|ref|XP_035596.1| hypothetical protein AF140225 [Homo sapiens] ref|XP_035597.1| 49482 [Homo sapiens] gb|AAH07829.1|AAH07829 (BC007829) Similar to hypothetical protein AF140225 [Homo sapiens]	2E-38

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
68	14727244	gi|14727244|ref|XP_035596.1| hypothetical protein AF140225 [Homo sapiens] ref|XP_035597.1| 49482 [Homo sapiens] gb|AAH07829.1|AAH07829 (BC007829) Similar to hypothetical protein AF140225 [Homo sapiens]	6E-60
69	14715574	gi|14715574|dbj|BAB62041.1| (AB065434) PRPK mutant1 [Homo sapiens]	2E-98
70	7491888	gi|7491888|pir||T41272 hypothetical protein SPCC297.05 - fission yeast (Schizosaccharomyces pombe) emb|CAB40785.1| (AL049609) hypothetical protein [Schizosaccharomyces pombe]	9.3
71	12843000	gi|12843000|dbj|BAB25820.1| (AK008666) putative [Mus musculus]	1E-86
72	13542310	gi|13542310|ref|NP_111998.1| Uncharacterized conserved protein [Thermoplasma volcanium]	6.6
73	14728906	gi|14728906|ref|XP_003327.3| hypothetical protein FLJ10858 [Homo sapiens]	7E-98
74	14749106	gi|14749106|ref|XP_031512.1| 14599 [Homo sapiens] dbj|BAB15298.1| (AK025963) unnamed protein product [Homo sapiens]	1E-26
76	1176169	gi|1176169|sp|P28636|YHBE_ECOLI HYPOTHETICAL 35.0 KDA PROTEIN IN DACB-RPMA INTERGENIC REGION pir||B65109 hypothetical 35.0K protein (dacB-rpmA intergenic region) - Escherichia coli gb|AAA57985.1| (U18997) ORF_f321 [Escherichia coli] gb|AAC76216.1| (AE000399) orf, hypothetical protein [Escherichia coli K12] gb|AAG58318.1|AE005547_4 (AE005547) orf, hypothetical protein [Escherichia coli O157:H7 EDL933] dbj|BAB37486.1| (AP002564) hypothetical protein [Escherichia coli O157:H7]	0.23
77	13161357	gi|13161357|dbj|BAB32948.1| (AP002908) hypothetical protein~similar to Arabidopsis thaliana F1P2.140 [Oryza sativa]	6.3
78	8922806	gi|8922806|ref|NP_060761.1| hypothetical protein FLJ10986 [Homo sapiens] dbj|BAA91940.1| (AK001848) unnamed protein product [Homo sapiens] gb|AAH00610.1|AAH00610 (BC000610) hypothetical protein FLJ10986 [Homo sapiens]	5E-83
82	14603356	gi|14603356|gb|AAH10136.1|AAH10136 (BC010136) Unknown (protein for MGC:19513) [Homo sapiens]	1E-74

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
83	12804667	gi|12804667|gb|AAH01758.1|AAH01758 (BC001758) hypothetical protein FLJ20758 [Homo sapiens]	0.000000005
90	9795608	gi|9795608|gb|AAF98426.1|AC021044_5 (AC021044) Unknown protein [Arabidopsis thaliana]	0.7
91	13631937	gi|13631937|ref|XP_001412.3| metal-regulatory transcription factor 1 [Homo sapiens]	0.0004
92	14574479	gi|14574479|gb|AAF60869.2| (AC024856) Hypothetical protein Y71G10AR.2 [Caenorhabditis elegans]	0.15
93	14970562	gi|14970562|emb|CAC44371.1| (AJ292465) WDR9 protein, form A [Homo sapiens]	2E-16
98	12855751	gi|12855751|dbj|BAB30445.1| (AK016814) putative [Mus musculus]	3.1
102	11498284	gi|11498284|ref|NP_069510.1| adenylate kinase (adk) [Archaeoglobus fulgidus] sp|O29581|KAD_ARCFU ADENYLATE KINASE (ATP-AMP TRANSPHOSPHORYLASE) pir||D69334 adenylate kinase (EC 2.7.4.3) - Archaeoglobus fulgidus gb|AAB90565.1| (AE001058) adenylate kinase (adk) [Archaeoglobus fulgidus]	4.00E-13
104	9910248	gi|9910248|ref|NP_064579.1| GL004 protein [Homo sapiens] gb|AAF86949.1|AF226049_1 (AF226049) GL004 [Homo sapiens]	1.00E-85
105	7302191	gi|7302191|gb|AAF57287.1| (AE003784) CG7856 gene product [Drosophila melanogaster]	1.00E+00
106	12005513	gi|12005513|gb|AAG44486.1|AF246239_1 (AF246239) AD030 [Homo sapiens] gb|AAG44658.1|AF258660_1 (AF258660) AD033 [Homo sapiens]	2.00E-73
108	13874435	gi|13874435|dbj|BAB46923.1| (AB000782) cerebral protein-10 [Homo sapiens]	4.00E-04
109	14783375	gi|14783375|ref|XP_045533.1| protein predicted by clone 23627 [Homo sapiens]	1.60E-01
110	7229532	gi|7229532|gb|AAF42865.1|AF225924_1 (AF225924) staufen [Drosophila virilis]	3.30E+00
112	14775931	gi|14775931|ref|XP_049935.1| hypothetical protein FLJ14950 [Homo sapiens]	3.00E-77
114	10140758	gi|10140758|gb|AAG13589.1|AC051633_5 (AC051633) putative ubiquitin protein [Oryza sativa]	2.10E+00

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
115	421058	gi|421058|pir||S34255 hypothetical protein 1a - Escherichia coli emb|CAA51036.1| (X72295) ORF1a [Escherichia coli]	6.50E+00
116	14775931	gi|14775931|ref|XP_049935.1| hypothetical protein FLJ14950 [Homo sapiens]	2.00E-74
117	14781316	gi|14781316|ref|XP_032533.1| hypothetical protein FLJ12787 [Homo sapiens]	e-101
118	13161938	gi|13161938|emb|CAC32991.1| (AJ309861) putative protein kinase WNK4 [Homo sapiens]	1.00E-30
119	7662028	gi|7662028|ref|NP_055557.1| KIAA0255 gene product [Homo sapiens] ref|XP_009540.1| KIAA0255 gene product [Homo sapiens] sp|Q92544|T9S4_HUMAN TRANSMEMBRANE 9 SUPERFAMILY PROTEIN MEMBER 4 dbj|BAA13385.1| (D87444) Similar to S.cerevisiae EMP70 protein precursor (S25110) [Homo sapiens] emb|CAB75607.2| (AL049539) dJ836N17.2 (KIAA0255 protein) [Homo sapiens]	7.00E-14
120	10179324	gi|10179324|dbj|BAB13674.1| (AB041351) type IV collagen alpha 6 chain [Mus musculus]	7.9
122	7160119	gi|7160119|emb|CAB76306.1| (AL158057) putative acetyltransferase (fragment). [Streptomyces coelicolor A3(2)]	0.1
123	14732244	gi|14732244|ref|XP_039960.1| PC3-96 protein [Homo sapiens] ref|XP_039961.1| PC3-96 protein [Homo sapiens] pir||T46276 hypothetical protein DKFZp564M1178.1 - human emb|CAB70781.1| (AL137515) hypothetical protein [Homo sapiens] gb|AAG35611.1|AF202092_1 (AF202092) PC3-96 [Homo sapiens]	9E-81
124	7020475	gi|7020475|dbj|BAA91144.1| (AK000407) unnamed protein product [Homo sapiens]	2.6
125	14775931	gi|14775931|ref|XP_049935.1| hypothetical protein FLJ14950 [Homo sapiens]	2E-72
127	226135	gi|226135|prf||1411303A GABA receptor alpha2 [Bos taurus]	0.046
136	4995818	gi|4995818|emb|CAB44313.1| (AJ131899) proline rich synapse associated protein 1 [Rattus norvegicus]	0.00003

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
138	13357869	gi|13357869|ref|NP_078143.1| unique hypothetical [Ureaplasma urealyticum] pir||D82907 hypothetical protein UU309 [imported] - Ureaplasma urealyticum gb|AAF30718.1|AE002128_6 (AE002128) unique hypothetical [Ureaplasma urealyticum]	2.7
139	1076802	gi|1076802|pir||S49915 extensin-like protein - maize emb|CAA84230.1| (Z34465) extensin-like protein [Zea mays] prf||2111476A extensin-like domain [Zea mays]	1.9
140	11466208	gi|11466208|ref|NP_066531.1| NADH dehydrogenase subunit 4 [Naegleria gruberi] gb|AAG17809.1|AF288092_34 (AF288092) NADH dehydrogenase subunit 4 [Naegleria gruberi]	6.6
145	7490290	gi|7490290|pir||T38644 conserved hypothetical protein SPAC323.07c - fission yeast (Schizosaccharomyces pombe) emb|CAB53410.1| (AL109988) conserved hypothetical protein; UPF0013 [Schizosaccharomyces pombe]	0.78
147	5813770	gi|5813770|gb|AAD52006.1|AF017304_1 (AF017304) FMVIB [Morone saxatilis]	6.8
149	2497311	gi|2497311|sp|P55803|MOG_BOVIN MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR pir||A47712 myelin/oligodendrocyte glycoprotein precursor - bovine	0.33
152	609342	gi|609342|gb|AAA58698.1| (U04946) nucleophosmin-anaplastic lymphoma kinase fusion protein [Homo sapiens]	2.7
153	7481152	gi|7481152|pir||T36795 probable penicillin acylase - Streptomyces coelicolor emb|CAB46792.1| (AL096811) putative penicillin acylase [Streptomyces coelicolor A3(2)]	8

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
154	12229694	gi|12229694|sp|O93830|BET2_CANAL TYPE II PROTEINS GERANYLGERANYLTRANSFERASE BETA SUBUNIT (TYPE II PROTEIN GERANYL-GERANYLTRANSFERASE BETA SUBUNIT) (GGTASE-II-BETA) (PGGT) (YPT1/SEC4 PROTEINS GERANYLGERANYLTRANSFERASE BETA SUBUNIT) dbj|BAA35193.1| (AB021171) Beta subunit of geranylgeranyl transferase type2 [Candida albicans]	4.7
156	9630058	gi|9630058|ref|NP_046276.1| unknown [Orgyia pseudotsugata single capsid nuclear polyhedrosis virus] sp|O10359|Y120_NPVOP HYPOTHETICAL 9.3 KD PROTEIN (ORF120) pir||T10389 hypothetical protein 120 - Orgyia pseudotsugata nuclear polyhedrosis virus gb|AAC59119.1| (U75930) unknown [Orgyia pseudotsugata single capsid nuclear polyhedrosis virus]	8.5
157	9965966	gi|9965966|gb|AAG10219.1|AF294433_1 (AF294433) coat protein [Alfalfa mosaic virus]	7
158	7296047	gi|7296047|gb|AAF51343.1| (AE003585) CG17711 gene product [Drosophila melanogaster]	4.6
161	13507856	gi|13507856|ref|NP_109805.1| ribosomal protein L20 [Mycoplasma pneumoniae] sp|P78023|RL20_MYCPN 50S RIBOSOMAL PROTEIN L20 pir||S73363 ribosomal protein L20 - Mycoplasma pneumoniae (strain ATCC 29342) gb|AAG34734.1|AE000004_3 (AE000004) ribosomal protein L20 [Mycoplasma pneumoniae]	0.86
162	8393641	gi|8393641|ref|NP_058889.1| kynurenine aminotransferase II [Rattus norvegicus] emb|CAA90507.1| (Z50144) kynurenine/alpha-aminoadipate aminotransferase [Rattus norvegicus]	4.2
169	1515448	gi|1515448|gb|AAC45559.1| (U63096) Description: pBF4 gene involved in Bacteroides spp. conjugal transfer [Bacteroides fragilis]	2.6
175	422832	gi|422832|pir||B46629 mucin 6, gastric (3-repeat clone) - human (fragment) gb|AAB61945.1| (L07518) mucin [Homo sapiens]	3.2

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
176	7504075	gi|7504075|pir||T22584 hypothetical protein F53F4.6 - Caenorhabditis elegans emb|CAB01215.1| (Z77663) F53F4.6 [Caenorhabditis elegans]	6.6
178	13385538	gi|13385538|ref|NP_080316.1| RIKEN cDNA 2810036K01 gene [Mus musculus] dbj|BAB28520.1| (AK012865) putative [Mus musculus]	2E-48
180	902377	gi|902377|gb|AAA82981.1| (U18059) polyprotein [pestivirus type 1]	0.53
181	13421499	gi|13421499|gb|AAK22335.1| (AE005708) conserved hypothetical protein [Caulobacter crescentus]	6.2
187	10803574	gi|10803574|ref|NP_045972.1| GvpN [Halobacterium sp. NRC-1] sp|Q9HI16|GVN1_HALN1 GVPN PROTEIN 1 pir||A47053 gas-vesicle operon protein gvpN [imported] - Halobacterium salinarum pir||T08244 gas-vesicle operon protein gvpN - Halobacterium sp. (strain NRC-1) plasmid pNRC100 gb|AAC82811.1| (AF016485) GvpN [Halobacterium sp. NRC-1] gb|AAD15044.1| (L03361) gas vesicle protein [Plasmid pNRC100] gb|AAG20728.1| (AE005142) GvpN protein, cluster A; GvpN1 [Halobacterium sp. NRC-1]	7.40E-01
192	7662532	gi|7662532|ref|NP_054838.1| PRO0195 protein [Homo sapiens] gb|AAF24025.1|AF090901_1 (AF090901) PRO0195 [Homo sapiens]	2.60E-01
194	5360226	gi|5360226|dbj|BAA36472.1| (AB015177) F0-ATPase subunit 6 [Beta vulgaris]	2.3
196	3024921	gi|3024921|sp|Q58312|Y902_METJA HYPOTHETICAL PROTEIN MJ0902 pir||F64412 hypothetical protein MJ0902 - Methanococcus jannaschii gb|AAB98907.1| (U67533) M. jannaschii predicted coding region MJ0902 [Methanococcus jannaschii]	6.5
198	7522108	gi|7522108|pir||T29097 pro-pol-dUTPase polyprotein - murine endogenous retrovirus ERV-L (fragment) emb|CAA73251.1| (Y12713) protease; reverse transcriptase; RNaseH; integrase; dUTPase; Pro-Pol-dUTPase polyprotein [Mus musculus]	1.7

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
199	9955592	gi|9955592|emb|CAC00653.1| (AJ292519) N-acylamino acid racemase [Amycolatopsis orientalis subsp. lurida]	4.5
203	4097932	gi|4097932|gb|AAD10321.1| (U72240) unknown [Choristoneura fumiferana nucleopolyhedrovirus]	6.5
205	11252252	gi|11252252|pir||D82079 pyruvate dehydrogenase, E1 component VC2414 [imported] - Vibrio cholerae (group O1 strain N16961) gb|AAF95557.1| (AE004311) pyruvate dehydrogenase, E1 component [Vibrio cholerae]	3.5
206	12963481	gi|12963481|ref|NP_061927.1| hypothetical protein MGC5560; hypothetical protein [Homo sapiens] dbj|BAB14342.1| (AK022978) unnamed protein product [Homo sapiens]	3E-73
207	14737646	gi|14737646|ref|XP_038048.1| similar to APICAL ENDOSOMAL GLYCOPROTEIN PRECURSOR (R. norvegicus) [Homo sapiens]	4
209	14742770	gi|14742770|ref|XP_039393.1| KIAA1550 protein [Homo sapiens]	8.4
213	12643499	gi|12643499|sp|P89202|RRPO_SHMV RNA-DIRECTED RNA POLYMERASE (186 KDA PROTEIN) [CONTAINS: METHYLTRANSFERASE/RNA HELICASE (MT/HEL) (128 KDA PROTEIN)]	6.5
223	9629141	gi|9629141|ref|NP_044299.1| putative transport protein [Soybean chlorotic mottle virus] sp|P15631|VMP_SOCMV MOVEMENT PROTEIN (CELL-TO-CELL TRANSPORT PROTEIN) (ORF IA) pir||JS0379 hypothetical 35.5K protein - soybean chlorotic mottle virus emb|CAA33833.1| (X15828) putative transport protein [Soybean chlorotic mottle virus]	4.3
226	7494266	gi|7494266|pir||T18485 hypothetical protein C0840w - malaria parasite (Plasmodium falciparum) emb|CAB11124.1| (Z98551) putative P-type ATPase [Plasmodium falciparum]	2.3
228	14042283	gi|14042283|dbj|BAB55184.1| (AK027535) unnamed protein product [Homo sapiens]	2E-30
229	14744326	gi|14744326|ref|XP_044812.1| NIMA (never in mitosis gene a)-related kinase 6 [Homo sapiens]	4E-13
232	98014	gi|98014|pir||S11148 amiA protein - Streptococcus pneumoniae	10

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
233	10178317	gi|10178317|emb|CAC08403.1| (AL121928) bA18I14.5.1 (novel protein isoform 1) [Homo sapiens]	7
234	630444	gi|630444|pir||S43955 probable NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 3, kinetoplast - Trypanosoma brucei mitochondrion (fragment) gb|AAA20887.1| (L26251) CR5 [Trypanosoma brucei]	6.2
239	7505826	gi|7505826|pir||T25816 hypothetical protein K12D9.2 - Caenorhabditis elegans	1.4
240	7434912	gi|7434912|pir||H71934 phosphatidylglycerophosphate synthase - Helicobacter pylori (strain J99) gb|AAD05990.1| (AE001475) PHOSPHATIDYLGLYCEROPHOSPHATE SYNTHASE [Helicobacter pylori J99]	5.8
243	6136155	gi|6136155|sp|O70546|UTX_MOUSE UBIQUITOUSLY TRANSCRIBED X CHROMOSOME TETRATRICOPEPTIDE REPEAT PROTEIN (UBIQUITOUSLY TRANSCRIBED TPR PROTEIN ON THE X CHROMOSOME) emb|CAA05692.1| (AJ002730) UTX [Mus musculus]	8.90E+00
246	2143962	gi|2143962|pir||I59422 rsec8 - rat (fragment) gb|AAC52265.1| (U32498) rsec8 [Rattus norvegicus]	1E-93
250	6136155	gi|6136155|sp|O70546|UTX_MOUSE UBIQUITOUSLY TRANSCRIBED X CHROMOSOME TETRATRICOPEPTIDE REPEAT PROTEIN (UBIQUITOUSLY TRANSCRIBED TPR PROTEIN ON THE X CHROMOSOME) emb|CAA05692.1| (AJ002730) UTX [Mus musculus]	7.1

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
255	12737603	gi|12737603|ref|XP_006839.2| activin A receptor type II-like 1 [Homo sapiens] ref|XP_050707.1| activin A receptor type II-like 1 [Homo sapiens] sp|P37023|KIR3_HUMAN SERINE/THREONINE-PROTEIN KINASE RECEPTOR R3 PRECURSOR (SKR3) (ACTIVIN RECEPTOR-LIKE KINASE 1) (ALK-1) (TGF-B SUPERFAMILY RECEPTOR TYPE I) (TSR-I) pir||A49431 activin/TGF-beta-like type I receptor - human gb|AAA16160.1| (L17075) TGF-b superfamily receptor type I [Homo sapiens] gb|AAB61900.1| (U77713) activin receptor like kinase 1 [Homo sapiens]	7.50E+00
265	2133974	gi|2133974|pir||S68425 SoxP1 protein - rainbow trout dbj|BAA11868.1| (D83256) SoxP1 [Oncorhynchus mykiss]	0.18
266	9838427	gi|9838427|ref|NP_064041.1| orf214 [Beta vulgaris]	2.2
268	5731737	gi|5731737|dbj|BAA83337.1| (AB021878) similar to yeast sodium/proton exchanger [Oryza sativa]	3.3
271	13642312	gi|13642312|ref|XP_002895.2| parathyroid hormone receptor 1 [Homo sapiens] ref|XP_033742.1| parathyroid hormone receptor 1 [Homo sapiens] ref|XP_033743.1| parathyroid hormone receptor 1 [Homo sapiens]	9
272	11545138	gi|11545138|emb|CAC08390.2| (AL121886) dJ1028D15.1 (continued from dJ138B7.1 in Em:Z98752) [Homo sapiens]	0.0000008
275	6323677	gi|6323677|ref|NP_013748.1| Ymr034cp [Saccharomyces cerevisiae] sp|Q05131|YMS4_YEAST HYPOTHETICAL 48.4 KD PROTEIN IN ARP9-IMP2 INTERGENIC REGION pir||S53951 probable membrane protein YMR034c - yeast (Saccharomyces cerevisiae) emb|CAA89150.1| (Z49213) unknown [Saccharomyces cerevisiae]	6.6
277	7297043	gi|7297043|gb|AAF52312.1| (AE003612) CG13992 gene product [Drosophila melanogaster]	8.1
282	1616595	gi|1616595|emb|CAA41710.1| (X58907) steroid 21-monooxygenase [Homo sapiens]	6.8
283	14089610	gi|14089610|emb|CAC13370.1| (AL445563) unknown; predicted coding region [Mycoplasma pulmonis]	2.1

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
284	139809	gi|139809|sp|P27571|XIST_MOUSE X INACTIVE SPECIFIC TRANSCRIPT PROTEIN pir||S15433 hypothetical protein - mouse emb|CAA41978.1| (X59289) ORF [Mus musculus] prf||1711440A xist gene [Mus musculus]	0.18
285	11355576	gi|11355576|pir||T44331 hypothetical protein wblD [imported] - Vibrio cholerae dbj|BAA33635.1| (AB012957) probable NADH dehydrogenase [Vibrio cholerae]	0.23
297	14389443	gi|14389443|ref|NP_116776.1| NADH dehydrogenase subunit 4 [Rana nigromaculata] dbj|BAB58996.1| (AB043889) NADH dehydrogenase subunit 4 [Rana nigromaculata]	9.2
300	4493987	gi|4493987|emb|CAB39046.1| (AL034559) hypothetical protein, PFC1030w [Plasmodium falciparum]	2.1
306	7494200	gi|7494200|pir||T18434 hypothetical protein C0375c - malaria parasite (Plasmodium falciparum) emb|CAB11111.1| (Z98547) predicted using hexExon; MAL3P3.10 (PFC0375c), Homologue of C.elegans T08A11.2 protein, len: 1387 aa; Similarity to C.elegans T08A11.2 protein. C.elegans T08A11.2 protein (WP:T08A11.2) BLAST Score: 2901, sum P(2) = 0.0; 66% identity in 839 aa >	1.3
308	10728064	gi|10728064|gb|AAF50455.2| (AE003556) CG7060 gene product [Drosophila melanogaster]	4.7
317	9631682	gi|9631682|ref|NP_048461.1| a113L [Paramecium bursaria Chlorella virus 1] pir||T17603 hypothetical protein a113L - Chlorella virus PBCV-1 gb|AAC96481.1| (U42580) a113L [Paramecium bursaria Chlorella virus 1]	7.7
318	4733986	gi|4733986|gb|AAD28666.1|AC007209_2 (AC007209) hypothetical protein [Arabidopsis thaliana]	5.30E+00
319	461649	gi|461649|sp|Q05004|BB61_RABIT BRUSH BORDER 61.9 KD PROTEIN PRECURSOR pir||B45665 adult-specific 61.9K brush border protein precursor - rabbit emb|CAA78302.1| (Z12840) protein of unknown function [Oryctolagus cuniculus]	3.00E-16

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
322	11466552	gi|11466552|ref|NP_044801.1| NADH dehydrogenase, subunit 4 [Reclinomonas americana] pir||S78183 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - Reclinomonas americana (ATCC 50394) mitochondrion gb|AAD11916.1| (AF007261) NADH dehydrogenase, subunit 4 [Reclinomonas americana]	9.1
323	13603897	gi|13603897|gb|AAK31986.1|AF295594_1 (AF295594) SKTx1 precursor [Buthus martensii]	9.3
325	11497767	gi|11497767|ref|NP_068989.1| hypothetical protein [Archaeoglobus fulgidus] sp|O30087|Y150_ARCFU HYPOTHETICAL PROTEIN AF0150 pir||F69268 hypothetical protein AF0150 - Archaeoglobus fulgidus gb|AAB91087.1| (AE001096) A. fulgidus predicted coding region AF0150 [Archaeoglobus fulgidus]	7.1
332	7506939	gi|7506939|pir||T24356 hypothetical protein T02D1.3 - Caenorhabditis elegans emb|CAB05908.1| (Z83319) T02D1.3 [Caenorhabditis elegans]	3.9
336	7510675	gi|7510675|pir||T29689 hypothetical protein ZC266.2 - Caenorhabditis elegans gb|AAA96101.1| (U53140) ZC266.2 gene product [Caenorhabditis elegans]	2.4
337	12697923	gi|12697923|dbj|BAB21780.1| (AB051476) KIAA1689 protein [Homo sapiens]	3E-21
338	630465	gi|630465|pir||S47042 protein kinase (EC 2.7.1.37) cdc2-related 1 - malaria parasite (Plasmodium falciparum)	5.7
340	7488318	gi|7488318|pir||T01191 RNA-directed DNA polymerase homolog F21E10.5 - Arabidopsis thaliana gb|AAC13599.1| (AF058914) similar to reverse transcriptase (Pfam: transcript_fact.hmm, score: 72.31) [Arabidopsis thaliana]	5
341	5804818	gi|5804818|emb|CAB52872.1| (AL021712) putative protein [Arabidopsis thaliana] emb|CAB79171.1| (AL161556) putative protein [Arabidopsis thaliana]	5
343	14579376	gi|14579376|gb|AAK69253.1|AF336309_48 (AF336309) SpyB [Yersinia enterocolitica]	8.2

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
344	11284162	gi|11284162|pir||H81077 hypothetical protein NMB1490 [imported] - Neisseria meningitidis (group B strain MD58) gb|AAF41846.1| (AE002498) hypothetical protein [Neisseria meningitidis MC58]	3
347	11361512	gi|11361512|pir||H82781 hypothetical protein XF0626 [imported] - Xylella fastidiosa (strain 9a5c) gb|AAF83436.1|AE003908_4 (AE003908) hypothetical protein [Xylella fastidiosa 9a5c]	7.6
348	7497054	gi|7497054|pir||T19739 hypothetical protein C35A5.4 - Caenorhabditis elegans emb|CAA94905.1| (Z71185) contains similarity to Pfam domain: PF00635 (MSP (Major sperm protein) domain), Score=66.4, E-value=2e 16, N=1 [Caenorhabditis elegans]	0.064
349	6531601	gi|6531601|gb|AAF15500.1| (AF167672) immunoglobulin heavy chain variable region [Homo sapiens]	1.6
352	12858471	gi|12858471|dbj|BAB31327.1| (AK018655) putative [Mus musculus]	3.9
353	2128157	gi|2128157|pir||C64319 hypothetical protein MJ0154 - Methanococcus jannaschii	0.98
355	14195575	gi|14195575|sp|P58114|YV78_CAUCR HYPOTHETICAL PROTEIN CC3178 gb|AAK25140.1| (AE005981) pirin-related protein [Caulobacter crescentus]	4.20E+00
359	7468435	gi|7468435|pir||B72015 metalloproteinase, insulinase family CP0903 [imported] - Chlamydophila pneumoniae (strains CWL029 and AR39) gb|AAD19093.1| (AE001675) Insulinase family/Protease III [Chlamydophila pneumoniae CWL029] gb|AAF38689.1| (AE002249) metalloprotease, insulinase family [Chlamydophila pneumoniae AR39] dbj|BAA99165.1| (AP002548) insulinase family/protease III [Chlamydophila pneumoniae J138]	4.1
360	461649	gi|461649|sp|Q05004|BB61_RABIT BRUSH BORDER 61.9 KD PROTEIN PRECURSOR pir||B45665 adult-specific 61.9K brush border protein precursor - rabbit emb|CAA78302.1| (Z12840) protein of unknown function [Oryctolagus cuniculus]	8E-45

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
363	12859685	gi|12859685|dbj|BAB31736.1| (AK019464) putative [Mus musculus]	6.1
365	11055982	gi|11055982|ref|NP_067633.1| PR domain containing 13; PR-domain containing protein 13 [Homo sapiens] ref|XP_011460.1| PR domain containing 13 [Homo sapiens] gb|AAG13448.1| (AY004253) PR-domain containing protein 13 [Homo sapiens]	3.4
368	3915305	gi|3915305|sp|Q96597|VP5_AHSV9 OUTER CAPSID PROTEIN VP5 gb|AAB17570.1| (U74489) VP5 [African horse sickness virus]	0.63
370	11466986	gi|11466986|ref|NP_041893.1| Orf635 [Euglena gracilis] sp|P31916|YCX3_EUGGR HYPOTHETICAL 78.0 KD PROTEIN IN PSBC INTRON 2 (ORF635) emb|CAA50080.1| (X70810) Orf635 [Euglena gracilis]	1.7
373	14766918	gi|14766918|ref|XP_034599.1| acid sphingomyelinase-like phosphodiesterase [Homo sapiens]	2E-99
375	5732610	gi|5732610|gb|AAD49190.1|AF115423_2 (AF115423) core protein [Hepatitis B virus]	3.4
377	2707661	gi|2707661|gb|AAB94699.1| (AF029934) IgM heavy chain VDJ region [Oryctolagus cuniculus]	4.7
379	7516819	gi|7516819|pir||C72580 hypothetical protein APE1923 - Aeropyrum pernix (strain K1) dbj|BAA80928.1| (AP000062) 105aa long hypothetical protein [Aeropyrum pernix]	6.80E+00
380	3859670	gi|3859670|emb|CAA22008.1| (AL033502) hypothetical membrane protein [Candida albicans]	9.90E+00
382	14784562	gi|14784562|ref|XP_040415.1| mutL (E. coli) homolog 3 [Homo sapiens] gb|AAF23905.1| (AF195658) DNA mismatch repair protein [Homo sapiens]	2E-25
383	14194519	gi|14194519|sp|Q9K920|CMGB_BACHD COMG OPERON PROTEIN 2 HOMOLOG dbj|BAB06550.1| (AP001516) DNA transport machinery [Bacillus halodurans]	2.7
386	7509624	gi|7509624|pir||T26676 hypothetical protein Y38F1A.1 - Caenorhabditis elegans emb|CAA21628.1| (AL032639) predicted using Genefinder~cDNA EST EMBL:AW057282 comes from this gene [Caenorhabditis elegans]	9.4

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
388	7508443	gi|7508443|pir||T25281 hypothetical protein T25E12.11 - Caenorhabditis elegans emb|CAB04829.1| (Z82052) contains similarity to Pfam domain: PF01827 (Domain of unknown function), Score=130.6, E-value=4.6e-36, N=1 [Caenorhabditis elegans]	3.4
389	7295832	gi|7295832|gb|AAF51133.1| (AE003580) CG3347 gene product [Drosophila melanogaster]	0.032
390	7510359	gi|7510359|pir||T27283 hypothetical protein Y64G10A.f - Caenorhabditis elegans	8.2
395	6679381	gi|6679381|ref|NP_032903.1| plasminogen [Mus musculus] sp|P20918|PLMN_MOUSE PLASMINOGEN PRECURSOR [CONTAINS: ANGIOSTATIN] pir||PLMS plasmin (EC 3.4.21.7) precursor - mouse gb|AAA50168.1| (J04766) plasminogen [Mus musculus]	2.2
396	8479518	gi|8479518|sp|Q89853|VGP_EBORS STRUCTURAL GLYCOPROTEIN PRECURSOR (VIRION SPIKE GLYCOPROTEIN) [CONTAINS: GP1; GP2] gb|AAC54889.1| (U23416) virion spike glycoprotein [Ebola virus] gb|AAC54891.1| (U23417) virion spike glycoprotein [Ebola virus]	3.1
403	14133247	gi|14133247|dbj|BAA86564.2| (AB033076) KIAA1250 protein [Homo sapiens]	6E-19
412	3293234	gi|3293234|gb|AAC25913.1| (U96413) T-DNA oncoprotein [Agrobacterium tumefaciens]	9.1
415	7023033	gi|7023033|dbj|BAA91809.1| (AK001649) unnamed protein product [Homo sapiens]	9E-85
416	12514130	gi|12514130|gb|AAG55434.1|AE005285_1 (AE005285) putative oxidoreductase [Escherichia coli O157:H7 EDL933] dbj|BAB34455.1| (AP002554) putative oxidoreductase [Escherichia coli O157:H7]	9.40E-01
418	4514359	gi|4514359|dbj|BAA75394.1| (AB013377) ComGB [Bacillus halodurans]	2.6
419	7510324	gi|7510324|pir||T27250 hypothetical protein Y5F2A.3 - Caenorhabditis elegans emb|CAA21648.1| (AL032641) Y5F2A.3 [Caenorhabditis elegans]	1.6

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
421	6981358	gi|6981358|ref|NP_037137.1| phosphoinositide 3-kinase p85 (other splicing variants: p55 and p50) [Rattus norvegicus] sp|Q63787|P85A_RAT PHOSPHATIDYLINOSITOL 3-KINASE REGULATORY ALPHA SUBUNIT (PI3-KINASE P85-ALPHA SUBUNIT) (PTDINS-3-KINASE P85-ALPHA) (PI3K) dbj|BAA18932.1| (D64045) phosphatidylinositol 3-kinase p85 alpha subunit [Rattus norvegicus]	2.4
423	6576738	gi|6576738|dbj|BAA88337.1| (AB005891) ORF2 [Platemys spixii]	3.4
424	6739553	gi|6739553|gb|AAF27299.1| (AF146429) DeltaC [Danio rerio]	3.9
425	13816283	gi|13816283|gb|AAK43020.1| (AE006883) Sulfate adenylyltransferase (sat) [Sulfolobus solfataricus]	3.6
428	11034774	gi|11034774|gb|AAG27071.1|AF105225_7 (AF030414) NifQ [Gluconacetobacter diazotrophicus]	3.6
433	13364676	gi|13364676|dbj|BAB38622.1| (AP002568) hypothetical protein [Escherichia coli O157:H7]	5.8
434	12845784	gi|12845784|dbj|BAB26898.1| (AK010380) putative [Mus musculus]	0.075
435	12513917	gi|12513917|gb|AAG55266.1|AE005270_2 (AE005270) Z1121 gene product [Escherichia coli O157:H7 EDL933] gb|AAG55675.1|AE005306_4 (AE005306) Z1560 gene product [Escherichia coli O157:H7 EDL933] dbj|BAB34723.1| (AP002554) putative membrane protein [Escherichia coli O157:H7]	8.3
436	7661654	gi|7661654|ref|NP_056444.1| DKFZP566J153 protein [Homo sapiens] emb|CAB43677.1| (AL050369) hypothetical protein [Homo sapiens]	0.42
437	1150678	gi|1150678|emb|CAA50971.1| (X72086) ORF20R; B21R in citation [3] [Variola virus]	5.10E+00
438	8928456	gi|8928456|sp|O51039|Y006_BORBU HYPOTHETICAL PROTEIN BB0006 pir||F70100 conserved hypothetical integral membrane protein BB0006 - Lyme disease spirochete gb|AAC66397.1| (AE001115) conserved hypothetical integral membrane protein [Borrelia burgdorferi]	4.2
440	7297273	gi|7297273|gb|AAF52536.1| (AE003618) Myo28B1 gene product [Drosophila melanogaster]	3.3

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
448	7495690	gi|7495690|pir||T19090 hypothetical protein C08F11.3 - Caenorhabditis elegans emb|CAB05674.1| (Z83216) C08F11.3 [Caenorhabditis elegans]	4.9
449	10438579	gi|10438579|dbj|BAB15281.1| (AK025916) unnamed protein product [Homo sapiens]	3.7
451	112200	gi|112200|pir||A32868 prolactin receptor - rat (fragments)	8.6
452	114987	gi|114987|sp|P17885|BIMA_EMENI BIMA PROTEIN pir||A53256 nuclear protein bimA - Emericella nidulans emb|CAA41959.1| (X59269) bimA [Emericella nidulans]	6.60E+00
457	4885039	gi|4885039|gb|AAD31932.1|U00058_6 (U00058) contains similarity to DNAJ domains (Pfam: PF00226, Score=44.9, E=1.8e-09, N=1) [Caenorhabditis elegans]	4.3
459	4505121	gi|4505121|ref|NP_003916.1| methyl-CpG binding domain protein 4; 3,N(4)-ethenocytosine glycosylase; G/T mismatch glycosylase; G/U mismatch glycosylase; G/5-fluorouracil mismatch glycosylase with biphasic kinetics [Homo sapiens] gb|AAC68879.1| (AF072250) methyl-CpG binding protein MBD4 [Homo sapiens] gb|AAD22195.1|AF114784_1 (AF114784) methyl-CpG binding endonuclease [Homo sapiens] gb|AAD50374.1| (AF120999) methyl-CpG binding protein 4 [Homo sapiens]	2.1
463	12644455	gi|12644455|sp|Q60751|IG1R_MOUSE INSULIN-LIKE GROWTH FACTOR I RECEPTOR PRECURSOR gb|AAC12782.1| (AF056187) insulin-like growth factor I receptor; IGF-I receptor [Mus musculus]	3.1
465	11465398	gi|11465398|ref|NP_045211.1| unknown; N-acetyl-glutamate-gamma-semialdehyde dehydrogenase [Cyanidium caldarium] sp|Q9TLQ8|HIS5_CYACA AMIDOTRANSFERASE HISH gb|AAF12883.1|AF022186_5 (AF022186) unknown; N-acetyl-glutamate-gamma-semialdehyde dehydrogenase [Cyanidium caldarium]	5
466	5761329	gi|5761329|dbj|BAA83473.1| (AB004819) cysteine endopeptidase [Oryza sativa]	5.70E+00

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
468	5306243	gi|5306243|gb|AAD41976.1|AC006438_8 (AC006438) hypothetical protein [Arabidopsis thaliana]	4.2
470	7304025	gi|7304025|gb|AAF59067.1| (AE003836) CG8639 gene product [Drosophila melanogaster]	3.20E-01
473	7303724	gi|7303724|gb|AAF58773.1| (AE003829) lola gene product [alt 2] [Drosophila melanogaster] gb|AAF58774.1| (AE003829) lola gene product [alt 3] [Drosophila melanogaster] gb|AAF58775.1| (AE003829) lola gene product [alt 4] [Drosophila melanogaster] gb|AAF58776.1| (AE003829) lola gene product [alt 5] [Drosophila melanogaster]	5.8
476	1098549	gi|1098549|gb|AAA82594.1| (U25703) immunoglobulin light chain F class [Ictalurus punctatus]	7
477	4262231	gi|4262231|gb|AAD14524.1| (AC006200) hypothetical protein [Arabidopsis thaliana]	3.8
478	5834894	gi|5834894|ref|NP_006964.1|ND5_10021 NADH dehydrogenase subunit 5 [Caenorhabditis elegans] sp|P24896|NU5M_CAEEL NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 pir||S26037 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Caenorhabditis elegans mitochondrion emb|CAA38162.1| (X54252) ND5 protein (AA 1 - 527) [Caenorhabditis elegans]	0.23
480	14776608	gi|14776608|ref|XP_033588.1| BAI1-associated protein 3 [Homo sapiens]	8.6
482	7448960	gi|7448960|pir||D72417 conserved hypothetical protein - Thermotoga maritima (strain MSB8) gb|AAD35211.1|AE001697_11 (AE001697) conserved hypothetical protein [Thermotoga maritima]	9.1
484	7497960	gi|7497960|pir||T15840 hypothetical protein C54G7.3 - Caenorhabditis elegans gb|AAA81392.1| (U40410) coded for by C. elegans cDNA yk9e10.5; coded for by C. elegans cDNA yk9e10.3; multiple regions of similarity to EGF-like repeats and cysteine-rich repeats [Caenorhabditis elegans]	5
487	14720884	gi|14720884|ref|XP_032180.1| hypothetical protein DKFZp434A171 [Homo sapiens]	7.7
490	3201900	gi|3201900|gb|AAC19365.1| (AF067420) SNC73 protein [Homo sapiens]	0.28

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
493	12018149	gi|12018149|gb|AAG45421.1|AF309495_1 (AF309495) gamete-specific hydroxyproline-rich glycoprotein a2 [Chlamydomonas reinhardtii]	3.7
494	467634	gi|467634|emb|CAA82856.1| (Z29969) HLY 4 [Entamoeba histolytica]	8.9
498	14726914	gi|14726914|ref|XP_037105.1| KIAA0622 protein; Drosophila 'multiple asters' (Mast)-like homolog 1 [Homo sapiens]	6.8
499	11692583	gi|11692583|gb|AAG39888.1|AF282303_1 (AF282303) odorant receptor M34 [Mus musculus]	9.5
502	7303064	gi|7303064|gb|AAF58132.1| (AE003810) CG12960 gene product [Drosophila melanogaster]	4.9
504	13701254	gi|13701254|dbj|BAB42549.1| (AP003133) ORFID:SA1289~hypothetical protein, similar to bifunctional biotin ligase/biotin operon repressor [Staphylococcus aureus subsp. aureus N315] dbj|BAB57618.1| (AP003362) hypothetical protein [Staphylococcus aureus subsp. aureus Mu50]	5.9
505	137073	gi|137073|sp|P17086|URE1_PROMI UREASE ALPHA SUBUNIT (UREA AMIDOHYDROLASE) pir||D43719 urease (EC 3.5.1.5) 62K chain - Proteus mirabilis gb|AAA25669.1| (M31834) urease subunit C [Proteus mirabilis]	8.5
512	14548038	gi|14548038|sp|Q9D952|EVPL_MOUSE ENVOPLAKIN (P210) (210 KDA CORNIFIED ENVELOPE PRECURSOR) emb|CAC38864.2| (AJ309317) envoplakin [Mus musculus]	4.2
516	14031018	gi|14031018|gb|AAK50523.1| (AY029684) NADH dehydrogenase F [Stenotaphrum secundatum]	4.6
518	14600836	gi|14600836|ref|NP_147359.1| hypothetical protein [Aeropyrum pernix] pir||D72647 hypothetical protein APE0610 - Aeropyrum pernix (strain K1) dbj|BAA79580.1| (AP000060) 376aa long hypothetical protein [Aeropyrum pernix]	2.8

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
519	4930062	gi|4930062|pdb|1MAA|D Chain D, Mouse Acetylcholinesterase Catalytic Domain, Glycosylated Protein pdb|1MAA|A Chain A, Mouse Acetylcholinesterase Catalytic Domain, Glycosylated Protein pdb|1MAA|C Chain C, Mouse Acetylcholinesterase Catalytic Domain, Glycosylated Protein pdb|1MAA|B Chain B, Mouse Acetylcholinesterase Catalytic Domain, Glycosylated Protein	8.8
522	9757603	gi|9757603|dbj|BAB08147.1| (AB030877) maturase [Lilium mackliniae]	0.62
526	7445887	gi|7445887|pir||T07052 probable potassium channel protein SKT2 - potato emb|CAA70870.1| (Y09699) putative inward rectifying potassium channel [Solanum tuberosum]	2.1
528	2897832	gi|2897832|dbj|BAA24910.1| (AB000134) cytochrome oxidase subunit I [Prorocentrum micans]	9.8
537	7446379	gi|7446379|pir||T14039 protein kinase (EC 2.7.1.37), myotonic dystrophy-associated - rat gb|AAC02941.1| (AF021935) mytonic dystrophy kinase-related Cdc42-binding kinase [Rattus norvegicus]	8E-52
544	14779648	gi|14779648|ref|XP_027140.1| hypothetical protein FLJ23239 [Homo sapiens]	6.3
546	7292503	gi|7292503|gb|AAF47906.1| (AE003481) CG15023 gene product [Drosophila melanogaster]	6.3
548	4758758	gi|4758758|ref|NP_004529.1| nucleosome assembly protein 1-like 3 [Homo sapiens] sp|Q99457|NPL3_HUMAN NUCLEOSOME ASSEMBLY PROTEIN 1-LIKE 3 dbj|BAA08904.1| (D50370) nucleosome assembly protein [Homo sapiens]	1.6
554	14530412	gi|14530412|emb|CAC42291.1| (Z69360) cDNA EST EMBL:U52071 comes from this gene [Caenorhabditis elegans]	7
559	6680788	gi|6680788|ref|NP_031576.1| Bloom syndrome protein homolog (human) [Mus musculus] sp|O88700|BLM_MOUSE BLOOM'S SYNDROME PROTEIN HOMOLOG emb|CAB10933.1| (Z98263) BLM protein [Mus musculus]	4.8

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
560	3294495	gi|3294495|gb|AAC25822.1| (AF038608) contains similarity to Mus musculus tumor susceptibility protein TSG101 (GB:U52945) [Caenorhabditis elegans]	0.78
561	6319273	gi|6319273|ref|NP_009356.1| pre-tRNA processing; Pta1p [Saccharomyces cerevisiae] sp|Q01329|PTA1_YEAST PTA1 PROTEIN pir||S31299 pre-tRNA processing protein PTA1 - yeast (Saccharomyces cerevisiae) gb|AAA34919.1| (M95673) pta1 [Saccharomyces cerevisiae] gb|AAC04988.1| (U12980) Pta1p: Pre-tRNA processing involved protein [Saccharomyces cerevisiae]	9.9
567	5817732	gi|5817732|gb|AAD52875.1|AF142703_1 (AF142703) maturase-like protein [Ophrestia radicosa]	6.6
569	126296	gi|126296|sp|P08548|LIN1_NYCCO LINE-1 REVERSE TRANSCRIPTASE HOMOLOG prf||1207289B reverse transcriptase related protein [Nycticebus coucang]	0.00000002
572	13816099	gi|13816099|gb|AAK42875.1| (AE006870) Hypothetical protein [Sulfolobus solfataricus]	2.1
574	12513361	gi|12513361|gb|AAG54834.1|AE005228_1 (AE005228) putative glutaminase [Escherichia coli O157:H7 EDL933] dbj|BAB33961.1| (AP002552) putative glutaminase [Escherichia coli O157:H7]	3.3
575	11350453	gi|11350453|pir||B82965 hypothetical protein PA5456 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG08841.1|AE004958_11 (AE004958) hypothetical protein [Pseudomonas aeruginosa]	9
584	1174945	gi|1174945|sp|P43109|VEXB_SALTI VI POLYSACCHARIDE EXPORT INNER-MEMBRANE PROTEIN VEXB pir||G36892 Vi polysaccharide capsule transporter VexB - Salmonella typhi dbj|BAA03197.1| (D14156) Wzm protein [Salmonella typhi]	4.5
586	4566616	gi|4566616|gb|AAD23408.1|AF113531_1 (AF113531) follicle-stimulating hormone receptor precursor [Coturnix coturnix]	2
589	14746756	gi|14746756|ref|XP_039102.1| similar to hypothetical protein FLJ20378 (H. sapiens) [Homo sapiens]	0.007

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
590	7429823	gi|7429823|pir||D69991 conserved hypothetical protein yteU - Bacillus subtilis gb|AAC00275.1| (AF008220) YteU [Bacillus subtilis] emb|CAB14987.1| (Z99119) similar to hypothetical proteins from B. subtilis [Bacillus subtilis]	0.49
592	11877309	gi|11877309|emb|CAC19023.1| (AJ278707) ORF 4 [Neisseria meningitidis phage 2120]	9.2
594	14193715	gi|14193715|gb|AAK56102.1|AF332074_1 (AF332074) peroxisome proliferator-activated receptor binding protein [Mus musculus]	0.000002
595	14625344	gi|14625344|gb|AAK71419.1|U80842_9 (U80842) Hypothetical protein ZC239.19 [Caenorhabditis elegans]	1.9
596	1107614	gi|1107614|emb|CAA62696.1| (X91351) viral infectivity factor protein [Human immunodeficiency virus type 1]	0.008
599	6324561	gi|6324561|ref|NP_014630.1| required to degrade misfolded ER lumenal and integral membrane proteins; Hrd1p [Saccharomyces cerevisiae] pir||S66695 probable membrane protein YOL013c - yeast (Saccharomyces cerevisiae) emb|CAA99012.1| (Z74755) ORF YOL013c [Saccharomyces cerevisiae]	6.7
600	7494878	gi|7494878|pir||T33047 hypothetical protein B0344.2 - Caenorhabditis elegans gb|AAC16982.1| (AF067209) B0344.2 gene product [Caenorhabditis elegans]	0.94
601	11347199	gi|11347199|pir||C81351 probable UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate--D-alanyl-D-alanine ligase (EC 6.3.2.15) Cj0795c [imported] - Campylobacter jejuni (strain NCTC 11168) emb|CAB73060.1| (AL139076) putative UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate- - ligase [Campylobacter jejuni]	0.55
604	1293067	gi|1293067|gb|AAB06014.1| (U50958) drosophila seven-in-absentia gene product homolog [Mus musculus]	7.9

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
606	5031975	gi|5031975|ref|NP_005875.1| p21-activated kinase 4; protein kinase related to S. cerevisiae STE20, effector for Cdc42Hs [Homo sapiens] ref|XP_041095.1| protein kinase related to S. cerevisiae STE20, effector for Cdc42Hs [Homo sapiens] ref|XP_041093.1| protein kinase related to S. cerevisiae STE20, effector for Cdc42Hs [Homo sapiens] sp|O96013|PAK4_HUMAN SERINE/THREONINE-PROTEIN KINASE PAK 4 (P21-ACTIVATED KINASE 4) (PAK-4) gb|AAD01210.1| (AF005046) serine/threonine kinase [Homo sapiens] emb|CAA09820.1| (AJ011855) PAK4 protein [Homo sapiens]	1.1
608	9280285	gi|9280285|dbj|BAB01686.1| (AB046104) unnamed protein product [Macaca fascicularis]	8.7
609	5869819	gi|5869819|emb|CAB55576.1| (AJ249395) NADH-ubiquinone oxidoreductase subunit 1 [Globodera pallida]	0.84
611	12045283	gi|12045283|ref|NP_073094.1| conserved hypothetical protein [Mycoplasma genitalium] sp|P47662|Y423_MYCGE HYPOTHETICAL PROTEIN MG423 pir||G64246 conserved hypothetical protein MG423 - Mycoplasma genitalium gb|AAC71647.1| (U39724) conserved hypothetical protein [Mycoplasma genitalium]	2.8
612	11289932	gi|11289932|pir||T50247 probable helicase [imported] - fission yeast (Schizosaccharomyces pombe) emb|CAB71840.1| (AL138666) putative helicase [Schizosaccharomyces pombe]	4.5
613	6119709	gi|6119709|emb|CAB59566.1| (AJ249986) C3G protein [Rattus norvegicus]	1.6
620	7144507	gi|7144507|gb|AAA58585.2| (U12823) hemolysin [Acanthamoeba polyphaga]	8.1
622	15011757	gi|15011757|gb|AAB04582.3| (U64603) Hypothetical protein C09B7.1 [Caenorhabditis elegans]	7
625	8923324	gi|8923324|ref|NP_060247.1| hypothetical protein FLJ20345 [Homo sapiens] ref|XP_008161.3| hypothetical protein FLJ20345 [Homo sapiens] dbj|BAA91105.1| (AK000352) unnamed protein product [Homo sapiens]	0.004

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
626	6960319	gi|6960319|gb|AAD43326.2|AF155156_1 (AF155156) adaptor-related protein complex AP-4 epsilon subunit [Homo sapiens]	0.00008
628	5739387	gi|5739387|gb|AAD50450.1|AF169388_1 (AF169388) alpha 4 collagen IV [Mus musculus]	5.5
631	3510234	gi|3510234|gb|AAC33487.1| (AC005581) R31237_1, partial CDS [Homo sapiens]	8.6
632	802150	gi|802150|gb|AAB32775.1| (S75037) pancreatic peptidylglycine alpha-amidating monooxygenase, PAM=membrane-bound isoform {alternatively spliced, clone PAM-3, transmembrane domain (Ba region)} [human, islet cell tumor cell line QGP-1, Peptide Partial, 971 aa] [Homo sapiens]	1E-13
636	2105238	gi|2105238|gb|AAB57954.1| (U86905) similar to variola and vaccinia E9L [Molluscum contagiosum virus subtype 1]	1.5
641	7576305	gi|7576305|emb|CAB88003.1| (AJ277410) NADH dehydrogenase subunit 1 [Taenia hydatigena]	9.3
643	12231395	gi|12231395|gb|AAG49078.1|AF216121_1 (AF216121) phytochrome B [Gyminda tonduzii]	7
647	281178	gi|281178|pir||JQ1580 major surface antigen - hepatitis B virus (subtype adw4q-, strains CNTS-38 and Fou) emb|CAA53344.1| (X75658) surface antigen [Hepatitis B virus]	6.7
652	7503145	gi|7503145|pir||T16315 hypothetical protein F41C3.6 - Caenorhabditis elegans gb|AAC46813.1| (U23521) asked finisher to look for frameshift because of discrepancy between prediction and EST CEESW76F; looks like there should be a splice from 21751 to 21706. But no problem was found in the area [Caenorhabditis elegans]	6.9
653	14773502	gi|14773502|ref|XP_043252.1| PCAF associated factor 65 alpha [Homo sapiens] gb|AAH08785.1|AAH08785 (BC008785) PCAF associated factor 65 alpha [Homo sapiens]	3E-10
658	14732840	gi|14732840|ref|XP_034110.1| hypothetical protein XP_034110 [Homo sapiens]	1.8
659	13442965	gi|13442965|gb|AAK26242.1|AF247132_1 (AF247132) putative chromatin remodeling factor [Mus musculus]	4

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
660	4512671	gi|4512671|gb|AAD21725.1| (AC006931) En/Spm-like transposon protein [Arabidopsis thaliana] gb|AAD33868.1|AF141375_1 (AF141375) protodermal factor 1 [Arabidopsis thaliana] gb|AAD33869.1|AF141376_1 (AF141376) protodermal factor 1 [Arabidopsis thaliana]	6.6
663	13385330	gi|13385330|ref|NP_080127.1| RIKEN cDNA 1700010I14 gene [Mus musculus] dbj|BAB24262.1| (AK005830) putative [Mus musculus]	0.33
665	14325583	gi|14325583|dbj|BAB60486.1| (AP000996) unknown product [Thermoplasma volcanium]	5.4
666	14779941	gi|14779941|ref|XP_007847.3| hypothetical protein from clone 24796 [Homo sapiens]	0.00000002
670	14330407	gi|14330407|emb|CAC41079.1| (AJ308518) P2X5 receptor [Gallus gallus]	3.3
672	13991595	gi|13991595|gb|AAK51427.1| (AF355796) BRCA1 [Echymipera kalubu]	6.9
681	14728540	gi|14728540|ref|XP_048261.1| similar to ring finger protein 23; RING-B box-coiled coil-B30.2 (M. musculus) [Homo sapiens]	0.026
683	14740222	gi|14740222|ref|XP_049918.1| similar to hypothetical protein MGC10940 (H. sapiens) [Homo sapiens]	1E-86
684	11359451	gi|11359451|pir||T51040 hypothetical protein B15I20.100 [imported] - Neurospora crassa emb|CAB97464.1| (AL389900) conserved hypothetical protein [Neurospora crassa]	9.2
685	14735526	gi|14735526|ref|XP_001804.4| guanylate binding protein 2, interferon-inducible [Homo sapiens]	2.3
687	7510353	gi|7510353|pir||T27275 hypothetical protein Y63D3A.9 - Caenorhabditis elegans emb|CAA21711.1| (AL032652) contains similarity to Pfam domain: PF00646 (F-box domain.), Score=43.2, E-value=1.9e-09, N=1 [Caenorhabditis elegans]	6.8
697	14773502	gi|14773502|ref|XP_043252.1| PCAF associated factor 65 alpha [Homo sapiens] gb|AAH08785.1|AAH08785 (BC008785) PCAF associated factor 65 alpha [Homo sapiens]	3E-10
700	7498998	gi|7498998|pir||T16057 hypothetical protein F13D11.2 - Caenorhabditis elegans	0.27

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
703	4493893	gi|4493893|emb|CAB39002.1| (AL034558) predicted using hexExon; MAL3P2.15 (PFC0230c), Hypothetical protein len: 3979 aa [Plasmodium falciparum]	9.2
706	7243081	gi|7243081|dbj|BAA92588.1| (AB037771) KIAA1350 protein [Homo sapiens]	1E-79
707	7496384	gi|7496384|pir||T33266 hypothetical protein C24B9.10 - Caenorhabditis elegans gb|AAC19256.1| (AF068709) Hypothetical protein C24B9.10 [Caenorhabditis elegans]	5.4
708	7492007	gi|7492007|pir||T41680 hypothetical protein SPCP1E11.01c - fission yeast (Schizosaccharomyces pombe) emb|CAB54860.1| (AL117183) hypothetical protein [Schizosaccharomyces pombe]	4.1
709	14758507	gi|14758507|ref|XP_044768.1| similar to death receptor 6 (H. sapiens) [Homo sapiens]	0.031
710	6513925	gi|6513925|gb|AAF14829.1|AC011664_11 (AC011664) unknown protein [Arabidopsis thaliana]	0.83
713	6434714	gi|6434714|emb|CAB61161.1| (AL132973) putative membrane protein. [Streptomyces coelicolor A3(2)]	1.2
714	8810476	gi|8810476|gb|AAF80137.1|AC024174_19 (AC024174) Contains similarity to a hypothetical protein F24K9.13 gi|6006885 from Arabidopsis thaliana gb|AC008153 and contains multiple PPR PF|01535 repeats	0.22
719	9626839	gi|9626839|ref|NP_041109.1| ORF 18 [ictalurid herpesvirus 1] sp|Q00120|VG18_HSVI1 HYPOTHETICAL GENE 18 PROTEIN pir||A36788 hypothetical protein ORF18 - ictalurid herpesvirus 1 (strain auburn 1) gb|AAA88121.1| (M75136) ORF 18 [ictalurid herpesvirus 1]	9.2
723	15004903	gi|15004903|gb|AAK77203.1|AC006622_3 (AC006622) Hypothetical protein C52D10.12 [Caenorhabditis elegans]	2.4
724	6677663	gi|6677663|ref|NP_033047.1| retinoic acid induced 1 [Mus musculus] pir||T30250 GT1 protein - mouse dbj|BAA06184.1| (D29801) Unknown [Mus musculus] prf||2123391A GT1 gene [Mus musculus]	0.12

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
729	2343183	gi|2343183|gb|AAB67715.1| (AF013243) zinc finger transcription factor [Lytechinus variegatus]	0.021
730	7465334	gi|7465334|pir||B71980 proline dehydrogenase (EC 1.5.99.8) / 1-pyrroline-5-carboxylate dehydrogenase (EC 1.5.1.12) putA [similarity] - Helicobacter pylori (strain J99) gb|AAD05632.1| (AE001444) Proline/pyrroline-5-carboxylate dehydrogenase [Helicobacter pylori J99]	4.9
733	9631436	gi|9631436|ref|NP_048287.1| ORF MSV216 SCG gene family protein [Melanoplus sanguinipes entomopoxvirus] pir||T28377 ORF MSV216 SCG gene family protein - Melanoplus sanguinipes entomopoxvirus gb|AAC97749.1| (AF063866) ORF MSV216 SCG gene family protein [Melanoplus sanguinipes entomopoxvirus]	0.52
734	13813168	gi|13813168|gb|AAK40402.1| (AE006645) Hypothetical protein [Sulfolobus solfataricus]	2.7
736	14776978	gi|14776978|ref|XP_033086.1| hypothetical protein XP_033086 [Homo sapiens]	5.4
737	7294863	gi|7294863|gb|AAF50194.1| (AE003550) CG6718 gene product [Drosophila melanogaster]	1.9
745	7465334	gi|7465334|pir||B71980 proline dehydrogenase (EC 1.5.99.8) / 1-pyrroline-5-carboxylate dehydrogenase (EC 1.5.1.12) putA [similarity] - Helicobacter pylori (strain J99) gb|AAD05632.1| (AE001444) Proline/pyrroline-5-carboxylate dehydrogenase [Helicobacter pylori J99]	3.9
750	5759216	gi|5759216|gb|AAD51030.1|AF172399_1 (AF172399) p75 neurotrophin receptor a-1 [Xenopus laevis] gb|AAD51031.1|AF172400_1 (AF172400) p75 neurotrophin receptor a-2 [Xenopus laevis]	3.9
751	6518511	gi|6518511|dbj|BAA87907.1| (AB021222) ketosynthase [Streptomyces rochei]	6.6
754	6679777	gi|6679777|ref|NP_032029.1| fibroblast growth factor 15 [Mus musculus] sp|O35622|FGFF_MOUSE FIBROBLAST GROWTH FACTOR-15 PRECURSOR (FGF-15) gb|AAB63197.1| (AF007268) fibroblast growth factor [Mus musculus] dbj|BAB30961.1| (AK017829) putative [Mus musculus]	7.7

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
755	7498881	gi|7498881|pir||T20748 hypothetical protein F11A5.2 - Caenorhabditis elegans emb|CAB07355.1| (Z92830) contains similarity to Pfam domain: PF01604 (7TM chemoreceptor), Score=428.7, E-value=1.7e-125, N=1 [Caenorhabditis elegans]	6.4
756	1378135	gi|1378135|gb|AAB02606.1| (U58466) putative fibroblast growth factor receptor 1-like protein; one of three possible open reading frames in the sequence [Rattus norvegicus]	5.1
758	7444901	gi|7444901|pir||B71630 hypothetical protein RP702 - Rickettsia prowazekii emb|CAA15138.1| (AJ235273) unknown [Rickettsia prowazekii]	2.2
759	12854427	gi|12854427|dbj|BAB30025.1| (AK015906) putative [Mus musculus]	6.6
763	4185892	gi|4185892|emb|CAA21831.1| (AL033125) 1-evidence=predicted by content~1-method=genefinder;084~1-evidence_end~2-evidence=predicted by match~2-match_accession=SWISS-PROT:P38205~2-match_description=HYPOTHETICAL 77.9 KD PROTEIN IN RRN10-MCM2 INTERGENIC REGION.~2-match_species=SACCHA>	9.1
766	14725855	gi|14725855|ref|XP_038865.1| similar to hypothetical protein PRO2822 (H. sapiens) [Homo sapiens]	9.2
770	7582302	gi|7582302|gb|AAF64271.1|AF208857_1 (AF208857) BM-015 [Homo sapiens]	8E-13
772	6594283	gi|6594283|dbj|BAA88419.1| (AB016615) hydrophobic transmembrane protein [Staphylococcus aureus]	1.7
783	12597803	gi|12597803|gb|AAG60115.1|AC073178_26 (AC073178) hypothetical protein [Arabidopsis thaliana]	0.62
784	8777303	gi|8777303|dbj|BAA96893.1| (AB018112) serine carboxypeptidase [Arabidopsis thaliana]	1.2
785	10045258	gi|10045258|emb|CAC07930.1| (AJ228487) cytochrome c oxidase subunit 3 [Acanthogammarus godlewskii]	1.5
786	1794167	gi|1794167|dbj|BAA11217.1| (D78137) unnamed protein product [Vibrio parahaemolyticus]	9.7
790	12835698	gi|12835698|dbj|BAB23329.1| (AK004489) putative [Mus musculus]	8.1

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
791	131761	gi|131761|sp|P11636|QAY_NEUCR QUINATE PERMEASE (QUINATE TRANSPORTER) pir||G31277 quinate transport protein - Neurospora crassa (tentative sequence) emb|CAA32752.1| (X14603) quinate transporter [Neurospora crassa]	1.7
794	11640576	gi|11640576|gb|AAG39285.1|AF113214_1 (AF113214) MSTP034 [Homo sapiens]	6.3
797	5306243	gi|5306243|gb|AAD41976.1|AC006438_8 (AC006438) hypothetical protein [Arabidopsis thaliana]	3.4
798	7511787	gi|7511787|pir||T29089 alpha-mannosidase (EC 3.2.1.-), class II - fall armyworm gb|AAB62719.1| (AF005034) alpha-mannosidase II [Spodoptera frugiperda]	7
800	3170793	gi|3170793|gb|AAC18201.1| (AF062165) immunoglobulin heavy chain variable region [Homo sapiens]	8.7
802	11466458	gi|11466458|ref|NP_038161.1| NADH dehydrogenase subunit 4L [Chrysodidymus synuroideus] gb|AAB95105.1| (U54633) NADH dehydrogenase subunit 4L [Chrysodidymus synuroideus] gb|AAF36927.1|AF222718_1 (AF222718) NADH dehydrogenase subunit 4L [Chrysodidymus synuroideus]	4.2
803	14779941	gi|14779941|ref|XP_007847.3| hypothetical protein from clone 24796 [Homo sapiens]	0.00000002
804	13430868	gi|13430868|ref|NP_077008.1| hypothetical protein MGC2615 [Homo sapiens] ref|XP_015759.1| hypothetical protein MGC2615 [Homo sapiens] gb|AAH01656.1|AAH01656 (BC001656) Unknown (protein for MGC:2615) [Homo sapiens]	4E-21
808	3293234	gi|3293234|gb|AAC25913.1| (U96413) T-DNA oncoprotein [Agrobacterium tumefaciens]	7.9
810	7299169	gi|7299169|gb|AAF54367.1| (AE003682) Fps85D gene product [alt 1] [Drosophila melanogaster]	5.6
814	11361627	gi|11361627|pir||H82736 hypothetical protein XF0992 [imported] - Xylella fastidiosa (strain 9a5c) gb|AAF83802.1|AE003937_6 (AE003937) hypothetical protein [Xylella fastidiosa 9a5c]	0.43
816	10803160	gi|10803160|emb|CAC13088.1| (AL445503) putative two component system response regulator [Streptomyces coelicolor]	6.4

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
819	2613090	gi|2613090|gb|AAB84279.1| (AF030317) OmpR [Proteus vulgaris]	1.7
821	2494232	gi|2494232|sp|Q62814|E2F5_RAT TRANSCRIPTION FACTOR E2F5 (E2F-5) gb|AAB00180.1| (U31668) E2F-5 [Rattus norvegicus]	7.8
822	14729752	gi|14729752|ref|XP_036388.1| hypothetical protein MGC5297 [Homo sapiens]	6.7
825	7024427	gi|7024427|emb|CAA87594.2| (Z47547) Pwi=orf234.1;Mpo=orf244;Angio=orfx~no ATG start codon [Chondrus crispus]	8
833	11691811	gi|11691811|emb|CAC11114.1| (AL121893) bA189K21.6 (Sec23 (S. cerevisiae) homolog B) [Homo sapiens]	5.6
834	117704	gi|117704|sp|P18246|CXA1_BOVIN GAP JUNCTION ALPHA-1 PROTEIN (CONNEXIN 43) (CX43) (VASCULAR SMOOTH MUSCLE CONNEXIN 43) pir||A36623 gap junction protein Cx43 - bovine gb|AAA30459.1| (J05535) vascular smooth muscle connexin43 [Bos taurus]	9.2
835	1170606	gi|1170606|sp|P43188|KADC_MAIZE ADENYLATE KINASE, CHLOROPLAST (ATP-AMP TRANSPHOSPHORYLASE) pir||S45634 adenylate kinase (EC 2.7.4.3), chloroplast - maize pdb|1ZAK|A Chain A, Adenylate Kinase From Maize In Complex With The Inhibitor P1,P5-Bis(Adenosine-5'-)pentaphosphate (Ap5a) pdb|1ZAK|B Chain B, Adenylate Kinase From Maize In Complex With The Inhibitor P1,P5-Bis(Adenosine-5'-)pentaphosphate (Ap5a)	0.0000001
836	7661750	gi|7661750|ref|NP_054866.1| HSPC047 protein [Homo sapiens] gb|AAF29019.1|AF161532_1 (AF161532) HSPC047 [Homo sapiens]	5E-28
838	13815530	gi|13815530|gb|AAK42398.1| (AE006828) Transport protein, hypothetical [Sulfolobus solfataricus]	5
839	14771844	gi|14771844|ref|XP_045585.1| hypothetical protein FLJ11085 [Homo sapiens] emb|CAB91047.2| (AL109935) dJ1022P6.2 (KIAA1434) [Homo sapiens]	0.089
843	4007786	gi|4007786|emb|CAA51374.1| (X72850) acetyl CoA acetyltransferase [Sphingomonas sp.]	4.6

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
847	9968471	gi|9968471|emb|CAC06698.1| (AJ275988) Kruppel like factor [Mus musculus]	6.2
848	7499805	gi|7499805|pir||T21337 hypothetical protein F25D7.1 - Caenorhabditis elegans emb|CAB01696.1| (Z78418) cDNA EST yk60g6.3 comes from this gene~cDNA EST yk60g6.5 comes from this gene~cDNA EST yk156b10.3 comes from this gene~cDNA EST yk156b10.5 comes from this gene~cDNA EST yk399f2.3 comes from this gene~cDNA EST yk399f2.5 comes from this gene~cDN>	7.1
849	6581093	gi|6581093|gb|AAF18453.1|AF205599_1 (AF205599) transposase-like protein [Mus musculus]	4.4
853	13651256	gi|13651256|ref|XP_015436.1| chloride channel 4 [Homo sapiens] ref|XP_045758.1| chloride channel 4 [Homo sapiens] ref|XP_045756.1| chloride channel 4 [Homo sapiens] ref|XP_045757.1| chloride channel 4 [Homo sapiens] dbj|BAA77327.1| (AB019432) chloride channel protein 4 [Homo sapiens] gb|AAD50981.1|AF170492_1 (AF170492) chloride channel CLC4 [Homo sapiens]	2.3
854	336159	gi|336159|gb|AAA46774.1| (M90520) polymerase protein [Woodchuck hepatitis B virus]	3.2
861	8979124	gi|8979124|dbj|BAA98959.1| (AP002547) CT651 hypothetical protein [Chlamydophila pneumoniae J138]	0.76
863	4758712	gi|4758712|ref|NP_004659.1| alpha-glucosidase; brush border hydrolase [Homo sapiens] sp|O43451|MGA_HUMAN MALTASE-GLUCOAMYLASE, INTESTINAL [INCLUDES: MALTASE (ALPHA-GLUCOSIDASE); GLUCOAMYLASE (GLUCAN 1,4-ALPHA-GLUCOSIDASE)] gb|AAC39568.1| (AF016833) maltase-glucoamylase [Homo sapiens]	0.1
864	13812050	gi|13812050|ref|NP_113184.1| hypothetical protein [Guillardia theta] gb|AAK39752.1|AF083031_109 (AF083031) hypothetical protein [Guillardia theta]	4.3
867	10726408	gi|10726408|gb|AAF54394.2| (AE003683) CG9381 gene product [Drosophila melanogaster]	5.5

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
870	7299899	gi|7299899|gb|AAF55074.1| (AE003705) CG7987 gene product [alt 1] [Drosophila melanogaster] gb|AAF55075.1| (AE003705) CG7987 gene product [alt 2] [Drosophila melanogaster]	9.7
872	6979325	gi|6979325|gb|AAF34418.1|AF172282_7 (AF172282) putative phosphatidylinositol 4-kinase [Oryza sativa]	4.8
873	13699930	gi|13699930|dbj|BAB41229.1| (AP003129) conserved hypothetical protein [Staphylococcus aureus subsp. aureus N315] dbj|BAB56175.1| (AP003358) conserved hypothetical protein [Staphylococcus aureus subsp. aureus Mu50]	3.7
877	6841256	gi|6841256|gb|AAF28981.1|AF161421_1 (AF161421) HSPC303 [Homo sapiens]	7E-64
879	2459878	gi|2459878|gb|AAC40459.1| (AF005734) glycoprotein precursor [Marburg virus]	2.5
880	14759292	gi|14759292|ref|XP_006700.2| checkpoint with forkhead and ring finger domains [Homo sapiens] gb|AAF91084.1|AF170724_1 (AF170724) cell cycle checkpoint protein CHFR [Homo sapiens]	0.000000002
886	141164	gi|141164|sp|P19297|YORM_TTV1 HYPOTHETICAL 38.6 KD PROTEIN emb|CAA32993.1| (X14855) URF (352 AA) [Thermoproteus tenax virus 1]	2.2
889	1755061	gi|1755061|gb|AAB50394.1| (U62737) photosystem I subunit XI [Synechococcus sp. PCC 7942]	3.6
890	7464739	gi|7464739|pir||G71920 hypothetical protein jhp0518 - Helicobacter pylori (strain J99) gb|AAD06099.1| (AE001485) putative [Helicobacter pylori J99]	7.6
891	14141161	gi|14141161|ref|NP_004492.2| heterogeneous nuclear ribonucleoprotein U, isoform b; hnRNP U protein; scaffold attachment factor A; p120 nuclear protein [Homo sapiens] gb|AAH03367.1|AAH03367 (BC003367) heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A) [Homo sapiens] gb|AAH03621.1|AAH03621 (BC003621) heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A) [Homo sapiens]	6.9
892	7649887	gi|7649887|dbj|BAA94165.1| (AP000422) tail fiber protein [Escherichia coli O157:H7]	0.63

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
901	7496871	gi|7496871|pir||T19650 hypothetical protein C32H11.7 - Caenorhabditis elegans emb|CAB05141.1| (Z82260) cDNA EST yk576f6.3 comes from this gene [Caenorhabditis elegans]	4.6
905	13400109	gi|13400109|gb|AAK21974.1| (U77931) rRNA promoter binding protein [Rattus norvegicus]	0.003
918	13235458	gi|13235458|emb|CAC33751.1| (AJ293322) ProP2 protein [Rickettsia typhi]	4.1
919	7292165	gi|7292165|gb|AAF47577.1| (AE003472) CG12023 gene product [Drosophila melanogaster]	0.25
920	12831207	gi|12831207|ref|NP_075579.1| gamma-aminobutyric acid (GABA-A) receptor, subunit epsilon [Rattus norvegicus] gb|AAF70383.1|AF189262_1 (AF189262) GABA-A receptor epsilon-like subunit [Rattus norvegicus]	4.5
926	10765285	gi|10765285|gb|AAG22971.1|AF183431_1 (AF183431) inhibitor of apoptosis protein 2 [Rattus norvegicus]	4.2
927	2832268	gi|2832268|gb|AAC15477.1| (AF043233) Caco-2 oligopeptide transporter [Homo sapiens]	5.1
928	6179898	gi|6179898|gb|AAF05702.1|AF190129_1 (AF190129) Na+/K+/2Cl- cotransporter [Callinectes sapidus]	6.1
931	12644035	gi|12644035|sp|Q9Z8M1|IF2_CHLPN TRANSLATION INITIATION FACTOR IF-2 pir||E81576 translation initiation factor 2 CP0440 [imported] - Chlamydophila pneumoniae (strain AR39) gb|AAF38279.1| (AE002205) translation initiation factor 2 [Chlamydophila pneumoniae AR39] dbj|BAA98527.1| (AP002546) initiation factor-2 [Chlamydophila pneumoniae J138]	0.91
932	10956362	gi|10956362|ref|NP_052811.1| pXO1-115 [Bacillus anthracis] pir||C59105 hypothetical protein pXO1-115 - Bacillus anthracis virulence plasmid pXO1 gb|AAD32419.1|AAD32419 (AF065404) pXO1-115 [Bacillus anthracis] gb|AAD41347.1|AF150965_1 (AF150965) resolvase X [Bacillus anthracis]	1.9
933	13814214	gi|13814214|gb|AAK41294.1| (AE006722) Conserved hypothetical protein [Sulfolobus solfataricus]	0.99

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
940	6320195	gi|6320195|ref|NP_010275.1| Ydl009cp [Saccharomyces cerevisiae] pir||S52510 probable membrane protein YDL009c - yeast (Saccharomyces cerevisiae) emb|CAA88350.1| (Z48432) unknown [Saccharomyces cerevisiae] emb|CAA98568.1| (Z74059) ORF YDL009c [Saccharomyces cerevisiae]	7
942	10181130	gi|10181130|ref|NP_065586.1| acid sphingomyelinase-like phosphodiesterase 3a [Mus musculus] emb|CAA69329.1| (Y08135) acid sphingomyelinase-like phosphodiesterase [Mus musculus]	6E-84
943	13124718	gi|13124718|sp|P54358|DPOD_DROME DNA POLYMERASE DELTA CATALYTIC SUBUNIT gb|AAF49555.1| (AE003529) DNApol-delta gene product [Drosophila melanogaster]	2.8
946	2258300	gi|2258300|gb|AAB63269.1| (AF001783) AgrC [Staphylococcus aureus]	1.9
947	7460037	gi|7460037|pir||T13431 hypothetical protein T17A13.20 Arabidopsis thaliana emb|CAB79678.1| (AL161574) hypothetical protein [Arabidopsis thaliana]	3.4
948	7494291	gi|7494291|pir||E71616 hypothetical protein PFB0365w - malaria parasite (Plasmodium falciparum) gb|AAC71862.1| (AE001390) hypothetical protein [Plasmodium falciparum]	1.9
950	1707627	gi|1707627|emb|CAA96381.1| (Z71701) cytochrome oxidase subunit III [Euhadra herklotsi]	9.1
952	6739602	gi|6739602|gb|AAF27330.1| (AF178534) talin [Homo sapiens]	1E-14

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
954	7498956	gi|7498956|pir||T20804 hypothetical protein F12F6.1 - Caenorhabditis elegans emb|CAA97791.1| (Z73425) cDNA EST yk30a8.3 comes from this gene~cDNA EST yk12d11.5 comes from this gene~cDNA EST yk30a8.5 comes from this gene~cDNA EST yk117g9.3 comes from this gene~cDNA EST yk113h11.5 comes from this gene~cDNA EST yk117g9.5 comes from this gene~cDNA> emb|CAA97796.1| (Z73426) cDNA EST yk30a8.3 comes from this gene~cDNA EST yk12d11.5 comes from this gene~cDNA EST yk30a8.5 comes from this gene~cDNA EST yk117g9.3 comes from this gene~cDNA EST yk113h11.5 comes from this gene~cDNA EST yk117g9.5 comes from this gene~cDNA>	6.6
955	9631417	gi|9631417|ref|NP_048325.1| ORF MSV254 leucine rich repeat gene family protein, similar to Amsacta moorei entomopoxvirus Q3 ORF SW:P28854 [Melanoplus sanguinipes entomopoxvirus] pir||T28415 ORF MSV254 leucine rich repeat gene family protein - Melanoplus sanguinipes entomopoxvirus gb|AAC97730.1| (AF063866) ORF MSV254 leucine rich repeat gene family protein, similar to Amsacta moorei entomopoxvirus Q3 ORF SW:P28854 [Melanoplus sanguinipes entomopoxvirus]	2.1
956	7160126	gi|7160126|emb|CAB76312.1| (AL158060) putative membrane protein. [Streptomyces coelicolor A3(2)]	0.25
959	1203965	gi|1203965|gb|AAA89173.1| (L42379) bone-derived growth factor [Homo sapiens]	1.4
960	585147	gi|585147|sp|P38094|FLUG_EMENI FLUG PROTEIN pir||A53186 fluG protein - Emericella nidulans gb|AAC37414.1| (L27817) FluG [Emericella nidulans]	5.4
963	11352695	gi|11352695|pir||D83270 transcription-repair coupling protein Mfd PA3002 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG06390.1|AE004725_3 (AE004725) transcription-repair coupling protein Mfd [Pseudomonas aeruginosa]	1.3

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
964	119777	gi|119777|sp|P16291|FA9_SHEEP COAGULATION FACTOR IX (CHRISTMAS FACTOR) pir||I47078 coagulation factor IXa (EC 3.4.21.22) - sheep (fragment) gb|AAA31520.1| (M26233) factor IX [Ovis aries]	8.2
965	7473507	gi|7473507|pir||F75587 probable glycosyltransferase - Deinococcus radiodurans (strain R1) gb|AAF12451.1|AE001863_76 (AE001863) glycosyltransferase, putative [Deinococcus radiodurans]	0.24
967	2494130	gi|2494130|gb|AAB80639.1| (AC002376) Contains similarity to Glycine SRC2 (gb|AB000130). [Arabidopsis thaliana]	5.2
972	10728660	gi|10728660|gb|AAF52603.2| (AE003620) CG8683 gene product [Drosophila melanogaster]	6E-12
980	7500037	gi|7500037|pir||T34063 chromosome segregation protein smc1 F28B3.7 [similarity] - Caenorhabditis elegans gb|AAK21378.1| (AF003136) contains similarity to ATP synthase subunit B [Caenorhabditis elegans]	0.68
981	7298917	gi|7298917|gb|AAF54122.1| (AE003675) CG10272 gene product [Drosophila melanogaster]	5.9
983	1170115	gi|1170115|sp|P46430|GTT1_MANSE GLUTATHIONE S-TRANSFERASE 1 (GST CLASS-THETA) gb|AAA92880.1| (L32091) glutathione S-transferase [Manduca sexta]	7.1
985	10864490	gi|10864490|gb|AAG24203.1| (AF022981) Hypothetical protein W03F9.6 [Caenorhabditis elegans]	5.3
987	105400	gi|105400|pir||A35648 B-cell adhesion protein CD22 alpha splice form precursor - human emb|CAA36988.1| (X52785) CD22 antigen [Homo sapiens] prf||1608208A B cell antigen DC22 [Homo sapiens]	6
989	14750376	gi|14750376|ref|XP_012394.3| myosin IXA [Homo sapiens]	3.9
990	6324560	gi|6324560|ref|NP_014629.1| Yol013w-ap [Saccharomyces cerevisiae] pir||S78736 protein YOL013w-a - yeast (Saccharomyces cerevisiae) delta remnant	9.3
991	7290503	gi|7290503|gb|AAF45956.1| (AE003431) CG3527 gene product [Drosophila melanogaster]	7.6

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
994	9964623	gi|9964623|ref|NP_064753.1| RP DNA pol [Roseophage SIO1] gb|AAG02598.1|AF189021_17 (AF189021) Roseophage SIO1 complete genome	3.5
996	2769538	gi|2769538|emb|CAA11217.1| (AJ223279) voltage-sensitive sodium channel [Plutella xylostella]	7.6
998	9628506	gi|9628506|ref|NP_043384.1| regulatory protein E2 [Human papillomavirus type 29] sp|P50772|VE2_HPV29 REGULATORY PROTEIN E2 gb|AAA79432.1| (U31784) regulatory protein E2 [Human papillomavirus type 29]	6.2
999	6566147	gi|6566147|dbj|BAA04745.2| (D21203) large Forked protein [Drosophila melanogaster]	0.085
1002	11346920	gi|11346920|pir||H81390 probable integral membrane protein Cj0461c [imported] - Campylobacter jejuni (strain NCTC 11168) emb|CAB75099.1| (AL139075) putative integral membrane protein [Campylobacter jejuni]	1.5
1005	9294038	gi|9294038|dbj|BAB01995.1| (AB020746) gene_id:MOB24.1~unknown protein [Arabidopsis thaliana]	9.8
1006	4505067	gi|4505067|ref|NP_002349.1| MAD2-like 1; mitotic arrest deficient, yeast, homolog-like 1 [Homo sapiens] sp|Q13257|MD21_HUMAN MITOTIC SPINDLE ASSEMBLY CHECKPOINT PROTEIN MAD2A (MAD2-LIKE 1) (HSMAD2) pir||G01942 mitotic feedback control protein Madp2 homolog - human gb|AAC52060.1| (U31278) mitotic feedback control protein Madp2 homolog [Homo sapiens] gb|AAC50781.1| (U65410) Mad2 [Homo sapiens] emb|CAA03943.1| (AJ000186) MAD2 [Homo sapiens] gb|AAH00356.1|AAH00356 (BC000356) MAD2 (mitotic arrest deficient, yeast, homolog)-like 1 [Homo sapiens] gb|AAH05945.1|AAH05945 (BC005945) MAD2 (mitotic arrest deficient, yeast, homolog)-like 1 [Homo sapiens] gb|AAK38174.1| (AF202273) MAD2-like protein 1 [Homo sapiens]	0.000005

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
1010	13994140	gi|13994140|ref|NP_038928.1| antigen p97 (melanoma associated) identified by monoclonal antibodies 133.2 and 96.5 [Mus musculus] dbj|BAA86655.1| (AB024336) membrane-bound transferrin-like protein p97 [Mus musculus] dbj|BAB41139.1| (AB047799) membrane-bound transferrin-like protein [Mus musculus]	4.1
1011	11465559	gi|11465559|ref|NP_045049.1| unknown [Cyanidium caldarium] gb|AAF12997.1|AF022186_169 (AF022186) unknown [Cyanidium caldarium]	1.8
1012	13421288	gi|13421288|gb|AAK22158.1| (AE005691) TonB-dependent receptor [Caulobacter crescentus]	0.65
1013	6978481	gi|6978481|ref|NP_036905.1| a-kinase anchoring protein [Rattus norvegicus] sp|Q62924|AK11_RAT A KINASE ANCHOR PROTEIN 11 (PROTEIN KINASE A ANCHORING PROTEIN 11) (PRKA11) (A KINASE ANCHOR PROTEIN 220 KDA) (AKAP 220) pir||T42732 A-kinase anchoring protein AKAP 220 - rat gb|AAB06559.1| (U48288) AKAP 220 [Rattus norvegicus]	3
1015	7498137	gi|7498137|pir||T31694 hypothetical protein D1065.2 - Caenorhabditis elegans	7.4
1017	9944230	gi|9944230|emb|CAC05416.1| (AJ400866) membrane tyrosine phosphatase [Bos indicus]	7
1023	14520862	gi|14520862|ref|NP_126337.1| hypothetical protein [Pyrococcus abyssi] pir||G75106 hypothetical protein PAB0444 - Pyrococcus abyssi (strain Orsay) emb|CAB49568.1| (AJ248285) hypothetical protein [Pyrococcus abyssi]	9.7
1025	11290247	gi|11290247|pir||D82039 conserved hypothetical protein VC2740 [imported] - Vibrio cholerae (group O1 strain N16961) gb|AAF95879.1| (AE004339) conserved hypothetical protein [Vibrio cholerae]	8.2
1027	12484269	gi|12484269|gb|AAG54048.1|AF224607_4 (AF224607) NADH dehydrogenase subunit 4 [Propithecus verreauxi deckeni]	7
1028	14329703	gi|14329703|emb|CAC40662.1| (AJ292926) anaerobic (class III) ribonucleotide reductase large subunit chain [Staphylococcus aureus]	1.7

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
1037	2636683	gi|2636683|gb|AAC06264.1| (U66333) pol [Schistosoma mansoni]	5.2
1039	6016240	gi|6016240|sp|O02100|HOP1_CAEEL INTEGRAL MEMBRANE PROTEIN HOP-1 pir||T15184 presenilin-beta homolog - Caenorhabditis elegans pir||T42237 presenilin-beta homolog - Caenorhabditis elegans gb|AAB52948.1| (AF000265) Hypothetical protein C18E3.8 [Caenorhabditis elegans] gb|AAB84394.1| (AF021905) presenilin [Caenorhabditis elegans]	8.5
1040	10047173	gi|10047173|dbj|BAB13380.1| (AB046774) KIAA1554 protein [Homo sapiens]	8.4
1043	14089928	gi|14089928|emb|CAC13687.1| (AL445564) HEMOLYSIN C [Mycoplasma pulmonis]	4.8
1045	7469269	gi|7469269|pir||S77245 bioY protein - Synechocystis sp. (strain PCC 6803) dbj|BAA17579.1| (D90907) BioY protein [Synechocystis sp. PCC 6803]	5.6
1046	10140780	gi|10140780|gb|AAG13610.1|AC078840_1 (AC078840) hypothetical protein [Oryza sativa]	2.2
1050	7496756	gi|7496756|pir||T19593 hypothetical protein C31A11.3 - Caenorhabditis elegans emb|CAB05685.1| (Z83218) contains similarity to Pfam domain: PF01838 (Domain of unknown function), Score=506.2, E-value=5.4e-154, N=2 [Caenorhabditis elegans]	4.1
1052	7500420	gi|7500420|pir||T32834 hypothetical protein F33H12.1 - Caenorhabditis elegans gb|AAB95002.1| (AF040649) Hypothetical protein F33H12.1 [Caenorhabditis elegans]	4
1054	14736828	gi|14736828|ref|XP_032481.1| hypothetical protein XP_032481 [Homo sapiens]	5.5
1056	7290674	gi|7290674|gb|AAF46122.1| (AE003436) CG4320 gene product [Drosophila melanogaster]	4.7
1060	14970757	gi|14970757|emb|CAC44464.1| (AJ313506) CtxX protein [Salmonella typhimurium]	5.5
1062	4115497	gi|4115497|dbj|BAA36391.1| (AB010426) AL1 like protein [Phytoplasma sp.]	3.4
1064	111816	gi|111816|pir||S21348 probable pol polyprotein-related protein 4 - rat emb|CAA37647.1| (X53581) ORF4 [Rattus norvegicus]	6.4

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
1067	14149940	gi|14149940|ref|NP_115610.1| hypothetical protein FLJ23059 [Homo sapiens] dbj|BAB15536.1| (AK026712) unnamed protein product [Homo sapiens]	8E-34
1072	6321761	gi|6321761|ref|NP_011837.1| Yhl026cp [Saccharomyces cerevisiae] sp|P38740|YHC6_YEAST HYPOTHETICAL 30.7 KD PROTEIN IN RIM1-SNF6 INTERGENIC REGION PRECURSOR pir||S48942 hypothetical protein YHL026c - yeast (Saccharomyces cerevisiae) gb|AAB65062.1| (U11583) YHL026c gene product [Saccharomyces cerevisiae]	0.26
1076	5932366	gi|5932366|gb|AAD56919.1|AF180145_11 (AF180145) hypothetical protein; zm12orf5 [Zymomonas mobilis]	7.2
1084	7106864	gi|7106864|gb|AAF36157.1|AF151071_1 (AF151071) HSPC237 [Homo sapiens]	8.3
1087	1173846	gi|1173846|gb|AAA86616.1| (U39455) envelope glycoprotein precursor [Crimean-Congo hemorrhagic fever virus]	6.1
1092	87765	gi|87765|pir||JU0033 hypothetical L1 protein (third intron of gene TS) - human prf||1510254A L1 repetitive element ORF [Homo sapiens]	2
1096	9506813	gi|9506813|ref|NP_062184.1| Inositol polyphosphate-5-phosphatase [Rattus norvegicus] gb|AAB40610.1| (U55192) inositol polyphosphate 5' phosphatase Ship [Rattus norvegicus]	3.3
1101	11496734	gi|11496734|ref|NP_045511.1| B. burgdorferi predicted coding region BBH18 [Borrelia burgdorferi] pir||C70237 hypothetical protein BBH18 - Lyme disease spirochete plasmid H/lp28-3 gb|AAC66022.1| (AE000784) B. burgdorferi predicted coding region BBH18 [Borrelia burgdorferi]	7
1102	9630723	gi|9630723|ref|NP_047269.1| putative virulence determinant Vir [Mycoplasma arthritidis bacteriophage MAV1] gb|AAC33779.1| (AF074945) putative virulence determinant Vir [Mycoplasma arthritidis bacteriophage MAV1]	9.9

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
1107	3638957	gi|3638957|gb|AAC36301.1| (AC004877) sco-spondin-mucin-like; similar to P98167 (PID:g1711548); details of intron/exon structure uncertain [Homo sapiens]	3.3
1110	14725582	gi|14725582|ref|XP_002477.3| hypothetical protein FLJ10829 [Homo sapiens]	0.85
1112	7298126	gi|7298126|gb|AAF53364.1| (AE003642) BG:DS00180.10 gene product [Drosophila melanogaster]	8.6
1120	15011489	gi|15011489|gb|AAK77584.1|AF396436_24 (AF396436) heme maturase [Tetrahymena thermophila]	0.077
1121	7500306	gi|7500306|pir||T21638 hypothetical protein F32B4.1 - Caenorhabditis elegans emb|CAB04238.1| (Z81522) predicted using Genefinder [Caenorhabditis elegans]	5.6
1123	170156	gi|170156|gb|AAA73078.1| (M73688) [Sorghum bicolor endosperm tissue mRNA, complete CDS.], gene product prf||1808331A gamma kafirin [Sorghum bicolor]	0.41
1125	348951	gi|348951|gb|AAC78248.1| (M77194) gag [Rat leukemia virus]	4.2
1127	14583262	gi|14583262|ref|NP_127506.1| replicase ORF1ab polyprotein [Equine arteritis virus] emb|CAA69187.2| (Y07862) replicase ORF1b polyprotein [Cloning vector pEAV030] emb|CAC42775.2| (X53459) replicase ORF1b polyprotein [Equine arteritis virus]	0.79
1128	6322140	gi|6322140|ref|NP_012215.1| involved in filamentous growth; Dfg10p [Saccharomyces cerevisiae] sp|P40526|YIE9_YEAST HYPOTHETICAL 30.3 KD PROTEIN IN RPL34B-SYG1 INTERGENIC REGION pir||S48430 probable membrane protein YIL049w - yeast (Saccharomyces cerevisiae) emb|CAA86173.1| (Z38060) orf, len: 253, CAI: 0.11 [Saccharomyces cerevisiae]	7.6
1129	14779404	gi|14779404|ref|XP_008099.4| integrin alpha L precursor [Homo sapiens]	0.004

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
1136	13928898	gi|13928898|ref|NP_113837.1| killer cell lectin-like receptor subfamily G, member 1 [Rattus norvegicus] pir||I59421 mast cell function associated antigen - rat emb|CAA56208.1| (X79812) mast cell function associated antigen [Rattus norvegicus] emb|CAA65829.1| (X97191) MAFA protein [Rattus norvegicus]	5
1138	11467057	gi|11467057|ref|NP_042533.1| NADH dehydrogenase, subunit 4 [Acanthamoeba castellanii] sp|Q37375|NU4M_ACACA NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 pir||S53834 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - Acanthamoeba castellanii mitochondrion gb|AAD11826.1| (U12386) NADH dehydrogenase, subunit 4 [Acanthamoeba castellanii]	0.63
1140	7331848	gi|7331848|gb|AAF60536.1| (AC024772) contains similarity to Pfam family PF00569 (Zinc finger present in dystrophin, CBP/p300), score=30.4, E=4.3e-05, N=1 [Caenorhabditis elegans]	4.5
1144	12725042	gi|12725042|gb|AAK06095.1|AE006429_13 (AE006429) UNKNOWN PROTEIN [Lactococcus lactis subsp. lactis]	0.82
1146	13122173	gi|13122173|emb|CAC32349.1| (AL583945) putative bifunctional protein (histidine kinase and regulator) [Streptomyces coelicolor]	1.3
1147	13925661	gi|13925661|gb|AAK49407.1|AF261233_1 (AF261233) sodium/calcium exchanger protein [Mus musculus]	5.3
1149	6552484	gi|6552484|gb|AAF16411.1|AF038572_1 (AF038572) jagged2 [Mus musculus]	0.83
1154	13489284	gi|13489284|gb|AAF16898.2|AF168614_1 (AF168614) HMG-box transcription factor Sox17 [Danio rerio]	9.8
1155	1170115	gi|1170115|sp|P46430|GTT1_MANSE GLUTATHIONE S-TRANSFERASE 1 (GST CLASS-THETA) gb|AAA92880.1| (L32091) glutathione S-transferase [Manduca sexta]	7.8
1159	13377412	gi|13377412|gb|AAK20674.1|AF316639_9 (AF316639) Wzy [Streptococcus pneumoniae] gb|AAK74527.1| (AE007347) hypothetical protein [Streptococcus pneumoniae]	4.1

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
1163	7298868	gi|7298868|gb|AAF54075.1| (AE003673) CG1105 gene product [Drosophila melanogaster]	5.5
1164	10178202	gi|10178202|dbj|BAB11626.1| (AB016875) gene_id:K9D7.13~unknown protein [Arabidopsis thaliana]	9.3
1166	7494379	gi|7494379|pir||C71610 probable membrane associated protein PFB0615c - malaria parasite (Plasmodium falciparum) gb|AAC71912.1| (AE001406) predicted membrane associated protein [Plasmodium falciparum]	6.5
1170	12408633	gi|12408633|ref|NP_074924.1| cytochrome c oxidase subunit 1 [Podospora anserina] sp|P20681|COX1_PODAN CYTOCHROME C OXIDASE POLYPEPTIDE I pir||A48327 cytochrome-c oxidase (EC 1.9.3.1) chain I - Podospora anserina mitochondrion emb|CAA38777.1| (X55026) cytochrome oxidase c [Podospora anserina]	3.1
1173	2144233	gi|2144233|pir||JC5010 nucleotide-binding protein F - Methanosarcina mazei emb|CAA62802.1| (X91502) ABC transporter [Methanosarcina mazei]	6.9
1174	10581460	gi|10581460|gb|AAG20195.1| (AE005096) Vng2034h [Halobacterium sp. NRC-1]	0.15
1176	13652647	gi|13652647|ref|XP_007000.3| solute carrier family 6 (neurotransmitter transporter, betaine/GABA), member 12 [Homo sapiens] ref|XP_029976.1| solute carrier family 6 (neurotransmitter transporter, betaine/GABA), member 12 [Homo sapiens]	9
1181	9631326	gi|9631326|ref|NP_048159.1| ORF MSV088 hypothetical protein [Melanoplus sanguinipes entomopoxvirus] pir||T28249 ORF MSV088 hypothetical protein - Melanoplus sanguinipes entomopoxvirus gb|AAC97639.1| (AF063866) ORF MSV088 hypothetical protein [Melanoplus sanguinipes entomopoxvirus]	3.2
1184	13897920	gi|13897920|gb|AAK48502.1|AF260966_1 (AF260966) IL-8 receptor [Oncorhynchus mykiss]	2.6
1185	12860694	gi|12860694|dbj|BAB32022.1| (AK020187) putative [Mus musculus]	0.86
1187	6671484	gi|6671484|gb|AAC49301.2| (U32444) phytochrome F [Lycopersicon esculentum]	3.4

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
1191	11358531	gi|11358531|pir||T51640 myb-related transcription factor MYB19 [imported] - Arabidopsis thaliana (fragment) gb|AAC83590.1| (AF062868) putative transcription factor [Arabidopsis thaliana]	0.95
1192	88462	gi|88462|pir||A27307 proline-rich phosphoprotein (gene PRH1, Db allele) - human	7.9
1193	7484909	gi|7484909|pir||T06608 disease resistance protein homolog F16J13.80 - Arabidopsis thaliana emb|CAB40942.1| (AL049638) putative disease resistance protein (TMV N-like) [Arabidopsis thaliana] emb|CAB78244.1| (AL161533) putative disease resistance protein (TMV N-like) [Arabidopsis thaliana]	3.4
1195	7492269	gi|7492269|pir||T39663 paired amphipathic helix, probable transcription regulator protein - fission yeast (Schizosaccharomyces pombe) emb|CAA21310.1| (AL031856) putative transcriptional rgulatory protein [Schizosaccharomyces pombe]	4.1
1197	134437	gi|134437|sp|P13823|SERA_PLAFG SERINE-REPEAT ANTIGEN PROTEIN PRECURSOR (P126) (111 KDA ANTIGEN) pir||A54505 serine-repeat antigen precursor - malaria parasite (Plasmodium falciparum) (strain FCR3) gb|AAA29763.1| (J03993) serine repeat protein [Plasmodium falciparum] gb|AAA16791.1| (J04000) serine-repeat antigen protein [Plasmodium falciparum] gb|AAA74911.1| (U08113) serine repeat antigen [Plasmodium falciparum]	4.6
1202	12841678	gi|12841678|dbj|BAB25308.1| (AK007856) putative [Mus musculus]	2E-31
1211	586120	gi|586120|sp|Q07283|TRHY_HUMAN TRICHOHYALIN pir||A45973 trichohyalin - human gb|AAA65582.1| (L09190) trichohyalin [Homo sapiens]	9.8
1214	3122611	gi|3122611|sp|O18417|A70A_DROSE ACCESSORY GLAND-SPECIFIC PEPTIDE 70A PRECURSOR (PARAGONIAL PEPTIDE B) emb|CAA67791.1| (X99414) sex-peptide [Drosophila sechellia]	6.1
1215	2190464	gi|2190464|emb|CAB09537.1| (Z96107) Uncx4.1 [Mus musculus]	7.6

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
1216	153930	gi|153930|gb|AAA27047.1| (M23007) NADPH-sulfite reductase hemoprotein component [Salmonella typhimurium]	1.3
1217	5091519	gi|5091519|dbj|BAA78754.1| (AB023482) Hypothetical protein [Oryza sativa]	0.95
1219	9759203	gi|9759203|dbj|BAB09740.1| (AB015476) heat shock transcription factor HSF30-like protein [Arabidopsis thaliana]	9.2
1224	1732073	gi|1732073|gb|AAC50901.1| (U75308) TBP-associated factor [Homo sapiens]	0.13
1225	7505421	gi|7505421|pir||T23399 hypothetical protein K07C10.1 - Caenorhabditis elegans emb|CAA87375.1| (Z47074) similarity to transmembranous domains of the drosophila protein patched (Swiss Prot accession number P18502) [Caenorhabditis elegans]	3.4
1228	140791	gi|140791|sp|P17369|YHR3_VACCV HYPOTHETICAL HOST RANGE 27.4 KDA PROTEIN pir||WZVZA3 27.4K HindIII-C protein - vaccinia virus (strain WR) gb|AAA69594.1| (M22812) unknown protein [Vaccinia virus]	4.6
1231	6831569	gi|6831569|sp|O84098|IF2_CHLTR TRANSLATION INITIATION FACTOR IF-2 pir||H71558 probable translation initiation factor IF-2 - Chlamydia trachomatis (serotype D, strain UW3/Cx) gb|AAC67687.1| (AE001283) Initiation Factor-2 [Chlamydia trachomatis]	7.8
1243	12725042	gi|12725042|gb|AAK06095.1|AE006429_13 (AE006429) UNKNOWN PROTEIN [Lactococcus lactis subsp. lactis]	0.91
1246	10178036	gi|10178036|dbj|BAB11519.1| (AB005245) pectinesterase [Arabidopsis thaliana]	0.28
1249	7494298	gi|7494298|pir||A71613 hypothetical protein PFB0530c - malaria parasite (Plasmodium falciparum) gb|AAC71895.1| (AE001400) hypothetical protein [Plasmodium falciparum]	2.6
1253	14721018	gi|14721018|ref|XP_051562.1| similar to agrin (H. sapiens) [Homo sapiens]	3.5
1255	6175163	gi|6175163|gb|AAF04889.1|AC011437_4 (AC011437) unknown protein [Arabidopsis thaliana]	8.7

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
1264	12320927	gi|12320927|gb|AAG50592.1|AC083891_6 (AC083891) ABC transporter, putative [Arabidopsis thaliana]	9.5
1265	13375919	gi|13375919|ref|NP_078940.1| hypothetical protein FLJ11838 [Homo sapiens] dbj|BAB13931.1| (AK021900) unnamed protein product [Homo sapiens]	4.2
1274	9369395	gi|9369395|gb|AAF87143.1|AC002423_8 (AC002423) T23E23.16 [Arabidopsis thaliana]	7.2
1275	7435789	gi|7435789|pir||T06276 benzothiadiazole-induced protein (clone WCI-4) - wheat gb|AAC49287.1| (U32430) thiol protease [Triticum aestivum]	5.4
1280	7497192	gi|7497192|pir||T19833 hypothetical protein C38D9.3 - Caenorhabditis elegans emb|CAB03949.1| (Z81481) C38D9.3 [Caenorhabditis elegans]	0.15
1284	14739967	gi|14739967|ref|XP_035107.1| v-raf murine sarcoma viral oncogene homolog B1 [Homo sapiens]	1.9
1289	7463772	gi|7463772|pir||F70103 signal peptidase I (lepB-1) homolog - Lyme disease spirochete gb|AAC66422.1| (AE001117) signal peptidase I (lepB-1) [Borrelia burgdorferi]	0.22
1292	4580388	gi|4580388|gb|AAD24366.1|AC007171_2 (AC007171) hypothetical protein [Arabidopsis thaliana]	5.5
1293	10437002	gi|10437002|dbj|BAB14954.1| (AK024666) unnamed protein product [Homo sapiens]	0.000000002
1296	4493974	gi|4493974|emb|CAB39033.1| (AL034559) hypothetical protein, PFC0930c [Plasmodium falciparum]	3.2
1301	482030	gi|482030|pir||S40544 hypothetical protein - Escherichia coli dbj|BAA01299.1| (D10483) IS1 hypothetical protein E-96(PIR:A04462) [Escherichia coli]	8.3
1306	4836719	gi|4836719|gb|AAD30537.1|AF133256_2 (AF133256) envelope protein precursor [Friend mink cell focus-forming virus]	8.6
1307	12843929	gi|12843929|dbj|BAB26168.1| (AK009250) putative [Mus musculus]	2.1
1308	10175999	gi|10175999|dbj|BAB07095.1| (AP001518) lipopolysaccharide biosynthesis [Bacillus halodurans]	2.8

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
1310	14767733	gi|14767733|ref|XP_030859.1| similar to TGF(beta)-induced transcription factor 2 (H. sapiens) [Homo sapiens]	1.5
1311	1351721	gi|1351721|sp|Q10105|YAQ5_SCHPO PUTATIVE TRANSLATIONAL ACTIVATOR C18G6.05C (GCN1 HOMOLOG) pir||T37919 GCN1 homolog - fission yeast (Schizosaccharomyces pombe) emb|CAA92385.1| (Z68198) GCN1 homologue [Schizosaccharomyces pombe]	0.48
1312	13376747	gi|13376747|ref|NP_079428.1| hypothetical protein FLJ12660 [Homo sapiens] ref|XP_017923.1| hypothetical protein FLJ12660 [Homo sapiens] dbj|BAB14203.1| (AK022722) unnamed protein product [Homo sapiens]	0.000000003
1315	9453886	gi|9453886|dbj|BAB03287.1| (AB045975) pro-alpha 1 type V/XI collagen [Pagrus major]	0.021
1320	11034630	gi|11034630|dbj|BAB17154.1| (AP002868) hypothetical protein [Oryza sativa] dbj|BAB55491.1| (AP002541) hypothetical protein [Oryza sativa]	0.49
1322	14727261	gi|14727261|ref|XP_027313.1| hypothetical protein FLJ22351 [Homo sapiens] ref|XP_027314.1| hypothetical protein FLJ22351 [Homo sapiens]	0.077
1327	2789430	gi|2789430|dbj|BAA24380.1| (D30612) repressor protein [Homo sapiens]	0.97
1328	7497494	gi|7497494|pir||T19963 hypothetical protein C46C2.4 - Caenorhabditis elegans emb|CAA92590.1| (Z68296) contains similarity to Pfam domain: PF00561 (alpha/beta hydrolase fold), Score=30.8, E-value=1e-05, N=1 [Caenorhabditis elegans]	0.2
1329	13129018	gi|13129018|ref|NP_076956.1| hypothetical protein MGC3077 [Homo sapiens] ref|XP_030116.1| hypothetical protein MGC3077 [Homo sapiens] gb|AAC23790.1| (AC005154) similar to protein U28928 (PID:g861306) [Homo sapiens] gb|AAH00625.1|AAH00625 (BC000625) Unknown (protein for MGC:3077) [Homo sapiens]	2E-89
1330	14647539	gi|14647539|gb|AAK71916.1|AF332040_1 (AF332040) growth hormone receptor [Jaculus jaculus]	4.8

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
1331	1584488	gi|1584488|prf||2123261AB chemosensory receptor [Caenorhabditis elegans]	0.68
1333	2326324	gi|2326324|emb|CAB10936.1| (Z98264) cytochrome c oxidase subunit III [Anabaena sp.]	4.1
1334	7434912	gi|7434912|pir||H71934 phosphatidylglycerophosphate synthase - Helicobacter pylori (strain J99) gb|AAD05990.1| (AE001475) PHOSPHATIDYLGLYCEROPHOSPHATE SYNTHASE [Helicobacter pylori J99]	5.9
1337	1335199	gi|1335199|emb|CAA26919.1| (X03145) pot. ORF V [Homo sapiens]	5.2
1340	7440285	gi|7440285|pir||T07994 ribosomal protein S9 - Chlamydomonas reinhardtii chloroplast emb|CAA74006.1| (Y13655) 30S ribosomal protein S9 [Chlamydomonas reinhardtii]	3
1341	8923088	gi|8923088|ref|NP_060127.1| hypothetical protein FLJ20080 [Homo sapiens] ref|XP_046636.1| hypothetical protein FLJ20080 [Homo sapiens] dbj|BAA90936.1| (AK000087) unnamed protein product [Homo sapiens]	0.000000008
1345	6958206	gi|6958206|gb|AAF32493.1|AF093132_1 (AF093132) kexin-like protease KEX1 [Pneumocystis carinii f. sp. muris]	2.3
1346	7496774	gi|7496774|pir||T32166 hypothetical protein C31B8.8 - Caenorhabditis elegans	2
1350	9366789	gi|9366789|emb|CAB95551.1| (AL359782) hypothetical protein, CHR1.313. [Trypanosoma brucei]	2.4
1352	10175488	gi|10175488|dbj|BAB06586.1| (AP001516) cation antiporter (Na+/Ca2+) [Bacillus halodurans]	0.72
1354	1119230	gi|1119230|dbj|BAA06595.1| (D31786) secretion protein Y [Acyrthosiphon kondoi endosymbiont]	8.5
1355	2897812	gi|2897812|dbj|BAA24894.1| (AB010996) G2-G1 polyprotein precursor [tomato spotted wilt virus]	8.9
1357	13111586	gi|13111586|gb|AAK12388.1|AF296094_1 (AF296094) polyprotein [Porcine teschovirus]	9.2
1359	13881823	gi|13881823|gb|AAK46426.1| (AE007064) hypothetical protein [Mycobacterium tuberculosis CDC1551]	1.3
1368	1362185	gi|1362185|pir||S56686 histone H2B123 - wheat dbj|BAA07158.1| (D37944) protein H2B123 [Triticum aestivum]	9.7

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
1369	13812308	gi|13812308|ref|NP_113426.1| hypothetical protein [Guillardia theta] emb|CAC26995.1| (AJ010592) hypothetical protein [Guillardia theta]	4.7
1370	13541057	gi|13541057|ref|NP_110745.1| Permease (major facilitator superfamily) [Thermoplasma volcanium] dbj|BAB59369.1| (AP000991) unknown product [Thermoplasma volcanium]	7.6
1371	9964353	gi|9964353|ref|NP_064821.1| AMV039 [Amsacta moorei entomopoxvirus] gb|AAG02745.1|AF250284_39 (AF250284) AMV039 [Amsacta moorei entomopoxvirus]	5.3
1373	902377	gi|902377|gb|AAA82981.1| (U18059) polyprotein [pestivirus type 1]	0.41
1374	8953748	gi|8953748|dbj|BAA98067.1| (AP000368) gene_id:F6B6.1~pir||C71410~similar to unknown protein [Arabidopsis thaliana]	0.27
1375	11291752	gi|11291752|pir||T47971 seven in absentia-like protein - Arabidopsis thaliana emb|CAB71109.1| (AL132959) seven in absentia-like protein [Arabidopsis thaliana]	10
1379	10177211	gi|10177211|dbj|BAB10286.1| (AB026650) protein kinase [Arabidopsis thaliana]	5
1384	7332073	gi|7332073|gb|AAF60760.1| (AC024810) Hypothetical protein Y54E10A.1 [Caenorhabditis elegans]	5.7
1388	11358814	gi|11358814|pir||T46130 RNA polymerase III subunit-like protein - Arabidopsis thaliana emb|CAB62010.1| (AL132967) RNA polymerase III subunit-like protein [Arabidopsis thaliana]	2.2
1389	4506569	gi|4506569|ref|NP_002932.1| roundabout (axon guidance receptor, Drosophila) homolog 1 [Homo sapiens] gb|AAC39575.1| (AF040990) roundabout 1 [Homo sapiens]	4E-17
1393	11761072	gi|11761072|dbj|BAB19062.1| (AP002744) hypothetical protein [Oryza sativa]	1.9
1398	461649	gi|461649|sp|Q05004|BB61_RABIT BRUSH BORDER 61.9 KD PROTEIN PRECURSOR pir||B45665 adult-specific 61.9K brush border protein precursor - rabbit emb|CAA78302.1| (Z12840) protein of unknown function [Oryctolagus cuniculus]	8E-52

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
1402	478809	gi|478809|pir||S29851 protein kinase 6 (EC 2.7.1.-) - soybean gb|AAA34002.1| (M67449) protein kinase [Glycine max] prf||1908223A protein kinase [Glycine max]	9.3
1406	1517936	gi|1517936|gb|AAB07000.1| (U52347) tachykinin-like receptor [Stomoxys calcitrans]	1.1
1407	9977929	gi|9977929|sp|Q05013|LIPA_NEIMB CAPSULE POLYSACCHARIDE MODIFICATION PROTEIN LIPA pir||D81240 capsule polysaccharide modification protein LipA NMB0082 [imported] - Neisseria meningitidis (group B strain MD58) gb|AAF40546.1| (AE002367) capsule polysaccharide modification protein LipA [Neisseria meningitidis MC58]	9.3
1412	14773348	gi|14773348|ref|XP_038450.1| 20849 [Homo sapiens]	1E-48
1413	13537363	gi|13537363|dbj|BAB40663.1| (AB051851) death receptor 3 [Homo sapiens]	3.9
1419	7477083	gi|7477083|pir||A70577 hypothetical protein Rv2133c - Mycobacterium tuberculosis (strain H37RV) emb|CAB08660.1| (Z95388) hypothetical protein Rv2133c [Mycobacterium tuberculosis] gb|AAK46475.1| (AE007067) conserved hypothetical protein [Mycobacterium tuberculosis CDC1551]	1.9
1422	7499021	gi|7499021|pir||T20846 hypothetical protein F13E9.9 - Caenorhabditis elegans emb|CAA93411.1| (Z69383) F13E9.9 [Caenorhabditis elegans]	4.1
1424	14723696	gi|14723696|ref|XP_035744.1| hypothetical protein XP_035744 [Homo sapiens]	1.5
1425	9961349	gi|9961349|ref|NP_005500.2| Dmx-like 1 [Homo sapiens]	0.94
1426	478302	gi|478302|pir||JN0835 carbonate dehydratase (EC 4.2.1.1) I - chimpanzee	1.6
1427	6649942	gi|6649942|gb|AAF21641.1|AF032379_1 (AF032379) gonadotrophin releasing hormone receptor; GnRH-R [Trichosurus vulpecula]	9.6
1432	6636500	gi|6636500|gb|AAF20201.1|AF205791_1 (AF205791) squalene synthase [Botryococcus braunii]	1.8
1434	7504070	gi|7504070|pir||T22586 hypothetical protein F53F4.14 - Caenorhabditis elegans	0.05

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
1437	102177	gi|102177|pir||S13141 hypothetical protein (ribosomal RNA repeat region) - Giardia lamblia	1.2
1439	13357869	gi|13357869|ref|NP_078143.1| unique hypothetical [Ureaplasma urealyticum] pir||D82907 hypothetical protein UU309 [imported] - Ureaplasma urealyticum gb|AAF30718.1|AE002128_6 (AE002128) unique hypothetical [Ureaplasma urealyticum]	5.4
1451	7468435	gi|7468435|pir||B72015 metalloproteinase, insulinase family CP0903 [imported] - Chlamydophila pneumoniae (strains CWL029 and AR39) gb|AAD19093.1| (AE001675) Insulinase family/Protease III [Chlamydophila pneumoniae CWL029] gb|AAF38689.1| (AE002249) metalloprotease, insulinase family [Chlamydophila pneumoniae AR39] dbj|BAA99165.1| (AP002548) insulinase family/protease III [Chlamydophila pneumoniae J138]	7.1
1452	9857712	gi|9857712|gb|AAG00902.1|AF176776_1 (AF176776) xyloglucan endotransglycosylase LeXET2 [Lycopersicon esculentum]	1.9
1453	4493974	gi|4493974|emb|CAB39033.1| (AL034559) hypothetical protein, PFC0930c [Plasmodium falciparum]	3.4
1454	4493900	gi|4493900|emb|CAB39009.1| (AL034558) predicted using hexExon; MAL3P2.22 (PFC0265c), Hypothetical protein, len: 637 aa [Plasmodium falciparum]	6.1
1456	7503603	gi|7503603|pir||T16375 hypothetical protein F46G11.1 - Caenorhabditis elegans gb|AAA81397.1| (U40412) Hypothetical protein F46G11.1 [Caenorhabditis elegans]	2.1
1462	9437954	gi|9437954|gb|AAF87502.1|AF250474_1 (AF250474) nucleoprotein [Influenza A virus (A/Duck/Hong Kong/P54/97(H11N9))]	6.7
1464	2129239	gi|2129239|pir||G64488 reverse gyrase (intein-containing) - Methanococcus jannaschii gb|AAB99531.1| (U67592) reverse gyrase, intein containing (rgy) [Methanococcus jannaschii]	9.2
1466	12232439	gi|12232439|ref|NP_073602.1| hypothetical protein FLJ11937 [Homo sapiens] dbj|BAB15124.1| (AK025392) unnamed protein product [Homo sapiens]	6.4

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
1468	7243247	gi|7243247|dbj|BAA92671.1| (AB037854) KIAA1433 protein [Homo sapiens]	2E-87
1472	12382242	gi|12382242|gb|AAG53080.1|AF263824_1 (AF263824) 5'A2rel-related protein [Leishmania donovani]	8.7
1473	13812383	gi|13812383|ref|NP_113501.1| seryl-tRNA synthetase (serin-tRNA ligase) [Guillardia theta] emb|CAC27070.1| (AJ010592) seryl-tRNA synthetase (serin-tRNA ligase) [Guillardia theta]	6.5
1476	6014998	gi|6014998|sp|O80164|DPA5_BPR69 DNA POLYMERASE PROCESSIVITY COMPONENT (DNA POLYMERASE ACCESSORY PROTEIN 45) (GP45) pdb|1B77|A Chain A, Building A Replisome Structure From Interacting Pieces: A Sliding Clamp Complexed With An Interaction Peptide From Dna Polymerase pdb|1B77|B Chain B, Building A Replisome Structure From Interacting Pieces: A Sliding Clamp Complexed With An Interaction Peptide From Dna Polymerase pdb|1B77|C Chain C, Building A Replisome Structure From Interacting Pieces: A Sliding Clamp Complexed With An Interaction Peptide From Dna Polymerase pdb|1B8H|A Chain A, Sliding Clamp, Dna Polymerase pdb|1B8H|B Chain B, Sliding Clamp, Dna Polymerase pdb|1B8H|C Chain C, Sliding Clamp, Dna Polymerase gb|AAC39310.1| (AF039565) DNA polymerase processivity component [Bacteriophage RB69]	6.9
1479	7706747	gi|7706747|ref|NP_057263.1| transient receptor potential 4 [Homo sapiens] sp|Q9UBN4|TRP4_HUMAN SHORT TRANSIENT RECEPTOR POTENTIAL CHANNEL 4 (TRPC4) (TRP-RELATED PROTEIN 4) (HTRP-4) (HTRP4) gb|AAD51736.1|AF175406_1 (AF175406) transient receptor potential 4 [Homo sapiens] gb|AAF22927.1|AF063822_1 (AF063822) trp-related protein 4 [Homo sapiens]	1.7
1480	9757550	gi|9757550|dbj|BAB08163.1| (AB030831) SrtT [Streptococcus pyogenes]	0.47
1483	13516917	gi|13516917|dbj|BAB40338.1| (AB044076) hybrid sensor [Myxococcus xanthus]	5

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
1487	5790208	gi|5790208|dbj|BAA83536.1| (AB031285) NADH dehydrogenase subunit 2 [Taenia saginata]	2.7
1489	14754352	gi|14754352|ref|XP_032294.1| hypothetical protein FLJ10775 [Homo sapiens]	0.0008
1490	3552028	gi|3552028|gb|AAC64946.1| (AF087130) siderophore regulation protein [Neurospora crassa]	7.2
1493	3913936	gi|3913936|sp|Q43652|IP27_SOLTU PROTEINASE INHIBITOR TYPE II CM7 PRECURSOR pir||S43105 proteinase inhibitor II - potato emb|CAA55082.1| (X78275) proteinase inhibitor II [Solanum tuberosum]	9.9
1494	6573777	gi|6573777|gb|AAF17697.1|AC009243_24 (AC009243) F28K19.17 [Arabidopsis thaliana]	2.2
1496	13622425	gi|13622425|gb|AAK34148.1| (AE006569) maltodextrin transport system permease [Streptococcus pyogenes M1 GAS]	3.7
1498	9910266	gi|9910266|ref|NP_064627.1| kinesin-like protein 2 [Homo sapiens] dbj|BAB03309.1| (AB035898) kinesin-like protein 2 [Homo sapiens]	5E-19
1503	7294128	gi|7294128|gb|AAF49482.1| (AE003527) CG4925 gene product [Drosophila melanogaster]	3.6
1506	14089610	gi|14089610|emb|CAC13370.1| (AL445563) unknown; predicted coding region [Mycoplasma pulmonis]	1.5
1507	2565196	gi|2565196|gb|AAB81938.1| (AF000381) non-functional folate binding protein [Homo sapiens]	0.0000004
1509	14753935	gi|14753935|ref|XP_040892.1| hypothetical protein XP_040892 [Homo sapiens]	3.3
1510	12545425	gi|12545425|ref|NP_074975.1| hypothetical protein [Astasia longa] sp|P34776|YCY2_ASTLO HYPOTHETICAL 34.5 KDA PROTEIN IN RPS12-TRNP INTERGENIC REGION (ORF288) emb|CAC24586.1| (AJ294725) hypothetical protein [Astasia longa]	7
1511	420215	gi|420215|pir||B45878 hypothetical protein 2 - mouse	7.1
1512	7512874	gi|7512874|pir||T08792 hypothetical protein DKFZp586E1422.1 - human (fragment) emb|CAB43306.1| (AL050170) hypothetical protein [Homo sapiens]	5.5
1514	221758	gi|221758|dbj|BAA01683.1| (D10879) UL37 [human herpesvirus 1]	0.18

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
1517	11466232	gi|11466232|ref|NP_062855.1| ORF9, contains 8 trans membrane regions, putative [Physarum polycephalum] dbj|BAB08089.1| (AB027295) ORF9, contains 8 trans membrane regions, putative [Physarum polycephalum]	0.43
1518	182710	gi|182710|gb|AAA52467.1| (M13918) fibronectin receptor alpha-subunit precursor [Homo sapiens]	1.3
1519	1142976	gi|1142976|gb|AAC52392.1| (U28769) odorant receptor [Mus musculus] prf||2207403C odorant receptor [Mus musculus]	5.6
1520	6912446	gi|6912446|ref|NP_036417.1| potassium voltage-gated channel, subfamily H (eag-related), member 4; ether-a-go-go K(+) channel family member [Homo sapiens] dbj|BAA83592.1| (AB022698) BEC2 [Homo sapiens]	8.4
1522	14601483	gi|14601483|ref|NP_148021.1| hypothetical protein [Aeropyrum pernix] pir||G72637 hypothetical protein APE1558 - Aeropyrum pernix (strain K1) dbj|BAA80557.1| (AP000061) 279aa long hypothetical protein [Aeropyrum pernix]	5.7
1526	12515306	gi|12515306|gb|AAG56369.1|AE005365_3 (AE005365) orf, hypothetical protein [Escherichia coli O157:H7 EDL933] dbj|BAB35435.1| (AP002557) hypothetical protein [Escherichia coli O157:H7]	7.4
1530	2765672	gi|2765672|emb|CAB06819.1| (Z86115) ArbX [Lactobacillus delbrueckii]	7.9
1532	13472514	gi|13472514|ref|NP_104081.1| unknown protein [Mesorhizobium loti] dbj|BAB49867.1| (AP003000) unknown protein [Mesorhizobium loti]	7.9
1533	3309522	gi|3309522|gb|AAC26098.1| (U18292) unknown [Borrelia burgdorferi]	2.1
1535	14520328	gi|14520328|ref|NP_125803.1| activator 1, replication factor C, small subunit [Pyrococcus abyssi] pir||C75198 activator 1, replication factor c, small chain PAB0068 - Pyrococcus abyssi (strain Orsay) emb|CAB49034.1| (AJ248283) activator 1, replication factor C, small subunit [Pyrococcus abyssi]	0.41
1536	7229605	gi|7229605|gb|AAF42902.1| (AF229961) NADH dehydrogenase subunit 1 [Taygetis andromede]	6.7

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
1537	6681261	gi|6681261|ref|NP_031926.1| ect2 oncogene [Mus musculus] sp|Q07139|ECT2_MOUSE ECT2 PROTEIN (ECT2 ONCOGENE) pir||S32372 transforming protein (ect2) - mouse gb|AAA37536.1| (L11316) ect2 [Mus musculus] prf||1911407A oncogene ect2 [Mus musculus]	6E-10
1538	12381848	gi|12381848|emb|CAC24715.1| (AJ297319) glucose-6-phosphate dehydrogenase-6-phosphogluconolactonase [Plasmodium berghei]	7
1540	7688657	gi|7688657|gb|AAF67469.1|AF146760_1 (AF146760) septin 2-like cell division control protein [Homo sapiens]	9.7
1541	13021853	gi|13021853|gb|AAK11564.1|AF318500_1 (AF318500) ent-kaurenoic acid hydroxylase [Arabidopsis thaliana]	0.091
1543	6900006	gi|6900006|emb|CAB71294.1| (AJ251917) chorion protein s18 [Ceratitis capitata]	2.1
1545	1076445	gi|1076445|pir||S53004 mitosis-specific cyclin CYC2 - rape gb|AAA51660.1| (L25406) cyclin [Brassica napus]	4.3
1548	7293274	gi|7293274|gb|AAF48655.1| (AE003503) CG9644 gene product [Drosophila melanogaster]	0.46
1549	11358961	gi|11358961|pir||T51243 Scl1 protein [imported] - rice (fragment) gb|AAC98091.1| (AF067401) Scl1 protein [Oryza sativa]	3.9
1550	8978966	gi|8978966|dbj|BAA98801.1| (AP002547) phenylalanyl tRNA synthetase beta [Chlamydophila pneumoniae J138]	4.1
1551	14010341	gi|14010341|gb|AAK51958.1|AF362013_1 (AF362013) ATP synthase F0 subunit 6 [Halichondria sp. RFW-2001]	8.2
1553	8923094	gi|8923094|ref|NP_060130.1| hypothetical protein FLJ20085 [Homo sapiens] ref|XP_009383.2| hypothetical protein FLJ20085 [Homo sapiens] dbj|BAA90939.1| (AK000092) unnamed protein product [Homo sapiens]	1.6
1557	14724725	gi|14724725|ref|XP_037600.1| hypothetical protein XP_037600 [Homo sapiens]	4.2

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
1561	14758684	gi|14758684|ref|XP_007211.4| retinoblastoma 1 (including osteosarcoma) [Homo sapiens] ref|XP_033825.1| retinoblastoma 1 (including osteosarcoma) [Homo sapiens] ref|XP_033826.1| retinoblastoma 1 (including osteosarcoma) [Homo sapiens] ref|XP_033827.1| retinoblastoma 1 (including osteosarcoma) [Homo sapiens]	0.91
1565	9635387	gi|9635387|ref|NP_059285.1| ORF137 [Xestia c-nigrum granulovirus] gb|AAF05251.1|AF162221_137 (AF162221) ORF137 [Xestia c-nigrum granulovirus]	5.9
1572	1730077	gi|1730077|sp|P18160|KYK1_DICDI NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (TYROSINE-PROTEIN KINASE 1) pir||T18276 non-receptor tyrosine kinase - slime mold (Dictyostelium discoideum) gb|AAB41125.1| (U32174) non-receptor tyrosine kinase [Dictyostelium discoideum]	6
1574	9622133	gi|9622133|gb|AAF89633.1|AF167719_1 (AF167719) transmembrane leptin receptor [Sus scrofa]	2.6
1578	139809	gi|139809|sp|P27571|XIST_MOUSE X INACTIVE SPECIFIC TRANSCRIPT PROTEIN pir||S15433 hypothetical protein - mouse emb|CAA41978.1| (X59289) ORF [Mus musculus] prf||1711440A xist gene [Mus musculus]	7.7
1579	8567792	gi|8567792|gb|AAF76364.1| (AC013428) I-box binding factor, putative [Arabidopsis thaliana]	5.7
1581	7638161	gi|7638161|gb|AAF65408.1|AF238312_1 (AF238312) putative serine-threonine protein kinase MkcB [Dictyostelium discoideum]	9.2
1583	12644495	gi|12644495|sp|Q9Z7G7|EX5B_CHLPN EXODEOXYRIBONUCLEASE V BETA CHAIN dbj|BAA98945.1| (AP002547) exodeoxyribonuclease V, beta [Chlamydophila pneumoniae J138]	7.2
1588	11350667	gi|11350667|pir||D83160 nitrite extrusion protein 1 PA3877 [imported] - Pseudomonas aeruginosa (strain PAO1) emb|CAA75538.1| (Y15252) nitrate extrusion protein [Pseudomonas aeruginosa] gb|AAG07264.1|AE004805_2 (AE004805) nitrite extrusion protein 1 [Pseudomonas aeruginosa]	9.7

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
1589	12644495	gi|12644495|sp|Q9Z7G7|EX5B_CHLPN EXODEOXYRIBONUCLEASE V BETA CHAIN dbj|BAA98945.1| (AP002547) exodeoxyribonuclease V, beta [Chlamydophila pneumoniae J138]	5.2
1590	305479	gi|305479|gb|AAC37807.1| (L11473) envelope glycoprotein [Human immunodeficiency virus type 1]	4.3
1591	9055244	gi|9055244|ref|NP_061256.1| huntington yeast partner C [Mus musculus] gb|AAD39464.1|AF135440_1 (AF135440) huntington yeast partner C [Mus musculus]	0.8
1593	12666210	gi|12666210|emb|CAC28083.1| (AL138875) bA103J18.2 (novel protein) [Homo sapiens]	4
1596	12855510	gi|12855510|dbj|BAB30362.1| (AK016654) putative [Mus musculus]	0.067
1597	133747	gi|133747|sp|P09899|RS12_MICLU 30S RIBOSOMAL PROTEIN S12 pir||A26956 ribosomal protein S12 - Micrococcus luteus gb|AAA25317.1| (M17788) ribosomal protein S12 (gtg start codon) [Micrococcus luteus]	9.9
1600	7292455	gi|7292455|gb|AAF47859.1| (AE003480) CG15005 gene product [Drosophila melanogaster]	0.43
1601	14748674	gi|14748674|ref|XP_038133.1| Prader-Willi/Angelman syndrome-5 [Homo sapiens]	8.9
1602	11278020	gi|11278020|pir||H82215 serine transporter VC1301 [imported] - Vibrio cholerae (group O1 strain N16961) gb|AAF94460.1| (AE004210) serine transporter [Vibrio cholerae]	7.8
1607	9757538	gi|9757538|dbj|BAB08122.1| (AB030852) maturase [Lilium rubellum]	6.6
1618	12249143	gi|12249143|ref|NP_066194.2| NADH dehydrogenase subunit 5 [Schistosoma japonicum] gb|AAG13134.2| (AF215860) NADH dehydrogenase subunit 5 [Schistosoma japonicum]	5.9
1620	7495508	gi|7495508|pir||T18993 hypothetical protein C06B8.1 - Caenorhabditis elegans emb|CAB03850.1| (Z81463) Similarity to C.elegans zinc finger proteins, contains similarity to Pfam domain: PF00104 (Ligand-binding domain of nuclear hormone receptor), Score=-13.7, E-value=0.051, N=1 [Caenorhabditis elegans]	2.9

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
1621	7288570	gi|7288570|gb|AAF45170.1|AF218963_1 (AF218963) period [Drosophila miranda]	4.3
1622	7707666	gi|7707666|dbj|BAA95343.1| (AB027560) ATPase subunit 6 [Echinococcus vogeli]	4.1
1625	4761646	gi|4761646|gb|AAD29428.1|AF139060_1 (AF139060) transmembrane cell adhesion receptor MUA-3 precursor [Caenorhabditis elegans] emb|CAA83226.2| (Z30974) contains similarity to Pfam domain: PF00057 (Low-density lipoprotein receptor domain class A), Score=52.9, E-value=2.2e-12, N=3, second half (former T20G5.3) contains similarity to Pfam domain: PF00008 (EGF-like domain), Score=326.3, E-value=1> emb|CAC42345.1| (Z30423) contains similarity to Pfam domain: PF00057 (Low-density lipoprotein receptor domain class A), Score=52.9, E-value=2.2e-12, N=3, second half (former T20G5.3) contains similarity to Pfam domain: PF00008 (EGF-like domain), Score=326.3, E-value=1>	1.7
1626	3582424	gi|3582424|dbj|BAA33057.1| (AB017255) arginine kinase two-domain chain [Pseudocardium sachalinensis]	4.5
1628	9758077	gi|9758077|dbj|BAB08521.1| (AB009052) sucrose cleavage protein-like [Arabidopsis thaliana]	6.2
1629	11610630	gi|11610630|gb|AAG37436.1| (AY013711) cyclin E [Mustela vison]	10
1631	4838093	gi|4838093|gb|AAD30838.1| (AF103278) immunoglobulin heavy chain variable region [Homo sapiens]	3.3
1635	12045265	gi|12045265|ref|NP_073076.1| ATP synthase F0, subunit B (atpF) [Mycoplasma genitalium] sp|P47643|ATPF_MYCGE ATP SYNTHASE B CHAIN PRECURSOR pir||F64244 ATP synthase B chain (atpF) - Mycoplasma genitalium gb|AAC71631.1| (U39722) ATP synthase F0, subunit B (atpF) [Mycoplasma genitalium]	8.5
1636	627406	gi|627406|pir||A54849 collagen alpha 1(VII) chain precursor - human	0.66
1643	2246540	gi|2246540|gb|AAB62665.1| (U93872) glycoprotein M [Human herpesvirus 8]	1.5
1644	2388576	gi|2388576|gb|AAB71457.1| (AC000098) YUP8H12.17 [Arabidopsis thaliana]	4.7

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
1645	7490184	gi|7490184|pir||T37997 carboxypeptidase y - fission yeast (Schizosaccharomyces pombe) pir||T43236 carboxypeptidase C (EC 3.4.16.5) precursor [validated] - fission yeast (Schizosaccharomyces pombe) emb|CAB10121.1| (Z97209) carboxypeptidase y [Schizosaccharomyces pombe] dbj|BAA25568.1| (D86560) carboxypeptidase Y [Schizosaccharomyces pombe]	0.009
1646	7415597	gi|7415597|dbj|BAA93452.1| (AB026494) acyltransferase homolog [Gentiana triflora]	6.1
1648	13541404	gi|13541404|ref|NP_111092.1| DNA helicase (superfamily II) [Thermoplasma volcanium] dbj|BAB59714.1| (AP000992) DNA helicase [Thermoplasma volcanium]	7.5
1649	6174902	gi|6174902|sp|Q24767|PER_DROYA PERIOD CIRCADIAN PROTEIN pir||S17286 period clock protein - fruit fly (Drosophila yakuba) emb|CAA43439.1| (X61127) period [Drosophila yakuba]	0.2
1650	14318508	gi|14318508|ref|NP_116641.1| Ies1p [Saccharomyces cerevisiae] sp|P43579|YFB3_YEAST HYPOTHETICAL 78.8 KD PROTEIN IN HSP12-HXT10 INTERGENIC REGION pir||S48316 probable membrane protein YFL013c - yeast (Saccharomyces cerevisiae) emb|CAA86347.1| (Z46255) orf, len: 692, CAI: 0.14 [Saccharomyces cerevisiae] dbj|BAA09225.1| (D50617) YFL013C [Saccharomyces cerevisiae]	8.8
1655	5052950	gi|5052950|gb|AAD38784.1|AF149422_1 (AF149422) unknown [Homo sapiens]	0.000000007
1660	2988422	gi|2988422|gb|AAC39776.1| (AF016903) agrin precursor [Homo sapiens]	3.4
1661	14756108	gi|14756108|ref|XP_029883.1| EGF-like-domain, multiple 4 [Homo sapiens]	5
1664	10047313	gi|10047313|dbj|BAB13444.1| (AB046838) KIAA1618 protein [Homo sapiens]	0.00001
1669	5902048	gi|5902048|ref|NP_008974.1| HIV-1 rev binding protein 2; Rev interacting protein [Homo sapiens] pir||G02629 Rev interacting protein Rip-1 - human gb|AAB00557.1| (U55766) Rev interacting protein Rip-1 [Homo sapiens]	0.009

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
1672	13122465	gi|13122465|gb|AAK12639.1|AF317654_1 (AF317654) G protein-coupled receptor [Homo sapiens]	2.4
1673	7296752	gi|7296752|gb|AAF52030.1| (AE003603) CG12147 gene product [Drosophila melanogaster]	2.1
1681	14767950	gi|14767950|ref|XP_040494.1| nuclear RNA export factor 5 [Homo sapiens] emb|CAC20428.1| (AJ277654) nuclear RNA export factor 5 [Homo sapiens]	6.9
1684	14740021	gi|14740021|ref|XP_033953.1| 32575 [Homo sapiens] ref|XP_033954.1| 32576 [Homo sapiens] ref|XP_033955.1| 32577 [Homo sapiens]	2.5
1685	13568988	gi|13568988|gb|AAK30843.1|AF254571_1 (AF254571) growth/differentiation factor 7 [Mus musculus]	5.8
1694	106323	gi|106323|pir||A34087 hypothetical protein (L1H 5' region) - human	0.005
1695	7444442	gi|7444442|pir||T02087 gag/pol polyprotein - maize retrotransposon Hopscotch gb|AAA57005.1| (U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]	0.49
1696	13569915	gi|13569915|ref|NP_112205.1| amnionless protein [Homo sapiens] gb|AAK28532.1|AF328788_1 (AF328788) amnionless [Homo sapiens]	4.4
1697	13812078	gi|13812078|ref|NP_113215.1| hypothetical protein [Guillardia theta] gb|AAF24011.1|AF083031_8 (AF083031) hypothetical protein [Guillardia theta]	5.2
1699	462193	gi|462193|sp|Q06003|GOLI_DROME GOLIATH PROTEIN (G1 PROTEIN) pir||JC1495 regulatory protein G1 - fruit fly (Drosophila melanogaster) gb|AAA28582.1| (M97204) goliath protein [Drosophila melanogaster]	9.3
1702	13376638	gi|13376638|ref|NP_079359.1| hypothetical protein FLJ21128 [Homo sapiens] dbj|BAB15001.1| (AK024781) unnamed protein product [Homo sapiens]	5E-49
1705	7445803	gi|7445803|pir||JC5348 cdd4 protein - Clostridium difficile emb|CAA63569.1| (X92982) cdd4 [Clostridium difficile]	0.28
1706	10175016	gi|10175016|dbj|BAB06115.1| (AP001515) BH2396~unknown [Bacillus halodurans]	9
1709	3953531	gi|3953531|dbj|BAA34722.1| (AB015856) ATF6 [Homo sapiens]	9.1

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
1712	14329676	gi|14329676|emb|CAC40651.1| (AJ242782) centaurin beta [Homo sapiens]	0.00003
1714	10432382	gi|10432382|emb|CAC10340.1| (AL139421) dJ717I23.1 (novel protein similar to Xenopus laevis Sojo protein) [Homo sapiens]	0.00006
1717	8247357	gi|8247357|emb|CAB92957.1| (AJ401026) hypothetical protein [Thermoanaerobacter thermohydrosulfuricus]	1.4
1719	7487043	gi|7487043|pir||T08926 hypothetical protein T15N24.50 - Arabidopsis thaliana emb|CAB77061.1| (AL078465) putative protein [Arabidopsis thaliana] emb|CAB79515.1| (AL161565) putative protein [Arabidopsis thaliana]	0.39
1721	13507765	gi|13507765|ref|NP_109714.1| similar to GTPases [Mycoplasma pneumoniae] sp|P75088|Y024_MYCPN PROBABLE GTP-BINDING PROTEIN MG024 HOMOLOG (B01_ORF362) pir||S73454 probable GTP-binding protein yyaF - Mycoplasma pneumoniae (strain ATCC 29342) gb|AAB95776.1| (AE000015) similar to GTPases [Mycoplasma pneumoniae]	6
1725	11071788	gi|11071788|emb|CAC14632.1| (AL449144) hypothetical protein P214.26 [Leishmania major]	9
1727	14325595	gi|14325595|dbj|BAB60498.1| (AP000996) hypothetical protein [Thermoplasma volcanium]	2.5

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
1728	6498442	gi|6498442|dbj|BAA87845.1| (AP000815) ESTs AU081301(E20138),C99280(E10593) correspond to a region of the predicted gene.~Similar to Arabidopsis thaliana chromosome II BAC T26B15 genomic sequence,unknown protein. (AC004681) [Oryza sativa] dbj|BAB00648.2| (AP002804) ESTs AU081301(E20138),C99280(E10593) correspond to a region of the predicted gene.~Similar to Arabidopsis thaliana chromosome II BAC T26B15 genomic sequence; unknown protein (AC004681) [Oryza sativa] dbj|BAB17744.1| (AP002862) contains ESTs AU081301(E20138),C99280(E10593)~similar to Arabidopsis thaliana chromosome 2, F12C20.11~unknown protein [Oryza sativa] dbj|BAB44118.1| (AP003103) contains ESTs AU081301(E20138),C99280(E10593)~similar to Arabidopsis thaliana chromosome 2, F12C20.11~unknown protein [Oryza sativa]	1.1
1741	11467083	gi|11467083|ref|NP_042559.1| NADH dehydrogenase, subunit 3 [Acanthamoeba castellanii] sp|Q37382|NU3M_ACACA NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 pir||S53860 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 3 - Acanthamoeba castellanii mitochondrion gb|AAD11852.1| (U12386) NADH dehydrogenase, subunit 3 [Acanthamoeba castellanii]	5
1742	12843826	gi|12843826|dbj|BAB26128.1| (AK009187) putative [Mus musculus]	0.00000002
1743	4928550	gi|4928550|gb|AAD33637.1| (AF133876) DBL alpha protein [Plasmodium falciparum]	6.2
1744	6503033	gi|6503033|gb|AAF14557.1|AF176666_1 (AF176666) F-box leucine-rich repeat protein 5 [Xenopus laevis]	3.8
1745	6562750	gi|6562750|emb|CAB62889.1| (AL035475) hypothetical protein, MAL4P2.48 [Plasmodium falciparum]	8.9
1750	7498998	gi|7498998|pir||T16057 hypothetical protein F13D11.2 - Caenorhabditis elegans	5.4
1751	6939792	gi|6939792|dbj|BAA90658.1| (AB037920) HA-17 [Clostridium botulinum]	7.3

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
1754	14195008	gi|14195008|sp|Q9JI55|PLE1_CRIGR PLECTIN 1 (PLTN) (PCN) (300-KDA INTERMEDIATE FILAMENT-ASSOCIATED PROTEIN) (IFAP300) gb|AAF70372.1| (AF260753) plectin [Cricetulus griseus]	1.6
1756	74519	gi|74519|pir||GNWVR4 structural polyprotein - rubella virus (strain Therien)	4.4
1760	6324076	gi|6324076|ref|NP_014146.1| Ynl253wp [Saccharomyces cerevisiae] sp|P53851|YNZ3_YEAST HYPOTHETICAL 47.2 KD PROTEIN IN SIP3-MRPL30 INTERGENIC REGION pir||S63226 hypothetical protein YNL253w - yeast (Saccharomyces cerevisiae) emb|CAA65491.1| (X96722) ORF N0860 [Saccharomyces cerevisiae] emb|CAA96160.1| (Z71529) ORF YNL253w [Saccharomyces cerevisiae]	3.6
1762	1708082	gi|1708082|sp|P50900|GUX2_CLOSR EXOGLUCANASE II PRECURSOR (EXOCELLOBIOHYDROLASE II) (1,4-BETA-CELLOBIOHYDROLASE II) (AVICELASE II) emb|CAA93280.1| (Z69359) avicelase II [Clostridium stercorarium]	1.9
1765	2224838	gi|2224838|emb|CAA45388.1| (X63974) putative protein-tyrosine phosphatase [Rhodobacter capsulatus]	5.2
1768	6513773	gi|6513773|gb|AAF14748.1|AF197756_1 (AF197756) maturase [Hedyosmum arborescens]	0.63
1775	14732870	gi|14732870|ref|XP_029018.1| hypothetical protein FLJ10647 [Homo sapiens] ref|XP_001969.2| hypothetical protein FLJ10647 [Homo sapiens]	1.3
1779	7521942	gi|7521942|pir||T29096 gag polyprotein - murine endogenous retrovirus ERV-L emb|CAA73250.1| (Y12713) Gag polyprotein [Mus musculus]	0.071
1785	7508408	gi|7508408|pir||T25251 hypothetical protein T24H10.4 - Caenorhabditis elegans emb|CAA90944.1| (Z54216) T24H10.4 [Caenorhabditis elegans]	2.9
1788	7460247	gi|7460247|pir||B71612 hypothetical protein PFB0555c - *malaria parasite (Plasmodium falciparum)* gb|AAC71900.1| (AE001402) hypothetical protein [Plasmodium falciparum]	6.4

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
1789	4337102	gi|4337102|gb|AAD18078.1|AAD18078 (AF129756) G6f [Homo sapiens]	2E-24
1792	1723494	gi|1723494|sp|Q10413|YD88_SCHPO VERY HYPOTHETICAL 13.3 KD PROTEIN C1F3.08C IN CHROMOSOME I pir||T38079 very hypothetical protein SPAC1F3.08c - fission yeast (Schizosaccharomyces pombe) emb|CAA94626.1| (Z70690) very hypothetical protein [Schizosaccharomyces pombe]	7.2
1793	4589921	gi|4589921|dbj|BAA76927.1| (AB017192) molybdopterin biosynthesis protein [Clostridium perfringens]	4.2
1799	7494302	gi|7494302|pir||E71611 hypothetical protein PFB0580w - malaria parasite (Plasmodium falciparum) gb|AAC71905.1| (AE001404) hypothetical protein [Plasmodium falciparum]	3.3
1800	14318508	gi|14318508|ref|NP_116641.1| Ies1p [Saccharomyces cerevisiae] sp|P43579|YFB3_YEAST HYPOTHETICAL 78.8 KD PROTEIN IN HSP12-HXT10 INTERGENIC REGION pir||S48316 probable membrane protein YFL013c - yeast (Saccharomyces cerevisiae) emb|CAA86347.1| (Z46255) orf, len: 692, CAI: 0.14 [Saccharomyces cerevisiae] dbj|BAA09225.1| (D50617) YFL013C [Saccharomyces cerevisiae]	6.6
1802	14325595	gi|14325595|dbj|BAB60498.1| (AP000996) hypothetical protein [Thermoplasma volcanium]	2
1809	7520399	gi|7520399|pir||T11689 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Graphium sarpedon mitochondrion (fragment) dbj|BAA28187.1| (AB013147) NADH dehydrogenase subunit 5 [Graphium sarpedon]	4.9
1816	423981	gi|423981|pir||A46193 88K E-26-specific domain protein Pok - fruit fly (Drosophila melanogaster) dbj|BAA01080.1| (D10228) Ets domain protein [Drosophila melanogaster]	0.23
1818	7463036	gi|7463036|pir||C70177 beta-glucosidase homolog - Lyme disease spirochete gb|AAC66976.1| (AE001163) beta-glucosidase, putative [Borrelia burgdorferi]	8.4
1819	3851471	gi|3851471|gb|AAC72292.1| (AF037295) sulfonylurea receptor-1 [Mus musculus]	3.4

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
1820	9845030	gi|9845030|dbj|BAB11914.1| (AB034726) 5-oxoprolinase precursor [Alcaligenes faecalis]	5.8
1821	6599044	gi|6599044|emb|CAB63584.1| (AJ251826) BMP2/4 protein [Asterias rubens]	6.7
1822	7715984	gi|7715984|gb|AAF68235.1|AF206244_1 (AF206244) seroreactive antigen BMN1-2 [Babesia microti]	0.067
1823	7293329	gi|7293329|gb|AAF48709.1| (AE003504) CG5162 gene product [Drosophila melanogaster]	2.8
1824	2136095	gi|2136095|pir||I58381 receptor tyrosine kinase isoform FLT4 long - human (fragment) gb|AAB28539.1| (S66407) receptor tyrosine kinase isoform FLT4 long, FLT41 {C-terminal} [human, Peptide Partial, 71 aa] [Homo sapiens]	0.0007
1826	7522093	gi|7522093|pir||T30809 plasminogen related growth factor receptor 3 - Fugu rubripes emb|CAA09086.1| (AJ010317) plasminogen related growth factor receptor 3 [Takifugu rubripes]	4.7
1832	13622999	gi|13622999|gb|AAK34670.1| (AE006621) hypothetical protein [Streptococcus pyogenes M1 GAS]	3.7
1834	6319504	gi|6319504|ref|NP_009586.1| Ybr030wp [Saccharomyces cerevisiae] sp|P38222|YBO0_YEAST HYPOTHETICAL 62.6 KD PROTEIN IN CDS1-RPL4A INTERGENIC REGION pir||S45886 hypothetical protein YBR030w - yeast (Saccharomyces cerevisiae) emb|CAA53686.1| (X76078) YBR0314 [Saccharomyces cerevisiae] emb|CAA84972.1| (Z35899) ORF YBR030w [Saccharomyces cerevisiae] prf||2206497K ORF YBR0314 [Saccharomyces cerevisiae]	0.65
1835	7290986	gi|7290986|gb|AAF46425.1| (AE003445) CG3898 gene product [Drosophila melanogaster]	3.1
1840	14725330	gi|14725330|ref|XP_002254.2| mitochondrial translational initiation factor 2 precursor [Homo sapiens]	4.2

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
1842	7509362	gi|7509362|pir||T31492 hypothetical protein Y116A8C.20 - Caenorhabditis elegans emb|CAB55126.1| (AL117204) predicted using Genefinder~contains similarity to Pfam domain: PF00642 (Zinc finger C-x8-C-x5-C-x3-H type (and similar).), Score=71.0, E-value=3.1e-19, N=2~cDNA EST yk247a8.5 comes from this gene [Caenorhabditis elegans]	8.4
1846	6093793	gi|6093793|sp|Q64181|PROP_CAVPO PROPERDIN PRECURSOR gb|AAB35918.1| (S81116) properdin [guinea pigs, spleen, Peptide, 470 aa] [Cavia]	4.1
1848	7300538	gi|7300538|gb|AAF55691.1| (AE003727) CG7411 gene product [Drosophila melanogaster]	2.7
1849	1730077	gi|1730077|sp|P18160|KYK1_DICDI NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (TYROSINE-PROTEIN KINASE 1) pir||T18276 non-receptor tyrosine kinase - slime mold (Dictyostelium discoideum) gb|AAB41125.1| (U32174) non-receptor tyrosine kinase [Dictyostelium discoideum]	8.4
1851	5326919	gi|5326919|emb|CAB46239.1| (AJ133488) SCO-spondin [Bos taurus]	2.7
1853	13811938	gi|13811938|emb|CAC03433.2| (AL118505) dJ1056H1.2.1 (novel protein similar to mitogen inducible protein MIG-2 (isoform 1)) [Homo sapiens]	2E-21
1859	8954377	gi|8954377|ref|NP_059365.1| haem lyase [Cyanidioschyzon merolae] pir||A58932 cytochrome C-type biogenesis protein CCMF - Cyanidioschyzon merolae mitochondrion dbj|BAA36527.1| (D89861) cytochrome C-type biogenesis protein CCMF [Cyanidioschyzon merolae]	2.3
1860	13376638	gi|13376638|ref|NP_079359.1| hypothetical protein FLJ21128 [Homo sapiens] dbj|BAB15001.1| (AK024781) unnamed protein product [Homo sapiens]	2E-47
1862	14602664	gi|14602664|gb|AAH09855.1|AAH09855 (BC009855) Similar to nucleolin [Homo sapiens]	4E-45

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
1864	7512078	gi|7512078|pir||T30879 dynein heavy chain isotype 5A - sea urchin (Tripneustes gratilla) (fragment) gb|AAA63591.1| (U03977) dynein heavy chain isotype 5A [Tripneustes gratilla]	1.7
1865	7688347	gi|7688347|emb|CAB89836.1| (AJ242516) AmpE protein [Salmonella typhimurium]	2.8
1867	4758568	gi|4758568|ref|NP_004497.1| heat shock transcription factor 2 [Homo sapiens] ref|XP_004466.2| heat shock transcription factor 2 [Homo sapiens] ref|XP_051573.1| heat shock transcription factor 2 [Homo sapiens] sp|Q03933|HSF2_HUMAN HEAT SHOCK FACTOR PROTEIN 2 (HSF 2) (HEAT SHOCK TRANSCRIPTION FACTOR 2) (HSTF 2) pir||A41138 heat shock transcription factor HSF2 - human gb|AAA36017.1| (M65217) HSF2 [Homo sapiens]	0.33
1869	13358509	gi|13358509|ref|NP_078688.1| orf107 [lymphocystis disease virus 1]	8.1
1870	6580323	gi|6580323|emb|CAB63392.1| (AL132864) cDNA EST EMBL:T00048 comes from this gene~cDNA EST EMBL:T00047 comes from this gene~cDNA EST yk390e6.3 comes from this gene~cDNA EST yk512a3.3 comes from this gene~cDNA EST yk512a3.5 comes from this gene~cDNA EST yk532a2.3 comes from this ge>	0.012
1871	11359776	gi|11359776|pir||T45059 hypothetical protein Y39B6B.gg [imported] - Caenorhabditis elegans emb|CAB60938.1| (AL132896) predicted using Genefinder; preliminary prediction [Caenorhabditis elegans]	3.6
1876	5453171	gi|5453171|gb|AAD43464.1| (AF113915) pre-mRNA splicing factor [Heterodera glycines]	2.1
1877	5453171	gi|5453171|gb|AAD43464.1| (AF113915) pre-mRNA splicing factor [Heterodera glycines]	2.1
1880	14752353	gi|14752353|ref|XP_050519.1| annexin A2 [Homo sapiens]	0.27
1881	7494821	gi|7494821|pir||T31996 hypothetical protein B0281.5 - Caenorhabditis elegans gb|AAB66084.1| (AF016666) similar to human tumor necrosis factor-alpha-induced protein B12 (NID:g179304) [Caenorhabditis elegans]	3.8

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
1883	480482	gi|480482|pir||S36953 cytochrome-c oxidase (EC 1.9.3.1) chain III - Herpetomonas samuelpessoai mitochondrion gb|AAD09166.1| (L10852) cytochrome oxidase subunit III [Herpetomonas pessoai]	0.78
1885	5174493	gi|5174493|ref|NP_006050.1| laminin, gamma 3 precursor [Homo sapiens] gb|AAD36991.1|AF041835_1 (AF041835) laminin gamma 3 chain precursor [Homo sapiens]	3E-12
1886	8922792	gi|8922792|ref|NP_060753.1| hypothetical protein FLJ10956 [Homo sapiens] ref|XP_007214.2| hypothetical protein FLJ10956 [Homo sapiens] dbj|BAA91925.1| (AK001818) unnamed protein product [Homo sapiens]	5E-39
1889	7479561	gi|7479561|pir||T35135 hypothetical protein SC4H8.04c SC4H8.04c - Streptomyces coelicolor emb|CAA15871.1| (AL020958) hypothetical protein SC4H8.04c [Streptomyces coelicolor A3(2)]	0.5
1890	7461128	gi|7461128|pir||T03057 hypothetical protein 032R - Chilo iridescent virus gb|AAB94431.1| (AF003534) hypothetical protein 032R [Chilo iridescent virus]	0.33
1891	8778367	gi|8778367|gb|AAF79375.1|AC007887_34 (AC007887) F15O4.28 [Arabidopsis thaliana]	6.6
1894	13475247	gi|13475247|ref|NP_106811.1| unknown protein [Mesorhizobium loti] dbj|BAB52597.1| (AP003008) unknown protein [Mesorhizobium loti]	2.3
1895	2285958	gi|2285958|emb|CAA70903.1| (Y09763) GABRE [Homo sapiens]	2.7
1896	14729939	gi|14729939|ref|XP_038475.1| DKFZP564J102 protein [Homo sapiens]	0.007
1898	7504499	gi|7504499|pir||T32750 hypothetical protein F57B10.1 - Caenorhabditis elegans gb|AAB96719.1| (AF039713) Hypothetical protein F57B10.1 [Caenorhabditis elegans]	4.2
1900	10581310	gi|10581310|gb|AAG20067.1| (AE005086) methionyl aminopeptidase; Map [Halobacterium sp. NRC-1]	8.9
1902	111814	gi|111814|pir||S21347 hypothetical protein 3 - rat emb|CAA37646.1| (X53581) ORF3 [Rattus norvegicus]	0.3
1903	7290766	gi|7290766|gb|AAF46211.1| (AE003439) CG4557 gene product [Drosophila melanogaster]	0.38

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
1904	5139521	gi|5139521|emb|CAB45562.1| (AJ238798) CTRP protein [Plasmodium berghei] dbj|BAA82322.1| (AB027129) adhesive protein-like molecule [Plasmodium berghei] gb|AAF73158.1|AF149771_1 (AF149771) ookinete protein [Plasmodium berghei]	8
1905	7489900	gi|7489900|pir||T18287 protein-tyrosine kinase (EC 2.7.1.112) - slime mold (Dictyostelium discoideum) gb|AAB04999.1| (U64830) protein tyrosine kinase [Dictyostelium discoideum]	5.3
1908	6002776	gi|6002776|gb|AAF00134.1|AF149806_1 (AF149806) hypothetical protein [Oryza sativa]	0.15
1913	14773348	gi|14773348|ref|XP_038450.1| 20849 [Homo sapiens]	2E-50
1916	7301187	gi|7301187|gb|AAF56319.1| (AE003748) CG5794 gene product [Drosophila melanogaster]	8
1918	3378685	gi|3378685|emb|CAA76071.1| (Y16104) replicase protein [Physalis mottle tymovirus]	0.13
1919	4501915	gi|4501915|ref|NP_003807.1| a disintegrin and metalloproteinase domain 9 preproprotein; meltrin gamma [Homo sapiens] gb|AAC50403.1| (U41766) metalloprotease/disintegrin/cysteine-rich protein precursor [Homo sapiens]	0.002
1922	14587070	gi|14587070|gb|AAK70463.1|AF387344_4 (AF387344) spore germination protein GerLC [Bacillus cereus]	8.4
1924	7291161	gi|7291161|gb|AAF46595.1| (AE003450) CG2892 gene product [Drosophila melanogaster]	6
1925	7446016	gi|7446016|pir||E70895 hypothetical glycine-rich protein Rv1087 - Mycobacterium tuberculosis (strain H37RV) emb|CAA17203.1| (AL021897) PE_PGRS [Mycobacterium tuberculosis]	3.6
1926	11595522	gi|11595522|emb|CAC18316.1| (AL451022) hypothetical protein [Neurospora crassa]	5.9
1930	14043326	gi|14043326|gb|AAH07658.1|AAH07658 (BC007658) Unknown (protein for MGC:747) [Homo sapiens]	8E-76
1931	13810543	gi|13810543|dbj|BAB43950.1| (AB051633) ookinete surface protein Pos28-2 [Plasmodium ovale]	3.1
1933	7206826	gi|7206826|gb|AAF39985.1| (AC006696) contains similarity to other proline-rich proteins [Caenorhabditis elegans]	6.6

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
1934	14749721	gi|14749721|ref|XP_027893.1| similar to ALU SUBFAMILY SB1 SEQUENCE CONTAMINATION WARNING ENTRY (H. sapiens) [Homo sapiens]	2.1
1935	12324211	gi|12324211|gb|AAG52077.1|AC012679_15 (AC012679) putative proline-rich protein precursor; 93710-91881 [Arabidopsis thaliana]	2.1
1940	4204305	gi|4204305|gb|AAD10686.1| (AC003027) Hypothetical protein [Arabidopsis thaliana]	5.4
1955	14783118	gi|14783118|ref|XP_043478.1| hypothetical protein XP_043478 [Homo sapiens]	4.7
1959	13375860	gi|13375860|ref|NP_078907.1| hypothetical protein FLJ23342 [Homo sapiens] dbj|BAB15618.1| (AK026995) unnamed protein product [Homo sapiens]	0.2
1962	7304316	gi|7304316|gb|AAF59348.1| (AE003844) CG2052 gene product [Drosophila melanogaster]	8.2
1963	7513579	gi|7513579|pir||T09064 1-acylglycerol-3-phosphate O-acyltransferase (EC 2.3.1.51) - mouse gb|AAB82009.1| (AF030001) lysophatidic acid acyl transferase-alpha [Mus musculus]	1.1
1964	7512671	gi|7512671|pir||T12545 hypothetical protein DKFZp434N074.1 - human (fragments) emb|CAB46377.1| (AL096732) hypothetical protein [Homo sapiens]	3.1
1972	13249541	gi|13249541|gb|AAK15414.1| (AY015597) dissimilatory sulfite reductase subunit B [uncultured sulfate-reducing bacterium]	2
1976	8134766	gi|8134766|sp|Q9ZES2|TRPE_BUCTC ANTHRANILATE SYNTHASE COMPONENT I emb|CAA09993.1| (AJ012333) anthranilate synthase large subunit [Buchnera aphidicola]	5.6
1977	7518768	gi|7518768|pir||A71111 hypothetical protein PH0656 - Pyrococcus horikoshii dbj|BAA29747.1| (AP000003) 107aa long hypothetical protein [Pyrococcus horikoshii]	9.3
1982	14749721	gi|14749721|ref|XP_027893.1| similar to ALU SUBFAMILY SB1 SEQUENCE CONTAMINATION WARNING ENTRY (H. sapiens) [Homo sapiens]	1.9

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
1983	2498123	gi|2498123|sp|O02833|ALS_PAPHA INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN PRECURSOR (ALS) pir||JC5239 insulin-like growth factor acid-labile chain - baboon	4.4
1990	2911545	gi|2911545|emb|CAA75449.1| (Y15173) E6 protein [Human papillomavirus type 75]	4.2
1992	1090764	gi|1090764|prf||2019432A cyclin-dependent kinase 5 activator [Bos taurus]	2.1
1993	7446170	gi|7446170|pir||T02529 myb-related protein F13M22.13 - Arabidopsis thaliana gb|AAC23633.1| (AC004684) putative MYB family transcription factor [Arabidopsis thaliana] gb|AAD53101.1|AF175996_1 (AF175996) putative transcription factor [Arabidopsis thaliana]	5.9
1994	4501915	gi|4501915|ref|NP_003807.1| a disintegrin and metalloproteinase domain 9 preproprotein; meltrin gamma [Homo sapiens] gb|AAC50403.1| (U41766) metalloprotease/disintegrin/cysteine-rich protein precursor [Homo sapiens]	0.002
1997	12853260	gi|12853260|dbj|BAB29697.1| (AK015063) putative [Mus musculus]	6.1
2000	6492289	gi|6492289|gb|AAF14258.1|AF137068_1 (AF137068) cubilin [Canis familiaris]	4.6
2001	2828501	gi|2828501|sp|P40899|ISP3_SCHPO SEXUAL DIFFERENTIATION PROCESS PROTEIN ISP3 pir||T38112 sexual differentiation process protein isp3 - fission yeast (Schizosaccharomyces pombe) emb|CAB03599.1| (Z81312) sexual differentiation process protein isp3; meiotic expression upregulated [Schizosaccharomyces pombe]	7.9
2022	4206157	gi|4206157|gb|AAD11433.1| (AF109404) transposase [Streptomyces scabiei]	3.4
2026	11466224	gi|11466224|ref|NP_062847.1| ORF1, contains 4 trans membrane regions, putative [Physarum polycephalum] dbj|BAB08081.1| (AB027295) ORF1, contains 4 trans membrane regions, putative [Physarum polycephalum]	1.2

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
2027	7507536	gi|7507536|pir||T24739 hypothetical protein T09E11.4 - Caenorhabditis elegans emb|CAB03533.1| (Z81147) contains similarity to Pfam domain: PF01757 (Domain of unknown function), Score=594.0, E-value=3e-175, N=1 [Caenorhabditis elegans]	4.3
2028	6102749	gi|6102749|emb|CAB59307.1| (AJ236287) NADH dehydrogenase subunit F [Carphalea glaucescens]	1.9
2031	7486224	gi|7486224|pir||T08553 hypothetical protein F27B13.160 - Arabidopsis thaliana emb|CAB43667.1| (AL050352) putative protein [Arabidopsis thaliana] emb|CAB79750.1| (AL161575) putative protein [Arabidopsis thaliana]	2.7
2032	7462619	gi|7462619|pir||F72210 hypothetical protein TM1801 - Thermotoga maritima (strain MSB8) gb|AAD36864.1|AE001817_11 (AE001817) hypothetical protein [Thermotoga maritima]	6.2
2035	7296128	gi|7296128|gb|AAF51422.1| (AE003587) CG4629 gene product [Drosophila melanogaster]	3.4
2038	14760974	gi|14760974|ref|XP_034809.1| similar to putative gag-pro-pol polyprotein (H. sapiens) [Homo sapiens]	1E-13
2041	14601134	gi|14601134|ref|NP_147662.1| hypothetical protein [Aeropyrum pernix] pir||H72698 hypothetical protein APE1008 - Aeropyrum pernix (strain K1) dbj|BAA79992.1| (AP000060) 123aa long hypothetical protein [Aeropyrum pernix]	2.6
2043	4507537	gi|4507537|ref|NP_003260.1| nuclear receptor subfamily 2, group E, member 1; tailless (Drosophila) homolog; tailless homolog (Drosophila) [Homo sapiens] ref|XP_004530.1| 54551 [Homo sapiens] ref|XP_038737.1| nuclear receptor subfamily 2, group E, member 1 [Homo sapiens] sp|Q9Y466|NR21_HUMAN ORPHAN NUCLEAR RECEPTOR NR2E1 (NUCLEAR RECEPTOR TLX) (TAILLESS HOMOLOG) (TLL) (HTLL) emb|CAA73725.1| (Y13276) Tailless protein [Homo sapiens] emb|CAB75626.1| (AL078596) dJ429G5.1 (nuclear receptor subfamily 2, group E, member 1) [Homo sapiens] gb|AAG31945.1|AF220532_1 (AF220532) orphan nuclear receptor [Homo sapiens]	9E-10

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
2044	7300319	gi|7300319|gb|AAF55480.1| (AE003719) CG7305 gene product [Drosophila melanogaster]	3.3
2046	7498832	gi|7498832|pir||T34212 hypothetical protein F10E7.4 - Caenorhabditis elegans gb|AAA82427.1| (U41264) coded for by C. elegans cDNA yk99a6.5; coded for by C. elegans cDNA yk72g6.5; coded for by C. elegans cDNA yk99a6.3; coded for by C. elegans cDNA yk72g6.3; coded for by C. elegans cDNA yk127a2.5; coded for by C. elegans cDNA yk127a2.3; Simila>	9.7
2050	13643847	gi|13643847|ref|XP_011044.2| 8-oxoguanine DNA glycosylase [Homo sapiens] ref|XP_016414.1| 8-oxoguanine DNA glycosylase [Homo sapiens] ref|XP_016415.1| 8-oxoguanine DNA glycosylase [Homo sapiens] ref|XP_031967.1| 8-oxoguanine DNA glycosylase [Homo sapiens] ref|XP_031959.1| 8-oxoguanine DNA glycosylase, isoform 2d [Homo sapiens] ref|XP_031961.1| 8-oxoguanine DNA glycosylase, isoform 1a [Homo sapiens] ref|XP_052277.1| similar to 8-oxoguanine DNA glycosylase (H. sapiens) [Homo sapiens]	1.2
2051	7474551	gi|7474551|pir||E69792 conserved hypothetical protein yeeA - Bacillus subtilis emb|CAB12496.1| (Z99107) similar to hypothetical proteins [Bacillus subtilis]	7
2060	3913201	gi|3913201|sp|Q58511|CCA_METJA TRNA NUCLEOTIDYLTRANSFERASE (TRNA ADENYLYLTRANSFERASE) (TRNA CCA-PYROPHOSPHORYLASE) (CCA-ADDING ENZYME) gb|AAB99114.1| (U67554) tRNA nucleotidyltransferase (cca) [Methanococcus jannaschii]	5.9
2072	13186342	gi|13186342|gb|AAK15384.1| (AF211134) valyl-tRNA synthetase [Carsonella ruddii]	2.8

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
2075	6225820	gi|6225820|sp|O04226|P5CS_ORYSA DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE (P5CS) [INCLUDES: GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK); GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDEHYDE DEHYDROGENASE)] pir||T03695 delta 1 pyrroline-5-carboxylate synthetase - rice dbj|BAA19916.1| (D49714) deltal-pyrroline-5-carboxylate synthetase [Oryza sativa]	9.4
2077	4028153	gi|4028153|gb|AAC96117.1| (AF083221) putative neurotransmitter receptor [Takifugu rubripes]	2
2080	4902680	gi|4902680|emb|CAB43550.1| (AL031673) dJ694B14.3 (novel haloacid dehalogenase-like hydrolase family protein similar to (archaea) bacterial proteins) [Homo sapiens]	2.9
2084	6322760	gi|6322760|ref|NP_012833.1| Ykl090wp [Saccharomyces cerevisiae] sp|P36075|YKJ0_YEAST HYPOTHETICAL 50.9 KD PROTEIN IN BUD2-MIF2 INTERGENIC REGION pir||S37915 hypothetical protein YKL090w - yeast (Saccharomyces cerevisiae) emb|CAA81928.1| (Z28090) ORF YKL090w [Saccharomyces cerevisiae]	2.8
2085	6635084	gi|6635084|emb|CAB64573.1| (AL135930) hypothetical protein L4738.02 [Leishmania major]	3.6
2086	7487726	gi|7487726|pir||T05814 hypothetical protein T5K18.90 - Arabidopsis thaliana emb|CAA18618.1| (AL022580) hypothetical protein [Arabidopsis thaliana] emb|CAB78933.1| (AL161550) hypothetical protein [Arabidopsis thaliana]	5.9
2089	13385468	gi|13385468|ref|NP_080247.1| RIKEN cDNA 2900001A12 gene [Mus musculus] dbj|BAB28377.1| (AK012645) putative [Mus musculus] dbj|BAB28865.1| (AK013457) putative [Mus musculus]	4E-11
2090	14742770	gi|14742770|ref|XP_039393.1| KIAA1550 protein [Homo sapiens]	3.2
2092	2982251	gi|2982251|gb|AAC32113.1| (AF051208) putative RNA-binding protein [Picea mariana]	7.6

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
2095	12718478	gi|12718478|emb|CAC28807.1| (AL513466) hypothetical protein [Neurospora crassa]	3.1
2096	5532964	gi|5532964|gb|AAD44957.1| (AF156655) MHC class I heavy chain [Ambystoma mexicanum]	9.3
2097	1711658	gi|1711658|sp|P54797|T10_MOUSE SER/THR-RICH PROTEIN T10 IN DGCR REGION pir||S37488 gene T10 protein - mouse emb|CAA52612.1| (X74504) T10 [Mus musculus]	4.3
2098	14193393	gi|14193393|gb|AAK55953.1|AF268062_2 (AF268062) RNA polymerase beta-prime subunit [Candidatus Carsonella ruddii]	2.1
2099	7243081	gi|7243081|dbj|BAA92588.1| (AB037771) KIAA1350 protein [Homo sapiens]	7E-97
2100	11357181	gi|11357181|pir||T49996 AtAGP4 - Arabidopsis thaliana gb|AAC77826.1| (AF082301) arabinogalactan-protein [Arabidopsis thaliana] gb|AAD38870.1|AF060874_1 (AF060874) AtAGP4 [Arabidopsis thaliana] emb|CAB89400.1| (AL353995) AtAGP4 [Arabidopsis thaliana] gb|AAK49601.1|AF372885_1 (AF372885) AT5g10430/F12B17_220 [Arabidopsis thaliana] gb|AAK68734.1| (AY042794) AtAGP4 [Arabidopsis thaliana]	1.2
2103	7497369	gi|7497369|pir||T32512 hypothetical protein C44B12.4 - Caenorhabditis elegans gb|AAB88327.1| (AF036692) Hypothetical protein C44B12.4 [Caenorhabditis elegans]	6.7
2109	14485227	gi|14485227|gb|AAK62977.1|AF384372_3 (AF384372) surface antigen [Hepatitis B virus]	5.7
2111	9711862	gi|9711862|dbj|BAB07956.1| (AP002524) putative extensin-like protein [Oryza sativa] dbj|BAB33013.1| (AP003118) putative extensin-like protein [Oryza sativa]	10
2114	9759203	gi|9759203|dbj|BAB09740.1| (AB015476) heat shock transcription factor HSF30-like protein [Arabidopsis thaliana]	8.4
2115	204070	gi|204070|gb|AAA41130.1| (M22030) electron transfer flavoprotein alpha-subunit [Rattus norvegicus]	0.75
2117	3638957	gi|3638957|gb|AAC36301.1| (AC004877) sco-spondin-mucin-like; similar to P98167 (PID:g1711548); details of intron/exon structure uncertain [Homo sapiens]	8.1

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
2121	14250436	gi|14250436|gb|AAH08653.1|AAH08653 (BC008653) Similar to LRP16 protein [Mus musculus]	9.3
2126	14760522	gi|14760522|ref|XP_038798.1| 7371 [Homo sapiens] gb|AAK01445.1| (AF334585) NIR3 [Homo sapiens]	5E-39
2134	3024944	gi|3024944|sp|Q58366|Y956_METJA HYPOTHETICAL PROTEIN MJ0956 pir||D64419 hypothetical protein MJ0956 - Methanococcus jannaschii gb|AAB98969.1| (U67539) M. jannaschii predicted coding region MJ0956 [Methanococcus jannaschii]	8.4
2135	6606266	gi|6606266|gb|AAF19148.1|AF158634_1 (AF158634) Vrga1 [Aegilops ventricosa]	7.1
2137	1729878	gi|1729878|sp|P54410|TCPH_TETTH T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA) pir||S71338 t-complex protein 1 theta chain - Tetrahymena thermophila (fragment) gb|AAC47007.1| (U46028) CCTeta [Tetrahymena thermophila] prf||2209286B chaperonin CCT-eta [Tetrahymena thermophila]	4.4
2141	3688193	gi|3688193|emb|CAA08995.1| (AJ010091) MAP3K alpha 1 protein kinase [Brassica napus]	6.9
2142	7491910	gi|7491910|pir||T41367 hypothetical protein SPCC4G3.09c - fission yeast (Schizosaccharomyces pombe) emb|CAB09776.1| (Z97052) hypothetical protein [Schizosaccharomyces pombe]	3.3
2144	6513832	gi|6513832|gb|AAF14807.1|AF197815_1 (AF197815) maturase [Alisma plantago-aquatica]	1.5
2148	6323084	gi|6323084|ref|NP_013156.1| transcription factor, probable member of histone acetyltransferase SAGA complex; Spt8p [Saccharomyces cerevisiae] sp|P38915|SPT8_YEAST TRANSCRIPTION FACTOR SPT8 pir||S47898 transcription factor SPT8 - yeast (Saccharomyces cerevisiae) gb|AAA53585.1| (M94955) transcription factor [Saccharomyces cerevisiae] emb|CAA64302.1| (X94607) transcription factor [Saccharomyces cerevisiae] emb|CAA97585.1| (Z73227) ORF YLR055c [Saccharomyces cerevisiae]	5.8

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
2151	1074219	gi|1074219|pir||S49239 hypothetical protein 2 (capsulation locus) - Haemophilus influenzae (strain RM107)	4
2153	10946710	gi|10946710|ref|NP_067350.1| Rhesus blood group-associated B glycoprotein; Rh type B glycoprotein [Mus musculus] gb|AAF19371.1| (AF193808) Rh type B glycoprotein [Mus musculus]	3.5
2159	9625644	gi|9625644|ref|NP_039895.1| BDLF2 late reading frame [Human herpesvirus 4] sp|P03225|BDL2_EBV PROTEIN BDLF2 pir||QQBE44 BDLF2 protein - human herpesvirus 4 (strain B95-8) emb|CAA24836.1| (V01555) BDLF2 late reading frame [Human herpesvirus 4]	3.7
2160	220578	gi|220578|dbj|BAA00447.1| (D00570) open reading frame (251 AA) [Mus musculus]	4.7
2165	9633076	gi|9633076|ref|NP_050182.1| B4 [Human herpesvirus 6B] pir||T44148 hypothetical protein B4 [imported] - human herpesvirus 6 (strain Z29) gb|AAD49620.1|AF157706_7 (AF157706) B4 [Human herpesvirus 6B]	0.057
2168	135838	gi|135838|sp|P01267|THYG_BOVIN THYROGLOBULIN PRECURSOR pir||UIBO thyroglobulin precursor - bovine emb|CAA26584.1| (X02815) thyroglobulin precursor [Bos taurus] prf||1109240A thyroglobulin [Bos taurus]	2
2173	11360154	gi|11360154|pir||T46337 hypothetical protein DKFZp434O2413.1 - human (fragment) emb|CAB70664.1| (AL137265) hypothetical protein [Homo sapiens]	3.7
2177	181400	gi|181400|gb|AAA35748.1| (M34225) cytokeratin 8 [Homo sapiens]	7E-53
2181	11347010	gi|11347010|pir||B81303 probable membrane protein Cj1013c [imported] - Campylobacter jejuni (strain NCTC 11168) emb|CAB73269.1| (AL139077) putative membrane protein [Campylobacter jejuni]	0.1
2182	8745261	gi|8745261|gb|AAF78857.1|AF134516_1 (AF134516) VP4 [Banna virus]	6

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
2183	285275	gi|285275|pir||A43963 envelope glycoprotein G(envelope glycoprotein G1, envelope glycoprotein G2) - Hantavirus sp.=Puumala virus gb|AAB22506.1| envelope glycoprotein G(envelope glycoprotein G1, envelope glycoprotein G2) [Hantavirus sp.=Puumala virus, Hallnas strain, Peptide, 1148 aa]	0.6
2186	7506378	gi|7506378|pir||T23989 hypothetical protein R07A4.3 - Caenorhabditis elegans emb|CAA91763.1| (Z67756) cDNA EST yk63e10.5 comes from this gene~cDNA EST yk63e10.3 comes from this gene [Caenorhabditis elegans]	8.9
2187	4511976	gi|4511976|gb|AAD21536.1| (AF088896) unknown [Zymomonas mobilis]	0.65
2188	14761847	gi|14761847|ref|XP_017198.2| hypothetical protein FLJ12085 [Homo sapiens]	3E-13
2192	5835478	gi|5835478|ref|NP_008404.1|CYTB_13475 cytochrome b [Balanoglossus carnosus] pir||T11138 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome b - acorn worm mitochondrion gb|AAD11951.1| (AF051097) cytochrome b [Balanoglossus carnosus]	0.95
2195	14906463	gi|14906463|gb|AAK72690.1| (AY039648) transcription factor Rel 1 [Crassostrea gigas]	9.3
2196	6680964	gi|6680964|ref|NP_031758.1| procollagen, type XVII, alpha 1 [Mus musculus] pir||A46053 bullous pemphigoid antigen, BPAG2, type XVII collagen alpha 1-chain - mouse gb|AAA37443.1| (L08407) collagen type XVII [Mus musculus]	6.8
2197	7206631	gi|7206631|gb|AAF39790.1| (AC006631) Hypothetical protein F27B3.2 [Caenorhabditis elegans]	4.3
2201	2564679	gi|2564679|gb|AAB81836.1| (AF023484) putative KP78 protein kinase [Drosophila melanogaster]	0.83
2204	9558143	gi|9558143|emb|CAC00269.1| (AL160371) possible f16d3.1 protein [Leishmania major]	5.3
2205	13813146	gi|13813146|gb|AAK40384.1| (AE006643) ATP-dependent helicase [Sulfolobus solfataricus]	4.3
2206	7662168	gi|7662168|ref|NP_055497.1| KIAA0535 gene product [Homo sapiens] dbj|BAA25461.1| (AB011107) KIAA0535 protein [Homo sapiens]	0.0003

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
2214	9229890	gi|9229890|dbj|BAB00618.1| (AB036841) prickle 2 [Ciona intestinalis]	4.4
2217	3435174	gi|3435174|gb|AAC32342.1| (AF061251) O antigen flippase Wzx [Escherichia coli] gb|AAG57097.1|AE005429_8 (AE005429) O antigen flippase Wzx [Escherichia coli O157:H7 EDL933]	2.5
2225	5725923	gi|5725923|gb|AAD48242.1|AF089987_1 (AF089987) four-loop conotoxin ABVIF [Conus abbreviatus] gb|AAD48243.1|AF089988_1 (AF089988) four-loop conotoxin ABVIF [Conus abbreviatus] gb|AAD48244.1|AF089989_1 (AF089989) four-loop conotoxin ABVIF [Conus abbreviatus] gb|AAD48245.1|AF089990_1 (AF089990) four-loop conotoxin ABVIF [Conus abbreviatus]	3.8
2228	1705523	gi|1705523|sp|P52650|C24A_PIG CYTOCHROME B-245 LIGHT CHAIN (P22 PHAGOCYTE B-CYTOCHROME) (NEUTROPHIL CYTOCHROME B, 22 KD POLYPEPTIDE) (P22-PHOX) (CYTOCHROME B(558) ALPHA CHAIN) (SUPEROXIDE-GENERATING NADPH OXIDASE LIGHT CHAIN SUBUNIT) gb|AAA64635.1| (U02477) NADPH oxidase light chain subunit [Sus scrofa]	0.48
2240	730885	gi|730885|sp|P07989|T1M_SALPO TYPE I RESTRICTION ENZYME STYSPI M PROTEIN (M.STYSPI) gb|AAA27143.1| (L02507) restriction-modification enzyme type I M subunit [Salmonella enterica]	4.9
2241	6753572	gi|6753572|ref|NP_034126.1| cytochrome P450, 24 [Mus musculus] sp|Q64441|CP24_MOUSE CYTOCHROME P450-CC24, MITOCHONDRIAL PRECURSOR (P450-CC24) (VITAMIN D(3) 24-HYDROXYLASE) (1,25-DIHYDROXYVITAMIN D(3) 24-HYDROXYLASE) (24-OHASE) pir||S60033 25-hydroxyvitamin D3 24-hydroxylase precursor - mouse dbj|BAA08416.1| (D49438) 25-hydroxyvitamin D3 24-hydroxylase precursor [Mus musculus] dbj|BAA21843.1| (D89669) vitamin D-24-hydroxylase [Mus musculus]	9.7

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
2243	14578299	gi|14578299|gb|AAF99465.1| (AY003872) PV1H14095_P [Plasmodium vivax]	3.7
2245	1916617	gi|1916617|gb|AAB51194.1| (U66003) ADAM 13 [Xenopus laevis]	0.45
2249	5739073	gi|5739073|gb|AAD50327.1| (AF063693) type XIII collagen [Mus musculus]	2.5
2254	3135611	gi|3135611|gb|AAC29067.1| (AF062485) cellulose synthase [Arabidopsis thaliana]	3.1
2256	281689	gi|281689|pir||S27657 hypothetical protein 1 - Rhizobium meliloti gb|AAA26255.1| (M94085) not homologous to known sequences as of 2/92; ORF1; putative [Sinorhizobium meliloti]	6
2257	10434352	gi|10434352|dbj|BAB14232.1| (AK022759) unnamed protein product [Homo sapiens]	2E-23
2258	1504022	gi|1504022|dbj|BAA13210.1| (D86974) KIAA0220 [Homo sapiens]	4E-21
2266	1871176	gi|1871176|gb|AAB63536.1| (U90439) unknown protein [Arabidopsis thaliana]	7.5
2270	12846015	gi|12846015|dbj|BAB26996.1| (AK010513) putative [Mus musculus]	8
2273	12860337	gi|12860337|dbj|BAB31923.1| (AK019929) putative [Mus musculus]	5
2276	994736	gi|994736|gb|AAA75561.1| (M18327) LacOPZ-alpha peptide from pUC9; putative [unidentified cloning vector] gb|AAA75563.1| (M18328) LacOPZ-alpha peptide from pUC9; putative [Cloning vector pBGS9+] gb|AAA75565.1| (M18329) LacOPZ-alpha peptide from pUC9; putative [Cloning vector pBGS9-]	0.00002
2280	11352313	gi|11352313|pir||G83376 probable trehalose synthase PA2152 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG05540.1|AE004642_7 (AE004642) probable trehalose synthase [Pseudomonas aeruginosa]	2
2285	7486992	gi|7486992|pir||T00831 hypothetical protein T13L16.5 - Arabidopsis thaliana gb|AAD20114.2| (AC006201) hypothetical protein [Arabidopsis thaliana]	1.4
2286	10173203	gi|10173203|dbj|BAB04308.1| (AP001509) BH0589~unknown conserved protein in others [Bacillus halodurans]	7.3

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
2289	7497857	gi|7497857|pir||T20180 hypothetical protein C53B4.4a - Caenorhabditis elegans emb|CAA92457.1| (Z68215) contains similarity to Pfam domain: PF00130 (Phorbol esters/diacylglycerol binding domain (C1 domain)), Score=12.8, E-value=0.0015, N=1; PF00595 (PDZ domain (Also known as DHR or GLGF).), Score=34.8, E-value=6.4e-07, N=1~cDNA EST CEMSC66F come>	9.6
2291	6424831	gi|6424831|gb|AAF08166.1| (AF130210) NADH dehydrogenase subunit F [Impatiens biflora]	6.1
2292	7489002	gi|7489002|pir||T07021 extensin-like protein Dif10 precursor - tomato (fragment) emb|CAA67813.1| (X99451) extensin-like protein Dif10 [Lycopersicon esculentum]	5.6
2294	1684828	gi|1684828|gb|AAB36537.1| (U77681) tyrosine kinase receptor [Xenopus laevis]	2
2297	12859724	gi|12859724|dbj|BAB31753.1| (AK019486) putative [Mus musculus]	0.0003
2301	11498284	gi|11498284|ref|NP_069510.1| adenylate kinase (adk) [Archaeoglobus fulgidus] sp|O29581|KAD_ARCFU ADENYLATE KINASE (ATP-AMP TRANSPHOSPHORYLASE) pir||D69334 adenylate kinase (EC 2.7.4.3) - Archaeoglobus fulgidus gb|AAB90565.1| (AE001058) adenylate kinase (adk) [Archaeoglobus fulgidus]	3E-13
2309	14725330	gi|14725330|ref|XP_002254.2| mitochondrial translational initiation factor 2 precursor [Homo sapiens]	4.5
2313	79651	gi|79651|pir||A30189 iron stress-induced hypothetical protein precursor - Synechococcus sp	2.8
2314	7500007	gi|7500007|pir||T16186 hypothetical protein F27D9.4 - Caenorhabditis elegans gb|AAA93383.1| (U49829) Hypothetical protein F27D9.4 [Caenorhabditis elegans]	7.1
2317	13517833	gi|13517833|gb|AAK29011.1| (AF344620) long-wavelength rhodopsin [Ceratina calcarata]	3.4

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
2318	7478661	gi|7478661|pir||F70662 probable plcC protein - Mycobacterium tuberculosis (strain H37RV) emb|CAB06146.1| (Z83860) plcC [Mycobacterium tuberculosis] gb|AAK46707.1| (AE007081) phospholipase C [Mycobacterium tuberculosis CDC1551]	4.4
2323	14768227	gi|14768227|ref|XP_012121.3| purinergic receptor P2X, ligand-gated ion channel, 7 [Homo sapiens]	4.3
2328	283032	gi|283032|pir||S22456 hydroxyproline-rich glycoprotein - perennial teosinte emb|CAA45514.1| (X64173) hydroxyproline-rich glycoprotein [Zea diploperennis]	5.4
2329	10241645	gi|10241645|emb|CAC09484.1| (AL442113) putative protein [Oryza sativa]	9.1
2330	14733085	gi|14733085|ref|XP_003575.3| soluble liver antigen/liver pancreas antigen [Homo sapiens]	1E-17
2335	12188796	gi|12188796|emb|CAC21494.1| (AJ278866) MchF protein [Escherichia coli]	4.7
2340	2492604	gi|2492604|sp|P78595|CDR2_CANAL MULTIDRUG RESISTANCE PROTEIN CDR2 gb|AAB96797.1| (U63812) drug resistance protein 2 [Candida albicans]	6.4
2345	13365569	gi|13365569|dbj|BAB39114.1| (AP002897) hypothetical protein~similar to Oryza sativa chromosome 1, P0665D10.16	1.8
2346	1334612	gi|1334612|emb|CAA41034.1| (X57968) nad1 [Triticum aestivum]	4.8
2351	1334612	gi|1334612|emb|CAA41034.1| (X57968) nad1 [Triticum aestivum]	4.8
2352	1334612	gi|1334612|emb|CAA41034.1| (X57968) nad1 [Triticum aestivum]	4.6
2353	1334612	gi|1334612|emb|CAA41034.1| (X57968) nad1 [Triticum aestivum]	4.8
2356	1334612	gi|1334612|emb|CAA41034.1| (X57968) nad1 [Triticum aestivum]	4.4
2357	14250644	gi|14250644|gb|AAH08786.1|AAH08786 (BC008786) integrin, alpha 5 (fibronectin receptor, alpha polypeptide) [Homo sapiens]	2
2367	7293054	gi|7293054|gb|AAF48440.1| (AE003498) Top1 gene product [Drosophila melanogaster]	1.2
2369	13959344	gi|13959344|sp|P82957|DM43_DIDMA VENOM METALLOPROTEINASE INHIBITOR DM43	8.2

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
2371	9082017	gi|9082017|gb|AAF82689.1|AF227196_1 (AF227196) ORF1a polyprotein [gill-associated virus]	7.8
2374	7498863	gi|7498863|pir||T20730 hypothetical protein F10G8.8 - Caenorhabditis elegans emb|CAB02286.2| (Z80216) Weak similarity with intermediate filament protein (TREMBL id G633240), contains similarity to Pfam domain: PF00169 (PH domain), Score=79.3, E-value=2.7e-21, N=2~cDNA EST EMBL:T01262 comes from this gene~cDNA EST yk23d5.3 comes from this gene~> emb|CAA19441.2| (AL023823) Weak similarity with intermediate filament protein (TREMBL id G633240), contains similarity to Pfam domain: PF00169 (PH domain), Score=79.3, E-value=2.7e-21, N=2~cDNA EST EMBL:T01262 comes from this gene~cDNA EST yk23d5.3 comes from this gen>	2.5
2375	321514	gi|321514|pir||S27931 Env/v-mpl fusion protein - myeloproliferative leukemia virus gb|AAA77654.1| (M60350) env:v-mpl fusion protein [Myeloproliferative leukemia virus]	2.8
2376	11348760	gi|11348760|pir||C83635 hypothetical protein PA0086 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG03476.1|AE004447_9 (AE004447) hypothetical protein [Pseudomonas aeruginosa]	4.6
2377	742234	gi|742234|prf||2009317A adhA upstream ORF [Acetobacter (subgen. Acetobacter) aceti]	8.2
2379	11466189	gi|11466189|ref|NP_066512.1| apocytochrome b [Naegleria gruberi] gb|AAG17790.1|AF288092_15 (AF288092) apocytochrome b [Naegleria gruberi]	7.2
2380	8250181	gi|8250181|emb|CAB93524.1| (AJ271740) D-Titin [Drosophila melanogaster]	4.2
2383	5870848	gi|5870848|gb|AAB03857.2| (U31864) stearyl-CoA desaturase [Cyprinus carpio]	7.7
2387	4063751	gi|4063751|gb|AAC98459.1| (AC005851) putative ABC transporter [Arabidopsis thaliana]	7.6
2389	7504822	gi|7504822|pir||T33371 hypothetical protein H02F09.1 - Caenorhabditis elegans gb|AAC64621.1| (AF077538) unknown [Caenorhabditis elegans]	3.6

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
2390	15011889	gi|15011889|ref|NP_077251.1| oxysterol binding protein 2 [Mus musculus] emb|CAC16404.2| (AJ278263) oxystyrol-binding protein homologue 1 [Mus musculus domesticus]	1.9
2393	450730	gi|450730|emb|CAA50838.1| (X71982) ORF j18L; potential membrane spanning region; potential glcosylation site [African swine fever virus]	2.5
2398	7445990	gi|7445990|pir||G72290 branched chain amino acid ABC transporter, ATP-binding protein - Thermotoga maritima (strain MSB8) gb|AAD36215.1|AE001771_8 (AE001771) branched chain amino acid ABC transporter, ATP-binding protein [Thermotoga maritima]	7.4
2401	11990448	gi|11990448|dbj|BAB19782.1| (AB052747) vascular cell adhesion molecule-1 6D variant lacking D7 [Bos taurus]	4.6
2402	12841678	gi|12841678|dbj|BAB25308.1| (AK007856) putative [Mus musculus]	1E-39
2403	5052967	gi|5052967|gb|AAD38786.1|AF151533_1 (AF151533) polyketide synthase [Nodulisporium sp. ATCC74245]	6.3
2407	8099350	gi|8099350|gb|AAF72105.1|AF154847_1 (AF154847) 33 kDa Vamp-associated protein [Homo sapiens]	5.2
2410	267344	gi|267344|sp|P29791|VGLF_BRSVA FUSION GLYCOPROTEIN PRECURSOR [CONTAINS: FUSION GLYCOPROTEIN F2; FUSION GLYCOPROTEIN F1] pir||VGNZBA cell fusion glycoprotein precursor - bovine respiratory syncytial virus (strain A51908) gb|AAA42804.1| (M82816) fusion protein F [Bovine respiratory syncytial virus]	1.4
2417	12856615	gi|12856615|dbj|BAB30727.1| (AK017396) putative [Mus musculus]	8E-49
2425	11347010	gi|11347010|pir||B81303 probable membrane protein Cj1013c [imported] - Campylobacter jejuni (strain NCTC 11168) emb|CAB73269.1| (AL139077) putative membrane protein [Campylobacter jejuni]	0.89
2426	7499991	gi|7499991|pir||T29526 hypothetical protein F27C1.7 - Caenorhabditis elegans gb|AAB37654.1| (U80441) Hypothetical protein F27C1.7 [Caenorhabditis elegans]	3.1

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
2427	2498043	gi|2498043|sp|Q57568|Y104_METJA HYPOTHETICAL ATP-BINDING PROTEIN MJ0104 pir||H64312 probable DNA helicase MJ0104 - Methanococcus jannaschii gb|AAB98084.1| (U67467) DNA-binding protein, probably DNA helicase [Methanococcus jannaschii]	1.5
2430	7494263	gi|7494263|pir||T18488 hypothetical protein C0825c - malaria parasite (Plasmodium falciparum) emb|CAB11127.1| (Z98551) putative cleavage and polyadenylation specificity factor protein [Plasmodium falciparum]	2.3
2434	493224	gi|493224|dbj|BAA03434.1| (D14581) fatty-acid desaturase [Anabaena variabilis]	9.1
2438	6755468	gi|6755468|ref|NP_036019.1| septin 3 [Mus musculus] sp|Q9Z1S5|SEP3_MOUSE NEURONAL-SPECIFIC SEPTIN 3 gb|AAD02884.1| (AF104411) neuronal-specific septin 3 [Mus musculus]	0.59
2440	9967295	gi|9967295|dbj|BAB12347.1| (AB047936) hypothetical protein [Macaca fascicularis]	0.063
2447	12847975	gi|12847975|dbj|BAB27780.1| (AK011690) putative [Mus musculus]	7E-65
2451	1730946	gi|1730946|sp|P50833|YPPE_BACSU HYPOTHETICAL 14.5 KDA PROTEIN IN PONA-COTD INTERGENIC REGION pir||B69940 hypothetical protein yppE - Bacillus subtilis gb|AAB38463.1| (L47838) putative [Bacillus subtilis] emb|CAB14144.1| (Z99115) yppE [Bacillus subtilis]	9.3
2452	401192	gi|401192|sp|P30975|TLR2_DROME TACHYKININ-LIKE PEPTIDES RECEPTOR 99D (DTKR) pir||S17783 tachykinin receptor homolog DTKR - fruit fly (Drosophila melanogaster) emb|CAA44595.1| (X62711) receptor for tachykinin-like peptides [Drosophila melanogaster]	4.8
2453	14768202	gi|14768202|ref|XP_018137.2| L1 cell adhesion molecule precursor [Homo sapiens]	0.11

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
2457	141028	gi|141028|sp|P04540|NU5M_TRYBB NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 pir||QQUTC5 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Trypanosoma brucei mitochondrion gb|AAB59225.1| (M14820) NADH dehydrogenase subunit 5 [Trypanosoma brucei] emb|CAB57807.1| (X01094) unidentified reading frame 10 [Trypanosoma brucei]	3.6
2461	7499039	gi|7499039|pir||T20867 hypothetical protein F13H10.5 - Caenorhabditis elegans emb|CAA92956.1| (Z68748) contains similarity to Pfam domain: PF01663 (Type I phosphodiesterase / nucleotide pyrophosphatase), Score=512.3, E-value=1.1e-150, N=1 [Caenorhabditis elegans] emb|CAA15977.1| (AL021176) contains similarity to Pfam domain: PF01663 (Type I phosphodiesterase / nucleotide pyrophosphatase), Score=512.3, E-value=1.1e-150, N=1 [Caenorhabditis elegans]	9.7
2462	3023956	gi|3023956|sp|Q00808|HET1_PODAN VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1 pir||T18521 beta transducin-like protein - Podospora anserina gb|AAA85775.1| (L28125) beta transducin-like protein [Podospora anserina]	8.7
2463	14972564	gi|14972564|gb|AAK75201.1| (AE007410) glutamine amidotransferase, class I [Streptococcus pneumoniae]	0.4
2470	13928966	gi|13928966|ref|NP_113882.1| heat shock factor 2 [Rattus norvegicus] gb|AAD51329.1|AF172640_1 (AF172640) heat shock factor 2 [Rattus norvegicus]	6E-14
2473	4521320	gi|4521320|dbj|BAA11580.1| (D82816) product is unknown [Gallus gallus]	0.29
2475	7507534	gi|7507534|pir||T24738 hypothetical protein T09E11.2 - Caenorhabditis elegans emb|CAB03532.1| (Z81147) Similarity to zinc finger proteins, contains similarity to Pfam domain: PF00104 (Ligand-binding domain of nuclear hormone receptor), Score=14.1, E-value=0.00047, N=1; PF00105 (Zinc finger, C4 type (two domains)), Score=42.6, E-value=5.5e-12, N>	6.7

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
2478	927030	gi|927030|gb|AAA73871.1| (L13287) kcrB4 gene product [Escherichia coli]	3.5
2481	6724309	gi|6724309|gb|AAF26929.1| (AF079967) NADH dehydrogenase subunit 4 [Phytomonas serpens]	7.9
2482	6319700	gi|6319700|ref|NP_009783.1| Ybr224wp [Saccharomyces cerevisiae] sp|P38320|YB74_YEAST HYPOTHETICAL 19.3 KDA PROTEIN IN FAT2-MCX1 INTERGENIC REGION PRECURSOR pir||S46100 probable membrane protein YBR224w - yeast (Saccharomyces cerevisiae) emb|CAA85187.1| (Z36092) ORF YBR224w [Saccharomyces cerevisiae]	2.4
2496	7503173	gi|7503173|pir||T31884 hypothetical protein F41E6.14 - Caenorhabditis elegans gb|AAB65962.1| (AF016448) weak similarity to several acyltransferases [Caenorhabditis elegans]	9.7
2498	11352621	gi|11352621|pir||E83187 tetrahydrodipicolinate succinylase PA3666 [imported] - Pseudomonas aeruginosa (strain PAO1) dbj|BAA75911.1| (AB024601) tetrahydrodipicolinate N-succinyletransferase [Pseudomonas aeruginosa] gb|AAG07054.1|AE004786_6 (AE004786) tetrahydrodipicolinate succinylase [Pseudomonas aeruginosa]	3.3
2500	7662214	gi|7662214|ref|NP_055604.1| KIAA0628 gene product [Homo sapiens] ref|XP_005044.3| KIAA0628 gene product [Homo sapiens] dbj|BAA31603.1| (AB014528) KIAA0628 protein [Homo sapiens]	3
2506	7508531	gi|7508531|pir||T25325 hypothetical protein T26H2.7 - Caenorhabditis elegans emb|CAB04848.1| (Z82055) contains similarity to Pfam domain: PF01757 (Domain of unknown function), Score=543.5, E-value=4.6e-160, N=1 [Caenorhabditis elegans]	9.2
2507	14730527	gi|14730527|ref|XP_051896.1| phospholipase A2, group IVA (cytosolic, calcium-dependent) [Homo sapiens] ref|XP_051897.1| phospholipase A2, group IVA (cytosolic, calcium-dependent) [Homo sapiens]	5E-26

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
2510	138394	gi|138394|sp|P27330|VHEL_LSV PROBABLE HELICASE (ORF 2) emb|CAA33398.1| (X15343) 25kD protein [Lily symptomless virus]	10
2519	13938116	gi|13938116|gb|AAH07173.1|AAH07173 (BC007173) Unknown (protein for IMAGE:3493127) [Mus musculus]	8E-22
2520	7486371	gi|7486371|pir||T00661 hypothetical protein F3I6.24 - Arabidopsis thaliana gb|AAC00591.1| (AC002396) Unknown protein [Arabidopsis thaliana]	0.16
2523	11358141	gi|11358141|pir||T48198 hypothetical protein T20L15.40 - Arabidopsis thaliana emb|CAB82747.1| (AL162351) putative protein [Arabidopsis thaliana]	9.1
2526	14485227	gi|14485227|gb|AAK62977.1|AF384372_3 (AF384372) surface antigen [Hepatitis B virus]	2.6
2527	6594617	gi|6594617|gb|AAF18559.1|U42380_1 (U42380) aminopeptidase [Aplysia californica]	5.3
2529	14193306	gi|14193306|gb|AAK55890.1|AF267211_2 (AF267211) ATP synthase gamma subunit [Candidatus Carsonella ruddii]	3.5
2531	3319680	gi|3319680|emb|CAA76809.1| (Y17614) N8 protein [Medicago truncatula]	1.5
2536	13811987	gi|13811987|ref|NP_113116.1| DNA repair helicase component of transcription factor b [Guillardia theta] gb|AAK39689.1|AF083031_46 (AF083031) DNA repair helicase component of transcription factor b [Guillardia theta]	4.8
2537	3122601	gi|3122601|sp|P93107|PF20_CHLRE FLAGELLAR WD-REPEAT PROTEIN PF20 pir||T08180 PF20 protein, microtubule-associated - Chlamydomonas reinhardtii gb|AAB41727.1| (U78547) PF20 [Chlamydomonas reinhardtii]	1.1
2540	7460001	gi|7460001|pir||G71079 hypothetical protein PH0903 - Pyrococcus horikoshii dbj|BAA29997.1| (AP000004) 141aa long hypothetical protein [Pyrococcus horikoshii]	6.3
2541	12330702	gi|12330702|gb|AAG52889.1|AF333769_1 (AF333769) cell recognition molecule CASPR3 [Homo sapiens]	2E-28

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
2547	6754652	gi|6754652|ref|NP_034904.1| methyl-CpG binding domain protein 4 [Mus musculus] gb|AAC68878.1| (AF072249) methyl-CpG binding protein MBD4 [Mus musculus] gb|AAD56595.1|AF120996_1 (AF120996) methyl-CpG binding protein 4 [Mus musculus domesticus]	7.1
2548	12655370	gi|12655370|emb|CAB57344.3| (AJ243708) prickle pk isoform [Drosophila melanogaster]	7.7
2551	12853631	gi|12853631|dbj|BAB29800.1| (AK015333) putative [Mus musculus]	0.61
2554	11466216	gi|11466216|ref|NP_066539.1| haem lyase [Naegleria gruberi] gb|AAG17817.1|AF288092_42 (AF288092) haem lyase [Naegleria gruberi]	1.5
2557	7321597	gi|7321597|gb|AAA32099.2| (L28677) unknown [Tetrahymena pyriformis]	3
2560	7304202	gi|7304202|gb|AAF59238.1| (AE003840) CG1602 gene product [Drosophila melanogaster]	1.6
2564	336831	gi|336831|gb|AAB02281.1| (M57910) NADH dehydrogenase subunit 2 [Drosophila melanogaster]	5.5
2566	7515231	gi|7515231|pir||T13518 hypothetical protein 29 - Bacillus phage phi-105 dbj|BAA36635.1| (AB016282) ORF29 [bacteriophage phi-105]	7.7
2568	12847263	gi|12847263|dbj|BAB27500.1| (AK011258) putative [Mus musculus]	6.6
2569	9964395	gi|9964395|ref|NP_064863.1| AMV081 [Amsacta moorei entomopoxvirus] gb|AAG02787.1|AF250284_81 (AF250284) AMV081 [Amsacta moorei entomopoxvirus]	2.4
2573	12060849	gi|12060849|gb|AAG48266.1|AF308299_1 (AF308299) serologically defined breast cancer antigen NY-BR-85 [Homo sapiens]	0.0006
2575	9633381	gi|9633381|ref|NP_050485.1| D5L protein [variola minor virus] pir||H72173 D5L protein - variola minor virus (strain Garcia-1966) gb|AAA69395.1| (U18339) D4L [Variola virus] emb|CAA50966.1| (X72086) ORF15L; B16L in citation [3] [Variola virus] emb|CAB54786.1| (Y16780) D5L protein [variola minor virus]	7.5
2576	7407131	gi|7407131|gb|AAF61923.1| (AF228524) SanE [Streptomyces ansochromogenes]	0.53
2577	14760789	gi|14760789|ref|XP_044332.1| piwi (Drosophila)-like 1 [Homo sapiens]	9E-42

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
2584	2764800	gi|2764800|emb|CAA54153.1| (X76738) 12s globulin [Avena sativa]	1.4
2585	12860337	gi|12860337|dbj|BAB31923.1| (AK019929) putative [Mus musculus]	5.3
2586	7768484	gi|7768484|emb|CAB90775.1| (AL355632) putative mitochondrial carrier protein [Schizosaccharomyces pombe]	2.8
2587	12620098	gi|12620098|gb|AAG60558.1| (AF250768) BioA-like protein [uncultured bacterium pCosFS1]	8.4
2591	2281181	gi|2281181|gb|AAB66275.1| (U58587) maturase [Lagoecia cuminoides]	3.8
2595	6573736	gi|6573736|gb|AAF17656.1|AC009398_5 (AC009398) F20B24.10 [Arabidopsis thaliana]	6.7
2596	31155	gi|31155|emb|CAA24999.1| (X00176) preproenkephalin part 1 [Homo sapiens]	9.5
2600	11278033	gi|11278033|pir||C81832 transferrin-binding protein A NMA2024 [imported] - Neisseria meningitidis (group A strain Z2491) gb|AAC13726.1| (AF058689) transferrin binding protein A precursor [Neisseria meningitidis] emb|CAB85243.1| (AL162757) transferrin-binding protein A [Neisseria meningitidis Z2491]	5
2613	7493138	gi|7493138|pir||T37964 probable ubiquitin ligase - fission yeast (Schizosaccharomyces pombe) emb|CAB16714.1| (Z99531) putative ubiquitin ligase [Schizosaccharomyces pombe]	0.21
2615	14625275	gi|14625275|gb|AAA80360.2| (U39644) Hypothetical protein T10E10.4 [Caenorhabditis elegans]	5.3
2617	7515479	gi|7515479|pir||S72298 hypothetical protein 91 - Plasmodium falciparum plastid emb|CAA64588.1| (X95276) ORF91 [Plasmodium falciparum]	0.66
2619	14091855	gi|14091855|gb|AAK53858.1|AC016781_12 (AC016781) Hypothetical protein [Oryza sativa]	0.69
2621	8393165	gi|8393165|ref|NP_035661.2| transiently-expressed axonal glycoprotein [Mus musculus]	0.11
2624	6754242	gi|6754242|ref|NP_034603.1| histidine rich calcium binding protein [Mus musculus] gb|AAD55250.1|AF158597_1 (AF158597) histidine-rich Ca2+ binding protein [Mus musculus]	8.1
2625	7959261	gi|7959261|dbj|BAA96024.1| (AB040933) KIAA1500 protein [Homo sapiens]	1E-36

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
2626	5508828	gi|5508828|gb|AAD43995.1| (U59485) AttU [Agrobacterium tumefaciens]	0.27
2627	3643603	gi|3643603|gb|AAC42250.1| (AC005395) unknown protein [Arabidopsis thaliana]	4.7
2630	5453906	gi|5453906|ref|NP_006310.1| CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase) [Homo sapiens] ref|XP_008065.1| CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase) [Homo sapiens] ref|XP_043951.1| CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase) [Homo sapiens] sp|O14735|PIS_HUMAN CDP-DIACYLGLYCEROL--INOSITOL 3-PHOSPHATIDYLTRANSFERASE (PHOSPHATIDYLINOSITOL SYNTHASE) (PTDINS SYNTHASE) (PI SYNTHASE) gb|AAB94860.1| (AF014807) phosphatidylinositol synthase [Homo sapiens] gb|AAH01444.1|AAH01444 (BC001444) CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase) [Homo sapiens]	7
2631	7515479	gi|7515479|pir||S72298 hypothetical protein 91 - Plasmodium falciparum plastid emb|CAA64588.1| (X95276) ORF91 [Plasmodium falciparum]	0.71
2636	11467075	gi|11467075|ref|NP_042551.1| ribosomal protein L5 [Acanthamoeba castellanii] sp|P46764|RM05_ACACA MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L5 pir||S53852 ribosomal protein L5 - Acanthamoeba castellanii mitochondrion gb|AAD11844.1| (U12386) ribosomal protein L5 [Acanthamoeba castellanii]	2.3
2639	1352549	gi|1352549|sp|P48906|NU2M_HANWI NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2	4.1
2642	13111580	gi|13111580|gb|AAK12385.1|AF296091_1 (AF296091) polyprotein [Porcine teschovirus]	2.4
2646	1314734	gi|1314734|gb|AAA99804.1| (U54641) 220 kDa silk protein [Chironomus thummi]	1.9
2651	7001374	gi|7001374|gb|AAF34871.1|AF112184_1 (AF112184) serine/threonine kinase NKIATRE alpha [Rattus norvegicus]	2.9
2653	2687582	gi|2687582|gb|AAB88853.1| (AF032875) protein kinase [Mus musculus]	7.2

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
2654	10636263	gi|10636263|emb|CAC10528.1| (AJ293919) putative inositol 1,4,5-trisphosphate receptor [Caenorhabditis briggsae]	5
2663	5902891	gi|5902891|dbj|BAA84474.1| (AB032367) type I polyketide synthase AVES 1 [Streptomyces avermitilis]	0.087
2664	4567214	gi|4567214|gb|AAD23629.1|AC007113_2 (AC007113) putative villin [Arabidopsis thaliana]	6.4
2665	2326816	gi|2326816|emb|CAA99382.1| (Z75081) ORF YOR172w [Saccharomyces cerevisiae]	0.46
2667	14285987	gi|14285987|sp|O83933|Y967_TREPA HYPOTHETICAL PROTEIN TP0967 pir||B71260 hypothetical protein TP0967 - syphilis spirochete gb|AAC65925.1| (AE001264) T. pallidum predicted coding region TP0967 [Treponema pallidum]	6.9
2669	6678247	gi|6678247|ref|NP_033358.1| transcription factor 7-like 1 [Mus musculus] emb|CAA11070.1| (AJ223069) TCF-3 protein [Mus musculus]	3.4
2671	7491697	gi|7491697|pir||T40527 hypothetical protein SPBC530.11c - fission yeast (Schizosaccharomyces pombe) emb|CAA19177.1| (AL023634) putative transcriptional regulator [Schizosaccharomyces pombe]	4.9
2673	5459308	gi|5459308|emb|CAB50693.1| (AJ238951) CE9 protein [Canis familiaris]	8.8
2675	7959261	gi|7959261|dbj|BAA96024.1| (AB040933) KIAA1500 protein [Homo sapiens]	1E-36
2680	14520279	gi|14520279|ref|NP_125754.1| hypothetical protein [Pyrococcus abyssi] pir||B75192 hypothetical protein PAB2304 - Pyrococcus abyssi (strain Orsay) emb|CAB48985.1| (AJ248283) hypothetical protein [Pyrococcus abyssi]	6.7
2681	12654531	gi|12654531|gb|AAH01098.1|AAH01098 (BC001098) Unknown (protein for IMAGE:3508043) [Homo sapiens]	2.8
2682	12657687	gi|12657687|gb|AAK01000.1| (AF178873) NADH dehydrogenase subunit 1 [Archiearis parthenias]	0.68

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
2686	6319517	gi|6319517|ref|NP_009599.1| Ybr043cp [Saccharomyces cerevisiae] sp|P38227|YBP3_YEAST HYPOTHETICAL 77.3 KDA PROTEIN IN FAT1-TCM62 INTERGENIC REGION pir||S45901 probable membrane protein YBR043c - yeast (Saccharomyces cerevisiae) emb|CAA84985.1| (Z35912) ORF YBR043c [Saccharomyces cerevisiae]	7.2
2691	7019565	gi|7019565|ref|NP_037528.1| ubiquitin specific protease 25; ubiquitin specific protease USP25 [Homo sapiens] ref|XP_047738.1| ubiquitin specific protease 25 [Homo sapiens] gb|AAF24998.1|AF134213_1 (AF134213) ubiquitin-specific protease [Homo sapiens]	2E-20
2693	2130214	gi|2130214|pir||S67381 tubulin-folding cofactor D homolog - fission yeast (Schizosaccharomyces pombe) pir||T39319 tubulin-folding cofactor D homolog - fission yeast (Schizosaccharomyces pombe) emb|CAA20686.1| (AL031528) tubulin-folding cofactor d. [Schizosaccharomyces pombe]	3.9
2696	2120601	gi|2120601|pir||JC6030 3-oxo-5alpha-steroid 4-dehydrogenase (EC 1.3.99.5) - Comamonas testosteroni gb|AAB08517.1| (L23428) delta 4, 5-alpha steroid dehydrogenase [Comamonas testosteroni]	4.6
2697	4263524	gi|4263524|gb|AAD15350.1| (AC004044) hypothetical protein [Arabidopsis thaliana] emb|CAB77761.1| (AL161495) hypothetical protein [Arabidopsis thaliana]	5.8
2698	5453072	gi|5453072|gb|AAD43426.1| (AF073977) olfactory receptor [Mus musculus domesticus]	1.1
2701	7298915	gi|7298915|gb|AAF54120.1| (AE003675) CG10267 gene product [Drosophila melanogaster]	0.86
2703	158148	gi|158148|gb|AAA28827.1| (M19537) RNA polymerase II largest subunit (, EC 2.7.7.6) [Drosophila melanogaster]	0.95
2706	7492334	gi|7492334|pir||T37965 probable 40s ribosomal protein - fission yeast (Schizosaccharomyces pombe) emb|CAB16715.1| (Z99531) putative component of U3 snoRNP, required for pre-18S rRNA processing [Schizosaccharomyces pombe]	6.8

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
2709	9366627	gi|9366627|emb|CAB95389.1| (AL359782) conserved hypothetical protein, CHR1.84 [Trypanosoma brucei]	9.2
2713	7436828	gi|7436828|pir||T00129 hypothetical protein 7 - Leptospira interrogans (fragment) dbj|BAA24376.1| (AB010203) ORF7; putative [Leptospira interrogans]	7.2
2715	3805770	gi|3805770|gb|AAC69148.1| (U78721) auxin response transcription factor 3 (ETTIN/ARF3) [Arabidopsis thaliana] gb|AAG53998.1|AF336917_1 (AF336917) ARF3 [Arabidopsis thaliana] gb|AAK26023.1|AF360313_1 (AF360313) ARF3 [Arabidopsis thaliana]	0.65
2716	5454158	gi|5454158|ref|NP_006286.1| valyl-tRNA synthetase 2 [Homo sapiens] sp|P26640|SYV2_HUMAN VALYL-TRNA SYNTHETASE 2 (VALINE--TRNA LIGASE 2) (VALRS 2) gb|AAD21819.1| (AF134726) G7A [Homo sapiens]	1.6
2721	7019565	gi|7019565|ref|NP_037528.1| ubiquitin specific protease 25; ubiquitin specific protease USP25 [Homo sapiens] ref|XP_047738.1| ubiquitin specific protease 25 [Homo sapiens] gb|AAF24998.1|AF134213_1 (AF134213) ubiquitin-specific protease [Homo sapiens]	8E-21
2722	13186335	gi|13186335|gb|AAK15378.1| (AF211133) tryptophanyl-tRNA synthetase [Carsonella ruddii]	8.9
2726	7514607	gi|7514607|pir||A71301 conserved hypothetical protein TP0636 - syphilis spirochete gb|AAC65610.1| (AE001238) conserved hypothetical protein [Treponema pallidum]	9.4
2727	13129046	gi|13129046|ref|NP_076972.1| hypothetical protein MGC2718 [Homo sapiens] ref|XP_017742.2| hypothetical protein MGC2718 [Homo sapiens] ref|XP_043040.1| hypothetical protein MGC2718 [Homo sapiens] gb|AAH01076.1|AAH01076 (BC001076) Unknown (protein for MGC:2718) [Homo sapiens] gb|AAH05121.1|AAH05121 (BC005121) hypothetical protein MGC2718 [Homo sapiens]	3.2

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
2730	11466216	gi|11466216|ref|NP_066539.1| haem lyase [Naegleria gruberi] gb|AAG17817.1|AF288092_42 (AF288092) haem lyase [Naegleria gruberi]	1.4
2734	14701844	gi|14701844|gb|AAK72251.1| (AF378136) MB2 [Plasmodium falciparum]	3.3
2739	7486489	gi|7486489|pir||T00671 hypothetical protein F6E13.4 - Arabidopsis thaliana gb|AAC23400.1| (AC004005) putative methyl chloride transferase [Arabidopsis thaliana] gb|AAK73255.1| (AY044314) putative methyl chloride transferase [Arabidopsis thaliana]	8.1
2747	7509946	gi|7509946|pir||T26972 hypothetical protein Y47H9C.4 - Caenorhabditis elegans emb|CAA21739.1| (AL032657) contains similarity to Pfam domain: PF00008 (EGF-like domain), Score=76.2, E-value=2.2e-19, N=17~cDNA EST yk20a5.3 comes from this gene~cDNA EST yk20a5.5 comes from this gene~cDNA EST yk299a12.3 comes from this gene~cDNA EST yk467g8.3 comes > gb|AAG60061.1|AF332568_1 (AF332568) CED-1 [Caenorhabditis elegans]	1.6
2749	8569100	gi|8569100|gb|AAF76445.1|AC015445_12 (AC015445) Contains Ribosomal S17 PF|00366 and DLH PF|01738 domains. [Arabidopsis thaliana]	9.5
2750	7293625	gi|7293625|gb|AAF48997.1| (AE003512) CG14223 gene product [Drosophila melanogaster]	2.9
2751	5454050	gi|5454050|ref|NP_006369.1| sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D; sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, 4D [Homo sapiens] sp|Q92854|SM4D_HUMAN SEMAPHORIN 4D PRECURSOR (LEUKOCYTE ACTIVATION ANTIGEN CD100) (BB18) (A8) (GR3) gb|AAC50810.1| (U60800) semaphorin [Homo sapiens]	9
2761	9964076	gi|9964076|gb|AAG09812.1|AF275943_1 (AF275943) avermectin polyketide synthase [Streptomyces avermitilis]	2.9
2762	4234794	gi|4234794|gb|AAD12962.1| (AF078135) unknown [Leptospira borgpetersenii]	1.3

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
2764	11131078	gi|11131078|sp|O15072|ATS3_HUMAN ADAM-TS 3 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 3) (ADAMTS-3) (ADAM-TS3) dbj|BAA20821.1| (AB002364) KIAA0366 [Homo sapiens]	4E-17
2765	6449069	gi|6449069|gb|AAF08806.1|AF192748_1 (AF192748) synapsin Ib [Lampetra fluviatilis]	0.008
2769	7300358	gi|7300358|gb|AAF55517.1| (AE003721) CG8045 gene product [alt 2] [Drosophila melanogaster] gb|AAB34837.2| (S78747) RK2 [Drosophila sp.]	3
2772	14731064	gi|14731064|ref|XP_036165.1| 40679 [Homo sapiens]	6E-20
2774	4927134	gi|4927134|gb|AAD33018.1|AF131999_1 (AF131999) putative erythrocyte binding protein EBL-1 [Plasmodium falciparum]	8.6
2775	11994465	gi|11994465|dbj|BAB02467.1| (AB025624) contains similarity to late embryogenesis abundant protein~gene_id:MLD14.16 [Arabidopsis thaliana]	7.5
2776	12852706	gi|12852706|dbj|BAB29508.1| (AK014697) putative [Mus musculus]	1
2777	9972373	gi|9972373|gb|AAG10623.1|AC022521_1 (AC022521) Unknown protein [Arabidopsis thaliana]	3.2
2779	12838769	gi|12838769|dbj|BAB24323.1| (AK005931) putative [Mus musculus]	7.6
2780	14743085	gi|14743085|ref|XP_050026.1| similar to immunoglobulin superfamily containing leucine-rich repeat (H. sapiens) [Homo sapiens]	3.4
2781	4581140	gi|4581140|gb|AAD24624.1|AC006919_4 (AC006919) unknown protein [Arabidopsis thaliana]	2.8
2792	7661684	gi|7661684|ref|NP_056277.1| DKFZP586L0724 protein [Homo sapiens] ref|XP_038194.1| DKFZP586L0724 protein [Homo sapiens] ref|XP_038195.1| 19734 [Homo sapiens] pir||T14789 hypothetical protein DKFZp586L0724.1 - human emb|CAB53709.1| (AL110271) hypothetical protein [Homo sapiens] gb|AAH01726.1|AAH01726 (BC001726) Similar to DKFZP586L0724 protein [Homo sapiens]	7
2793	13624635	gi|13624635|emb|CAA10856.2| (AJ222584) maturase-like protein [Euglena viridis]	1.3

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
2800	9622888	gi|9622888|gb|AAF89968.1|AF200532_1 (AF200532) cellulose synthase-8 [Zea mays]	3.8
2803	7499161	gi|7499161|pir||T25690 hypothetical protein F15A8.6 - Caenorhabditis elegans gb|AAB52848.1| (U97549) strong similarity to the type-B carboxylesterase/lipase family [Caenorhabditis elegans]	3.1
2806	14746401	gi|14746401|ref|XP_031955.1| ring finger protein 27 [Homo sapiens]	0.3
2809	14731173	gi|14731173|ref|XP_017730.2| IQ motif containing GTPase activating protein 2 [Homo sapiens]	2E-11
2813	4567214	gi|4567214|gb|AAD23629.1|AC007113_2 (AC007113) putative villin [Arabidopsis thaliana]	3.5
2817	2500866	gi|2500866|sp|Q20411|SA11_CAEEL SRA-11 PROTEIN pir||T22192 hypothetical protein F44F4.13 - Caenorhabditis elegans emb|CAA85461.1| (Z37092) contains similarity to Pfam domain: PF02117 (C.elegans Sra family integral membrane protein), Score=675.6, E-value=8.3e-200, N=1 [Caenorhabditis elegans]	3.1
2818	15011503	gi|15011503|gb|AAK77598.1|AF396436_38 (AF396436) ymf71 [Tetrahymena thermophila]	5.9
2823	11278033	gi|11278033|pir||C81832 transferrin-binding protein A NMA2024 [imported] - Neisseria meningitidis (group A strain Z2491) gb|AAC13726.1| (AF058689) transferrin binding protein A precursor [Neisseria meningitidis] emb|CAB85243.1| (AL162757) transferrin-binding protein A [Neisseria meningitidis Z2491]	5
2825	3913143	gi|3913143|sp|O23913|AX1B_ARATH ALTERNATIVE OXIDASE 1B PRECURSOR dbj|BAA22624.1| (D89875) alternative oxidase [Arabidopsis thaliana] dbj|BAB01774.1| (AB022215) alternative oxidase 1b precursor [Arabidopsis thaliana]	1.2
2827	12842679	gi|12842679|dbj|BAB25689.1| (AK008476) putative [Mus musculus]	7.8
2835	12848636	gi|12848636|dbj|BAB28031.1| (AK012100) putative [Mus musculus]	0.083
2839	7292152	gi|7292152|gb|AAF47564.1| (AE003472) Dhc62B gene product [Drosophila melanogaster]	4.6

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
2846	9628099	gi|9628099|ref|NP_042686.1| alternative tat protein [Jembrana disease virus] gb|AAA64395.1| (U21603) alternative tat protein [Jembrana disease virus] prf||2116345E tat gene [Jembrana disease virus]	3.3
2855	4165313	gi|4165313|dbj|BAA37146.1| (AB022083) SOX30 protein [Homo sapiens]	9.2
2859	14388365	gi|14388365|dbj|BAB60739.1| (AB062957) hypothetical protein [Macaca fascicularis]	0.55
2864	14739019	gi|14739019|ref|XP_005626.3| deleted in bladder cancer chromosome region candidate 1 [Homo sapiens]	6.3
2867	6319950	gi|6319950|ref|NP_010031.1| Transcription regulator; Ycr106wp [Saccharomyces cerevisiae] sp|P25611|YCZ6_YEAST PUTATIVE 95.7 KD TRANSCRIPTIONAL REGULATORY PROTEIN IN PAU3-AAD3 INTERGENIC REGION pir||S19418 probable membrane protein YCR106w - yeast (Saccharomyces cerevisiae) emb|CAA42238.1| (X59720) hypothetical protein [Saccharomyces cerevisiae]	9.1
2870	14724850	gi|14724850|ref|XP_050192.1| 29140 [Homo sapiens]	2.2
2871	4587097	gi|4587097|dbj|BAA76616.1| (AB019045) OMPdecarboxylase [Rhizomucor pusillus]	9.7
2873	7522108	gi|7522108|pir||T29097 pro-pol-dUTPase polyprotein - murine endogenous retrovirus ERV-L (fragment) emb|CAA73251.1| (Y12713) protease; reverse transcriptase; RNaseH; integrase; dUTPase; Pro-Pol-dUTPase polyprotein [Mus musculus]	0.003
2875	7482073	gi|7482073|pir||B69010 conserved hypothetical protein MTH1078 - Methanobacterium thermoautotrophicum (strain Delta H) gb|AAB85567.1| (AE000879) conserved protein [Methanothermobacter thermautotrophicus]	4.6
2876	11360401	gi|11360401|pir||T42759 Munc13-3 protein - rat	0.000000005
2879	5091521	gi|5091521|dbj|BAA78756.1| (AB023482) Hypothetical protein [Oryza sativa]	2.1
2881	13810543	gi|13810543|dbj|BAB43950.1| (AB051633) ookinete surface protein Pos28-2 [Plasmodium ovale]	3
2882	5091521	gi|5091521|dbj|BAA78756.1| (AB023482) Hypothetical protein [Oryza sativa]	2.1

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
2887	6723244	gi|6723244|dbj|BAA89640.1| (AB036666) similar to terminase large subunit of phage lambda [Wolbachia sp. wKue]	7.1
2889	7494347	gi|7494347|pir||E71625 variant-specific surface protein 1 truncated homolog PFB0020c - malaria parasite (Plasmodium falciparum) gb|AAC71794.1| (AE001366) PfEMP1 fragment [Plasmodium falciparum]	5
2890	6942188	gi|6942188|gb|AAF32349.1|AF220008_1 (AF220008) coilin p80 [Danio rerio]	0.11
2891	10639397	gi|10639397|emb|CAC11399.1| (AL445063) hypothetical membrane protein [Thermoplasma acidophilum]	8.5
2898	10800417	gi|10800417|ref|NP_006759.2| BRCA1 associated protein [Homo sapiens]	0.98
2901	7488089	gi|7488089|pir||T02283 probable disease resistance protein T13D8.20 - Arabidopsis thaliana gb|AAC24071.1| (AC004473) Contains similarity to TMV resistance protein N homolog gb|2245048 from A. thaliana chromosome 4 contig gb|Z97342. [Arabidopsis thaliana]	8.5
2904	10728394	gi|10728394|gb|AAF45654.2| (AE003421) EG:171E4.2 gene product [Drosophila melanogaster]	1.4
2905	10956333	gi|10956333|ref|NP_052782.1| pXO1-86 [Bacillus anthracis] pir||F59101 hypothetical protein pXO1-86 - Bacillus anthracis virulence plasmid pXO1 gb|AAD32390.1|AAD32390 (AF065404) pXO1-86 [Bacillus anthracis]	9.7
2906	4028153	gi|4028153|gb|AAC96117.1| (AF083221) putative neurotransmitter receptor [Takifugu rubripes]	2.8
2909	12836120	gi|12836120|dbj|BAB23511.1| (AK004729) putative [Mus musculus]	5.3
2911	1778844	gi|1778844|gb|AAB40929.1| (U83086) LimA [Dictyostelium discoideum]	1.3
2913	3192956	gi|3192956|gb|AAC41298.1| (AF033670) T-Box protein 4 [Gallus gallus]	3.1
2914	7506147	gi|7506147|pir||T33303 hypothetical protein R01B10.4 - Caenorhabditis elegans gb|AAC17768.1| (AF068718) R01B10.4 gene product [Caenorhabditis elegans]	0.4

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
2915	6041793	gi|6041793|gb|AAF02113.1|AC009755_6 (AC009755) putative auxin-independent growth promoter [Arabidopsis thaliana]	2.1
2916	5803098	gi|5803098|ref|NP_006757.1| zinc finger protein 220; Monocytic leukemia zinc finger protein [Homo sapiens] sp|Q92794|MOZ_HUMAN MONOCYTIC LEUKEMIA ZINC FINGER PROTEIN (ZINC FINGER PROTEIN 220) gb|AAC50662.1| (U47742) monocytic leukaemia zinc finger protein [Homo sapiens]	0.084
2919	10639353	gi|10639353|emb|CAC11355.1| (AL445063) hypothetical membrane protein [Thermoplasma acidophilum]	3.1
2920	13235586	gi|13235586|emb|CAC33776.1| (AJ301807) SclB protein [Streptococcus pyogenes]	9.7
2925	7507618	gi|7507618|pir||T33548 hypothetical protein T10D4.8 - Caenorhabditis elegans	4.3
2928	7522108	gi|7522108|pir||T29097 pro-pol-dUTPase polyprotein - murine endogenous retrovirus ERV-L (fragment) emb|CAA73251.1| (Y12713) protease; reverse transcriptase; RNaseH; integrase; dUTPase; Pro-Pol-dUTPase polyprotein [Mus musculus]	1.2
2932	13542796	gi|13542796|gb|AAH05601.1|AAH05601 (BC005601) Similar to RIKEN cDNA 1110061A19 gene [Mus musculus]	6.4
2934	417869	gi|417869|sp|P33007|TERP_PSESP TERPREDOXIN (TDX) pir||E42971 terpredoxin - Pseudomonas sp gb|AAA25998.1| (M91440) terpredoxin [Pseudomonas sp.]	3.7
2938	7433891	gi|7433891|pir||T00981 flavonol 3-O-glucosyltransferase homolog T9J22.15 - Arabidopsis thaliana gb|AAC14497.1| (AC002505) putative glucosyltransferase [Arabidopsis thaliana]	6.8
2939	15021546	gi|15021546|gb|AAK77823.1|AF369029_154 (AF369029) ORF154 [white spot syndrome virus]	0.25
2944	11466694	gi|11466694|ref|NP_039290.1| ORF370i [Marchantia polymorpha] sp|P12174|MATK_MARPO PROBABLE INTRON MATURASE pir||A05034 hypothetical protein 370i - liverwort (Marchantia polymorpha) chloroplast emb|CAA28076.1| (X04465) ORF370i [Marchantia polymorpha]	4.3

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
2945	7302236	gi|7302236|gb|AAF57330.1| (AE003786) CG10416 gene product [Drosophila melanogaster]	1.4
2950	2495638	gi|2495638|sp|P76511|YFDO_ECOLI HYPOTHETICAL 14.4 KDA PROTEIN IN INTC-DSDC INTERGENIC REGION pir||C65009 hypothetical protein b2358 - Escherichia coli (strain K-12) gb|AAC75417.1| (AE000324) orf, hypothetical protein [Escherichia coli K12]	4.5
2955	220578	gi|220578|dbj|BAA00447.1| (D00570) open reading frame (251 AA) [Mus musculus]	4.2
2958	12855573	gi|12855573|dbj|BAB30384.1| (AK016695) putative [Mus musculus]	0.007
2963	2981631	gi|2981631|dbj|BAA25253.1| (AB012223) ORF2 [Canis familiaris]	0.29
2966	7657401	gi|7657401|ref|NP_056616.1| neuropathy target esterase; Swiss cheese [Mus musculus] gb|AAD51700.1|AF173829_1 (AF173829) neuropathy target esterase homolog [Mus musculus]	1.5
2967	14285535	gi|14285535|sp|P71399|LSG1_HAEIN LSG LOCUS PUTATIVE PROTEIN 1	4.8
2973	14423780	gi|14423780|sp|O95013|O4F3_HUMAN OLFACTORY RECEPTOR 4F3 gb|AAD05195.1| (AC004908) similar to rat olfactory receptor OR18; similar to S29710 (PID:g423702) [Homo sapiens]	3E-35
2975	14771691	gi|14771691|ref|XP_045484.1| 67354 [Homo sapiens]	1.3
2978	6573738	gi|6573738|gb|AAF17658.1|AC009398_7 (AC009398) F20B24.13 [Arabidopsis thaliana]	8.5
2982	13811437	gi|13811437|gb|AAK40121.1| (AF354707) type II deodinase [Xenopus laevis]	2.4
2986	7522108	gi|7522108|pir||T29097 pro-pol-dUTPase polyprotein - murine endogenous retrovirus ERV-L (fragment) emb|CAA73251.1| (Y12713) protease; reverse transcriptase; RNaseH; integrase; dUTPase; Pro-Pol-dUTPase polyprotein [Mus musculus]	0.00001
2990	12722927	gi|12722927|gb|AAK04181.1|AE006247_3 (AE006247) UNKNOWN PROTEIN [Lactococcus lactis subsp. lactis]	1.3

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
2994	11346713	gi|11346713|pir||F81302 hypothetical protein Cj1009c [imported] - Campylobacter jejuni (strain NCTC 11168) emb|CAB73265.1| (AL139077) hypothetical protein Cj1009c [Campylobacter jejuni]	4.1
2995	7321945	gi|7321945|gb|AAC60504.2| (S68356) action potential broadening potassium channel [Aplysia sp.]	4.2
3003	11360394	gi|11360394|pir||T42731 atrophin-1 related protein - rat gb|AAA98970.1| (U44091) atrophin-1 related protein [Rattus norvegicus]	7.6
3005	10765337	gi|10765337|gb|AAG22997.1| (AF188579) glycoprotein [Bovine respiratory syncytial virus]	1.9
3006	5803252	gi|5803252|dbj|BAA83562.1| (AP000399) hypothetical protein [Oryza sativa]	0.046
3007	7662688	gi|7662688|gb|AAF66138.1| (L00016) urf4 [Homo sapiens]	1.7
3013	14150037	gi|14150037|ref|NP_115666.1| hypothetical protein DKFZp761C121 [Homo sapiens] ref|XP_027894.1| hypothetical protein DKFZp761C121 [Homo sapiens] emb|CAB66495.1| (AL136560) hypothetical protein [Homo sapiens]	0.00000001
3014	7243706	gi|7243706|gb|AAF43421.1|AF233291_1 (AF233291) epsin-like protein [Drosophila melanogaster]	6.5
3019	7293274	gi|7293274|gb|AAF48655.1| (AE003503) CG9644 gene product [Drosophila melanogaster]	0.47
3025	11414881	gi|11414881|dbj|BAB18568.1| (AB028173) HCCA2 [Homo sapiens]	8.6
3026	11359423	gi|11359423|pir||T48729 hypothetical protein 8D4.30 [imported] - Neurospora crassa emb|CAB88545.1| (AL353819) conserved hypothetical protein [Neurospora crassa]	0.66
3028	2118405	gi|2118405|pir||I51018 cobra venom factor precursor - monocled cobra gb|AAA68989.1| (U09969) cobra venom factor precursor [Naja naja]	3.1
3029	2739145	gi|2739145|gb|AAC98522.1| (AF030306) envelope protein; ORF4 [Porcine reproductive and respiratory syndrome virus]	4.3
3030	13549158	gi|13549158|gb|AAK29672.1|AF353095_1 (AF353095) protein synthesis initiation factor eIF2 beta [Arabidopsis thaliana]	6.3

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
3034	14753542	gi|14753542|ref|XP_046011.1| 53288 [Homo sapiens]	0.000000006
3042	3150471	gi|3150471|gb|AAC16989.1| (AF067211) Hypothetical protein B0205.2 [Caenorhabditis elegans]	0.56
3044	14734012	gi|14734012|ref|XP_051005.1| KIAA1297 protein [Homo sapiens]	0.16
3047	7493994	gi|7493994|pir||JC6564 cellobiose oxidase (EC 1.1.3.25) precursor - white-rot fungus (Trametes versicolor)	6.1
3056	114351	gi|114351|sp|P08314|ATI2_HSV1F ALPHA TRANS-INDUCING FACTOR 77 KD PROTEIN pir||TNBE77 77K alpha trans-inducing protein - human herpesvirus 1 (strain F) gb|AAA45768.1| (M15621) alpha trans-inducing factor 77kb [human herpesvirus 1]	7
3069	6562755	gi|6562755|emb|CAB62894.1| (AL035475) possible ribosomal protein [Plasmodium falciparum]	6.4
3071	804764	gi|804764|gb|AAA65999.1| (M27826) neutral protease large subunit [Homo sapiens]	0.00003
3079	14768311	gi|14768311|ref|XP_048396.1| methyl CpG binding protein 2 [Homo sapiens]	0.65
3080	11994604	gi|11994604|dbj|BAB02658.1| (AP002062) gene_id:T22B15.11~unknown protein [Arabidopsis thaliana]	5
3083	7302673	gi|7302673|gb|AAF57753.1| (AE003800) stau gene product [alt 2] [Drosophila melanogaster]	9.2
3085	7494170	gi|7494170|pir||D71613 GAF domain protein (cyclic nt signal transduct.) PFB0510w - malaria parasite (Plasmodium falciparum) gb|AAC71891.1| (AE001399) GAF domain protein (cyclic nt signal transduct.) [Plasmodium falciparum]	8.1
3087	14590168	gi|14590168|ref|NP_142233.1| hypothetical protein [Pyrococcus horikoshii] pir||F71247 hypothetical protein PH0237 - Pyrococcus horikoshii dbj|BAA29309.1| (AP000001) 230aa long hypothetical protein [Pyrococcus horikoshii]	2.3
3097	14326099	gi|14326099|gb|AAK60138.1|AF365405_1 (AF365405) ribosomal protein S14 [Schizosaccharomyces pombe]	3

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
3098	2499244	gi|2499244|sp|Q35140|NU2M_NEUCR NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 pir||A25096 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Neurospora crassa mitochondrion emb|CAA27418.1| (X03793) put. URF-2 like protein (aa 1-583) [Neurospora crassa]	8.1
3101	113668	gi|113668|sp|P23961|ALUC_HUMAN !!!! ALU CLASS C WARNING ENTRY !!!!	6.5
3105	12721131	gi|12721131|gb|AAK02908.1| (AE006121) unknown [Pasteurella multocida]	9.2
3107	12621134	gi|12621134|ref|NP_075244.1| MEGF6 [Rattus norvegicus] pir||T13954 MEGF6 protein - rat dbj|BAA32462.1| (AB011532) MEGF6 [Rattus norvegicus]	2.1
3108	1346666	gi|1346666|sp|P48305|NB5M_BOVIN NADH-UBIQUINONE OXIDOREDUCTASE B15 SUBUNIT (COMPLEX I-B15) (CI-B15) pir||S28237 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain B15 - bovine emb|CAA46107.1| (X64898) B15 subunit of the NADH: ubiquinone oxidoreductase complex [Bos taurus]	0.47
3111	462022	gi|462022|sp|P33948|ERD2_PLAFA ER LUMEN PROTEIN RETAINING RECEPTOR pir||S39609 ERD2 protein - malaria parasite (Plasmodium falciparum) emb|CAA81128.1| (Z26043) ERD2 [Plasmodium falciparum] emb|CAA52861.1| (X74869) PFERD2 [Plasmodium falciparum]	0.95
3114	12831427	gi|12831427|gb|AAK02082.1| (AY014401) site-specific recombinase IntIA [Listonella pelagia]	8.3
3117	7657530	gi|7657530|ref|NP_055248.1| rhabdoid tumor deletion region protein 1 [Homo sapiens] ref|XP_009866.1| rhabdoid tumor deletion region protein 1 [Homo sapiens] ref|XP_037053.1| rhabdoid tumor deletion region protein 1 [Homo sapiens] gb|AAF02484.1|AF133587_1 (AF133587) rhabdoid tumor deletion region protein 1 [Homo sapiens] gb|AAH08986.1|AAH08986 (BC008986) rhabdoid tumor deletion region protein 1 [Homo sapiens]	7.8
3123	12083527	gi|12083527|gb|AAG48836.1|AC084218_6 (AC084218) similar to Arabidopsis thaliana DNA-directed RNA polymerase (EC 2.7.7.6) II largest chain (JDMU1) [Oryza sativa]	6.9

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
3126	2565196	gi|2565196|gb|AAB81938.1| (AF000381) non-functional folate binding protein [Homo sapiens]	8.8
3132	8923808	gi|8923808|ref|NP_060941.1| uncharacterized hypothalamus protein HT010 [Homo sapiens] gb|AAF67649.1|AF220184_1 (AF220184) uncharacterized hypothalamus protein HT010 [Homo sapiens]	7E-13
3138	14755072	gi|14755072|ref|XP_048449.1| hypothetical protein XP_048449 [Homo sapiens]	9.5
3141	1085507	gi|1085507|pir||S52306 zinc finger protein 10 - mouse emb|CAA85283.1| (Z36270) GC Binding Protein - 23b [Mus musculus]	6.7
3142	4417278	gi|4417278|gb|AAD20403.1| (AC007019) unknown protein [Arabidopsis thaliana]	2.8
3148	12084884	gi|12084884|ref|NP_073349.1| UL54 post-translational gene regulation protein [Meleagrid herpesvirus 1] gb|AAG45793.1|AF291866_60 (AF291866) UL54 post-translational gene regulation protein [Meleagrid herpesvirus 1]	8.2
3151	13122204	gi|13122204|emb|CAB89584.2| (AL354512) possible non-canonical ubiquitin conjugating enzyme 1 [Leishmania major]	0.65
3153	418745	gi|418745|pir||S34959 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - Crithidia oncopelti mitochondrion emb|CAA39491.1| (X56015) NADH dehydrogenase subunit 4 [Crithidia oncopelti]	1
3157	6015766	gi|6015766|emb|CAB57593.1| (Y18930) hypothetical protein [Sulfolobus solfataricus]	7.7
3162	6983867	gi|6983867|dbj|BAA90802.1| (AP001168) Similar to putative salt-inducible protein (AC006248) [Oryza sativa]	2.8
3163	11467948	gi|11467948|sp|O65404|ER11_ARATH SQUALENE MONOOXYGENASE 1,1 (SQUALENE EPOXIDASE 1,1) (SE 1,1) dbj|BAB08406.1| (AB016883) squalene monooxygenase [Arabidopsis thaliana]	6.1
3167	3461813	gi|3461813|gb|AAC32907.1| (AC004138) putative sucrose-proton symporter [Arabidopsis thaliana] emb|CAB92307.1| (AJ289165) sucrose transporter [Arabidopsis thaliana]	4.4

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
3168	6753576	gi|6753576|ref|NP_034128.1| cytochrome P450, 2b10, phenobarbitol inducible, type b [Mus musculus] sp|P12791|CPBA_MOUSE CYTOCHROME P450 2B10 (CYPIIB10) (TESTOSTERONE 16-ALPHA HYDROXYLASE) (P450-16-ALPHA) (CLONE PF3/46) pir||B31047 testosterone 16alpha-hydroxylase (EC 1.14.14.-) cytochrome P450 2B10 - mouse gb|AAA40425.1| (M21856) testosterone 16-alpha-hydroxylase [Mus musculus]	7.6
3174	585811	gi|585811|sp|Q08517|REFR_SPVKA RIFAMPICIN RESISTANCE PROTEIN (62 KD PROTEIN) gb|AAA16176.1| (L22012) ORF H1L [Swinepox virus]	6.9
3176	14714688	gi|14714688|gb|AAH10485.1|AAH10485 (BC010485) Unknown (protein for MGC:7224) [Mus musculus]	2.1
3178	10047191	gi|10047191|dbj|BAB13389.1| (AB046783) KIAA1563 protein [Homo sapiens]	4E-26
3180	6324246	gi|6324246|ref|NP_014316.1| Ynl083wp [Saccharomyces cerevisiae] pir||S57539 probable membrane protein YNL083w - yeast (Saccharomyces cerevisiae) emb|CAA61427.1| (X89016) ORF N2312 [Saccharomyces cerevisiae] emb|CAA95958.1| (Z71359) ORF YNL083w [Saccharomyces cerevisiae]	0.24
3184	7494290	gi|7494290|pir||C71618 hypothetical protein PFB0315w - malaria parasite (Plasmodium falciparum) gb|AAC71852.1| (AE001386) hypothetical protein [Plasmodium falciparum]	0.084
3185	6754948	gi|6754948|ref|NP_036089.1| origin recognition complex, subunit 5 homolog (S. cerevisiae); mouse origin recognition complex 5 [Mus musculus] sp|Q9WUV0|ORC5_MOUSE ORIGIN RECOGNITION COMPLEX SUBUNIT 5 emb|CAB43767.1| (AJ007360) ORC5-related protein [Mus musculus] gb|AAH06927.1|AAH06927 (BC006927) origin recognition complex, subunit 5 homolog (S. cerevisiae) [Mus musculus]	8.5
3199	7295489	gi|7295489|gb|AAF50803.1| (AE003567) CG10671 gene product [Drosophila melanogaster]	4.3

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
3203	14741894	gi|14741894|ref|XP_049656.1| hypothetical protein XP_049656 [Homo sapiens]	4
3208	14520989	gi|14520989|ref|NP_126464.1| hypothetical protein [Pyrococcus abyssi] pir||F75122 hypothetical protein PAB1844 - Pyrococcus abyssi (strain Orsay) emb|CAB49695.1| (AJ248285) hypothetical protein [Pyrococcus abyssi]	4.1
3210	9911016	gi|9911016|sp|P76543|YFFL_ECOLI HYPOTHETICAL 25.1 KDA PROTEIN IN EUTB-EUTH INTERGENIC REGION pir||B65019 hypothetical protein b2443 - Escherichia coli (strain K-12) gb|AAC75496.1| (AE000331) orf, hypothetical protein [Escherichia coli K12]	7.9
3211	9626990	gi|9626990|ref|NP_056868.1| No definition line found gb|AAB92648.1| (AF035403) No definition line found [Turnip yellow mosaic virus]	3.7
3213	7504416	gi|7504416|pir||T16477 hypothetical protein F56D2.5 - Caenorhabditis elegans gb|AAB52683.1| (U13644) F56D2.5 gene product [Caenorhabditis elegans]	8.4
3216	14746120	gi|14746120|ref|XP_005163.2| cadherin 17, LI cadherin (liver-intestine) [Homo sapiens] ref|XP_043524.1| cadherin 17, LI cadherin (liver-intestine) [Homo sapiens]	1E-18
3217	9366835	gi|9366835|emb|CAB95597.1| (AL359782) hypothetical protein, CHR1.368 [Trypanosoma brucei]	4.1
3218	6272295	gi|6272295|gb|AAF06072.1|AF072715_3 (AF072715) unknown [Mycoplasma mycoides subsp. capri]	0.17
3220	7293488	gi|7293488|gb|AAF48863.1| (AE003509) CG15040 gene product [Drosophila melanogaster]	2.8
3223	7662432	gi|7662432|ref|NP_055769.1| KIAA0985 protein [Homo sapiens] ref|XP_007006.3| KIAA0985 protein [Homo sapiens] sp|Q9Y2J0|RP3A_HUMAN RABPHILIN-3A dbj|BAA76829.1| (AB023202) KIAA0985 protein [Homo sapiens]	0.18
3225	7504860	gi|7504860|pir||T33299 hypothetical protein H05B21.4 - Caenorhabditis elegans gb|AAC17764.1| (AF068717) Hypothetical protein H05B21.4 [Caenorhabditis elegans]	3.7

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
3226	6708056	gi|6708056|gb|AAF25780.1|AF163311_1 (AF163311) Kal1.2 [Danio rerio]	2.5
3229	13473697	gi|13473697|ref|NP_105265.1| acyl-CoA thioesterase [Mesorhizobium loti] dbj|BAB51051.1| (AP003004) acyl-CoA thioesterase [Mesorhizobium loti]	5.4
3230	12964703	gi|12964703|gb|AAK11280.1|AF315035_1 (AF315035) phosphocholine cytidylyltransferase [Plasmodium falciparum]	2.1
3231	7521951	gi|7521951|pir||T30180 hypothetical protein - Shewanella sp gb|AAB81120.1| (U73935) unknown [Shewanella sp. SCRC-2738]	6
3232	3249620	gi|3249620|gb|AAC24120.1| (AF067182) IDI-2 precursor [Podospora anserina]	3.1
3233	7493160	gi|7493160|pir||T40507 probable vacuolar protein sorting-associated pro tein - fission yeast (Schizosaccharomyces pombe) emb|CAA20730.1| (AL031534) putative vacuolar protein sorting-associated protein [Schizosaccharomyces pombe]	5.5
3237	7462822	gi|7462822|pir||C72269 hypothetical protein TM1297 - Thermotoga maritima (strain MSB8) gb|AAD36371.1|AE001785_2 (AE001785) oxidoreductase, putative [Thermotoga maritima]	5.5
3241	1531651	gi|1531651|gb|AAC61662.1| (U67083) KRAB-zinc finger protein KZF-2 [Rattus norvegicus]	4.6
3247	2118405	gi|2118405|pir||I51018 cobra venom factor precursor - monocled cobra gb|AAA68989.1| (U09969) cobra venom factor precursor [Naja naja]	9.2
3253	11499508	gi|11499508|ref|NP_070749.1| LSU ribosomal protein L4P (rpl4P) [Archaeoglobus fulgidus] sp|O28355|RL4_ARCFU 50S RIBOSOMAL PROTEIN L4/L1E pir||C69490 LSU ribosomal protein L4P (rpl4P) homolog - Archaeoglobus fulgidus gb|AAB89332.1| (AE000971) LSU ribosomal protein L4P (rpl4P) [Archaeoglobus fulgidus]	2.9

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
3258	461509	gi|461509|sp|Q03045|AMYG_HORRE GLUCOAMYLASE P PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE) pir||S33908 glucan 1,4-alpha-glucosidase (EC 3.2.1.3) P precursor - creosote fungus emb|CAA47945.1| (X67708) 1, 4-alpha-D-glucan glucohydrolase; glucan 1,4-alpha-glucosidase [Amorphotheca resinae] emb|CAA48243.1| (X68143) glucan 1,4-alpha-glucosidase [Amorphotheca resinae] prf||1907167A glucoamylase P [Amorphotheca resinae] prf||2113213A glucoamylase P [Amorphotheca resinae]	5.8
3260	5817900	gi|5817900|gb|AAD52976.1| (AF176771) reverse transcriptase [Human immunodeficiency virus type 2]	6.1
3262	12804147	gi|12804147|gb|AAH02928.1|AAH02928 (BC002928) Unknown (protein for MGC:11357) [Homo sapiens]	3E-14
3266	6323756	gi|6323756|ref|NP_013827.1| myosin I; Myo5p [Saccharomyces cerevisiae] sp|Q04439|YMZ9_YEAST HYPOTHETICAL MYOSIN-LIKE PROTEIN IN ILV2-ADE17 INTERGENIC REGION pir||S54570 probable membrane protein YMR109w - yeast (Saccharomyces cerevisiae) emb|CAA89745.1| (Z49702) unknown [Saccharomyces cerevisiae] gb|AAB37419.1| Myo5p=actin patch localized myosin I variant/MYO5 product [Saccharomyces cerevisiae=yeast, Peptide, 1219 aa]	0.24
3271	12848866	gi|12848866|dbj|BAB28115.1| (AK012246) putative [Mus musculus]	0.011
3273	4758842	gi|4758842|ref|NP_004551.1| receptor tyrosine kinase-like orphan receptor 2; Ror2; neurotrophic tyrosine kinase, receptor-related 2 [Homo sapiens] sp|Q01974|ROR2_HUMAN TYROSINE-PROTEIN KINASE TRANSMEMBRANE RECEPTOR ROR2 PRECURSOR (NEUROTROPHIC TYROSINE KINASE, RECEPTOR-RELATED 2) pir||B45082 neurotrophic receptor ror2 precursor - human gb|AAA60276.1| (M97639) transmembrane receptor [Homo sapiens]	5.6

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
3274	913140	gi|913140|gb|AAB33486.1| ARK2 product/receptor-like serine/threonine protein kinase ARK2 [Arabidopsis thaliana, Columbia, Peptide, 850 aa]	1.7
3276	11357726	gi|11357726|pir||T51437 hypothetical protein F2G14_40 - Arabidopsis thaliana emb|CAC01811.1| (AL391146) putative protein [Arabidopsis thaliana] gb|AAK49610.1|AF372894_1 (AF372894) AT5g14920/F2G14_40 [Arabidopsis thaliana] gb|AAK74054.1| (AY045696) AT5g14920/F2G14_40 [Arabidopsis thaliana]	2
3277	7511204	gi|7511204|pir||T27899 hypothetical protein ZK546.5 - Caenorhabditis elegans gb|AAA68738.1| (U29380) Hypothetical protein ZK546.5 [Caenorhabditis elegans]	3.4
3279	7492154	gi|7492154|pir||T38426 major facilitator protein homolog - fission yeast (Schizosaccharomyces pombe)	6
3285	14764251	gi|14764251|ref|XP_011989.3| ELKL motif kinase 1 isoform a [Homo sapiens]	9E-18
3286	126686	gi|126686|sp|P27424|MGP1_BOVIN MICROFIBRIL-ASSOCIATED GLYCOPROTEIN PRECURSOR (MAGP) (MAGP-1) (TROPOELASTIN-BINDING PROTEIN) pir||A54151 microfibril-associated glycoprotein precursor - bovine gb|AAA62715.1| (M59851) microfibril-associated glycoprotein [Bos taurus] gb|AAB29686.1| (S68064) microfibril-associated glycoprotein, MAGP=tropoelastin-binding protein [cattle, Peptide Partial, 183 aa] [Bos taurus]	5.4
3293	13622462	gi|13622462|gb|AAK34181.1| (AE006573) conserved hypothetical protein [Streptococcus pyogenes M1 GAS]	6
3295	7523494	gi|7523494|dbj|BAA94222.1| (AP001633) hypothetical protein [Oryza sativa]	0.16
3301	5815436	gi|5815436|gb|AAD52672.1|AF178772_1 (AF178772) 98kDa HDM allergen [Dermatophagoides farinae]	8.3

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
3302	7522146	gi|7522146|pir||T17467 rifamycin polyketide synthase modules 9-10 - Amycolatopsis mediterranei emb|CAA11039.1| (AJ223012) rifamycin polyketide synthase, type 1 [Amycolatopsis mediterranei] gb|AAC01714.1| (AF040570) polyketide synthase [Amycolatopsis mediterranei]	8.5
3313	14737876	gi|14737876|ref|XP_031833.1| collagen, type V, alpha 1 [Homo sapiens]	9.6
3316	10092673	gi|10092673|ref|NP_064709.1| hypothetical protein [Homo sapiens] ref|XP_048065.1| hypothetical protein [Homo sapiens] gb|AAC24312.1| (AC004382) Unknown gene product [Homo sapiens]	0.000002
3317	135937	gi|135937|sp|P04924|TNFA_RABIT TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN) gb|AAA31482.1| (M12846) tumor necrosis factor [Oryctolagus cuniculus] gb|AAA31484.1| (M60340) tumor necrosis factor [Oryctolagus cuniculus]	8.2
3318	11282039	gi|11282039|pir||C82096 aminoacyl-histidine dipeptidase VC2279 [imported] - Vibrio cholerae (group O1 strain N16961) gb|AAF95423.1| (AE004299) aminoacyl-histidine dipeptidase [Vibrio cholerae]	0.73
3320	11360605	gi|11360605|pir||A81752 conserved hypothetical protein TC0009 [imported] - Chlamydia muridarum (strain Nigg) gb|AAF38902.1| (AE002269) conserved hypothetical protein [Chlamydia muridarum]	9.2
3321	7491033	gi|7491033|pir||T38495 hypothetical protein SPAC29B12.07 - fission yeast (Schizosaccharomyces pombe)	0.46
3322	102425	gi|102425|pir||B41132 collagen-related protein 2 - Hydra magnipapillata (fragment) pir||S21930 mini-collagen - Hydra sp emb|CAA43380.1| (X61046) mini-collagen [Hydra sp.]	0.99
3328	7507644	gi|7507644|pir||T25887 hypothetical protein T10H10.2 - Caenorhabditis elegans gb|AAB37989.1| (U80848) T10H10.2 gene product [Caenorhabditis elegans]	4.3

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
3331	3738325	gi|3738325|gb|AAC63666.1| (AC005170) cyclic nucleotide and calmodulin-regulated ion channel [Arabidopsis thaliana]	9.1
3332	8978523	gi|8978523|dbj|BAA98360.1| (AP002545) CT147 hypothetical protein [Chlamydophila pneumoniae J138]	8.3
3337	12382001	gi|12382001|dbj|BAB21270.1| (AP002844) hypothetical protein [Oryza sativa]	2.6
3338	11466493	gi|11466493|ref|NP_038196.1| cytochrome c oxidase subunit 3 [Chrysodidymus synuroideus] gb|AAF36962.1|AF222718_36 (AF222718) cytochrome c oxidase subunit 3 [Chrysodidymus synuroideus]	5.4
3339	7475952	gi|7475952|pir||H69754 two-component sensor histidine kinase homolog yccG - Bacillus subtilis dbj|BAA22234.1| (AB000617) YccG [Bacillus subtilis] emb|CAB12067.1| (Z99105) similar to two-component sensor histidine kinase [YccH] [Bacillus subtilis]	5.9
3344	340613	gi|340613|gb|AAA31881.1| (L07545) A 'c' was inserted after nt 369 (=nt 10459 in genomic sequence (M10126)) to correct -1 frameshift probably due to gel compression [Leishmania tarentolae]	1.4
3345	10121788	gi|10121788|gb|AAG13373.1| (AF268180) polyprotein [bovine viral diarrhea virus type 2]	5.4
3346	3641252	gi|3641252|gb|AAC36318.1| (AF053127) leucine-rich receptor-like protein kinase [Malus x domestica]	0.49
3347	6226170	gi|6226170|sp|O67271|SYE_AQUAE GLUTAMYL-TRNA SYNTHETASE (GLUTAMATE--TRNA LIGASE) (GLURS) pir||D70405 glutamate--tRNA ligase (EC 6.1.1.17) - Aquifex aeolicus gb|AAC07230.1| (AE000729) glutamyl-tRNA synthetase [Aquifex aeolicus]	3
3348	2127912	gi|2127912|pir||B64428 formate hydrogenlyase, subunit 5 - Methanococcus jannaschii gb|AAB99031.1| (U67545) formate hydrogenlyase, subunit 5 [Methanococcus jannaschii]	2.9

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
3351	7507391	gi|7507391|pir||T24665 hypothetical protein T07F10.4 - Caenorhabditis elegans emb|CAB01241.1| (Z77669) predicted using Genefinder~Similarity to Human mRNA (KIAA0033) (TR:G436224) [Caenorhabditis elegans]	6.3
3355	7476137	gi|7476137|pir||A70989 hypothetical glycine-rich protein Rv1768 - Mycobacterium tuberculosis (strain H37RV) emb|CAB09311.1| (Z95890) PE_PGRS [Mycobacterium tuberculosis]	4.1
3359	6782280	gi|6782280|emb|CAB70102.1| (AL132949) Y53F4B.7 [Caenorhabditis elegans] emb|CAB70113.2| (AL132949) Y53F4B.26 [Caenorhabditis elegans]	5.6
3361	14133241	gi|14133241|dbj|BAA86438.2| (AB032950) KIAA1124 protein [Homo sapiens]	0.28
3362	117000	gi|117000|sp|P04371|COX1_TRYBB CYTOCHROME C OXIDASE POLYPEPTIDE I pir||ODUTMB cytochrome-c oxidase (EC 1.9.3.1) chain I - Trypanosoma brucei mitochondrion gb|AAB59223.1| (M14820) cytochrome c oxidase subunit I [Trypanosoma brucei] emb|CAB57806.1| (X01094) put. gene for cytochrome c oxidase subunit I gene [Trypanosoma brucei]	1.7
3369	2072972	gi|2072972|gb|AAC51276.1| (U93572) putative p150 [Homo sapiens]	0.000008
3371	13476092	gi|13476092|ref|NP_107662.1| ABC transporter permease protein [Mesorhizobium loti] dbj|BAB53448.1| (AP003011) ABC transporter permease protein [Mesorhizobium loti]	0.43
3372	13385538	gi|13385538|ref|NP_080316.1| RIKEN cDNA 2810036K01 gene [Mus musculus] dbj|BAB28520.1| (AK012865) putative [Mus musculus]	2E-58
3376	14765434	gi|14765434|ref|XP_030354.1| similar to KIAA0220 protein (H. sapiens) [Homo sapiens]	8
3393	10641134	gi|10641134|dbj|BAB16313.1| (AB049587) fork head/HNF-3 homologue [Ciona savignyi]	9.2
3396	11358605	gi|11358605|pir||T49882 pectin methyl-esterase-like protein - Arabidopsis thaliana emb|CAB87932.1| (AL163912) pectin methyl-esterase-like protein [Arabidopsis thaliana]	4.1

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
3397	4493932	gi|4493932|emb|CAB38968.1| (AL034556) Hypothetical protein, PFC0580c [Plasmodium falciparum]	7
3400	11496667	gi|11496667|ref|NP_045466.1| conserved hypothetical protein [Borrelia burgdorferi] pir||F70231 conserved hypothetical protein BBG06 - Lyme disease spirochete plasmid G/lp28-2 gb|AAC66054.1| (AE000786) conserved hypothetical protein [Borrelia burgdorferi]	7.3
3403	7020787	gi|7020787|dbj|BAA91274.1| (AK000589) unnamed protein product [Homo sapiens]	5E-19
3404	12045115	gi|12045115|ref|NP_072926.1| lipoprotein, putative [Mycoplasma genitalium] sp|P47502|Y260_MYCGE HYPOTHETICAL LIPOPROTEIN MG260 PRECURSOR pir||G64228 hypothetical protein homolog MG260 - Mycoplasma genitalium gb|AAC71481.1| (U39705) lipoprotein, putative [Mycoplasma genitalium]	3.4
3407	13959004	gi|13959004|gb|AAK51055.1|AF361075_2 (AF361075) UL24 [Canine herpesvirus]	0.89
3408	13814730	gi|13814730|gb|AAK41724.1| (AE006765) Hypothetical protein [Sulfolobus solfataricus]	9.1
3415	12744896	gi|12744896|gb|AAK06840.1|AF329637_1 (AF329637) mitofusin 1 precursor [Homo sapiens]	0.16
3416	8922500	gi|8922500|ref|NP_060600.1| hypothetical protein FLJ10539 [Homo sapiens] dbj|BAA91669.1| (AK001401) unnamed protein product [Homo sapiens]	7.1
3418	6635084	gi|6635084|emb|CAB64573.1| (AL135930) hypothetical protein L4738.02 [Leishmania major]	3.5
3419	296559	gi|296559|emb|CAA49925.1| (X70529) ORF YBR1730 [Saccharomyces cerevisiae]	0.42
3422	5579432	gi|5579432|gb|AAD45553.1|U70376_18 (U70376) SpcH [Streptomyces netropsis]	6.3
3423	11466493	gi|11466493|ref|NP_038196.1| cytochrome c oxidase subunit 3 [Chrysodidymus synuroideus] gb|AAF36962.1|AF222718_36 (AF222718) cytochrome c oxidase subunit 3 [Chrysodidymus synuroideus]	6
3424	1084985	gi|1084985|pir||S51908 cryptogene protein G1(ND9) - Leishmania tarentolae (strain LEM125)	6.6
3426	8778413	gi|8778413|gb|AAF79421.1|AC025808_3 (AC025808) F18O14.6 [Arabidopsis thaliana]	4.2

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
3430	13992688	gi|13992688|gb|AAK51582.1|AC022352_18 (AC022352) Putative retroelement [Oryza sativa]	9.3
3431	9280694	gi|9280694|gb|AAF86563.1|AC069252_22 (AC069252) F2E2.6 [Arabidopsis thaliana]	3.3
3437	4115918	gi|4115918|gb|AAD03429.1| (AF118222) similar to nascent polypeptide associated complex alpha chain [Arabidopsis thaliana]	4.4
3438	7433244	gi|7433244|pir||T01751 gibberellin 20-oxidase - common tobacco dbj|BAA31690.1| (AB016084) Ntc16 [Nicotiana tabacum]	1.2
3439	3978489	gi|3978489|gb|AAC83366.1| (AF092918) unknown [Pseudomonas alcaligenes]	8.5
3441	7506359	gi|7506359|pir||T23969 hypothetical protein R06C7.5 - Caenorhabditis elegans emb|CAA95843.1| (Z71266) Similarity to Human adenylosuccinate lyase (SW:PUR8_HUMAN), contains similarity to Pfam domain: PF00206 (Lyase), Score=165.2, E-value=3.5e-46, N=1~cDNA EST EMBL:Z14522 comes from this gene~cDNA EST yk67g5.3 comes from this gene~cDNA EST yk67g5>	5.9
3443	12852662	gi|12852662|dbj|BAB29494.1| (AK014667) putative [Mus musculus]	2E-28
3448	9256527	gi|9256527|ref|NP_061764.1| ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation) [Homo sapiens] gb|AAF13115.1|AF123757_1 (AF123757) putative transmembrane protein [Homo sapiens] gb|AAF13116.1|AF123758_1 (AF123758) putative transmembrane protein [Homo sapiens] gb|AAF13117.1|AF123759_1 (AF123759) putative transmembrane protein [Homo sapiens] gb|AAF13118.1|AF123760_1 (AF123760) putative transmembrane protein [Homo sapiens] gb|AAF13119.1|AF123761_1 (AF123761) putative transmembrane protein [Homo sapiens]	2.7
3457	7705167	gi|7705167|gb|AAC60545.2| (S54379) sucrose-phosphate synthase; SPS [Spinacia oleracea]	8.6
3461	10179322	gi|10179322|dbj|BAB13673.1| (AB041350) type IV collagen alpha 5 chain [Mus musculus]	0.25
3462	13882453	gi|13882453|gb|AAK47018.1| (AE007102) hypothetical protein [Mycobacterium tuberculosis CDC1551]	3.6

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
3466	2499996	gi|2499996|sp|Q45298|PTGA_CORGL PTS SYSTEM, GLUCOSE-SPECIFIC IIABC COMPONENT (EIIABC-GLC) (GLUCOSE-PERMEASE IIABC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, ABC COMPONENT) (EII-GLC/EIII-GLC) gb|AAA22992.1| (L18875) phosphoenolpyruvate sugar phosphotransferase [Corynebacterium glutamicum]	9.9
3467	7503384	gi|7503384|pir||T31714 probable zinc proteinase (EC 3.4.24.-) F44E7.4 - Caenorhabditis elegans gb|AAC25789.1| (AF016421) Hypothetical protein F44E7.4 [Caenorhabditis elegans]	5.1
3472	225485	gi|225485|prf||1304284B beejin [Dictyostelium discoideum]	5
3482	7302644	gi|7302644|gb|AAF57724.1| (AE003800) fj gene product [Drosophila melanogaster]	0.19
3487	3121914	gi|3121914|sp|Q37679|COX3_THEAN CYTOCHROME C OXIDASE POLYPEPTIDE III gb|AAA73631.1| (U32225) cytochrome oxidase polypeptide III [Theileria annulata]	6.9
3489	1351243	gi|1351243|sp|P47749|THRR_XENLA THROMBIN RECEPTOR PRECURSOR pir||I51667 thrombin receptor - African clawed frog gb|AAA18498.1| (U09632) thrombin receptor [Xenopus laevis]	6.2
3491	12517831	gi|12517831|gb|AAG58344.1|AE005549_1 (AE005549) aerobic respiration sensor-response protein; histidine protein kinase/phosphatase, sensor for arcA [Escherichia coli O157:H7 EDL933] dbj|BAB37512.1| (AP002564) aerobic respiration sensor-response protein [Escherichia coli O157:H7]	6.9
3492	2240037	gi|2240037|gb|AAB66910.1| (AF005356) integrin subunit betaCn1 [Acropora millepora]	5.5
3494	14742385	gi|14742385|ref|XP_046349.1| 33219 [Homo sapiens]	4.6
3501	12847027	gi|12847027|dbj|BAB27408.1| (AK011113) putative [Mus musculus]	5.6
3505	1763691	gi|1763691|gb|AAB39835.1| (U72048) glycoprotein [Classical swine fever virus]	1.2
3507	13470696	gi|13470696|ref|NP_102265.1| unknown protein [Mesorhizobium loti] dbj|BAB48051.1| (AP002994) unknown protein [Mesorhizobium loti]	5.1

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
3511	7706335	gi|7706335|ref|NP_057140.1| CGI-119 protein [Homo sapiens] gb|AAD34114.1|AF151877_1 (AF151877) CGI-119 protein [Homo sapiens]	2.3
3512	13812236	gi|13812236|ref|NP_113367.1| hypothetical protein [Guillardia theta] gb|AAK39923.1|AF165818_131 (AF165818) hypothetical protein [Guillardia theta]	2.4
3513	7510320	gi|7510320|pir||T33571 hypothetical protein Y59C2A.2 - Caenorhabditis elegans gb|AAC68742.1| (AF099003) Y59C2A.2 gene product [Caenorhabditis elegans]	0.37
3517	12724149	gi|12724149|gb|AAK05281.1|AE006350_8 (AE006350) HYPOTHETICAL PROTEIN [Lactococcus lactis subsp. lactis]	1.7
3519	2342679	gi|2342679|gb|AAB70402.1| (AC000106) Similar to Vicia sativa ENBP1 (gb|X95995). [Arabidopsis thaliana]	5.2
3520	7305389	gi|7305389|ref|NP_038658.1| polycystic kidney disease 1 homolog; polycystin-1 [Mus musculus] gb|AAC53207.1| (U70209) polycystic kidney disease 1 protein [Mus musculus]	2.2
3523	1353257	gi|1353257|gb|AAB06234.1| (U26665) dimethyl sulphoxide reductase subunit B [Haemophilus influenzae]	3.9
3524	14794474	gi|14794474|gb|AAK73355.1|AF390546_1 (AF390546) gut-enriched kruppel-like factor [Rattus norvegicus]	0.47
3527	7510320	gi|7510320|pir||T33571 hypothetical protein Y59C2A.2 - Caenorhabditis elegans gb|AAC68742.1| (AF099003) Y59C2A.2 gene product [Caenorhabditis elegans]	0.89
3530	10173181	gi|10173181|dbj|BAB04286.1| (AP001509) nickel transport system (nickel-binding protein) [Bacillus halodurans]	4.6
3531	7442453	gi|7442453|pir||G72215 oligopeptide ABC transporter, permease protein - Thermotoga maritima (strain MSB8) gb|AAD36813.1|AE001813_5 (AE001813) oligopeptide ABC transporter, permease protein [Thermotoga maritima]	8.7
3532	11136027	gi|11136027|sp|O88553|ZF37_RAT ZINC FINGER PROTEIN 37 (ZFP-37) gb|AAC24590.1| (AF072439) zinc-finger protein-37; ZFP-37 [Rattus norvegicus]	1.8

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
3538	14732500	gi|14732500|ref|XP_041698.1| hypothetical protein FLJ10904 [Homo sapiens] ref|XP_041699.1| 50659 [Homo sapiens]	8.5
3540	7438506	gi|7438506|pir||T09963 mitosis-specific cyclin B-type - Madagascar periwinkle dbj|BAA20411.1| (D86386) B-type cyclin [Catharanthus roseus]	0.75
3541	7495199	gi|7495199|pir||T31857 hypothetical protein C02E7.14 - Caenorhabditis elegans gb|AAC24171.1| (AF016446) Hypothetical protein C02E7.14 [Caenorhabditis elegans]	4.9
3542	162223	gi|162223|gb|AAA30233.1| (M27163) RNA polymerase III [Trypanosoma brucei]	4.9
3546	6635084	gi|6635084|emb|CAB64573.1| (AL135930) hypothetical protein L4738.02 [Leishmania major]	2.7
3549	13095647	gi|13095647|ref|NP_076562.1| unknown [Bovine herpesvirus 4] gb|AAK07989.1|AF318573_69 (AF318573) unknown [Bovine herpesvirus 4]	6.9
3551	11359423	gi|11359423|pir||T48729 hypothetical protein 8D4.30 [imported] - Neurospora crassa emb|CAB88545.1| (AL353819) conserved hypothetical protein [Neurospora crassa]	5.3
3556	13241881	gi|13241881|gb|AAK16450.1| (AF327992) cytochrome oxidase subunit I [Platycryptus undatus]	9.7
3562	4589564	gi|4589564|dbj|BAA76804.1| (AB023177) KIAA0960 protein [Homo sapiens]	4.8
3563	7486330	gi|7486330|pir||T05113 hypothetical protein F28M20.240 - Arabidopsis thaliana emb|CAA19766.1| (AL031004) putative protein [Arabidopsis thaliana] emb|CAB79875.1| (AL161579) putative protein [Arabidopsis thaliana]	8.3
3569	118965	gi|118965|sp|P23098|DYHC_TRIGR DYNEIN BETA CHAIN, CILIARY pir||S17653 dynein beta heavy chain, ciliary - sea urchin (Tripneustes gratilla) emb|CAA42170.1| (X59603) Beta heavy chain of outer-arm axonemal dynein ATPase [Tripneustes gratilla] prf||1714372A dynein:SUBUNIT=beta heavy chain [Tripneustes gratilla]	7.7
3571	7662078	gi|7662078|ref|NP_055454.1| KIAA0372 gene product [Homo sapiens] dbj|BAA20827.1| (AB002370) KIAA0372 [Homo sapiens]	5E-65

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
3576	5803098	gi|5803098|ref|NP_006757.1| zinc finger protein 220; Monocytic leukemia zinc finger protein [Homo sapiens] sp|Q92794|MOZ_HUMAN MONOCYTIC LEUKEMIA ZINC FINGER PROTEIN (ZINC FINGER PROTEIN 220) gb|AAC50662.1| (U47742) monocytic leukaemia zinc finger protein [Homo sapiens]	4.6
3582	9964384	gi|9964384|ref|NP_064852.1| AMV070 [Amsacta moorei entomopoxvirus] gb|AAG02776.1|AF250284_70 (AF250284) AMV070 [Amsacta moorei entomopoxvirus]	9
3583	13272342	gi|13272342|gb|AAK17105.1|AF291051_2 (AF291051) ATP synthase subunit a [Candidatus Carsonella ruddii]	1.3
3586	7505649	gi|7505649|pir||T28783 hypothetical protein K09E10.1 - Caenorhabditis elegans gb|AAC48044.1| (AF003149) Hypothetical protein K09E10.1 [Caenorhabditis elegans]	2.9
3587	2981631	gi|2981631|dbj|BAA25253.1| (AB012223) ORF2 [Canis familiaris]	0.98
3590	6018210	gi|6018210|gb|AAF01791.1| (AF143853) 82 kD heat shock protein [Moniliformis moniliformis]	0.15
3593	7160719	gi|7160719|emb|CAA88053.2| (Z48007) contains similarity to Pfam domain: PF00069 (Eukaryotic protein kinase domain), Score=49.7, E-value=3.4e-13, N=3; PF00211 (Adenylate and Guanylate cyclase catalytic domain), Score=325.1, E-value=2.5e-94, N=1; PF01094 (Receptor family ligand bi>	4.3
3599	7470593	gi|7470593|pir||S75491 hypothetical protein slr2115 - Synechocystis sp. (strain PCC 6803) dbj|BAA18052.1| (D90911) ORF_ID:slr2115~unknown protein [Synechocystis sp. PCC 6803]	5.5
3600	1334398	gi|1334398|emb|CAA33190.1| (X15081) MURF2 protein (AA 1-348) [Crithidia fasciculata]	2.2

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
3602	118965	gi|118965|sp|P23098|DYHC_TRIGR DYNEIN BETA CHAIN, CILIARY pir||S17653 dynein beta heavy chain, ciliary - sea urchin (Tripneustes gratilla) emb|CAA42170.1| (X59603) Beta heavy chain of outer-arm axonemal dynein ATPase [Tripneustes gratilla] prf||1714372A dynein:SUBUNIT=beta heavy chain [Tripneustes gratilla]	9.8
3603	14578630	gi|14578630|gb|AAK68919.1|AF189282_9 (AF189282) putative glycosyltransferase [Bacteroides fragilis]	0.29
3606	14318569	gi|14318569|ref|NP_116702.1| Yfr044cp [Saccharomyces cerevisiae] sp|P43616|YFL4_YEAST HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION pir||S56299 hypothetical protein YFR044c - yeast (Saccharomyces cerevisiae) dbj|BAA09283.1| (D50617) YFR044C [Saccharomyces cerevisiae]	3
3609	10581847	gi|10581847|gb|AAG20525.1| (AE005124) Vng2444c [Halobacterium sp. NRC-1]	4.5
3616	1363925	gi|1363925|pir||S57662 hypothetical protein 2 - North American opossum (fragment) emb|CAA88817.1| (Z48955) ORF-2, putative RT [Didelphis virginiana]	3.6
3618	1808609	gi|1808609|emb|CAA64091.1| (X94355) D6L [Cowpox virus] emb|CAA72556.1| (Y11842) C6L [Cowpox virus]	9.6
3619	14775653	gi|14775653|ref|XP_045559.1| similar to KIAA0565 gene product (H. sapiens) [Homo sapiens]	4.7
3621	7475003	gi|7475003|pir||G69801 hypothetical protein yfhO - Bacillus subtilis emb|CAB12689.1| (Z99108) yfhO [Bacillus subtilis] dbj|BAA24481.1| (D85082) YfhO [Bacillus subtilis]	8.1
3626	5902895	gi|5902895|dbj|BAA84478.1| (AB032367) type I polyketide synthase AVES 3 [Streptomyces avermitilis]	4.3
3627	7444049	gi|7444049|pir||F72275 phosphate regulon transcription regulator PhoB - Thermotoga maritima (strain MSB8) gb|AAD36333.1|AE001781_4 (AE001781) phosphate regulon transcriptional regulatory protein PhoB [Thermotoga maritima]	2.8

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
3630	7507776	gi|7507776|pir||T16867 probable cytochrome P450 T13C5.1 [similarity] - Caenorhabditis elegans	1.6
3632	11360480	gi|11360480|pir||H82745 acyl-[ACP]-UDP-N-acetylglucosamine XF0918 [imported] - Xylella fastidiosa (strain 9a5c) gb|AAF83728.1|AE003931_5 (AE003931) acyl-[ACP]-UDP-N-acetylglucosamine [Xylella fastidiosa 9a5c]	1.3
3633	13873167	gi|13873167|gb|AAK43406.1| (AF196891) polygalacturonase inhibitor protein [Fragaria vesca] gb|AAK43407.1| (AF196892) polygalacturonase inhibitor protein [Fragaria vesca] gb|AAK43408.1| (AF196893) polygalacturonase inhibitor protein [Fragaria vesca]	3.7
3636	10946710	gi|10946710|ref|NP_067350.1| Rhesus blood group-associated B glycoprotein; Rh type B glycoprotein [Mus musculus] gb|AAF19371.1| (AF193808) Rh type B glycoprotein [Mus musculus]	4.9
3638	7447412	gi|7447412|pir||T06201 xyloglucan endo-1,4-beta-D-glucanase (EC 3.2.1.-) - barley emb|CAA63662.1| (X93174) xyloglucan endotransglycosylase (XET) [Hordeum vulgare]	5.5
3639	12620601	gi|12620601|gb|AAG60877.1|AF322012_182 (AF322013) ID409 [Bradyrhizobium japonicum]	6.4
3640	1175418	gi|1175418|sp|Q09743|ST16_SCHPO STE16 PROTEIN pir||T39379 sexual differentiation and meiosis protein ste20 - fission yeast (Schizosaccharomyces pombe) emb|CAA90815.1| (Z54140) required for sexual differentiation and meiosis [Schizosaccharomyces pombe] emb|CAA11758.1| (AJ223984) Ste20 protein [Schizosaccharomyces pombe]	4.6
3641	1172876	gi|1172876|sp|P35906|RDS_FELCA PERIPHERIN (RETINAL DEGENERATION SLOW PROTEIN) pir||I46087 peripherin - cat gb|AAA19175.1| (M94047) peripherin [Felis catus]	5.1
3643	825671	gi|825671|emb|CAA34809.1| (X16934) B23 nucleophosmin (280 AA) [Homo sapiens]	2E-10
3645	2388576	gi|2388576|gb|AAB71457.1| (AC000098) YUP8H12.17 [Arabidopsis thaliana]	3.7

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
3648	7498664	gi|7498664|pir||T20598 hypothetical protein F08G2.4 - Caenorhabditis elegans emb|CAB04058.1| (Z81495) predicted using Genefinder~cDNA EST yk401a9.3 comes from this gene~cDNA EST yk401a9.5 comes from this gene~cDNA EST yk523d8.3 comes from this gene~cDNA EST yk523d8.5 comes from this gene [Caenorhabditis elegans] gb|AAG50226.1|AF303268_1 (AF303268) 2O123 [Caenorhabditis elegans]	9.4
3654	225992	gi|225992|prf||1405326A GLI gene [Homo sapiens]	3.2
3657	422532	gi|422532|pir||A45407 collagen alpha 3(IV) chain - sea urchin (Strongylocentrotus purpuratus)	0.94
3658	14149807	gi|14149807|ref|NP_115517.1| hypothetical protein DKFZp434K1421 [Homo sapiens] emb|CAB66740.1| (AL136806) hypothetical protein [Homo sapiens]	4E-65
3665	134872	gi|134872|sp|P13666|SRCA_RABIT SARCALUMENIN PRECURSOR gb|AAA31189.1| (M25750) sarcolumenin precursor [Oryctolagus cuniculus]	8.1
3670	14734955	gi|14734955|ref|XP_046758.1| tensin [Homo sapiens]	0.47
3675	14742385	gi|14742385|ref|XP_046349.1| 33219 [Homo sapiens]	2.1
3676	2197085	gi|2197085|gb|AAD04635.1| (AF003535) ORF2-like protein [Homo sapiens]	0.14
3690	1711034	gi|1711034|gb|AAB38323.1| (U78953) basic helix-loop-helix DNA binding protein HLH-3 [Caenorhabditis elegans]	5.4
3692	2072964	gi|2072964|gb|AAC51271.1| (U93569) putative p150 [Homo sapiens]	0.15
3693	1857258	gi|1857258|gb|AAB48409.1| (U75538) putative viral polymerase [tobacco streak virus]	5.3
3694	8573079	gi|8573079|ref|NP_059567.1| NADH dehydrogenase subunit 1 [Sciurus vulgaris] emb|CAB93985.1| (AJ238588) NADH dehdrogenase subunit 1 [Sciurus vulgaris]	3E-15
3699	12654875	gi|12654875|gb|AAH01281.1|AAH01281 (BC001281) tumor necrosis factor receptor superfamily, member 10b [Homo sapiens]	7.9
3704	2961586	gi|2961586|gb|AAC05758.1| (AF051294) NADH dehydrogenase subunit 1 [Dalbulus gelbus]	4.3

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
3707	1504016	gi|1504016|dbj|BAA13207.1| (D86971) no similarities to reported gene products [Homo sapiens]	6E-11
3709	11466493	gi|11466493|ref|NP_038196.1| cytochrome c oxidase subunit 3 [Chrysodidymus synuroideus] gb|AAF36962.1|AF222718_36 (AF222718) cytochrome c oxidase subunit 3 [Chrysodidymus synuroideus]	5.7
3710	14089788	gi|14089788|emb|CAC13547.1| (AL445564) LIPOPROTEIN [Mycoplasma pulmonis]	2.4
3724	8978260	gi|8978260|dbj|BAA98151.1| (AB025612) CLP protease regulatory subunit CLPX-like [Arabidopsis thaliana]	5.4
3727	14748431	gi|14748431|ref|XP_018068.2| hypothetical protein MGC3199 [Homo sapiens]	0.000009
3734	10727054	gi|10727054|gb|AAF46943.2| (AE003459) CG3037 gene product [Drosophila melanogaster]	3.8
3735	6323629	gi|6323629|ref|NP_013700.1| Yml013c-ap [Saccharomyces cerevisiae] pir||S69871 hypothetical protein YML012c-a - yeast (Saccharomyces cerevisiae)	9
3736	4502081	gi|4502081|ref|NP_001626.1| amphiphysin; amphiphysin (Stiff-Man syndrome with breast cancer 128kD autoantigen) [Homo sapiens] ref|XP_035768.1| amphiphysin [Homo sapiens] ref|XP_035767.1| amphiphysin [Homo sapiens] sp|P49418|AMPH_HUMAN AMPHIPHYSIN pir||S62400 amphiphysin (clone 22-2) - human gb|AAA21865.1| (U07616) amphiphysin [Homo sapiens] emb|CAA57197.1| (X81438) amphiphysin [Homo sapiens]	0.61
3741	7492913	gi|7492913|pir||T40695 probable ribosomal protein precursor, mitochondrial - fission yeast (Schizosaccharomyces pombe) emb|CAB36868.1| (AL035536) mitochondrial ribosomal protein L36 [Schizosaccharomyces pombe]	6.7
3743	1168945	gi|1168945|sp|P30572|CHS2_CANAL CHITIN SYNTHASE 2 (CHITIN-UDP ACETYL-GLUCOSAMINYL TRANSFERASE 2) gb|AAB59308.2| (M82937) chitin synthase 2 [Candida albicans]	1.2

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
3745	12722927	gi|12722927|gb|AAK04181.1|AE006247_3 (AE006247) UNKNOWN PROTEIN [Lactococcus lactis subsp. lactis]	2.9
3747	6090792	gi|6090792|gb|AAF03328.1| (AF101747) olfactory receptor [Pan paniscus]	4.1
3750	12846356	gi|12846356|dbj|BAB27137.1| (AK010713) putative [Mus musculus]	0.000000004
3754	4240279	gi|4240279|dbj|BAA74918.1| (AB020702) KIAA0895 protein [Homo sapiens]	10
3755	543715	gi|543715|sp|P36875|2AAA_PEA PROTEIN PHOSPHATASE PP2A REGULATORY SUBUNIT A (PR65) pir||S40171 phosphoprotein phosphatase 2A 65kDa regulatory chain - garden pea (fragment) pir||S43776 phosphoprotein phosphatase 2A 65kDa regulatory subunit - garden pea (fragment) emb|CAA81107.1| (Z25888) phosphoprotein phosphatase 2A 65kDa regulatory subunit [Pisum sativum]	6E-12
3756	11353649	gi|11353649|pir||D81094 hypothetical protein NMB1340 [imported] - Neisseria meningitidis (group B strain MD58) gb|AAF41715.1| (AE002482) hypothetical protein [Neisseria meningitidis MC58]	3.4
3761	11276053	gi|11276053|gb|AAG33872.1|AF319939_1 (AF319939) enhancin [Choristoneura fumiferana granulovirus]	4.3
3763	13812312	gi|13812312|ref|NP_113430.1| 40S ribosomal protein SSA [Guillardia theta] emb|CAC26999.1| (AJ010592) 40S ribosomal protein SSA [Guillardia theta]	9.3
3764	4115943	gi|4115943|gb|AAD03453.1| (AF118223) contains similarity to eukaryotic protein kinase domains (Pfam: PF00069, score=312.6, E=4.7e-90, N=1) and EF hand domains (Pfam: PF00036, score=131, E=2.1e-35, N=4) [Arabidopsis thaliana] emb|CAB80837.1| (AL161501) putative calcium dependent protein kinase [Arabidopsis thaliana]	1.2
3765	7494381	gi|7494381|pir||H71613 probable multiple transmembrane domain protein PFB0475c - malaria parasite (Plasmodium falciparum) gb|AAC71884.1| (AE001397) predicted multiple transmembrane domain protein [Plasmodium falciparum]	8.5

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
3768	3930075	gi|3930075|gb|AAC82262.1| (U81928) envelope glycoprotein [Human immunodeficiency virus type 1]	2.5
3769	4493896	gi|4493896|emb|CAB39005.1| (AL034558) predicted using hexExon; MAL3P2.18 (PFC0245c), Hypothetical protein, len: 3934 aa [Plasmodium falciparum]	9.2
3770	14193274	gi|14193274|gb|AAK55866.1|AF267203_2 (AF267203) ATP synthase gamma subunit [Candidatus Carsonella ruddii]	6.3
3771	11499055	gi|11499055|ref|NP_070289.1| hypothetical protein [Archaeoglobus fulgidus] sp|O28812|YE60_ARCFU HYPOTHETICAL PROTEIN AF1460 pir||C69432 hypothetical protein AF1460 - Archaeoglobus fulgidus gb|AAB89791.1| (AE001002) A. fulgidus predicted coding region AF1460 [Archaeoglobus fulgidus]	5.9
3773	7301453	gi|7301453|gb|AAF56578.1| (AE003755) CG12290 gene product [Drosophila melanogaster]	9.3
3777	11467606	gi|11467606|ref|NP_050068.1| NH2 terminus uncertain [Leishmania tarentolae] pir||B26696 hypothetical protein 1 (CYb-COII intergenic region) - Leishmania tarentolae mitochondrion (fragment) gb|AAA96601.1| (M10126) NH2 terminus uncertain [Leishmania tarentolae]	0.4
3780	7507710	gi|7507710|pir||T23023 hypothetical protein T12A7.5 - Caenorhabditis elegans emb|CAB07423.1| (Z92847) cDNA EST yk26a3.5 comes from this gene~cDNA EST yk29g7.5 comes from this gene~cDNA EST yk29g8.5 comes from this gene~cDNA EST yk50c8.5 comes from this gene~cDNA EST yk52f12.5 comes from this gene~cDNA EST yk53c1.5 comes from this gene~cDNA EST> emb|CAA98143.1| (Z73911) cDNA EST yk26a3.5 comes from this gene~cDNA EST yk29g7.5 comes from this gene~cDNA EST yk29g8.5 comes from this gene~cDNA EST yk50c8.5 comes from this gene~cDNA EST yk52f12.5 comes from this gene~cDNA EST yk53c1.5 comes from this gene~cDNA EST>	2.6

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
3783	13994312	gi|13994312|ref|NP_114137.1| testis transcript Y 13 [Homo sapiens] ref|XP_040549.1| testis transcript Y 13 [Homo sapiens] gb|AAK13492.1|AF332242_1 (AF332242) transcript Y 13 [Homo sapiens]	2.6
3786	1169093	gi|1169093|sp|P45815|CRF1_YARLI COPPER RESISTANCE PROTEIN CRF1 emb|CAA80803.1| (Z23265) Product required for copper resistance [Yarrowia lipolytica]	7.1
3787	3599476	gi|3599476|gb|AAC69336.1| (AF084637) serendipity alpha protein [Drosophila virilis]	2.5
3793	14728817	gi|14728817|ref|XP_047357.1| KIAA0342 gene product [Homo sapiens]	9.5
3795	11281706	gi|11281706|pir||B81937 competence protein NMA0906 [imported] - Neisseria meningitidis (group A strain Z2491) emb|CAB84183.1| (AL162754) competence protein [Neisseria meningitidis Z2491]	5.5
3797	11096149	gi|11096149|gb|AAG30214.1|AF296334_1 (AF296334) collagen-like surface protein [Streptococcus pyogenes]	2.4
3798	1827933	gi|1827933|pdb|1PCA| Procarboxypeptidase A (E.C.3.4.12.2)	1.3
3800	6320364	gi|6320364|ref|NP_010444.1| regulator of transporters; Ssy1p [Saccharomyces cerevisiae] sp|Q03770|SSY1_YEAST PUTATIVE AMINO-ACID PERMEASE SSY1 pir||S57984 probable membrane protein YDR160w - yeast (Saccharomyces cerevisiae) emb|CAA90380.1| (Z50046) unknown [Saccharomyces cerevisiae]	0.92
3803	14973521	gi|14973521|gb|AAK76078.1| (AE007490) ribosomal large subunit pseudouridine synthase, RluD subfamily [Streptococcus pneumoniae]	7.4
3807	10834955	gi|10834955|ref|NP_066916.1| ICP4 protein [Gallid herpesvirus 3] dbj|BAB16594.1| (AB049735) ICP4 protein [Gallid herpesvirus 3]	1.6
3817	13430085	gi|13430085|gb|AAK25738.1|AF291747_1 (AF291747) zinc-finger transcription factor KROX20 [Gallus gallus]	0.63
3822	7462422	gi|7462422|pir||A72258 hypothetical protein - Thermotoga maritima (strain MSB8) gb|AAD36479.1|AE001793_9 (AE001793) hypothetical protein [Thermotoga maritima]	9.7

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
3828	7517565	gi|7517565|pir||A70328 hypothetical protein aq_311 - Aquifex aeolicus gb|AAC06616.1| (AE000683) putative protein [Aquifex aeolicus]	3.7
3830	3924618	gi|3924618|gb|AAC79121.1| (U88902) putative envelope protein [Homo sapiens]	0.0000006
3835	7023029	gi|7023029|dbj|BAA91807.1| (AK001647) unnamed protein product [Homo sapiens]	4E-80
3836	12698001	gi|12698001|dbj|BAB21819.1| (AB051515) KIAA1728 protein [Homo sapiens]	0.0004
3837	5281354	gi|5281354|gb|AAD41491.1|AF136456_1 (AF136456) transcription factor Tcf3b [Danio rerio]	5
3838	9628045	gi|9628045|ref|NP_042639.1| ORF 42 [Equine herpesvirus 2] pir||S55637 hypothetical protein 42 - equine herpesvirus 2 gb|AAC13830.1| (U20824) ORF 42 [Equine herpesvirus 2]	7.1
3839	9964462	gi|9964462|ref|NP_064930.1| AMV148 [Amsacta moorei entomopoxvirus] gb|AAG02854.1|AF250284_148 (AF250284) AMV148 [Amsacta moorei entomopoxvirus]	5.8
3844	13357611	gi|13357611|ref|NP_077885.1| membrane nuclease A - hypothetical [Ureaplasma urealyticum] pir||A82939 membrane nuclease A, hypothetical UU055 [imported] - Ureaplasma urealyticum gb|AAF30460.1|AE002105_1 (AE002105) membrane nuclease A - hypothetical [Ureaplasma urealyticum]	2.9
3845	2425188	gi|2425188|dbj|BAA22281.1| (AB007035) FGF receptor 3 [Xenopus laevis]	2.5
3848	11351069	gi|11351069|pir||H83232 probable ATP-dependent helicase PA3297 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG06685.1|AE004752_1 (AE004752) probable ATP-dependent helicase [Pseudomonas aeruginosa]	4.2
3850	7141304	gi|7141304|gb|AAF37281.1| (AF225702) RSH1 [Arabidopsis thaliana]	9.3
3852	11352313	gi|11352313|pir||G83376 probable trehalose synthase PA2152 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG05540.1|AE004642_7 (AE004642) probable trehalose synthase [Pseudomonas aeruginosa]	3

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
3856	9453863	gi|9453863|dbj|BAB03284.1| (AB037278) complement C4A [Cyprinus carpio]	5.5
3859	11466282	gi|11466282|ref|NP_049597.1| orf1386 [Tetrahymena pyriformis] gb|AAD41942.1|AF160864_30 (AF160864) orf1386 [Tetrahymena pyriformis]	7.5
3861	9626695	gi|9626695|ref|NP_040967.1| overlapping out-of-phase protein [Eggplant mosaic virus] sp|P20129|V70K_EPMV 70 KD PROTEIN gb|AAA43038.1| (J04374) overlapping out-of-phase protein [Eggplant mosaic virus]	5.6
3862	7473683	gi|7473683|pir||H75456 probable succinate dehydrogenase, hydrophobic subunit SdhD - Deinococcus radiodurans (strain R1) gb|AAF10526.1|AE001947_9 (AE001947) succinate dehydrogenase, hydrophobic subunit SdhD, putative [Deinococcus radiodurans]	5.2
3864	11359953	gi|11359953|pir||T46330 hypothetical protein DKFZp434D0513.1 - human (fragment) emb|CAB70660.1| (AL137259) hypothetical protein [Homo sapiens]	6E-28
3867	3056600	gi|3056600|gb|AAC13911.1|AAC13911 (AC004255) T1F9.21 [Arabidopsis thaliana]	5.5
3872	11358605	gi|11358605|pir||T49882 pectin methyl-esterase-like protein - Arabidopsis thaliana emb|CAB87932.1| (AL163912) pectin methyl-esterase-like protein [Arabidopsis thaliana]	3.9
3873	5917666	gi|5917666|gb|AAD55980.1|AF159297_1 (AF159297) extensin-like protein [Zea mays]	9.2
3879	15011489	gi|15011489|gb|AAK77584.1|AF396436_24 (AF396436) heme maturase [Tetrahymena thermophila]	3
3880	5835877	gi|5835877|ref|NP_008647.1|ND2_15072 NADH dehydrogenase subunit 2 [Ceratitis capitata] emb|CAB45088.1| (AJ242872) NADH dehydrogenase (ubiquinone) chain 2 [Ceratitis capitata]	0.85

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
3881	10956089	gi|10956089|ref|NP_052581.1| Orf2 [Pediococcus pentosaceus] ref|NP_037562.1| mobilization protein [Pediococcus pentosaceus] gb|AAD25894.1|AF069302_2 (AF069302) Orf2 [Pediococcus pentosaceus] gb|AAD39619.1|AF033858_2 (AF033858) mobilization protein [Pediococcus pentosaceus]	5.5
3883	9294238	gi|9294238|dbj|BAB02140.1| (AP000411) contains similarity to reverse transcriptase~gene_id:K11J14.5 [Arabidopsis thaliana]	6.3
3885	975667	gi|975667|emb|CAA61500.1| (X89213) RNA polymerase [Infectious hematopoietic necrosis virus] prf||2121413F RNA polymerase [Infectious hematopoietic necrosis virus]	4.3
3886	138293	gi|138293|sp|P23041|VGLG_HRSV8 MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G) pir||MGNZ60 major surface glycoprotein G - human respiratory syncytial virus (strain 8/60) gb|AAA47408.1| (M73545) attachment protein [Human respiratory syncytial virus] gb|AAA47413.1| (M55633) attachment glycoprotein [Human respiratory syncytial virus]	2.1
3888	9628729	gi|9628729|ref|NP_043760.1| U4 [Human herpesvirus 7] sp|P52521|VU4_HSV7J U4 PROTEIN pir||T41908 hypothetical protein U4 - human herpesvirus 7 (strain JI) gb|AAC54668.1| (U43400) U4 gene product [Human herpesvirus 7] gb|AAC40722.1| (AF037218) U4 [Human herpesvirus 7]	0.77
3891	13376093	gi|13376093|ref|NP_079033.1| hypothetical protein FLJ12879 [Homo sapiens] dbj|BAB14321.1| (AK022941) unnamed protein product [Homo sapiens]	6.5
3892	7508715	gi|7508715|pir||T26003 hypothetical protein VC27A7L.1 - Caenorhabditis elegans emb|CAB09130.1| (Z95621) contains similarity to Pfam domain: PF01461 (7TM chemoreceptor), Score=-47.3, E-value=1.9e-12, N=1 [Caenorhabditis elegans]	4.7
3893	2961421	gi|2961421|dbj|BAA25153.1| (AB011027) Pns10-2 [oat sterile dwarf virus]	7.5

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
3899	11276053	gi|11276053|gb|AAG33872.1|AF319939_1 (AF319939) enhancin [Choristoneura fumiferana granulovirus]	3.7
3904	10177870	gi|10177870|dbj|BAB11240.1| (AB010074) potassium/proton antiporter-like protein [Arabidopsis thaliana]	2.7
3907	9629709	gi|9629709|ref|NP_045001.1| methyltransferase (MT) and helicase (HEL) domains [Little cherry closterovirus] emb|CAA71285.1| (Y10237) methyltransferase (MT) and helicase (HEL) domains [Little cherry closterovirus]	4.1
3908	14756677	gi|14756677|ref|XP_040326.1| absent in melanoma 1 [Homo sapiens]	0.96
3911	9630708	gi|9630708|ref|NP_047255.1| gag-pol precursor polyprotein gPr80 [Feline leukemia virus] gb|AAC31801.1| (AF052723) gag-pol precursor polyprotein gPr80 [Feline leukemia virus]	0.021
3913	91039	gi|91039|pir||S04847 leukocyte adhesion protein CD18 precursor - mouse emb|CAA33077.1| (X14951) CD18 antigen preprotein [Mus musculus]	4.6
3916	5107943	gi|5107943|gb|AAD40185.1|AF157488_1 (AF157488) 36DE accessory gland protein [Drosophila melanogaster] gb|AAF53664.1| (AE003658) Acp36DE gene product [Drosophila melanogaster]	5.8
3919	4809000	gi|4809000|gb|AAD30054.1| (AF133052) pol polyprotein [walleye epidermal hyperplasia virus type 2]	0.000004
3920	7262603	gi|7262603|gb|AAF43901.1|AF162134_1 (AF162134) immunoglobulin epsilon heavy chain constant region [Felis catus]	8.9
3927	12963481	gi|12963481|ref|NP_061927.1| hypothetical protein MGC5560; hypothetical protein [Homo sapiens] dbj|BAB14342.1| (AK022978) unnamed protein product [Homo sapiens]	2E-66
3929	13651251	gi|13651251|ref|XP_017240.1| 15060 [Homo sapiens]	0.00000003
3930	11466329	gi|11466329|ref|NP_051157.1| ATP synthase F0 subunit 6 [Cafeteria roenbergensis] gb|AAF05808.1|AF193903_31 (AF193903) ATP synthase F0 subunit 6 [Cafeteria roenbergensis]	8.3

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
3933	7452186	gi|7452186|pir||S75936 hypothetical protein slr0023 - Synechocystis sp. (strain PCC 6803) dbj|BAA10783.1| (D64006) ORF_ID:slr0023~unknown protein [Synechocystis sp. PCC 6803]	7.7
3935	12720861	gi|12720861|gb|AAK02675.1| (AE006095) unknown [Pasteurella multocida]	1.2
3937	8919178	gi|8919178|emb|CAB96077.1| (AJ277244) alpha-glucosidase [Solanum tuberosum subsp. tuberosum]	5.7
3938	12830385	gi|12830385|emb|CAC29069.1| (AJ408289) immunoglobulin lambda light chain variable region [Homo sapiens]	2.1
3942	13385576	gi|13385576|ref|NP_080353.1| RIKEN cDNA 3110040N11 gene [Mus musculus] dbj|BAB29184.1| (AK014163) putative [Mus musculus] dbj|BAB31031.1| (AK018003) putative [Mus musculus] dbj|BAB31634.1| (AK019261) putative [Mus musculus]	5E-48
3945	13476785	gi|13476785|ref|NP_108354.1| transcription regulator [Mesorhizobium loti] dbj|BAB53815.1| (AP003013) transcription regulator [Mesorhizobium loti]	5.6
3947	13357649	gi|13357649|ref|NP_077923.1| unique hypothetical membrane lipoprotein [Ureaplasma urealyticum] pir||E82934 hypothetical protein UU092 [imported] - Ureaplasma urealyticum gb|AAF30498.1|AE002109_1 (AE002109) unique hypothetical membrane lipoprotein [Ureaplasma urealyticum]	4.1
3951	13358144	gi|13358144|ref|NP_078418.1| conserved hypothetical membrane lipoprotein [Ureaplasma urealyticum] pir||G82873 conserved hypothetical membrane lipoprotein UU579 [imported] - Ureaplasma urealyticum gb|AAF30993.1|AE002156_8 (AE002156) conserved hypothetical membrane lipoprotein [Ureaplasma urealyticum]	8.1
3956	7299437	gi|7299437|gb|AAF54626.1| (AE003691) KP78b gene product [Drosophila melanogaster]	5.5
3961	6729023	gi|6729023|gb|AAF27019.1|AC009177_9 (AC009177) hypothetical protein [Arabidopsis thaliana]	9.8

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
3962	2645329	gi|2645329|gb|AAB87213.1| (U83821) NADH dehydrogenase subunit 4 [Oryzomys palustris]	6.6
3965	11280919	gi|11280919|pir||T46939 hypothetical protein 1 [imported] - Agrobacterium tumefaciens plasmid pAtK84b gb|AAD31598.1|AF065244_2 (AF065244) unknown [Agrobacterium tumefaciens]	0.33
3966	7305249	gi|7305249|ref|NP_038748.1| MAX-interacting protein [Mus musculus] gb|AAF24761.1| (AF205935) MGA protein [Mus musculus]	3E-51
3969	5901753	gi|5901753|gb|AAD55397.1| (AF177905) hypothetical protein [Candida glabrata]	1.6
3973	9635492	gi|9635492|ref|NP_059583.1| gtrA [Enterobacteria phage P22] sp|P57021|GTRA_BPP22 BACTOPRENOL-LINKED GLUCOSE TRANSLOCASE gb|AAF75001.1| (AF217253) gtrA [Enterobacteria phage P22]	4
3975	2143428	gi|2143428|pir||I58123 aggrecan - mouse (fragment) gb|AAB32159.1| (S73720) aggrecan=cmd(aggrecan) [mice, cmd/cmd, liver, Peptide Partial Mutant, 112 aa] [Mus sp.]	3.3
3979	14767565	gi|14767565|ref|XP_027089.1| N-acetylated alpha-linked acidic dipeptidase 2 [Homo sapiens] emb|CAB39967.1| (AJ012370) NAALADase II protein [Homo sapiens]	1.3
3980	11359267	gi|11359267|pir||T50192 probable pseudouridylate synthase [imported] - fission yeast (Schizosaccharomyces pombe) emb|CAB61771.1| (AL133225) probable pseudouridylate synthase [Schizosaccharomyces pombe]	1.7
3982	13652498	gi|13652498|ref|XP_007053.3| tubby like protein 3 [Homo sapiens] ref|XP_045148.1| 8937 [Homo sapiens]	5.1
3983	9978891	gi|9978891|sp|P57059|SN1L_HUMAN PROBABLE SERINE/THREONINE PROTEIN KINASE SNF1LK dbj|BAA95536.1| (AP001751) gene similar to rat protein kinase (KID2) [Homo sapiens]	1.6
3986	7448436	gi|7448436|pir||E71674 hypothetical protein RP682 - Rickettsia prowazekii emb|CAA15119.1| (AJ235272) unknown [Rickettsia prowazekii]	2.2
3987	13815874	gi|13815874|gb|AAK42697.1| (AE006854) Hypothetical protein [Sulfolobus solfataricus]	3.8

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
3989	7485330	gi|7485330|pir||T04802 hypothetical protein F10M23.130 - Arabidopsis thaliana emb|CAB36525.1| (AL035440) putative APG protein [Arabidopsis thaliana] emb|CAB79534.1| (AL161565) putative APG protein [Arabidopsis thaliana]	4.5
3991	7295073	gi|7295073|gb|AAF50399.1| (AE003555) Talin gene product [Drosophila melanogaster] gb|AAG22814.1| (AF299248) talin [Drosophila melanogaster]	3.8
3992	14456133	gi|14456133|emb|CAC41650.1| (AJ315577) putative nitrate reductase [Ustilago maydis]	8
3993	533179	gi|533179|gb|AAA56944.1| (L33090) pol protein [Human immunodeficiency virus type 2]	7.4
3996	14250408	gi|14250408|gb|AAH08638.1|AAH08638 (BC008638) Similar to aspartyl-tRNA synthetase [Mus musculus]	4.1
4000	14775307	gi|14775307|ref|XP_042250.1| similar to nuclear pore complex interacting protein (H. sapiens) [Homo sapiens]	3.5
4002	7507695	gi|7507695|pir||T24847 hypothetical protein T11G6.7 - Caenorhabditis elegans emb|CAA93415.1| (Z69384) predicted using Genefinder [Caenorhabditis elegans]	8.3
4008	1173359	gi|1173359|sp|P45287|SAPC_HAEIN PEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN SAPC pir||C64134 sapC protein homolog - Haemophilus influenzae (strain Rd KW20) gb|AAC23287.1| (U32837) peptide ABC transporter, permease protein (sapC) [Haemophilus influenzae Rd]	0.83
4009	13385538	gi|13385538|ref|NP_080316.1| RIKEN cDNA 2810036K01 gene [Mus musculus] dbj|BAB28520.1| (AK012865) putative [Mus musculus]	1E-41
4011	13639013	gi|13639013|ref|XP_012007.2| dual specificity phosphatase 8 [Homo sapiens]	9.1
4015	1079359	gi|1079359|pir||JC2394 phospholipase A2 inhibitor 25K chain - monocled cobra gb|AAB32583.1| phospholipase A2 25 kda subunit, PLA2 25 kda subunit=urokinase-type plasminogen activator receptor homolog [Naja naja kaouthia=Thailand cobras, blood, Peptide, 185 aa]	5

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
4016	284079	gi|284079|pir||E41925 hypothetical protein 3 - human gb|AAA58464.1| (M69297) ORF 3 [Homo sapiens]	0.005
4017	7293601	gi|7293601|gb|AAF48973.1| (AE003512) CG14217 gene product [Drosophila melanogaster]	2.9
4020	11352313	gi|11352313|pir||G83376 probable trehalose synthase PA2152 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG05540.1|AE004642_7 (AE004642) probable trehalose synthase [Pseudomonas aeruginosa]	2.9
4023	11386701	gi|11386701|sp|Q9V773|C6AK_DROME PROBABLE CYTOCHROME P450 6A20 (CYPVIA20)	9
4030	7332064	gi|7332064|gb|AAF60751.1| (AC006801) contains similarity to Loligo pealei microtubule-associated protein H1 (PIR:S28831) [Caenorhabditis elegans]	1.7
4034	13242494	gi|13242494|ref|NP_077507.1| EsV-1-22 [Ectocarpus siliculosus virus]	1.6
4035	7522108	gi|7522108|pir||T29097 pro-pol-dUTPase polyprotein - murine endogenous retrovirus ERV-L (fragment) emb|CAA73251.1| (Y12713) protease; reverse transcriptase; RNaseH; integrase; dUTPase; Pro-Pol-dUTPase polyprotein [Mus musculus]	0.025
4042	12045115	gi|12045115|ref|NP_072926.1| lipoprotein, putative [Mycoplasma genitalium] sp|P47502|Y260_MYCGE HYPOTHETICAL LIPOPROTEIN MG260 PRECURSOR pir||G64228 hypothetical protein homolog MG260 - Mycoplasma genitalium gb|AAC71481.1| (U39705) lipoprotein, putative [Mycoplasma genitalium]	3.2
4044	14249544	gi|14249544|ref|NP_116223.1| hypothetical protein FLJ14751 [Homo sapiens] dbj|BAB55272.1| (AK027657) unnamed protein product [Homo sapiens]	0.27
4046	6474685	gi|6474685|dbj|BAA87286.1| (AB027982) Protein kinase C-like 1 [Schizosaccharomyces pombe]	1.9
4049	1514669	gi|1514669|emb|CAA87082.1| (Z46958) adenyl cyclase [Xenopus laevis]	0.56
4050	1514669	gi|1514669|emb|CAA87082.1| (Z46958) adenyl cyclase [Xenopus laevis]	0.85

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
4051	2499547	gi|2499547|sp|P77153|WZB_ECOLI PROBABLE LOW MOLECULAR WEIGHT PROTEIN-TYROSINE-PHOSPHATASE WZB pir||D64972 probable protein-tyrosine-phosphatase (EC 3.1.3.48) wzb, low molecular weight - Escherichia coli gb|AAC77834.1| (U38473) putative acid phosphatase [Escherichia coli] gb|AAC75122.1| (AE000296) probable protein-tyrosine-phosphatase [Escherichia coli K12] gb|AAG57121.1|AE005432_2 (AE005432) probable protein-tyrosine-phosphatase [Escherichia coli O157:H7 EDL933] dbj|BAB36289.1| (AP002560) probable protein-tyrosine-phosphatase [Escherichia coli O157:H7]	2.8
4052	14916565	gi|14916565|sp|Q9XHG2|FLS_MALDO FLAVONOL SYNTHASE (FLS) gb|AAD26261.1|AF119095_1 (AF119095) flavonol synthase [Malus x domestica]	3.8
4053	3769667	gi|3769667|gb|AAC64604.1| (AF093797) unknown [Norwalk virus]	2.8
4060	14335082	gi|14335082|gb|AAK59820.1| (AY037220) AT4g24060/T19F6_50 [Arabidopsis thaliana]	1.3
4061	12838540	gi|12838540|dbj|BAB24237.1| (AK005786) putative [Mus musculus]	4.3
4066	7549797	gi|7549797|ref|NP_035731.1| T lymphoma oncogene [Mus musculus] sp|P17408|TLM_MOUSE TLM PROTEIN (TLM ONCOGENE) pir||S10151 transforming protein tlm - mouse (strain balb/c) emb|CAA36859.1| (X52634) tlm protein [Mus musculus]	0.58
4067	11357726	gi|11357726|pir||T51437 hypothetical protein F2G14_40 - Arabidopsis thaliana emb|CAC01811.1| (AL391146) putative protein [Arabidopsis thaliana] gb|AAK49610.1|AF372894_1 (AF372894) AT5g14920/F2G14_40 [Arabidopsis thaliana] gb|AAK74054.1| (AY045696) AT5g14920/F2G14_40 [Arabidopsis thaliana]	1.8
4070	8218109	gi|8218109|emb|CAB92762.1| (AL121883) dJ545K15.1.3 (novel protein similar to KIAA0512 (contains translation of cDNAs Em:AK000818 and Em:L20773) (isoform 3)) [Homo sapiens]	5.5

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
4072	13096854	gi|13096854|gb|AAH03224.1|AAH03224 (BC003224) Similar to chromosome condensation 1-like [Mus musculus]	9.1
4073	103076	gi|103076|pir||B21124 Bkm-like sex-determining region hypothetical protein CS314 - fruit fly (Drosophila melanogaster) (fragment)	0.3
4074	14722732	gi|14722732|ref|XP_017441.2| hypothetical protein FLJ21477 [Homo sapiens]	6.6
4076	3378554	gi|3378554|emb|CAA76192.1| (Y16404) multidrug resistance protein [Candida albicans]	0.33
4081	6983946	gi|6983946|gb|AAF34740.1|AF200327_1 (AF200327) unknown [Plasmodium chabaudi]	8.5
4082	5524754	gi|5524754|emb|CAB50786.1| (AJ011801) Rx protein [Solanum tuberosum]	2.6
4086	7959271	gi|7959271|dbj|BAA96029.1| (AB040938) KIAA1505 protein [Homo sapiens]	3E-58
4087	130687	gi|130687|sp|P27536|POST_XENLA POSTERIOR PROTEIN pir||A43784 Xpo protein - African clawed frog emb|CAA41397.1| (X58487) Xpo [Xenopus laevis]	1.2
4092	2406633	gi|2406633|gb|AAB70469.1| (AF005630) adenylyl cyclase isoform DAC9 [Drosophila melanogaster]	7.3
4095	13812388	gi|13812388|ref|NP_113506.1| cell division cycle 2 homolog [Guillardia theta] emb|CAC27075.1| (AJ010592) cell division cycle 2 homolog [Guillardia theta]	9.7
4096	14530932	gi|14530932|gb|AAG37978.2| (AC087081) Hypothetical protein Y82E9BL.13 [Caenorhabditis elegans]	3.1
4097	14760316	gi|14760316|ref|XP_045601.1| 7324 [Homo sapiens]	0.83
4098	7305361	gi|7305361|ref|NP_038652.1| otogelin [Mus musculus] pir||T42214 otogelin - mouse gb|AAB96561.1| (U96411) otogelin; MLEMP [Mus musculus]	1E-10
4103	8953656	gi|8953656|emb|CAB96704.1| (AL360354) vir15, rpg1, putative transmembrane protein, similar to rpg2, vir9 MW:34499 (294 aa), fasta scores: opt: 398, E(): 0.023, 26.0% identity in 289 aa overlap, and to vir2: MW:35019 (292 aa), fasta scores: opt: 380, E(): 0.037, 28.0% identity in>	3.6
4108	3659615	gi|3659615|gb|AAC61684.1| (AF052517) diguanylate cyclase [Gluconacetobacter xylinus]	6.5

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
4110	11465871	gi|11465871|ref|NP_066420.1| NADH dehydrogenase subunit 2 [Ochromonas danica] gb|AAG18386.1|AF287134_11 (AF287134) NADH dehydrogenase subunit 2 [Ochromonas danica]	9.3
4112	13786586	gi|13786586|ref|NP_112718.1| ORF55 [Bacteriophage TP901-1] gb|AAK38072.1| (AF304433) ORF55 [Bacteriophage TP901-1]	1.4
4115	14743649	gi|14743649|ref|XP_036116.1| KIAA0594 protein [Homo sapiens]	2E-46
4121	7491991	gi|7491991|pir||T41608 hypothetical protein SPCC790.03 - fission yeast (Schizosaccharomyces pombe) emb|CAA21293.1| (AL031855) hypothetical protein [Schizosaccharomyces pombe]	2.9
4122	6647413	gi|6647413|sp|Q9ZE52|ALR_RICPR ALANINE RACEMASE pir||F71718 alanine racemase (alr) RP095 - Rickettsia prowazekii emb|CAA14565.1| (AJ235270) ALANINE RACEMASE (alr) [Rickettsia prowazekii]	9.1
4125	7293814	gi|7293814|gb|AAF49181.1| (AE003517) nes gene product [Drosophila melanogaster]	7.7
4128	7505316	gi|7505316|pir||T23351 hypothetical protein K05D4.2 - Caenorhabditis elegans emb|CAB07252.1| (Z92804) contains similarity to Pfam domain: PF01461 (7TM chemoreceptor), Score=118.9, E-value=3.1e-32, N=1 [Caenorhabditis elegans]	9.3
4139	4335719	gi|4335719|gb|AAD17397.1| (AC006248) putative C3HC4-type RING zinc finger protein [Arabidopsis thaliana]	5.1
4140	9625775	gi|9625775|ref|NP_040024.1| Conserved herpesvirus spliced gene [human herpesvirus 5] sp|P16732|VTER_HCMVA PROBABLE DNA PACKAGING PROTEIN emb|CAA35363.1| (X17403) Conserved herpesvirus spliced gene [human herpesvirus 5]	4.3
4144	7510388	gi|7510388|pir||T27298 hypothetical protein Y68A4A.7 - Caenorhabditis elegans emb|CAA16418.1| (AL021503) predicted using Genefinder~contains similarity to Pfam domain: PF01604 (7TM chemoreceptor), Score=-48.3, E-value=7.1e-07, N=1 [Caenorhabditis elegans]	3.4

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
4145	7243081	gi|7243081|dbj|BAA92588.1| (AB037771) KIAA1350 protein [Homo sapiens]	e-112
4149	13812221	gi|13812221|ref|NP_113352.1| hypothetical protein [Guillardia theta] gb|AAK39908.1|AF165818_116 (AF165818) hypothetical protein [Guillardia theta]	5.1
4150	7706557	gi|7706557|ref|NP_057604.1| hepatocellular carcinoma-associated antigen 59; hypothetical protein [Homo sapiens] ref|XP_017552.1| hypothetical protein [Homo sapiens] ref|XP_052691.1| hypothetical protein [Homo sapiens] gb|AAF37561.1| (AF218421) hepatocellular carcinoma-associated antigen 59 [Homo sapiens] gb|AAH07664.1|AAH07664 (BC007664) hepatocellular carcinoma-associated antigen 59 [Homo sapiens]	3E-81
4151	984305	gi|984305|gb|AAA75468.1| (U25975) hPAK65 [Homo sapiens]	1E-11
4153	14729667	gi|14729667|ref|XP_029101.1| KIAA0947 protein [Homo sapiens]	0.47
4154	3355648	gi|3355648|emb|CAA08785.1| (AJ009688) tungsten formylmethanofuran dehydrogenase subunit fwdB [Methanothermobacter wolfeii]	0.54
4156	12513192	gi|12513192|gb|AAG54704.1|AE005215_1 (AE005215) putative transport protein [Escherichia coli O157:H7 EDL933] dbj|BAB33831.1| (AP002551) putative transport protein [Escherichia coli O157:H7]	4.1
4159	7472450	gi|7472450|pir||D75370 hypothetical protein - Deinococcus radiodurans (strain R1) gb|AAF11218.1|AE002008_13 (AE002008) hypothetical protein [Deinococcus radiodurans]	7.9
4160	13876525	gi|13876525|gb|AAK43501.1|AC020666_11 (AC020666) hypothetical protein [Oryza sativa]	4.6
4162	6665675	gi|6665675|gb|AAF22966.1|AF175308_1 (AF175308) acetyl-CoA carboxylase [Sus scrofa]	2E-11
4163	7509105	gi|7509105|pir||T31728 probable cysteine proteinase (EC 3.4.22.-) W07B8.4 - Caenorhabditis elegans gb|AAB65345.1| (AF016426) Hypothetical protein W07B8.4 [Caenorhabditis elegans]	1.4
4164	7510169	gi|7510169|pir||T31555 hypothetical protein Y53H1C.2 - Caenorhabditis elegans emb|CAB55064.1| (AL117201) predicted using Genefinder [Caenorhabditis elegans]	7

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
4166	6683126	gi|6683126|dbj|BAA20797.2| (AB002337) KIAA0339 protein [Homo sapiens]	9.8
4167	7485930	gi|7485930|pir||T10623 hypothetical protein F21C20.160 - Arabidopsis thaliana emb|CAB45847.1| (AL080254) putative protein [Arabidopsis thaliana] emb|CAB79081.1| (AL161553) putative protein [Arabidopsis thaliana]	5.9
4171	11348277	gi|11348277|pir||C83019 conserved hypothetical protein PA5019 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG08404.1|AE004914_5 (AE004914) conserved hypothetical protein [Pseudomonas aeruginosa]	3.5
4172	1150480	gi|1150480|emb|CAA91110.1| (Z54312) hypothetical protein [Lactobacillus sakei]	3.2
4173	14776432	gi|14776432|ref|XP_050788.1| similar to KIAA0133 gene product (H. sapiens) [Homo sapiens]	0.3
4175	13569915	gi|13569915|ref|NP_112205.1| amnionless protein [Homo sapiens] gb|AAK28532.1|AF328788_1 (AF328788) amnionless [Homo sapiens]	8.9
4180	6978481	gi|6978481|ref|NP_036905.1| a-kinase anchoring protein [Rattus norvegicus] sp|Q62924|AK11_RAT A KINASE ANCHOR PROTEIN 11 (PROTEIN KINASE A ANCHORING PROTEIN 11) (PRKA11) (A KINASE ANCHOR PROTEIN 220 KDA) (AKAP 220) pir||T42732 A-kinase anchoring protein AKAP 220 - rat gb|AAB06559.1| (U48288) AKAP 220 [Rattus norvegicus]	3.1
4187	14738118	gi|14738118|ref|XP_048649.1| Apobec-1 complementation factor; APOBEC-1 stimulating protein [Homo sapiens] emb|CAB94754.1| (AJ272078) APOBEC-1 stimulating protein [Homo sapiens]	1E-37
4189	13183342	gi|13183342|gb|AAK15157.1|AF284034_1 (AF284034) vitellogenin B [Melanogrammus aeglefinus]	9.4

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
4192	13123985	gi|13123985|sp|Q9N293|B3G5_GORGO BETA-1,3-GALACTOSYLTRANSFERASE 5 (BETA-1,3-GALTASE 5) (BETA3GAL-T5) (B3GAL-T5) (UDP-GALACTOSE:BETA-N-ACETYLGLUCOSAMINE BETA-1,3-GALACTOSYLTRANSFERASE 5) (UDP-GAL:BETA-GLCNAC BETA-1,3-GALACTOSYLTRANSFERASE 5) (BETA-3-GX-T5) dbj|BAA94501.1| (AB041416) UDP-Gal:GlcNAc beta1,3-galactosyltransferase 5 [Homo sapiens]	4
4194	7295768	gi|7295768|gb|AAF51070.1| (AE003579) CG3410 gene product [Drosophila melanogaster]	1.5
4195	7290544	gi|7290544|gb|AAF45996.1| (AE003432) CG6903 gene product [Drosophila melanogaster]	6
4200	9966502	gi|9966502|gb|AAG10295.1|AF275272_1 (AF275272) unknown [Schizophyllum commune]	0.83
4213	6010435	gi|6010435|gb|AAF01135.1| (AF087699) erythrocyte membrane protein 3 [Plasmodium falciparum]	2.2
4216	14775884	gi|14775884|ref|XP_043964.1| similar to KIAA0220 protein (H. sapiens) [Homo sapiens]	5E-12
4218	7511578	gi|7511578|pir||T19209 probable protein kinase E02H4.3 - Caenorhabditis elegans emb|CAA94122.1| (Z70205) Similarity to Drosophila Doa kinase (PIR Acc. No. S44077), contains similarity to Pfam domain: PF00069 (Eukaryotic protein kinase domain), Score=184.6, E-value=5.2e-52, N=1~cDNA EST yk5d6.3 comes from this gene~cDNA EST yk5d6.5 comes from this> emb|CAA91979.1| (Z68003) Similarity to Drosophila Doa kinase (PIR Acc. No. S44077), contains similarity to Pfam domain: PF00069 (Eukaryotic protein kinase domain), Score=184.6, E-value=5.2e-52, N=1~cDNA EST yk5d6.3 comes from this gene~cDNA EST yk5d6.5 comes from this>	0.069
4220	7471938	gi|7471938|pir||G75366 glucose-1-phosphate adenylyltransferase - Deinococcus radiodurans (strain R1) gb|AAF11244.1|AE002010_7 (AE002010) glucose-1-phosphate adenylyltransferase [Deinococcus radiodurans]	2.6

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
4224	4506051	gi|4506051|ref|NP_000937.1| primase, polypeptide 1 (49kD); primase polypeptide 1 (49kD) [Homo sapiens] ref|XP_048930.1| primase, polypeptide 1 (49kD) [Homo sapiens] ref|XP_006706.3| primase, polypeptide 1 (49kD) [Homo sapiens] sp|P49642|PRI1_HUMAN DNA PRIMASE SMALL SUBUNIT (DNA PRIMASE 49 KDA SUBUNIT) (P49) pir||S45630 DNA primase chain p48 - human emb|CAA52377.1| (X74330) DNA primase (subunit p48) [Homo sapiens] gb|AAH05266.1|AAH05266 (BC005266) primase, polypeptide 1 (49kD) [Homo sapiens]	0.014
4228	13812048	gi|13812048|ref|NP_113182.1| putative protein kinase [Guillardia theta] gb|AAK39750.1|AF083031_107 (AF083031) putative protein kinase [Guillardia theta]	1.8
4229	7465475	gi|7465475|pir||S70173 autoinducer synthesis protein - Pseudomonas aeruginosa	1.3
4236	11288518	gi|11288518|pir||T49586 related to nif-specific regulatory protein [imported] - Neurospora crassa emb|CAB91387.1| (AL355930) related to nif-specific regulatory protein [Neurospora crassa]	6.8
4237	2072951	gi|2072951|gb|AAC51263.1| (U93564) putative p150 [Homo sapiens]	3.1
4244	1903416	gi|1903416|gb|AAC53095.1| (U76112) translation repressor NAT1 [Mus musculus]	2E-15
4248	14749171	gi|14749171|ref|XP_038309.1| hypothetical protein XP_038309 [Homo sapiens]	4.3
4251	7432367	gi|7432367|pir||T13881 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - Chlorogonium elongatum mitochondrion emb|CAA73990.1| (Y13644) NADH dehydrogenase subunit 4 [Chlorogonium elongatum]	1.2
4255	13621755	gi|13621755|gb|AAK33536.1| (AE006511) putative nucleotide sugar dehydrogenase [Streptococcus pyogenes M1 GAS]	2.7
4259	9880	gi|9880|emb|CAA36427.1| (X52177) RNA polymerase beta subunit (697 AA) [Plasmodium falciparum]	1.1
4260	10314010	gi|10314010|ref|NP_066241.1| replicase polyprotein [acute bee paralysis virus] gb|AAG13118.1|AF150629_1 (AF150629) replicase polyprotein [acute bee paralysis virus]	7.5

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
4261	1170902	gi|1170902|sp|P43245|MDR1_RAT MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1) pir||JH0502 p-glycoprotein - rat	5.2
4265	10180785	gi|10180785|gb|AAG14273.1|AF243438_88 (AF243438) RS1 immediate-early gene transactivator-like protein [Gallid herpesvirus 2] gb|AAG14284.1|AF243438_99 (AF243438) RS1 immediate-early gene transactivator ICP4-like protein [Gallid herpesvirus 2]	1.3
4267	1353257	gi|1353257|gb|AAB06234.1| (U26665) dimethyl sulphoxide reductase subunit B [Haemophilus influenzae]	4.8
4268	4240315	gi|4240315|dbj|BAA74936.1| (AB020720) KIAA0913 protein [Homo sapiens]	3.3
4269	4493991	gi|4493991|emb|CAB39050.1| (AL034559) hypothetical protein, PFC1060c [Plasmodium falciparum]	6.3
4272	4557503	gi|4557503|ref|NP_001072.1| cubilin precursor; cubilin; intrinsic factor-cobalamin receptor; intrinsic factor B12-receptor [Homo sapiens] pir||T09456 intrinsic factor-B12 receptor Cubilin precursor - human gb|AAC82612.1| (AF034611) intrinsic factor-B12 receptor precursor; cubilin [Homo sapiens]	5E-10
4277	7504212	gi|7504212|pir||T22670 hypothetical protein F54F11.1 - Caenorhabditis elegans emb|CAB05738.1| (Z83229) Weak similarity with glycerol phospholipid-cholesterol acyltransferase~cDNA EST yk479h12.3 comes from this gene~cDNA EST yk479h12.5 comes from this gene [Caenorhabditis elegans]	8
4279	421548	gi|421548|pir||B47013 butanol dehydrogenase (EC 1.1.1.) II - Clostridium acetobutylicum	1.7
4284	7497553	gi|7497553|pir||T19999 hypothetical protein C47D12.2 - Caenorhabditis elegans emb|CAA93767.1| (Z69902) predicted using Genefinder~cDNA EST yk14e2.3 comes from this gene~cDNA EST yk88e3.3 comes from this gene~cDNA EST yk132h1.3 comes from this gene~cDNA EST yk88e3.5 comes from this gene~cDNA EST yk132h1.5 comes from this gene~cDNA EST yk422c3.3 >	6.7

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
4292	5042237	gi|5042237|emb|CAB44655.1| (Y18605) hypothetical protein RvD1-Rv2024c' [Mycobacterium bovis BCG] gb|AAK46361.1| (AE007059) helicase, putative/conserved hypothetical protein [Mycobacterium tuberculosis CDC1551]	6.3
4298	14746217	gi|14746217|ref|XP_011563.2| hypothetical protein FLJ21634 [Homo sapiens] dbj|BAB15338.1| (AK026056) unnamed protein product [Homo sapiens]	0.000000002
4299	6005978	gi|6005978|ref|NP_009098.1| zinc finger protein 258 [Homo sapiens] gb|AAD15797.1| (AF055470) ZNF258 [Homo sapiens]	9E-26
4303	9845291	gi|9845291|ref|NP_063945.1| phosphatidylinositol polyphosphate 5-phosphatase type IV [Homo sapiens] gb|AAF81404.1|AF187891_1 (AF187891) phosphatidylinositol polyphosphate 5-phosphatase type IV [Homo sapiens]	7.7
4305	13620879	gi|13620879|dbj|BAB40992.1| (AB049938) alpha1,3-fucosyltransferase [Rattus norvegicus]	2.7
4308	6424813	gi|6424813|gb|AAF08148.1| (AF130192) NADH dehydrogenase subunit F [Valeriana fauriei]	9.6
4311	5834894	gi|5834894|ref|NP_006964.1|ND5_10021 NADH dehydrogenase subunit 5 [Caenorhabditis elegans] sp|P24896|NU5M_CAEEL NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 pir||S26037 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Caenorhabditis elegans mitochondrion emb|CAA38162.1| (X54252) ND5 protein (AA 1 - 527) [Caenorhabditis elegans]	1.6
4314	11135954	gi|11135954|sp|Q9TC94|YM16_NEPOL HYPOTHETICAL PROTEIN YMF16 gb|AAF03203.1|AF110138_35 (AF110138) homolog of E. coli MttB, a protein involved in folded protein translocation and targeting across bacterial membranes [Nephroselmis olivacea]	2.2
4316	14089831	gi|14089831|emb|CAC13590.1| (AL445564) unknown; predicted coding region [Mycoplasma pulmonis]	6.5
4317	10728595	gi|10728595|gb|AAF52302.2| (AE003611) CG9011 gene product [Drosophila melanogaster]	4E-19

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
4318	9187479	gi|9187479|emb|CAB96962.1| (AJ007508) magnesium-chelatase subunit chlI [Gnetum gnemon]	2.4
4322	7469635	gi|7469635|pir||S76563 hypothetical protein - Synechocystis sp. (strain PCC 6803) dbj|BAA10409.1| (D64002) ORF_ID:sll0188~unknown protein [Synechocystis sp. PCC 6803]	1.6
4324	15021476	gi|15021476|gb|AAK77753.1|AF369029_84 (AF369029) ORF84 [white spot syndrome virus]	1.7
4333	11466210	gi|11466210|ref|NP_066533.1| NADH dehydrogenase subunit 2 [Naegleria gruberi] gb|AAG17811.1|AF288092_36 (AF288092) NADH dehydrogenase subunit 2 [Naegleria gruberi]	0.46
4336	127494	gi|127494|sp|P25127|MT_ESOLU METALLOTHIONEIN (MT) pir||S17175 Metallothionein - Northern pike pir||S38334 metallothionein - northern pike pir||S31723 metallothionein - northern pike emb|CAA42035.1| (X59392) metallothionein [Esox lucius] emb|CAA49636.1| (X70042) Metallothioein [Esox lucius]	1
4341	6009729	gi|6009729|dbj|BAA85039.1| (AB026129) alpha-2-macroglobulin-2 [Cyprinus carpio]	0.00002
4342	1170606	gi|1170606|sp|P43188|KADC_MAIZE ADENYLATE KINASE, CHLOROPLAST (ATP-AMP TRANSPHOSPHORYLASE) pir||S45634 adenylate kinase (EC 2.7.4.3), chloroplast - maize pdb|1ZAK|A Chain A, Adenylate Kinase From Maize In Complex With The Inhibitor P1,P5-Bis(Adenosine-5'-)pentaphosphate (Ap5a) pdb|1ZAK|B Chain B, Adenylate Kinase From Maize In Complex With The Inhibitor P1,P5-Bis(Adenosine-5'-)pentaphosphate (Ap5a)	5E-13
4345	543537	gi|543537|pir||JN0720 glucosyl transferase - Shigella flexneri phage X gb|AAA71895.1| (L05001) glucosyl transferase [bacteriophage SfX]	8.1
4347	7297011	gi|7297011|gb|AAF52281.1| (AE003611) CG11149 gene product [Drosophila melanogaster]	0.93
4348	11558496	gi|11558496|emb|CAC17816.1| (AJ276292) sodium iodide symporter [Sus scrofa]	2.6

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
4351	7293017	gi|7293017|gb|AAF48404.1| (AE003497) CG12398 gene product [Drosophila melanogaster]	9
4352	7486021	gi|7486021|pir||T06133 hypothetical protein F23E12.200 - Arabidopsis thaliana emb|CAA18745.1| (AL022604) putative protein [Arabidopsis thaliana] emb|CAB80241.1| (AL161587) putative protein [Arabidopsis thaliana]	0.085
4353	10047323	gi|10047323|dbj|BAB13449.1| (AB046843) KIAA1623 protein [Homo sapiens]	2.7
4359	262249	gi|262249|gb|AAB24620.1| (S52010) orf1 5' of EpoR [Mus sp.]	0.67
4361	14589828	gi|14589828|gb|AAK70656.1|AC024771_1 (AC024771) Hypothetical protein Y40B10A.1 [Caenorhabditis elegans]	0.45
4364	543537	gi|543537|pir||JN0720 glucosyl transferase - Shigella flexneri phage X gb|AAA71895.1| (L05001) glucosyl transferase [bacteriophage SfX]	6.6
4366	14587208	gi|14587208|dbj|BAB61142.1| (AP003199) hypothetical protein [Oryza sativa]	5.1
4370	13385738	gi|13385738|ref|NP_080509.1| RIKEN cDNA 4933434I20 gene [Mus musculus] dbj|BAB30173.1| (AK016272) putative [Mus musculus]	0.046
4372	7507823	gi|7507823|pir||T24908 hypothetical protein T14D7.2 - Caenorhabditis elegans emb|CAB03365.1| (Z81123) cDNA EST EMBL:M88978 comes from this gene~cDNA EST yk419b8.3 comes from this gene~cDNA EST yk285a8.3 comes from this gene~cDNA EST yk398c1.3 comes from this gene~cDNA EST yk350c8.3 comes from this gene~cDNA EST yk350c8.5 comes from this gene~c>	0.33
4376	7302573	gi|7302573|gb|AAF57655.1| (AE003798) CG15086 gene product [Drosophila melanogaster]	1.1
4377	531764	gi|531764|emb|CAA56961.1| (X81072) hypothetical protein in YTA7 5'region [Saccharomyces cerevisiae]	5.4

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
4378	585100	gi|585100|sp|Q07287|ZPB_PIG ZONA PELLUCIDA SPERM-BINDING PROTEIN B PRECURSOR (ZONA PELLUCIDA 3-ALPHA) (ZONA PELLUCIDA GLYCOPROTEIN ZP3-ALPHA) pir||S35712 sperm-binding glycoprotein ZP3-alpha precursor - pig gb|AAA50164.1| (L11000) zp3-alpha sperm-binding glycoprotein [Sus scrofa]	2.5
4382	2148043	gi|2148043|pir||S51527 S-receptor kinase (EC 2.7.1.-) A14 precursor - rape gb|AAA62232.1| (U00443) S-receptor kinase [Brassica napus]	6
4383	2257556	gi|2257556|dbj|BAA21448.1| (AB004539) probable membrane protein YOL130w [Schizosaccharomyces pombe]	7.9
4386	8928528	gi|8928528|sp|Q44601|YTR1_BUCSC HYPOTHETICAL 35.1 KDA PROTEIN IN TRPA 3'REGION gb|AAA92793.1| (U09185) unknown [Buchnera aphidicola]	9.3
4389	12518050	gi|12518050|gb|AAG58518.1|AE005564_3 (AE005564) maltodextrin phosphorylase [Escherichia coli O157:H7 EDL933] dbj|BAB37682.1| (AP002565) maltodextrin phosphorylase [Escherichia coli O157:H7]	4.8
4391	13813161	gi|13813161|gb|AAK40397.1| (AE006644) Hypothetical protein [Sulfolobus solfataricus]	0.64
4393	13626090	gi|13626090|sp|P78704|ACR2_NEUCR ACRIFLAVINE SENSITIVITY CONTROL PROTEIN ACR-2	3
4394	6680736	gi|6680736|ref|NP_031522.1| AT motif binding factor 1 [Mus musculus] dbj|BAA05046.1| (D26046) AT motif-binding factor [Mus musculus] prf||2207230A transcription factor ATBF1 [Mus musculus]	1.1
4395	7269957	gi|7269957|emb|CAB79774.1| (AL161577) cyclic nucleotide and calmodulin-regulated ion channel-like protein [Arabidopsis thaliana]	5
4396	13812152	gi|13812152|ref|NP_113279.1| hypothetical protein [Guillardia theta] gb|AAK39839.1|AF165818_47 (AF165818) hypothetical protein [Guillardia theta]	2

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
4398	11350074	gi|11350074|pir||G83141 hypothetical protein PA4035 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG07422.1|AE004820_7 (AE004820) hypothetical protein [Pseudomonas aeruginosa]	1.8
4399	6601484	gi|6601484|gb|AAF18995.1|AF211856_1 (AF211856) pulmonary surfactant protein A [Ovis aries] gb|AAF31148.1|AF076633_1 (AF076633) pulmonary surfactant-associated protein A [Ovis aries]	2.3
4402	7480194	gi|7480194|pir||T37054 hypothetical protein SCJ21.05 - Streptomyces coelicolor emb|CAB52351.1| (AL109747) hypothetical SCJ21.05 [Streptomyces coelicolor A3(2)]	6.9
4403	123346	gi|123346|sp|P16393|HMDH_STRPU 3-HYDROXY-3-METHYLGLUTARYL-COENZYME A REDUCTASE (HMG-COA REDUCTASE) pir||A31898 hydroxymethylglutaryl-CoA reductase (NADPH) (EC 1.1.1.34) - sea urchin (Strongylocentrotus purpuratus) gb|AAA30060.1| (J04200) HMGCoA reductase (EC 1.1.1.34) [Strongylocentrotus purpuratus]	4.2
4404	1870163	gi|1870163|emb|CAB05927.1| (Z83335) unknown [Streptococcus pneumoniae]	8.3
4408	5739524	gi|5739524|ref|NP_000544.1| Werner syndrome protein [Homo sapiens] sp|Q14191|WRN_HUMAN WERNER SYNDROME HELICASE gb|AAC41981.1| (L76937) Homo sapiens Werner syndrome gene, complete cds gb|AAC63361.1| (AF091214) WRN [Homo sapiens] gb|AAF06162.1| (AF181897) WRN [Homo sapiens]	7.2
4409	7494315	gi|7494315|pir||C71607 hypothetical protein PFB0745w - malaria parasite (Plasmodium falciparum) gb|AAC71938.1| (AE001415) hypothetical protein [Plasmodium falciparum]	2.4
4414	13477147	gi|13477147|gb|AAH05031.1|AAH05031 (BC005031) Unknown (protein for IMAGE:3532103) [Homo sapiens]	9.1
4415	6650234	gi|6650234|gb|AAF21778.1| (AF072567) zinc finger protein 74 isoform III [Homo sapiens]	3.3

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
4419	7498637	gi|7498637|pir||T32474 hypothetical protein F08F1.3 - Caenorhabditis elegans gb|AAB71303.1| (AF026213) Hypothetical protein F08F1.3 [Caenorhabditis elegans]	9.9
4420	6016842	gi|6016842|dbj|BAA85182.1| (AB033168) nuclear protein ZAP [Mus musculus]	2.2
4422	125704	gi|125704|sp|P08630|SRC2_DROME TYROSINE-PROTEIN KINASE SRC28C pir||TVFFDS protein-tyrosine kinase (EC 2.7.1.112) src2 - fruit fly (Drosophila melanogaster) gb|AAA28912.1| (M16599) Dsrc28C protein [Drosophila melanogaster]	8.9
4423	14746157	gi|14746157|ref|XP_046163.1| T-cell lymphoma-1 [Homo sapiens]	8.6
4424	13235641	gi|13235641|emb|CAC33768.1| (AJ308570) S-adenosyl-L-methionine:salicylic acid carboxyl methyltransferase [Stephanotis floribunda]	6.3
4426	12805257	gi|12805257|gb|AAH02091.1|AAH02091 (BC002091) Unknown (protein for MGC:6342) [Mus musculus]	5.5
4428	7488979	gi|7488979|pir||T07612 cellulase (EC 3.2.1.4) Cel3, membrane-anchored - tomato gb|AAC49704.1| (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]	9.5
4429	14741807	gi|14741807|ref|XP_049622.1| KIAA1630 protein [Homo sapiens]	2E-16
4434	6324137	gi|6324137|ref|NP_014207.1| chitin synthase 1; Chs1p [Saccharomyces cerevisiae] sp|P08004|CHS1_YEAST CHITIN SYNTHASE 1 (CHITIN-UDP ACETYL-GLUCOSAMINYL TRANSFERASE 1) pir||A23944 chitin synthase (EC 2.4.1.16) CHS1 - yeast (Saccharomyces cerevisiae) gb|AAA34491.1| (M14045) chitin synthase [Saccharomyces cerevisiae] emb|CAA96086.1| (Z71468) ORF YNL192w [Saccharomyces cerevisiae]	6.8
4436	6678958	gi|6678958|ref|NP_032667.1| microtubule associated testis specific serine/threonine protein kinase [Mus musculus] pir||A54602 microtubule-associated serine/threonine protein kinase MAST205 - mouse gb|AAC04312.1| (U02313) protein kinase [Mus musculus]	0.41

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
4445	7494262	gi|7494262|pir||T18489 hypothetical protein C0820w - malaria parasite (Plasmodium falciparum) emb|CAB11128.1| (Z98551) hypothetical protein, PFC0820w [Plasmodium falciparum]	6.3
4454	11245201	gi|11245201|gb|AAG33502.1|AF302058_1 (AF302058) cytochrome oxidase I [Apocrypta sp. MSPAR2]	9.1
4457	6752960	gi|6752960|ref|NP_033743.1| a disintegrin and metalloprotease domain 11; a disintegrin and metalloprotease domain (ADAM) 11 [Mus musculus] sp|Q9R1V4|AD11_MOUSE ADAM 11 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE DOMAIN 11) (METALLOPROTEINASE-LIKE, DISINTEGRIN-LIKE, AND CYSTEINE-RICH PROTEIN) (MDC) dbj|BAA83384.1| (AB009676) ADAM11 [Mus musculus]	3.8
4462	103076	gi|103076|pir||B21124 Bkm-like sex-determining region hypothetical protein CS314 - fruit fly (Drosophila melanogaster) (fragment)	0.14
4463	14742023	gi|14742023|ref|XP_039778.1| HSPC047 protein [Homo sapiens]	1E-65
4464	13816057	gi|13816057|gb|AAK42842.1| (AE006867) Agmatinase (agmatine ureohydrolase) (speB-2) [Sulfolobus solfataricus]	6.5
4466	295359	gi|295359|gb|AAA21303.1| (L14824) surface antigen [Trypanosoma cruzi]	4.2
4471	2429459	gi|2429459|gb|AAB70995.1| (AF025461) contains similarity to Canis familiaris (dog) 180k ribosome receptor (NID:g984113) [Caenorhabditis elegans]	2.2
4474	7296176	gi|7296176|gb|AAF51469.1| (AE003588) CG2839 gene product [Drosophila melanogaster]	8.9
4475	14736857	gi|14736857|ref|XP_005322.2| KIAA0967 protein [Homo sapiens]	0.33
4480	13959004	gi|13959004|gb|AAK51055.1|AF361075_2 (AF361075) UL24 [Canine herpesvirus]	0.35

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
4483	7511539	gi|7511539|pir||T18770 probable calcium channel protein - Caenorhabditis elegans emb|CAA90091.1| (Z49907) similar to calcium channel alpha-2 subunit~cDNA EST yk134g4.5 comes from this gene~cDNA EST yk49c7.3 comes from this gene~cDNA EST yk134g4.3 comes from this gene~cDNA EST yk49c7.5 comes from this gene~cDNA EST yk349a4.3 comes from this gene~cD> emb|CAA90141.1| (Z49912) similar to calcium channel alpha-2 subunit~cDNA EST yk134g4.5 comes from this gene~cDNA EST yk49c7.3 comes from this gene~cDNA EST yk134g4.3 comes from this gene~cDNA EST yk49c7.5 comes from this gene~cDNA EST yk349a4.3 comes from this gene~cD>	6
4484	11288486	gi|11288486|pir||T49552 hypothetical protein B21J21.300 [imported] - Neurospora crassa emb|CAB91353.1| (AL355929) hypothetical protein [Neurospora crassa]	9.5
4488	11120676	gi|11120676|ref|NP_068546.1| putative envelope polyprotein [DG-75 Murine leukemia virus] gb|AAG29094.1|AF221065_2 (AF221065) putative envelope polyprotein [DG-75 Murine leukemia virus]	1.8
4489	3901274	gi|3901274|gb|AAC78630.1| (AF077821) inducible nitric oxide synthase; iNOS [Canis familiaris]	3.5
4491	11595582	gi|11595582|emb|CAC18184.1| (AL451014) conserved hypothetical protein [Neurospora crassa]	3
4493	5835447	gi|5835447|ref|NP_008371.1|ND6_13186 NADH dehydrogenase subunit 6 [Onchocerca volvulus] pir||T11066 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 6 - nematode (Onchocerca volvulus) mitochondrion gb|AAC61613.1| (AF015193) NADH dehydrogenase subunit 6 [Onchocerca volvulus]	1
4494	13814848	gi|13814848|gb|AAK41824.1| (AE006774) SSV1 hypothetical 14.8 kd protein (orf B-129) homolog [Sulfolobus solfataricus]	5.4
4500	14529727	gi|14529727|emb|CAC42176.1| (AL135758) dM117J5.1 (novel protein similar to anonymous human, fly, worm and yeast proteins) [Mus musculus]	7E-97

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
4504	13512594	gi|13512594|gb|AAK28688.1| (AF078553) unknown function U3 [Ehrlichia canis]	8.8
4506	6635084	gi|6635084|emb|CAB64573.1| (AL135930) hypothetical protein L4738.02 [Leishmania major]	3.2
4508	11467470	gi|11467470|ref|NP_043616.1| 50S ribosomal protein L4 [Odontella sinensis] sp|P49546|RK4_ODOSI CHLOROPLAST 50S RIBOSOMAL PROTEIN L4 pir||S78275 ribosomal protein L4, chloroplast - Odontella sinensis chloroplast emb|CAA91648.1| (Z67753) 50S ribosomal protein L4 [Odontella sinensis]	5.9
4509	4512681	gi|4512681|gb|AAD21735.1| (AC006931) hypothetical protein [Arabidopsis thaliana]	0.73
4510	5835704	gi|5835704|ref|NP_008519.1|ND4_15045 NADH dehydrogenase subunit 4 [Rhipicephalus sanguineus] sp|O99825|NU4M_RHISA NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 pir||T11162 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 [similarity] - hardbacked tick (Rhipicephalus sanguineus) mitochondrion gb|AAD05526.1| (AF081829) NADH dehydrogenase 4 [Rhipicephalus sanguineus]	6.8
4511	8922500	gi|8922500|ref|NP_060600.1| hypothetical protein FLJ10539 [Homo sapiens] dbj|BAA91669.1| (AK001401) unnamed protein product [Homo sapiens]	2E-13
4514	12018296	gi|12018296|ref|NP_072138.1| CDC10 (cell division cycle 10, S.cerevisiae, homolog) [Rattus norvegicus] sp|Q9WVC0|SEP7_RAT SEPTIN 7 (CDC10 PROTEIN HOMOLOG) gb|AAD37861.1|AF142759_1 (AF142759) CDC10 [Rattus norvegicus]	6.9
4518	11357368	gi|11357368|pir||T48358 hypothetical protein F12E4.100 - Arabidopsis thaliana emb|CAB83293.1| (AL162751) putative protein [Arabidopsis thaliana]	1.1
4520	6754038	gi|6754038|ref|NP_034456.1| glycoprotein 1a, alpha polypeptide [Mus musculus] gb|AAC53320.1| (U91967) platelet glycoprotein Ib-alpha [Mus musculus]	0.53

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
4521	7437434	gi|7437434|pir||D72038 DNA topoisomerase I CP1103 [imported] - Chlamydophila pneumoniae (strains CWL029 and AR39) gb|AAD18907.1| (AE001658) DNA Topoisomerase I-Fused to SWI Domain [Chlamydophila pneumoniae CWL029] gb|AAF38871.1| (AE002266) DNA topoisomerase I [Chlamydophila pneumoniae AR39] dbj|BAA98977.1| (AP002547) DNA topoisomerase I-fused to SWI domain [Chlamydophila pneumoniae J138]	8.2
4525	1514669	gi|1514669|emb|CAA87082.1| (Z46958) adenyl cyclase [Xenopus laevis]	0.86
4526	6321382	gi|6321382|ref|NP_011459.1| similar to S. pombe sds23; Sds23p [Saccharomyces cerevisiae] sp|P53172|YGF6_YEAST HYPOTHETICAL 58.1 KD PROTEIN IN UBC2-OLE1 INTERGENIC REGION pir||S64060 probable membrane protein YGL056c - yeast (Saccharomyces cerevisiae) emb|CAA96759.1| (Z72578) ORF YGL056c [Saccharomyces cerevisiae]	4.2
4528	7487690	gi|7487690|pir||T01961 hypothetical protein T5H22.5 - Arabidopsis thaliana gb|AAC62796.1| (AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana] emb|CAB80803.1| (AL161498) similarity to [Arabidopsis thaliana]	3.9
4530	12839203	gi|12839203|dbj|BAB24467.1| (AK006222) putative [Mus musculus]	9.2
4531	1177607	gi|1177607|emb|CAA63219.1| (X92485) pva1 [Plasmodium vivax]	0.11
4534	7506781	gi|7506781|pir||T24250 hypothetical protein R53.3a - Caenorhabditis elegans emb|CAA91353.1| (Z66515) contains similarity to Pfam domain: PF00096 (Zinc finger, C2H2 type), Score=105.7, E-value=2.9e-28, N=5 [Caenorhabditis elegans]	3.2
4538	14041637	gi|14041637|emb|CAC38421.1| (AJ302647) POL protein [Human immunodeficiency virus type 1]	2.8

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
4546	6324843	gi|6324843|ref|NP_014912.1| Required for viability in the absence of Cin8p; Pac1p [Saccharomyces cerevisiae] sp|P39946|PAC1_YEAST PAC1 PROTEIN pir||S67166 PAC1 protein - yeast (Saccharomyces cerevisiae) emb|CAA61775.1| (X89633) hypothetical protein [Saccharomyces cerevisiae] gb|AAB00685.1| (U16827) Pac1p [Saccharomyces cerevisiae] emb|CAA99493.1| (Z75177) ORF YOR269w [Saccharomyces cerevisiae]	4.2
4555	14424433	gi|14424433|ref|NP_077816.1| ATPase, Class V, type 10C; ATPase type IV, phospholipid transporting (P-type) (putative) [Homo sapiens] gb|AAK33100.1| (AY029504) aminophospholipid-transporting ATPase [Homo sapiens] dbj|BAB47392.1| (AB051358) putative aminophospholipid translocase [Homo sapiens]	3E-10
4560	6714740	gi|6714740|emb|CAB66205.1| (AL136502) putative prolyl aminopeptidase. [Streptomyces coelicolor A3(2)]	4.7
4562	6724176	gi|6724176|gb|AAF26878.1|AF196232_1 (AF196232) T cell receptor V delta 6 [Rattus norvegicus]	7.4
4563	14783807	gi|14783807|ref|XP_027541.1| hypothetical protein FLJ21858 [Homo sapiens]	3.1
4564	6478266	gi|6478266|gb|AAF13781.1|AF129403_2 (AF129403) gamma subunit of membrane-bound ATP synthase [Buchnera aphidicola]	2
4566	7509812	gi|7509812|pir||T26861 hypothetical protein Y43F8B.5 - Caenorhabditis elegans emb|CAA21513.1| (AL032623) contains similarity to Pfam domain: PF00188 (SCP-like extracellular protein), Score=34.9, E-value=4.2e-09, N=2 [Caenorhabditis elegans]	5.7
4567	5230656	gi|5230656|gb|AAD40953.1|AF148934_1 (AF148934) phantastica [Lycopersicon esculentum]	7.9
4578	14732381	gi|14732381|ref|XP_050222.1| hypothetical protein XP_050222 [Homo sapiens]	0.0009
4581	14349161	gi|14349161|dbj|BAB60707.1| (AB049622) ficolin 4 [Halocynthia roretzi]	2.5
4585	3599476	gi|3599476|gb|AAC69336.1| (AF084637) serendipity alpha protein [Drosophila virilis]	2.4

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
4586	145512	gi|145512|gb|AAC41418.1| (M55661) colonisation factor antigen d' [Escherichia coli]	8.9
4590	7499104	gi|7499104|pir||T20906 hypothetical protein F14F7.1 - Caenorhabditis elegans emb|CAB04111.1| (Z81503) predicted using Genefinder~contains similarity to Pfam domain: PF01484 (Nematode cuticle collagen N-terminal domain), Score=31.5, E-value=6.2e-06, N=1~cDNA EST yk56g5.3 comes from this gene~cDNA EST yk56g5.5 comes from this gene [Caenorhabditi>	9.8
4591	7267234	gi|7267234|emb|CAB80841.1| (AL161501) putative sugar transporter [Arabidopsis thaliana]	9.9
4593	401050	gi|401050|sp|Q01656|RSP4_CHLRE FLAGELLAR RADIAL SPOKE PROTEIN 4 pir||A44498 radial spoke protein 4 - Chlamydomonas reinhardtii gb|AAA33092.1| (M87526) flagellar radial spoke protein [Chlamydomonas reinhardtii]	0.31
4594	7300719	gi|7300719|gb|AAF55865.1| (AE003734) CG5862 gene product [Drosophila melanogaster]	1.5
4596	12851516	gi|12851516|dbj|BAB29072.1| (AK013941) putative [Mus musculus]	1.1
4598	14193314	gi|14193314|gb|AAK55896.1|AF267213_2 (AF267213) ATP synthase gamma subunit [Candidatus Carsonella ruddii]	5.2
4599	13898998	gi|13898998|gb|AAK48930.1|AF359251_1 (AF359251) extracellular polypeptide Ecp76 [Chlamydomonas reinhardtii]	0.17
4601	8922500	gi|8922500|ref|NP_060600.1| hypothetical protein FLJ10539 [Homo sapiens] dbj|BAA91669.1| (AK001401) unnamed protein product [Homo sapiens]	4.7
4605	7494152	gi|7494152|pir||T18410 carbamoyl-phosphate synthase (glutamine-hydrolyzing) (EC 6.3.5.5) II - malaria parasite (Plasmodium falciparum) gb|AAA29522.1| (L32150) carbamoyl phosphate synthetase II [Plasmodium falciparum]	8.7
4607	6178092	gi|6178092|dbj|BAA86168.1| (AB031705) ORF2 protein [TT virus]	3.4
4608	122078	gi|122078|sp|P02301|H34_MOUSE HISTONE H3.4 (EMBRYONIC) emb|CAA24131.1| (V00754) reading frame histone H3 [Mus musculus]	0.059

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
4610	2598224	gi|2598224|emb|CAA69955.1| (Y08696) aldehyde dehydrogenase [Gluconacetobacter europaeus]	2.1
4612	12382242	gi|12382242|gb|AAG53080.1|AF263824_1 (AF263824) 5'A2rel-related protein [Leishmania donovani]	3.2
4613	1405336	gi|1405336|dbj|BAA13060.1| (D86240) hypothethecal membrane transporter [Staphylococcus aureus] gb|AAD21958.1| (AF101234) putative membrane protein DltB [Staphylococcus aureus] dbj|BAB42033.1| (AP003132) DltB membrane protein [Staphylococcus aureus subsp. aureus N315] dbj|BAB57095.1| (AP003360) DltB membrane protein [Staphylococcus aureus subsp. aureus Mu50]	7.4
4616	6321803	gi|6321803|ref|NP_011879.1| PolyA-binding protein; Mip6p [Saccharomyces cerevisiae] sp|P38760|YHH5_YEAST HYPOTHETICAL 75.9 KDA PROTEIN IN SPO13-ARG4 INTERGENIC REGION pir||S46788 PES4 protein homolog YHR015w - yeast (Saccharomyces cerevisiae) gb|AAB68942.1| (U10400) Yhr015wp [Saccharomyces cerevisiae]	5.3
4618	14749154	gi|14749154|ref|XP_031524.1| AF15q14 protein [Homo sapiens]	9E-94
4621	12837658	gi|12837658|dbj|BAB23899.1| (AK005241) putative [Mus musculus] dbj|BAB26680.1| (AK010067) putative [Mus musculus]	6.8
4622	9628166	gi|9628166|ref|NP_042752.1| CD2 homolog [African swine fever virus] pir||A40678 T-cell adhesion receptor CD2 homolog - African swine fever virus gb|AAA42691.1| (L16864) cd2 homologue [African swine fever virus] gb|AAA65288.1| (U18466) CD2 homolog [African swine fever virus] prf||2113434BJ CD2-like protein [African swine fever virus]	7.6
4625	56691	gi|56691|emb|CAA68549.1| (Y00497) precursor (AA - 24 to 198) [Rattus norvegicus]	4.2
4628	10946710	gi|10946710|ref|NP_067350.1| Rhesus blood group-associated B glycoprotein; Rh type B glycoprotein [Mus musculus] gb|AAF19371.1| (AF193808) Rh type B glycoprotein [Mus musculus]	9.9

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
4631	7507118	gi|7507118|pir||T24482 hypothetical protein T05A1.2 - Caenorhabditis elegans emb|CAA92476.1| (Z68219) contains similarity to Pfam domain: PF01391 (Collagen triple helix repeat (20 copies)), Score=86.4, E-value=1.8e-22, N=2; PF01484 (Nematode cuticle collagen N-terminal domain), Score=23.9, E-value=0.0012, N=1~cDNA EST CEMSE21F comes from this >	3.6
4634	2072964	gi|2072964|gb|AAC51271.1| (U93569) putative p150 [Homo sapiens]	0.12
4636	13385228	gi|13385228|ref|NP_080036.1| RIKEN cDNA 4933428I03 gene [Mus musculus] dbj|BAB30529.1| (AK016968) putative [Mus musculus] dbj|BAB30656.1| (AK017257) putative [Mus musculus]	2.1
4639	13637800	gi|13637800|ref|XP_017899.1| hypothetical protein FLJ12673 [Homo sapiens]	2E-11
4645	14759884	gi|14759884|ref|XP_010198.3| 64448 [Homo sapiens] sp|Q9BZS1|FXP3_HUMAN FORKHEAD BOX PROTEIN P3 (ZINC FINGER PROTEIN JM2) (SCURFIN) gb|AAG53607.1|AF277993_1 (AF277993) scurfin [Homo sapiens]	0.000002
4651	9758192	gi|9758192|dbj|BAB08666.1| (AB018109) pectinesterase [Arabidopsis thaliana]	5.5
4653	9989055	gi|9989055|gb|AAG10818.1|AC011808_6 (AC011808) Hypothetical protein [Arabidopsis thaliana]	6E-11
4658	560700	gi|560700|gb|AAB31458.1| gibbon ape leukemia virus receptor [Mus musculus=Japanese feral mice, spp. molossinus, susceptible cells, Peptide, 680 aa]	7
4659	3878238	gi|3878238|emb|CAA81588.1| (Z27078) cDNA EST yk181g1.5 comes from this gene~cDNA EST yk153a11.5 comes from this gene~cDNA EST yk465b1.5 comes from this gene [Caenorhabditis elegans]	1.3

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
4663	141028	gi|141028|sp|P04540|NU5M_TRYBB NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 pir||QQUTC5 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Trypanosoma brucei mitochondrion gb|AAB59225.1| (M14820) NADH dehydrogenase subunit 5 [Trypanosoma brucei] emb|CAB57807.1| (X01094) unidentified reading frame 10 [Trypanosoma brucei]	0.54
4664	5442110	gi|5442110|gb|AAD43259.1|AF126468_2 (AF126468) protease [Simian retrovirus type 2]	0.3
4666	12860471	gi|12860471|dbj|BAB31968.1| (AK020018) putative [Mus musculus]	7.6
4669	4103974	gi|4103974|gb|AAD05047.1| (AF030414) FeMo protein of nitrogenase alpha subunit; NifD [Gluconacetobacter diazotrophicus]	9.1
4678	2072953	gi|2072953|gb|AAC51264.1| (U93565) putative p150 [Homo sapiens]	0.057
4679	7208454	gi|7208454|gb|AAF40208.1|AF233885_1 (AF233885) phospholipase C-like protein [Mus musculus]	9.6
4680	14193286	gi|14193286|gb|AAK55875.1|AF267206_2 (AF267206) ATP synthase gamma subunit [Candidatus Carsonella ruddii]	9
4681	11361549	gi|11361549|pir||A82772 hypothetical protein XF0722 [imported] - Xylella fastidiosa (strain 9a5c) gb|AAF83532.1|AE003914_13 (AE003914) hypothetical protein [Xylella fastidiosa 9a5c]	3.1
4682	7463298	gi|7463298|pir||A70144 hypothetical protein BB0354 - Lyme disease spirochete gb|AAC66737.1| (AE001141) B. burgdorferi predicted coding region BB0354 [Borrelia burgdorferi]	5.4
4685	9631610	gi|9631610|ref|NP_048389.1| contains Pro-rich Px motif, PAPK (8X); similar to Thermoproteus virus protein TPX, corresponds to Swiss-Prot Accession Number P19275 [Paramecium bursaria Chlorella virus 1] pir||T17531 proline-rich protein A41R - Chlorella virus PBCV-1 gb|AAC96409.1| (U42580) contains Pro-rich Px motif, PAPK (8X); similar to Thermoproteus virus protein TPX, corresponds to Swiss-Prot Accession Number P19275 [Paramecium bursaria Chlorella virus 1]	1.8

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
4688	14754644	gi|14754644|ref|XP_030896.1| similar to hypothetical protein MGC5384 (H. sapiens) [Homo sapiens]	9E-48
4689	2865163	gi|2865163|dbj|BAA24799.1| (AB007836) Hic-5 [Homo sapiens]	2E-16
4693	6760239	gi|6760239|gb|AAF28263.1|AF178655_4 (AF178655) fusion F [Bovine parainfluenza virus 3]	9.8
4698	13446199	gi|13446199|emb|CAC34985.1| (AL035536) very hypothetical protein [Schizosaccharomyces pombe]	5.2
4699	6320491	gi|6320491|ref|NP_010571.1| synaptonemal complex protein; Zip1p [Saccharomyces cerevisiae] sp|P31111|ZIP1_YEAST SYNAPTONEMAL COMPLEX PROTEIN ZIP1 pir||S70115 ZIP1 protein - yeast (Saccharomyces cerevisiae) gb|AAB64474.1| (U51031) Zip1p: Synaptonemal complex protein (Swiss Prot. accession number P31111). [Saccharomyces cerevisiae]	0.001
4703	416704	gi|416704|sp|Q03376|BAR3_CHITE BALBIANI RING PROTEIN 3 PRECURSOR pir||S08167 Balbiani ring 3 protein - midge (Chironomus tentans) emb|CAA36506.1| (X52263) balbiani ring 3 (BR3) [Chironomus tentans]	5.4
4709	6005948	gi|6005948|ref|NP_009118.1| WW domain-containing binding protein 4; formin binding protein 21 [Homo sapiens] ref|XP_007153.1| WW domain-containing binding protein 4 [Homo sapiens] ref|XP_049374.1| WW domain-containing binding protein 4 [Homo sapiens] ref|XP_049375.1| WW domain-containing binding protein 4 [Homo sapiens] gb|AAC34811.1| (AF071185) formin binding protein 21 [Homo sapiens]	0.007
4713	629166	gi|629166|pir||S39791 neurotoxin - Clostridium botulinum	2.5
4719	4096360	gi|4096360|gb|AAC99858.1| (U31159) CR16 [Rattus norvegicus] gb|AAC99859.1| (U31169) SH3 domain binding protein [Rattus norvegicus]	4.3
4723	11352438	gi|11352438|pir||F83161 pyocin protein PA3866 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG07253.1|AE004804_1 (AE004804) pyocin protein [Pseudomonas aeruginosa]	9.1
4725	14761847	gi|14761847|ref|XP_017198.2| hypothetical protein FLJ12085 [Homo sapiens]	0.0007

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
4726	7475497	gi|7475497|pir||B70045 hypothetical protein yvpB - Bacillus subtilis gb|AAC67292.1| (AF017113) YvpB [Bacillus subtilis] emb|CAB15499.1| (Z99121) yvpB [Bacillus subtilis]	9
4731	11466185	gi|11466185|ref|NP_066508.1| NADH dehydrogenase subunit 11 [Naegleria gruberi] gb|AAG17786.1|AF288092_11 (AF288092) NADH dehydrogenase subunit 11 [Naegleria gruberi]	6.2
4735	9802589	gi|9802589|gb|AAF99791.1|AC012463_8 (AC012463) T2E6.16 [Arabidopsis thaliana]	7.7
4741	7512245	gi|7512245|pir||T03849 Fas-binding protein Daxx - green monkey gb|AAB66586.1| (AF015957) Fas-binding protein Daxx [Cercopithecus aethiops]	7.1
4746	345660	gi|345660|pir||A45031 cysteine-rich fibroblast growth factor receptor - chicken gb|AAA48769.1| (M95766) cysteine-rich fibroblast growth factor receptor [Gallus gallus]	1
4750	6324550	gi|6324550|ref|NP_014619.1| mitochondrial initiation factor 2; Ifm1p [Saccharomyces cerevisiae] sp|P25038|IF2M_YEAST TRANSLATION INITIATION FACTOR IF-2, MITOCHONDRIAL PRECURSOR (IF-2MT) (IF-2(MT)) pir||S66706 translation initiation factor IF-2, mitochondrial - yeast (Saccharomyces cerevisiae) emb|CAA99023.1| (Z74765) ORF YOL023w [Saccharomyces cerevisiae]	8.1
4751	12249161	gi|12249161|ref|NP_066211.2| cytochrome c oxidase subunit III [Schistosoma mansoni] gb|AAG13163.2| (AF216698) cytochrome c oxidase subunit 3 [Schistosoma mansoni]	6.6
4758	10835218	gi|10835218|ref|NP_004609.1| topoisomerase (DNA) III alpha [Homo sapiens] ref|XP_008635.1| topoisomerase (DNA) III alpha [Homo sapiens] sp|Q13472|TP3A_HUMAN DNA TOPOISOMERASE III ALPHA gb|AAB03694.1| (U43431) DNA topoisomerase III [Homo sapiens]	9.4
4759	9294528	gi|9294528|dbj|BAB02791.1| (AB024034) gb|AAF50915.1~gene_id:MDC11.5~similar to unknown protein [Arabidopsis thaliana]	7.1
4760	6624755	gi|6624755|emb|CAB63872.1| (AJ251846) OTX5b protein [Xenopus laevis]	8.8

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
4762	14768465	gi|14768465|ref|XP_038469.1| hypothetical protein XP_038469 [Homo sapiens]	0.88
4768	7290081	gi|7290081|gb|AAF45547.1| (AE003418) fz3 gene product [alt 2] [Drosophila melanogaster]	4.7
4770	13358052	gi|13358052|ref|NP_078326.1| unique hypothetical membrane lipoprotein [Ureaplasma urealyticum] pir||H82883 hypothetical protein UU489 [imported] - Ureaplasma urealyticum gb|AAF30901.1|AE002147_2 (AE002147) unique hypothetical membrane lipoprotein [Ureaplasma urealyticum]	0.95
4774	12698025	gi|12698025|dbj|BAB21831.1| (AB051527) KIAA1740 protein [Homo sapiens]	0.24
4784	116910	gi|116910|sp|P10169|CON8_NEUCR CONIDIATION-SPECIFIC PROTEIN 8 pir||S02210 con-8 protein - Neurospora crassa emb|CAA30092.1| (X07040) con-8 [Neurospora crassa]	4.3
4788	3694664	gi|3694664|gb|AAC62434.1| (AC004893) similar to NEDD-4 (KIA0093); similar to P46934 (PID:g1171682) [Homo sapiens]	8.2
4790	1731439	gi|1731439|sp|P51505|ZN80_MACMU ZINC FINGER PROTEIN 80 emb|CAA61771.1| (X89629) znf80 [Macaca mulatta]	1.3
4794	11257183	gi|11257183|pir||F82319 transketolase 1 VC0473 [imported] - Vibrio cholerae (group O1 strain N16961) gb|AAF93646.1| (AE004133) transketolase 1 [Vibrio cholerae]	9.1
4795	11466520	gi|11466520|ref|NP_044769.1| SecY-type transporter protein [Reclinomonas americana] pir||S78151 secY protein homolog - Reclinomonas americana (ATCC 50394) mitochondrion gb|AAD11884.1| (AF007261) SecY-type transporter protein [Reclinomonas americana]	2.3
4799	5869811	gi|5869811|emb|CAB55552.1| (AJ243538) Fox2 protein [Glomus mosseae]	8.5

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
4801	6324187	gi|6324187|ref|NP_014257.1| Ammonia transport protein; Mep2p [Saccharomyces cerevisiae] sp|P41948|MEP2_YEAST AMMONIUM TRANSPORTER MEP2 pir||S51089 ammonium transport protein MEP2 - yeast (Saccharomyces cerevisiae) emb|CAA58587.1| (X83608) ammonium transporter [Saccharomyces cerevisiae] emb|CAA86884.1| (Z46843) NH3 permease [Saccharomyces cerevisiae] emb|CAA96025.1| (Z71418) ORF YNL142w [Saccharomyces cerevisiae]	8.3
4805	14738182	gi|14738182|ref|XP_038231.1| KIAA0793 gene product [Homo sapiens]	3E-16
4806	481861	gi|481861|pir||S39796 aggrecan precursor - chicken	0.065
4808	462116	gi|462116|sp|Q05394|FMLR_RABIT FMET-LEU-PHE RECEPTOR (FMLP RECEPTOR) (N-FORMYL PEPTIDE RECEPTOR) (FPR) (N-FORMYLPEPTIDE CHEMOATTRACTANT RECEPTOR) pir||A46520 N-formyl peptide receptor - rabbit gb|AAA31254.1| (M94549) N-formyl peptide receptor [Oryctolagus cuniculus]	2.2
4809	12832739	gi|12832739|dbj|BAB22236.1| (AK002621) putative [Mus musculus]	1.1
4813	464359	gi|464359|sp|P33295|PEPC_ASPNG SUBTILISIN-LIKE SERINE PROTEASE PEPC PRECURSOR pir||JU0146 serine proteinase (EC 3.4.21.-) precursor - Aspergillus niger gb|AAA32702.1| (M96758) serine protease [Aspergillus niger]	0.91
4814	14741436	gi|14741436|ref|XP_032168.1| hypothetical protein XP_032168 [Homo sapiens]	1.3
4821	6322061	gi|6322061|ref|NP_012136.1| Yil130wp [Saccharomyces cerevisiae] sp|P40467|YIN0_YEAST PUTATIVE 108.8 KD TRANSCRIPTIONAL REGULATORY PROTEIN IN FKH1-STH1 INTERGENIC REGION pir||S48404 probable membrane protein YIL130w - yeast (Saccharomyces cerevisiae) emb|CAA86148.1| (Z38059) orf, len: 964, CAI: 0.15, possible regulatory protein [Saccharomyces cerevisiae]	6.7
4822	14784569	gi|14784569|ref|XP_016395.2| 11729 [Homo sapiens]	5E-26

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
4825	13926079	gi|13926079|gb|AAK49526.1|AF356082_1 (AF356082) C2H2 zinc finger transcription factor JING [Drosophila melanogaster]	2.7
4827	1209370	gi|1209370|gb|AAA91081.1| (L33971) EBV BKRF4 homologue [Leporid herpesvirus 1]	8
4829	11359537	gi|11359537|pir||T51023 hypothetical protein B7F21.40 [imported] - Neurospora crassa emb|CAB97476.1| (AL389901) conserved hypothetical protein [Neurospora crassa]	0.57
4832	13629392	gi|13629392|sp|P97523|MET_RAT HEPATOCYTE GROWTH FACTOR RECEPTOR PRECURSOR (MET PROTO-ONCOGENE TYROSINE KINASE) (C-MET) (HGF RECEPTOR) (HGF-SF RECEPTOR) emb|CAA65582.1| (X96786) c-met [Rattus norvegicus]	1.3
4834	4508019	gi|4508019|ref|NP_003449.1| bassoon (presynaptic cytomatrix protein); neuronal double zinc finger protein; zinc finger protein 231 [Homo sapiens] gb|AAC83555.1| (AF052224) neuronal double zinc finger protein [Homo sapiens]	1.5
4835	5734374	gi|5734374|emb|CAB52680.1| (AJ133723) Ran-binding protein 2 [Bos taurus]	4.7
4837	3281932	gi|3281932|emb|CAA76796.1| (Y17584) beta-lactamase class A [Escherichia coli] emb|CAC43180.1| (AJ277416) TEM-29 ES-beta-lactamase [Escherichia coli]	9.4
4839	15021417	gi|15021417|gb|AAK77694.1|AF369029_25 (AF369029) ORF25, gene family 4 [white spot syndrome virus]	9.4
4841	7507283	gi|7507283|pir||T32024 hypothetical protein T06D4.4 - Caenorhabditis elegans gb|AAB66123.1| (AF016673) similar to endothelin-converting enzymes [Caenorhabditis elegans]	6.7
4843	1165132	gi|1165132|emb|CAA64491.1| (X95193) homeobox-leucine zipper protein [Pimpinella brachycarpa]	8.5

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
4845	11466755	gi|11466755|ref|NP_039351.1| ORF191 [Marchantia polymorpha] sp|P06266|NU6C_MARPO NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 6, CHLOROPLAST pir||DELVN6 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 6 - liverwort (Marchantia polymorpha) chloroplast emb|CAA28137.1| (X04465) ORF191 [Marchantia polymorpha]	9.5
4849	14010605	gi|14010605|gb|AAK52051.1|AF363973_1 (AF363973) semaphorin 6C [Mus musculus]	6.3
4853	14755906	gi|14755906|ref|XP_044358.1| similar to cleft lip and palate associated transmembrane protein 1 (H. sapiens) [Homo sapiens]	2.7
4859	13647785	gi|13647785|ref|XP_018036.1| hypothetical protein FLJ13166 [Homo sapiens] ref|XP_051378.1| similar to hypothetical protein FLJ13166 (H. sapiens) [Homo sapiens]	6.1
4866	11994373	gi|11994373|dbj|BAB02332.1| (AB019229) gene_id:MDC16.14~unknown protein [Arabidopsis thaliana]	4.7
4872	12514590	gi|12514590|gb|AAG55801.1|AE005316_6 (AE005316) orf, hypothetical protein [Escherichia coli O157:H7 EDL933] dbj|BAB34856.1| (AP002555) hypothetical protein [Escherichia coli O157:H7]	6
4873	14017847	gi|14017847|dbj|BAB47444.1| (AB058718) KIAA1815 protein [Homo sapiens]	6E-18
4878	7506698	gi|7506698|pir||T24214 hypothetical protein R134.2 - Caenorhabditis elegans	7.3
4880	7505750	gi|7505750|pir||T23590 hypothetical protein K10H10.1 - Caenorhabditis elegans emb|CAB05777.1| (Z83236) contains similarity to Pfam domain: PF00083 (Sugar (and other) transporter), Score=-89.7, E-value=0.00037, N=1~cDNA EST yk503h12.5 comes from this gene~cDNA EST yk653a11.3 comes from this gene~cDNA EST yk653a11.5 comes from this gene [Caenorha>	1.4
4882	2500112	gi|2500112|sp|P71359|RECQ_HAEIN ATP-DEPENDENT DNA HELICASE RECQ gb|AAC22387.1| (U32756) ATP-dependent DNA helicase (recQ) [Haemophilus influenzae Rd]	8.7

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
4883	13447070	gi|13447070|gb|AAK26617.1| (AF340025) NADH dehydrogenase subunit V [Coturnix chinensis]	3.1
4886	14775307	gi|14775307|ref|XP_042250.1| similar to nuclear pore complex interacting protein (H. sapiens) [Homo sapiens]	4.2
4888	6434530	gi|6434530|emb|CAB61080.1| (AL132949) predicted using Genefinder~cDNA EST yk51g5.3 comes from this gene~cDNA EST yk62d6.3 comes from this gene~cDNA EST yk51g5.5 comes from this gene~cDNA EST yk62d6.5 comes from this gene~cDNA EST yk105f8.5 comes from this gene~cDNA EST yk99f8.3 >	0.28
4896	12832739	gi|12832739|dbj|BAB22236.1| (AK002621) putative [Mus musculus]	1.1
4903	11281764	gi|11281764|pir||C81739 conserved hypothetical protein TC0120 [imported] - Chlamydia muridarum (strain Nigg) gb|AAF38998.1| (AE002279) conserved hypothetical protein [Chlamydia muridarum]	2.7
4908	12838194	gi|12838194|dbj|BAB24118.1| (AK005558) putative [Mus musculus]	1.7
4911	12721131	gi|12721131|gb|AAK02908.1| (AE006121) unknown [Pasteurella multocida]	8.3
4913	10638457	gi|10638457|emb|CAC12644.1| (AL136442) bA25J23.1 (KIAA1165 protein, similar to Drosophila CG8056 protein) [Homo sapiens]	1E-18
4916	11346431	gi|11346431|pir||T47803 mitogen-activated protein kinase-like protein - Arabidopsis thaliana emb|CAB75798.1| (AL138647) mitogen-activated protein kinase-like protein [Arabidopsis thaliana]	4

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
4924	14758601	gi|14758601|ref|XP_010183.3| protein phosphatase, EF hand calcium-binding domain 1 [Homo sapiens] ref|XP_040201.1| protein phosphatase, EF hand calcium-binding domain 1 [Homo sapiens] ref|XP_040202.1| protein phosphatase, EF hand calcium-binding domain 1 [Homo sapiens] sp|O14829|PPE1_HUMAN SERINE/THREONINE PROTEIN PHOSPHATASE WITH EF-HANDS-1 (PPEF-1) (PROTEIN PHOSPHATASE WITH EF CALCIUM-BINDING DOMAIN) (PPEF) (SERINE/THREONINE PROTEIN PHOSPHATASE 7) (PP7) gb|AAB82795.1| (AF023455) protein phosphatase with EF-hands-1 [Homo sapiens] gb|AAC05825.1| (AF027977) serine/threonine protein phosphatase 7 catalytic subunit [Homo sapiens]	0.08
4932	12007365	gi|12007365|gb|AAG45157.1|AF316823_1 (AF316823) cellulase Cel9-H [Clostridium cellulolyticum]	3.2
4933	8745051	gi|8745051|emb|CAB95305.1| (AL359781) dynein heavy chain, cytosolic [Leishmania major]	8
4934	7499345	gi|7499345|pir||T21083 hypothetical protein F18A11.4 - Caenorhabditis elegans emb|CAB04136.1| (Z81507) cDNA EST yk651h1.5 comes from this gene [Caenorhabditis elegans] emb|CAA21639.1| (AL032639) cDNA EST yk651h1.5 comes from this gene [Caenorhabditis elegans]	0.4
4935	14133229	gi|14133229|dbj|BAA76843.2| (AB023216) KIAA0999 protein [Homo sapiens]	0.91
4936	5835447	gi|5835447|ref|NP_008371.1|ND6_13186 NADH dehydrogenase subunit 6 [Onchocerca volvulus] pir||T11066 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 6 - nematode (Onchocerca volvulus) mitochondrion gb|AAC61613.1| (AF015193) NADH dehydrogenase subunit 6 [Onchocerca volvulus]	2.8
4940	6978439	gi|6978439|ref|NP_036622.1| acrosin [Rattus norvegicus] emb|CAA41441.2| (X58550) preproacrosin [Rattus sp.]	9.1

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
4946	11349140	gi|11349140|pir||G83492 hypothetical protein PA1232 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG04621.1|AE004552_11 (AE004552) hypothetical protein [Pseudomonas aeruginosa]	1
4950	12862434	gi|12862434|dbj|BAB32470.1| (AB047280) Pol-like protein Pol-2 [Tricholoma matsutake]	4.6
4956	15011489	gi|15011489|gb|AAK77584.1|AF396436_24 (AF396436) heme maturase [Tetrahymena thermophila]	2.8
4958	1944163	gi|1944163|dbj|BAA19637.1| (AB002668) unnamed protein product [Actinobacillus actinomycetemcomitans]	0.84
4966	7522108	gi|7522108|pir||T29097 pro-pol-dUTPase polyprotein - murine endogenous retrovirus ERV-L (fragment) emb|CAA73251.1| (Y12713) protease; reverse transcriptase; RNaseH; integrase; dUTPase; Pro-Pol-dUTPase polyprotein [Mus musculus]	0.0005
4968	12963743	gi|12963743|ref|NP_076085.1| equilibrative nucleoside transporter 3 [Mus musculus] gb|AAK00957.1|AF326986_1 (AF326986) equilibrative nucleoside transporter 3 [Mus musculus]	9.3
4971	6503300	gi|6503300|gb|AAF14676.1|AC011713_24 (AC011713) Contains PF|01535 Domain of unknown function. [Arabidopsis thaliana]	3.1
4976	7498863	gi|7498863|pir||T20730 hypothetical protein F10G8.8 - Caenorhabditis elegans emb|CAB02286.2| (Z80216) Weak similarity with intermediate filament protein (TREMBL id G633240), contains similarity to Pfam domain: PF00169 (PH domain), Score=79.3, E-value=2.7e-21, N=2~cDNA EST EMBL:T01262 comes from this gene~cDNA EST yk23d5.3 comes from this gene~> emb|CAA19441.2| (AL023823) Weak similarity with intermediate filament protein (TREMBL id G633240), contains similarity to Pfam domain: PF00169 (PH domain), Score=79.3, E-value=2.7e-21, N=2~cDNA EST EMBL:T01262 comes from this gene~cDNA EST yk23d5.3 comes from this gen>	7

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
4981	436923	gi|436923|gb|AAA62274.1| (U01849) ORF1 [Trypanosoma brucei]	1.2
4982	2827416	gi|2827416|gb|AAB99843.1| (AF043083) glycoprotein B [human herpesvirus 5]	9.1
4989	11135234	gi|11135234|sp|P57642|SYK3_BUCAI PUTATIVE LYSYL-TRNA SYNTHETASE (LYSINE--TRNA LIGASE) (LYSRS) (GX) dbj|BAB13271.1| (AP001119) hypothetical lysyl-tRNA synthetase homolog [Buchnera sp. APS]	1.4
4990	2129953	gi|2129953|pir||JC5229 laccase (EC 1.10.3.2) precursor - common tobacco gb|AAC49536.1| (U43542) diphenol oxidase [Nicotiana tabacum]	9.1
4995	13786443	gi|13786443|gb|AAK39568.1|AC025296_3 (AC025296) hypothetical protein [Oryza sativa]	0.83
4998	7494262	gi|7494262|pir||T18489 hypothetical protein C0820w - malaria parasite (Plasmodium falciparum) emb|CAB11128.1| (Z98551) hypothetical protein, PFC0820w [Plasmodium falciparum]	0.81
5000	10121788	gi|10121788|gb|AAG13373.1| (AF268180) polyprotein [bovine viral diarrhea virus type 2]	7.4
5007	6906704	gi|6906704|dbj|BAA90553.1| (AB032551) proline-rich inositol polyphosphate 5-phosphatase [Rattus norvegicus]	1.6
5008	8978523	gi|8978523|dbj|BAA98360.1| (AP002545) CT147 hypothetical protein [Chlamydophila pneumoniae J138]	7.4
5009	9630127	gi|9630127|ref|NP_046554.1| putative lipoprotein [Bacteriophage SPBc2] pir||T12766 probable lipoprotein yokB - Bacillus subtilis phage SPBc2 emb|CAB14083.1| (Z99115) yokB [Bacillus subtilis] gb|AAC12975.1| (AF020713) putative lipoprotein [Bacteriophage SPBc2]	2.7
5011	8978523	gi|8978523|dbj|BAA98360.1| (AP002545) CT147 hypothetical protein [Chlamydophila pneumoniae J138]	7.4
5012	13636469	gi|13636469|ref|XP_016747.1| latent transforming growth factor beta binding protein 1 precursor [Homo sapiens]	1.7
5016	3694664	gi|3694664|gb|AAC62434.1| (AC004893) similar to NEDD-4 (KIA0093); similar to P46934 (PID:g1171682) [Homo sapiens]	7.9
5020	14751816	gi|14751816|ref|XP_034239.1| hypothetical protein XP_034239 [Homo sapiens]	0.064

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
5022	4768840	gi|4768840|gb|AAD29638.1|AF117611_1 (AF117611) DosA protein [Dictyostelium discoideum]	9.9
5023	7442182	gi|7442182|pir||T04989 pathogenesis-related protein 1 precursor, 19.3K - Arabidopsis thaliana emb|CAA20585.1| (AL031394) pathogenesis-related protein 1 precursor, 19.3K [Arabidopsis thaliana] emb|CAB80089.1| (AL161584) pathogenesis-related protein 1 precursor, 19.3K [Arabidopsis thaliana] gb|AAG40056.1|AF324705_1 (AF324705) AT4g33720 [Arabidopsis thaliana] gb|AAG42009.1|AF327419_1 (AF327419) putative pathogenesis-related protein 1 precursor protein [Arabidopsis thaliana] gb|AAK00381.1|AF339699_1 (AF339699) putative pathogenesis-related protein 1 precursor protein [Arabidopsis thaliana] gb|AAK62632.1| (AY039577) AT4g33720/T16L1_210 [Arabidopsis thaliana]	9.3
5029	4884674	gi|4884674|gb|AAD31763.1|AF121945_1 (AF121945) aldehyde oxidase [Mus musculus]	7.9
5031	2133751	gi|2133751|pir||S66610 sulfakinin - bluebottle fly (Calliphora vomitoria) prf||2120269A sulfakinin [Calliphora vomitoria]	9
5033	975667	gi|975667|emb|CAA61500.1| (X89213) RNA polymerase [Infectious hematopoietic necrosis virus] prf||2121413F RNA polymerase [Infectious hematopoietic necrosis virus]	4.1
5035	11267434	gi|11267434|pir||F82853 DNA helicase II XF0050 [imported] - Xylella fastidiosa (strain 9a5c) gb|AAF82863.1|AE003859_4 (AE003859) DNA helicase II [Xylella fastidiosa 9a5c]	3.1
5036	11994373	gi|11994373|dbj|BAB02332.1| (AB019229) gene_id:MDC16.14~unknown protein [Arabidopsis thaliana]	4.8
5050	1082778	gi|1082778|pir||A56395 secretory phospholipase A2 receptor precursor, transmembrane form - human gb|AAA70110.1| (U17033) 180 kDa transmembrane PLA2 receptor precursor [Homo sapiens]	3.5

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
5051	13518480	gi|13518480|ref|NP_084839.1| hypothetical protein [Lotus japonicus] ref|NP_084856.1| hypothetical protein [Lotus japonicus] dbj|BAB33238.1| (AP002983) hypothetical protein [Lotus japonicus] dbj|BAB33256.1| (AP002983) hypothetical protein [Lotus japonicus]	5
5065	7460247	gi|7460247|pir||B71612 hypothetical protein PFB0555c - malaria parasite (Plasmodium falciparum) gb|AAC71900.1| (AE001402) hypothetical protein [Plasmodium falciparum]	7.1
5069	13486795	gi|13486795|dbj|BAB40028.1| (AP003021) hypothetical protein [Oryza sativa]	2.6
5072	6166049	gi|6166049|sp|O55017|CCAB_MOUSE VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL III) (BIII) gb|AAB97840.1| (AF042317) neuronal type calcium channel alpha-1 subunit [Mus musculus]	1.2
5074	7495367	gi|7495367|pir||T33395 hypothetical protein C04F2.1 - Caenorhabditis elegans gb|AAC26911.1| (AF078780) Similar to chemoreceptor; C04F2.1 [Caenorhabditis elegans]	3.1
5075	9507739	gi|9507739|ref|NP_061405.1| 23 pct identical(9 gaps) to 343 residues of 1286 aa protein sp:AIDA_ECOLI[Adhesin AidA-I precursor] [Plasmid F] dbj|BAA97896.1| (AP001918) 23 pct identical(9 gaps) to 343 residues of 1286 aa protein sp:AIDA_ECOLI[Adhesin AidA-I precursor] [Plasmid F]	9.7
5076	7495508	gi|7495508|pir||T18993 hypothetical protein C06B8.1 - Caenorhabditis elegans emb|CAB03850.1| (Z81463) Similarity to C.elegans zinc finger proteins, contains similarity to Pfam domain: PF00104 (Ligand-binding domain of nuclear hormone receptor), Score=-13.7, E-value=0.051, N=1 [Caenorhabditis elegans]	4.2
5077	14018037	gi|14018037|ref|NP_114377.1| ATP synthase F0 subunit 6 [Hymenolepis diminuta] gb|AAK51337.1|AF314223_9 (AF314223) ATP synthase subunit 6 [Hymenolepis diminuta]	4.9

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
5086	6562005	gi|6562005|emb|CAB62499.1| (AJ250586) chitinase [Arthrobacter sp.]	1.5
5087	9631327	gi|9631327|ref|NP_048161.1| ORF MSV090 putative Molluscum contagiosum virus MC121L (vaccinia A16L) homolog, similar to GB:U60315 [Melanoplus sanguinipes entomopoxvirus] pir||T28251 ORF MSV090 probable Molluscum contagiosum virus MC121L (vaccinia A16L) homolog - Melanoplus sanguinipes entomopoxvirus gb|AAC97640.1| (AF063866) ORF MSV090 putative Molluscum contagiosum virus MC121L (vaccinia A16L) homolog, similar to GB:U60315 [Melanoplus sanguinipes entomopoxvirus]	8.7
5088	4321813	gi|4321813|gb|AAD15835.1| (AF063236) variant 2 major surface glycoprotein [Pneumocystis carinii]	6.5
5089	12853765	gi|12853765|dbj|BAB29840.1| (AK015427) putative [Mus musculus]	0.0003
5094	732059	gi|732059|sp|P39372|YJHA_ECOLI HYPOTHETICAL 28.3 KDA PROTEIN IN FECI-FIMB INTERGENIC REGION PRECURSOR pir||S56536 hypothetical protein f241 (fecI-fimB intergenic region) - Escherichia coli gb|AAA97207.1| (U14003) ORF_f241 [Escherichia coli] gb|AAC77267.1| (AE000501) orf, hypothetical protein [Escherichia coli K12] gb|AAG59493.1|AE005662_5 (AE005662) orf, hypothetical protein [Escherichia coli O157:H7 EDL933] dbj|BAB38693.1| (AP002569) hypothetical protein [Escherichia coli O157:H7]	1.4
5095	84124	gi|84124|pir||B24785 hypothetical protein 1028 - slime mold (Dictyostelium discoideum) transposon DIRS-1 (fragment)	2.9
5096	84043	gi|84043|pir||C22845 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - Trypanosoma brucei mitochondrion	2.3
5100	5441886	gi|5441886|dbj|BAA82384.1| (AP000367) EST AU069246(C53478) corresponds to a region of the predicted gene.; hypothetical protein [Oryza sativa]	4.9

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
5102	6678810	gi|6678810|ref|NP_032581.1| mannan-binding lectin serine protease 1 [Mus musculus] sp|P98064|CRAR_MOUSE COMPLEMENT-ACTIVATING COMPONENT OF RA-REACTIVE FACTOR PRECURSOR (RA-REACTIVE FACTOR SERINE PROTEASE P100) (RARF) (MANNAN-BINDING LECTIN SERINE PROTEASE 1) dbj|BAA03944.1| (D16492) P100 serine protease of Ra-reactive factor (RaRF) [Mus musculus]	7.3
5106	13357651	gi|13357651|ref|NP_077925.1| unique hypothetical membrane lipoprotein [Ureaplasma urealyticum] pir||G82934 hypothetical protein UU094 [imported] - Ureaplasma urealyticum gb|AAF30500.1|AE002109_3 (AE002109) unique hypothetical membrane lipoprotein [Ureaplasma urealyticum]	2.4
5108	2499547	gi|2499547|sp|P77153|WZB_ECOLI PROBABLE LOW MOLECULAR WEIGHT PROTEIN-TYROSINE-PHOSPHATASE WZB pir||D64972 probable protein-tyrosine-phosphatase (EC 3.1.3.48) wzb, low molecular weight - Escherichia coli gb|AAC77834.1| (U38473) putative acid phosphatase [Escherichia coli] gb|AAC75122.1| (AE000296) probable protein-tyrosine-phosphatase [Escherichia coli K12] gb|AAG57121.1|AE005432_2 (AE005432) probable protein-tyrosine-phosphatase [Escherichia coli O157:H7 EDL933] dbj|BAB36289.1| (AP002560) probable protein-tyrosine-phosphatase [Escherichia coli O157:H7]	1.4
5109	5292165	gi|5292165|gb|AAB01085.2| (U34402) single-subunit RNA polymerase C [Triticum aestivum]	2.9
5112	2598890	gi|2598890|dbj|BAA23297.1| (D86277) VP7 [Human rotavirus 3]	0.52
5115	7301702	gi|7301702|gb|AAF56815.1| (AE003767) wdn gene product [Drosophila melanogaster]	2
5116	12853765	gi|12853765|dbj|BAB29840.1| (AK015427) putative [Mus musculus]	0.0003
5121	4009428	gi|4009428|gb|AAD11553.1| (AF019894) replication protein A [Helicobacter pylori]	4.2
5128	12849716	gi|12849716|dbj|BAB28451.1| (AK012761) putative [Mus musculus]	7.3

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
5129	7496182	gi|7496182|pir||T19344 hypothetical protein C17D12.4 - Caenorhabditis elegans emb|CAB03892.1| (Z81473) predicted using Genefinder [Caenorhabditis elegans]	5.7
5130	9634540	gi|9634540|ref|NP_038078.1| TA35L [Vaccinia virus (strain Tian Tan)] gb|AAF34031.1| (AF095689) TA35L [Vaccinia virus (strain Tian Tan)]	9.5
5136	12045115	gi|12045115|ref|NP_072926.1| lipoprotein, putative [Mycoplasma genitalium] sp|P47502|Y260_MYCGE HYPOTHETICAL LIPOPROTEIN MG260 PRECURSOR pir||G64228 hypothetical protein homolog MG260 - Mycoplasma genitalium gb|AAC71481.1| (U39705) lipoprotein, putative [Mycoplasma genitalium]	3.3
5138	2144796	gi|2144796|pir||I36912 involucrin S - douroucouli (fragment) gb|AAA35376.1| (M25314) involucrin (small allele) [Aotus trivirgatus]	4.3
5140	7509951	gi|7509951|pir||T33900 hypothetical protein Y48A5A.1 - Caenorhabditis elegans gb|AAD12829.1| (AF125455) Y48A5A.1 gene product [Caenorhabditis elegans]	1.3
5143	13701664	gi|13701664|dbj|BAB42957.1| (AP003135) ORFID:SA1688~hypothetical protein, similar to teichoic acid translocation ATP-binding protein tagH [Staphylococcus aureus subsp. aureus N315] dbj|BAB58033.1| (AP003363) hypothetical protein [Staphylococcus aureus subsp. aureus Mu50]	6.1
5147	7243223	gi|7243223|dbj|BAA92659.1| (AB037842) KIAA1421 protein [Homo sapiens]	6E-96
5148	14771907	gi|14771907|ref|XP_045594.1| hypothetical protein MGC4816 [Homo sapiens]	5E-30
5163	6056374	gi|6056374|gb|AAF02838.1|AC009894_9 (AC009894) Similar to serine/threonine kinases [Arabidopsis thaliana]	9.5

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
5164	6322278	gi|6322278|ref|NP_012352.1| mannosyltransferase complex component; Mnn11p [Saccharomyces cerevisiae] sp|P46985|YJS3_YEAST HYPOTHETICAL 47.8 KD PROTEIN IN SWE1-ATP12 INTERGENIC REGION pir||S56966 probable membrane protein YJL183w - yeast (Saccharomyces cerevisiae) emb|CAA89478.1| (Z49458) ORF YJL183w [Saccharomyces cerevisiae]	0.5
5168	14738479	gi|14738479|ref|XP_027836.1| general transcription factor IIIC, polypeptide 4 (90kD) [Homo sapiens]	7
5169	4505321	gi|4505321|ref|NP_003862.1| myelin transcription factor 2; cerebrin-50 [Homo sapiens] pir||I52374 cerebrin-50 - human gb|AAB34231.1| (S76853) cerebrin-50=cerebrospinal fluid protein [human, cerebral brain, Peptide, 435 aa] [Homo sapiens]	5
5171	14336722	gi|14336722|gb|AAK61254.1|AE006464_22 (AE006464) Similar to pre-pro-megakarycyte potentiating factor precursor [Homo sapiens]	0.22
5173	13700778	gi|13700778|dbj|BAB42074.1| (AP003132) ORFID:SA0834~hypothetical protein, similar to lipopolysaccharide modification acyltransferase [Staphylococcus aureus subsp. aureus N315] dbj|BAB57136.1| (AP003360) hypothetical protein [Staphylococcus aureus subsp. aureus Mu50]	5.7
5174	8894607	gi|8894607|emb|CAB94193.2| (AJ289710) envelope protein [HERV-H/env60]	0.0002
5176	14772400	gi|14772400|ref|XP_045944.1| hypothetical protein XP_045944 [Homo sapiens]	2.5
5181	8248741	gi|8248741|gb|AAB20211.2| (S61973) NMDA receptor glutamate-binding subunit [Rattus sp.]	7.4
5186	12329963	gi|12329963|emb|CAC24680.1| (AL513062) possible high molecular mass nuclear antigen [Leishmania major]	9.7
5187	3915815	gi|3915815|sp|Q45032|PRIA_BORBU PRIMOSOMAL PROTEIN N' (REPLICATION FACTOR Y) pir||F70101 primosomal protein N (priA) homolog - Lyme disease spirochete gb|AAC66393.1| (AE001115) primosomal protein N (priA) [Borrelia burgdorferi]	0.86

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
5191	7516796	gi|7516796|pir||H72575 hypothetical protein APE1888 - Aeropyrum pernix (strain K1) dbj|BAA80893.1| (AP000062) 107aa long hypothetical protein [Aeropyrum pernix]	9.9
5192	4691710	gi|4691710|gb|AAD28038.1|AF119712_1 (AF119712) bone morphogenetic protein BMP2/4 [Lytechinus variegatus]	4.5
5198	10639274	gi|10639274|emb|CAC11276.1| (AL445063) amylopullulanase related protein [Thermoplasma acidophilum]	2.4
5199	10998836	gi|10998836|gb|AAG26008.1|AF312017_1 (AF312017) beta-glucosidase precursor [Tenebrio molitor]	3.1
5205	7657228	gi|7657228|ref|NP_055258.1| interleukin 17B [Homo sapiens] ref|XP_003898.3| 50367 [Homo sapiens] ref|XP_046987.1| interleukin 17B [Homo sapiens] ref|XP_046984.1| interleukin 17B [Homo sapiens] ref|XP_046985.1| interleukin 17B [Homo sapiens] ref|XP_046986.1| 50372 [Homo sapiens] gb|AAF01318.1|AF184969_1 (AF184969) cytokine-like protein ZCYTO7 [Homo sapiens] gb|AAF28104.1|AF152098_1 (AF152098) interleukin 17B [Homo sapiens] gb|AAF78775.1|AF212311_1 (AF212311) interleukin 20 [Homo sapiens] gb|AAG39637.1|AF110385_1 (AF110385) interleukin-17 beta; IL-17 beta [Homo sapiens] gb|AAG44136.1|AF218727_1 (AF218727) neuronal interleukin-17 related factor [Homo sapiens] gb|AAK60336.1|AF386077_1 (AF386077) interleukin 17B [Homo sapiens]	5.5
5207	12311878	gi|12311878|emb|CAC22694.1| (AL389894) hypothetical protein L779.02 [Leishmania major]	1.6

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
5208	7657683	gi|7657683|ref|NP_055146.1| solute carrier family 7, (cationic amino acid transporter, y+ system) member 11; cystine/glutamate transporter [Homo sapiens] sp|Q9UPY5|XCT_HUMAN CYSTINE/GLUTAMATE TRANSPORTER (AMINO ACID TRANSPORT SYSTEM XC-) (XCT) dbj|BAA82628.1| (AB026891) cystine/glutamate transporter [Homo sapiens] gb|AAG35592.1|AF200708_1 (AF200708) calcium channel blocker resistance protein CCBR1 [Homo sapiens] gb|AAK49111.1|AF252872_1 (AF252872) cystine/glutamate transporter xCT [Homo sapiens]	2.2
5212	2388574	gi|2388574|gb|AAB71455.1| (AC000098) Strong similarity to Phalaenopsis homeobox protein (gb|U34743). [Arabidopsis thaliana]	7
5221	14740481	gi|14740481|ref|XP_045136.1| similar to cadherin related 23 (H. sapiens) [Homo sapiens]	1E-18
5222	12852452	gi|12852452|dbj|BAB29417.1| (AK014534) putative [Mus musculus]	8E-21
5224	2119250	gi|2119250|pir||I38857 microtubule-associated protein 1A - human gb|AAA81362.1| (U14577) microtubule-associated protein 1A [Homo sapiens]	0.99
5226	1304610	gi|1304610|gb|AAC59915.1| (U41783) cytochrome b [Cynolebias affinis]	4.7
5227	12311878	gi|12311878|emb|CAC22694.1| (AL389894) hypothetical protein L779.02 [Leishmania major]	1.3
5228	6650047	gi|6650047|gb|AAF21692.1|AF051987_1 (AF051987) maturase K [Hyobanche sanguinea]	1.9
5232	3859671	gi|3859671|emb|CAA22009.1| (AL033502) hypothetical protein [Candida albicans]	0.0009
5240	9963891	gi|9963891|gb|AAG09748.1|AF233276_1 (AF233276) peroxin-1 [Penicillium chrysogenum]	9.3
5242	3024924	gi|3024924|sp|Q58315|Y905_METJA HYPOTHETICAL PROTEIN MJ0905 pir||A64413 hypothetical protein MJ0905 - Methanococcus jannaschii gb|AAB98915.1| (U67534) M. jannaschii predicted coding region MJ0905 [Methanococcus jannaschii]	1.8
5245	11279021	gi|11279021|pir||T47996 hypothetical protein F21F14.210 - Arabidopsis thaliana emb|CAB71911.1| (AL138642) putative protein [Arabidopsis thaliana]	5.2

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
5255	2746323	gi|2746323|gb|AAB97896.1| (AF037166) major surface glycoprotein [Leishmania panamensis]	2.2
5260	7506750	gi|7506750|pir||T16770 hypothetical protein R153.2 - Caenorhabditis elegans gb|AAA68293.1| (U28729) Hypothetical protein R153.2 [Caenorhabditis elegans]	4.1
5264	14737112	gi|14737112|ref|XP_046972.1| hypothetical protein XP_046972 [Homo sapiens]	3.4
5266	7432465	gi|7432465|pir||T13677 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Santolina chamaecyparissus chloroplast gb|AAC37776.1| (L39444) NADH dehydrogenase [Santolina chamaecyparissus]	8.1
5267	9845030	gi|9845030|dbj|BAB11914.1| (AB034726) 5-oxoprolinase precursor [Alcaligenes faecalis]	6.8
5268	7429144	gi|7429144|pir||GNMSLL retrovirus-related reverse transcriptase homolog - mouse retrotransposon gb|AAA66024.1| (M13002) 2855 is the position of the first start codon in ORF 2; putative [Mus musculus]	0.0003
5269	6689319	gi|6689319|emb|CAB65444.1| (AJ238583) penicillin binding protein 2x [Streptococcus pneumoniae]	0.37
5274	7522099	gi|7522099|pir||T28658 polyketide synthase - Sorangium cellulosum (fragment)	3.9
5278	13786182	gi|13786182|ref|NP_112634.1| delta-6 fatty acid desaturase [Rattus norvegicus] pir||JG0180 Delta6 fatty acid desaturase (EC 1.14.99.-) [imported] - rat dbj|BAA75496.1| (AB021980) delta-6 fatty acid desaturase [Rattus norvegicus]	4E-12
5279	7674158	gi|7674158|sp|O76942|PTP_ENCCU MAJOR POLAR TUBE PROTEIN PRECURSOR (MAJOR PTP) emb|CAA06662.1| (AJ005666) polar tube protein [Encephalitozoon cuniculi]	1.2
5280	10726396	gi|10726396|gb|AAF54288.2| (AE003680) CG11773 gene product [Drosophila melanogaster]	1.1
5282	14767779	gi|14767779|ref|XP_007023.2| G protein-coupled receptor kinase-interactor 2 [Homo sapiens] gb|AAD28047.1|AF124491_1 (AF124491) ARF GTPase-activating protein GIT2 [Homo sapiens]	4E-13
5284	14602920	gi|14602920|gb|AAH09955.1|AAH09955 (BC009955) Unknown (protein for IMAGE:4297851) [Homo sapiens]	1.4

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
5287	7487876	gi|7487876|pir||T02741 hypothetical protein T9I4.19 - Arabidopsis thaliana gb|AAC33237.1| (AC005315) putative ligand-gated ion channel protein [Arabidopsis thaliana]	9.9
5288	14423780	gi|14423780|sp|O95013|O4F3_HUMAN OLFACTORY RECEPTOR 4F3 gb|AAD05195.1| (AC004908) similar to rat olfactory receptor OR18; similar to S29710 (PID:g423702) [Homo sapiens]	0.000002
5290	14764967	gi|14764967|ref|XP_049605.1| KIAA1467 protein [Homo sapiens]	0.00003
5291	7496712	gi|7496712|pir||T15708 hypothetical protein C30B5.1 - Caenorhabditis elegans gb|AAK31466.1| (U23450) Hypothetical protein C30B5.1 [Caenorhabditis elegans]	2.6
5292	4468835	gi|4468835|emb|CAB38221.1| (AJ232783) hairless [Drosophila hydei]	1.3
5298	7481600	gi|7481600|pir||T36589 probable transmembrane protein - Streptomyces coelicolor emb|CAB42730.1| (AL049826) putative transmembrane protein [Streptomyces coelicolor A3(2)]	5.6
5301	4885323	gi|4885323|ref|NP_005293.1| G protein-coupled receptor 37 (endothelin receptor type B-like); endothelin receptor type B-like; hET(B)R-LP [Homo sapiens] ref|XP_004804.1| G protein-coupled receptor 37 (endothelin receptor type B-like) [Homo sapiens] ref|XP_032150.1| 58490 [Homo sapiens] ref|XP_032151.1| G protein-coupled receptor 37 (endothelin receptor type B-like) [Homo sapiens] sp|O15354|GP37_HUMAN PROBABLE G PROTEIN-COUPLED RECEPTOR GPR37 PRECURSOR (ENDOTHELIN B RECEPTOR-LIKE PROTEIN-1) (ETBR-LP-1) emb|CAA73080.1| (Y12476) G protein coupled receptor 37 [Homo sapiens] gb|AAD08853.1| (AC004925) G protein coupled receptor 37 [Homo sapiens]	1.9

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
5304	11467524	gi|11467524|ref|NP_043670.1| PSI, subunit III, plastocyanin-binding [Odontella sinensis] sp|P49483|PSAF_ODOSI PHOTOSYSTEM I REACTION CENTRE SUBUNIT III (PSI-F) pir||S78329 photosystem I chain III - Odontella sinensis chloroplast emb|CAA91702.1| (Z67753) PSI, subunit III, plastocyanin-binding [Odontella sinensis]	6.2
5306	7292767	gi|7292767|gb|AAF48162.1| (AE003489) CG15927 gene product [Drosophila melanogaster]	6.3
5309	14601766	gi|14601766|ref|NP_148307.1| hypothetical protein [Aeropyrum pernix] pir||C72501 hypothetical protein APE1985 - Aeropyrum pernix (strain K1) dbj|BAA80995.1| (AP000063) 160aa long hypothetical protein [Aeropyrum pernix]	1.8
5310	13661965	gi|13661965|gb|AAK38127.1|AC058781_4 (AC058781) L344.4 [Leishmania major]	7.1
5312	6320879	gi|6320879|ref|NP_010958.1| Transcriptional activator of nitrogen-regulated genes; Gln3p [Saccharomyces cerevisiae] sp|P18494|GLN3_YEAST NITROGEN REGULATORY PROTEIN GLN3 pir||S50543 GLN3 protein - yeast (Saccharomyces cerevisiae) gb|AAB64575.1| (U18796) Gln3p: Nitrogen regulatory protein [Saccharomyces cerevisiae]	8.5
5313	4493990	gi|4493990|emb|CAB39049.1| (AL034559) hypothetical protein, PFC1045c [Plasmodium falciparum]	0.74
5314	10047245	gi|10047245|dbj|BAB13411.1| (AB046805) KIAA1585 protein [Homo sapiens]	2E-69
5317	14762995	gi|14762995|ref|XP_044123.1| cadherin 20, type 2 [Homo sapiens]	4E-17
5321	14773348	gi|14773348|ref|XP_038450.1| 20849 [Homo sapiens]	3E-45
5326	4691710	gi|4691710|gb|AAD28038.1|AF119712_1 (AF119712) bone morphogenetic protein BMP2/4 [Lytechinus variegatus]	5.4
5328	13161382	gi|13161382|dbj|BAB32977.1| (AB034197) lamin B3 [Carassius auratus]	6.9
5333	12654811	gi|12654811|gb|AAH01248.1|AAH01248 (BC001248) hypothetical protein FLJ20272 [Homo sapiens]	6.2

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
5334	4504455	gi|4504455|ref|NP_000183.1| T-box 5 [Homo sapiens] emb|CAA70592.1| (Y09445) transcription factor [Homo sapiens]	2.5
5337	6642649	gi|6642649|gb|AAF20230.1|AC012395_17 (AC012395) putative glucan synthase [Arabidopsis thaliana]	1.7
5342	7330072	gi|7330072|gb|AAF60061.1|AF210726_82 (AF210726) ORFRU4-R [Macaca mulatta rhadinovirus 26-95]	0.012
5344	90587	gi|90587|pir||PS0135 H-2 class I histocompatibility antigen T7 - mouse (fragment) emb|CAA34332.1| (X16213) MHC T7 class I antigen (64 AA) (119 is 2nd base in codon) [Mus musculus]	6.4
5345	14749813	gi|14749813|ref|XP_041197.1| integrin, alpha 11 [Homo sapiens]	0.48
5348	2143962	gi|2143962|pir||I59422 rsec8 - rat (fragment) gb|AAC52265.1| (U32498) rsec8 [Rattus norvegicus]	3E-96
5349	7549797	gi|7549797|ref|NP_035731.1| T lymphoma oncogene [Mus musculus] sp|P17408|TLM_MOUSE TLM PROTEIN (TLM ONCOGENE) pir||S10151 transforming protein tlm - mouse (strain balb/c) emb|CAA36859.1| (X52634) tlm protein [Mus musculus]	1.9
5351	7505043	gi|7505043|pir||T33641 hypothetical protein K01A2.7 - Caenorhabditis elegans gb|AAC69507.1| (AF099925) Hypothetical protein K01A2.7 [Caenorhabditis elegans]	0.71
5357	6677735	gi|6677735|ref|NP_033084.1| ral guanine nucleotide dissociation stimulator [Mus musculus] sp|Q03385|GNDS_MOUSE RAL GUANINE NUCLEOTIDE DISSOCIATION STIMULATOR (RALGEF) (RALGDS) pir||S28415 guanine nucleotide dissociation stimulator ralGDS - mouse gb|AAA37714.1| (L07924) guanine nucleotide dissociation stimulator [Mus musculus]	4
5360	11499595	gi|11499595|ref|NP_070837.1| coenzyme F390 synthetase (ftsA-3) [Archaeoglobus fulgidus] pir||D69501 coenzyme F390 synthetase (ftsA-3) homolog - Archaeoglobus fulgidus gb|AAB89243.1| (AE000964) coenzyme F390 synthetase (ftsA-3) [Archaeoglobus fulgidus]	4.8

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
5365	12383066	gi|12383066|ref|NP_073737.1| hypothetical protein DKFZp586F1122 similar to axotrophin [Homo sapiens] ref|XP_016117.2| hypothetical protein DKFZp586F1122 similar to axotrophin [Homo sapiens] dbj|BAB14340.1| (AK022973) unnamed protein product [Homo sapiens]	8E-61
5368	7500833	gi|7500833|pir||T21991 hypothetical protein F39B2.10 - Caenorhabditis elegans emb|CAB07390.1| (Z92834) contains similarity to Pfam domain: PF00226 (DnaJ domain), Score=132.3, E-value=2.8e-36, N=1; PF00684 (DnaJ central domain (4 repeats)), Score=103.9, E-value=9.9e-28, N=1; PF01556 (DnaJ C terminal region), Score=35.8, E-value=1.5e-08, N=1~cDNA>	3.2
5370	11499595	gi|11499595|ref|NP_070837.1| coenzyme F390 synthetase (ftsA-3) [Archaeoglobus fulgidus] pir||D69501 coenzyme F390 synthetase (ftsA-3) homolog - Archaeoglobus fulgidus gb|AAB89243.1| (AE000964) coenzyme F390 synthetase (ftsA-3) [Archaeoglobus fulgidus]	5.5
5371	11387290	gi|11387290|sp|P57436|Y355_BUCAI PUTATIVE DEOXYRIBONUCLEASE BU355 dbj|BAB13059.1| (AP001119) hypothetical protein [Buchnera sp. APS]	7.1
5374	8923462	gi|8923462|ref|NP_060317.1| hypothetical protein FLJ20505 [Homo sapiens] dbj|BAA91218.1| (AK000512) unnamed protein product [Homo sapiens]	5E-76
5376	7491381	gi|7491381|pir||T39498 hypothetical protein SPBC1604.16c - fission yeast (Schizosaccharomyces pombe) emb|CAA22349.1| (AL034433) hypothetical protein [Schizosaccharomyces pombe]	5.1
5378	5835229	gi|5835229|ref|NP_008273.1|ND4_10703 NADH dehydrogenase subunit 4 [Protopterus dolloi] pir||S68137 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - Protopterus dolloi mitochondrion gb|AAC38030.1| (L42813) NADH dehydrogenase subunit 4 [Protopterus dolloi]	7.9
5381	12861366	gi|12861366|dbj|BAB32182.1| (AK020701) putative [Mus musculus]	1E-20

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
5387	12957488	gi|12957488|ref|NP_075463.1| putative gene product [Homo sapiens] emb|CAB42442.1| (AL049784) hypothetical protein [Homo sapiens]	1E-23
5390	13621158	gi|13621158|ref|NP_112433.1| NADH dehydrogenase subunit 1 [Tetrodontophora bielanensis] gb|AAK30952.1|AF272824_13 (AF272824) NADH dehydrogenase subunit 1 [Tetrodontophora bielanensis]	8.5
5391	14720363	gi|14720363|ref|XP_042844.1| similar to ALU SUBFAMILY SC SEQUENCE CONTAMINATION WARNING ENTRY (H. sapiens) [Homo sapiens]	5.5
5399	14916308	gi|14916308|gb|AAK73874.1|U00067_3 (U00067) Hypothetical protein F54E7.3a [Caenorhabditis elegans]	7.6
5401	12856615	gi|12856615|dbj|BAB30727.1| (AK017396) putative [Mus musculus]	1E-91
5406	625580	gi|625580|pir||A49626 transregulatory protein IE-1 - Autographa californica nuclear polyhedrosis virus gb|AAB29676.1| (S68091) IE-1=transregulatory protein [Autographa californica nuclear polyhedrosis virus AcNPV, tsB821, Peptide Mutant, 582 aa] [Autographa californica nucleopolyhedrovirus]	2.9
5408	7511058	gi|7511058|pir||T27805 hypothetical protein ZK262.11 - Caenorhabditis elegans emb|CAB16552.1| (Z99288) contains similarity to Pfam domain: PF01604 (7TM chemoreceptor), Score=138.5, E-value=3.8e-38, N=1 [Caenorhabditis elegans]	8
5412	5869818	gi|5869818|emb|CAB55575.1| (AJ249395) NADH-ubiquinone oxidoreductase subunit 6 [Globodera pallida]	0.36
5413	7492086	gi|7492086|pir||T41670 hypothetical zinc finger protein - fission yeast (Schizosaccharomyces pombe) emb|CAA20703.1| (AL031530) hypothetical zinc finger protein; C3HC4 type (RING finger) family [Schizosaccharomyces pombe]	8.5
5416	6056374	gi|6056374|gb|AAF02838.1|AC009894_9 (AC009894) Similar to serine/threonine kinases [Arabidopsis thaliana]	9.5

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
5417	7464490	gi|7464490|pir||E64666 hypothetical protein HP1173 - Helicobacter pylori (strain 26695) gb|AAD08225.1| (AE000623) H. pylori predicted coding region HP1173 [Helicobacter pylori 26695]	4
5418	13812393	gi|13812393|ref|NP_113511.1| hypothetical protein [Guillardia theta] emb|CAC27080.1| (AJ010592) hypothetical protein [Guillardia theta]	1.9
5420	6041669	gi|6041669|ref|NP_004538.2| NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4 (15kD, B15) [Homo sapiens] ref|XP_002929.1| NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4 (15kD, B15) [Homo sapiens] ref|XP_041367.1| NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4 (15kD, B15) [Homo sapiens] sp|O95168|NB5M_HUMAN NADH-UBIQUINONE OXIDOREDUCTASE B15 SUBUNIT (COMPLEX I-B15) (CI-B15) pir||JE0383 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain NDUFB4 - human gb|AAD05421.1| (AF044957) NADH:ubiquinone oxidoreductase B15 subunit [Homo sapiens] gb|AAH00855.1|AAH00855 (BC000855) NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4 (15kD, B15) [Homo sapiens]	0.00002
5422	7296624	gi|7296624|gb|AAF51905.1| (AE003600) CG10303 gene product [Drosophila melanogaster]	4.2
5429	6453299	gi|6453299|emb|CAA04499.2| (AJ001045) P-type cation-transporting ATPase [Blastocladiella emersonii]	6.2
5430	14784393	gi|14784393|ref|XP_033306.1| sodium channel, nonvoltage-gated 1 alpha [Homo sapiens]	7.6
5438	7657956	gi|7657956|dbj|BAA94876.1| (AB028668) ORF1 [TT virus]	3.4
5449	7206840	gi|7206840|gb|AAF39999.1| (AC006832) similar to a family of C. elegans proteins; see (GB:AF016684) [Caenorhabditis elegans]	6.3
5451	13636619	gi|13636619|ref|XP_002437.3| cAMP-regulated guanine nucleotide exchange factor II [Homo sapiens]	0.000001
5454	7303178	gi|7303178|gb|AAF58242.1| (AE003814) CG17390 gene product [Drosophila melanogaster]	3.1

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
5457	7446747	gi|7446747|pir||T07607 phosphate transport protein 2 - potato emb|CAA67396.1| (X98891) inorganic phosphate transporter 2 [Solanum tuberosum]	4.2
5458	7471296	gi|7471296|pir||A75450 conserved hypothetical protein - Deinococcus radiodurans (strain R1) gb|AAF10584.1|AE001952_12 (AE001952) conserved hypothetical protein [Deinococcus radiodurans]	0.32
5460	11267150	gi|11267150|pir||A81338 H+/K+-exchanging ATPase (EC 3.6.1.36) B chain Cj0677 [imported] - Campylobacter jejuni (strain NCTC 11168) emb|CAB72951.1| (AL139076) potassium-transporting ATPase B chain [Campylobacter jejuni]	0.37
5467	1246530	gi|1246530|emb|CAA64368.1| (X94742) olfactory receptor 2 [Gallus gallus]	0.00000001
5475	1353257	gi|1353257|gb|AAB06234.1| (U26665) dimethyl sulphoxide reductase subunit B [Haemophilus influenzae]	4.2
5476	585053	gi|585053|sp|P37202|DIS3_SCHPO MITOTIC CONTROL PROTEIN DIS3 pir||A41944 mitotic control protein dis3+ - fission yeast (Schizosaccharomyces pombe) gb|AAA35302.1| (M74094) mitotic control protein [Schizosaccharomyces pombe] emb|CAA21102.1| (AL031743) mitotic control protein dis3 [Schizosaccharomyces pombe]	2.6
5477	7388318	gi|7388318|sp|Q9ZL01|THIE_HELPJ PROBABLE THIAMINE-PHOSPHATE PYROPHOSPHORYLASE (TMP PYROPHOSPHORYLASE) (TMP-PPASE) (THIAMINE-PHOSPHATE SYNTHASE) pir||G71889 thiamin-phosphate pyrophosphorylase (EC 2.5.1.3) - Helicobacter pylori (strain J99) gb|AAD06361.1| (AE001508) THIAMINE PHOSPHATE PYROPHOSPHORYLASE [Helicobacter pylori J99]	7
5483	6754362	gi|6754362|ref|NP_035962.1| insulin receptor-related receptor [Mus musculus] dbj|BAA77835.1| (AB007135) insulin receptor-related receptor [Mus musculus]	7.5

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
5486	10697032	gi|10697032|emb|CAC12661.1| (AJ296086) cytochrome c oxidase subunit 1 [Anabaena variabilis]	0.96
5491	8919908	gi|8919908|emb|CAB96228.1| (AJ133067) env polypeptide [Human immunodeficiency virus type 1]	7.4
5496	7658073	gi|7658073|dbj|BAA94924.1| (AB028715) ORF1 [TT virus]	3.8
5500	9437326	gi|9437326|gb|AAF87312.1|AF124441_1 (AF124441) NBC-like protein [Rattus norvegicus]	6.5
5501	6707844	gi|6707844|gb|AAF25692.1| (AF113517) ventral anterior homeobox 3 [Xenopus laevis]	3.1
5502	12698075	gi|12698075|dbj|BAB21856.1| (AB051552) KIAA1765 protein [Homo sapiens]	1.9
5503	7673065	gi|7673065|gb|AAF66723.1|AF146723_1 (AF146723) cytochrome b [Tapinoma sp. ACBJ.1]	4.2
5508	6754932	gi|6754932|ref|NP_035121.1| olfactory receptor 49 [Mus musculus] gb|AAD13315.1| (AF102523) olfactory receptor C6 [Mus musculus]	8E-12
5512	7296803	gi|7296803|gb|AAF52080.1| (AE003604) CG2008 gene product [Drosophila melanogaster]	3.7
5514	5824783	gi|5824783|emb|CAB54433.1| (AL110487) contains similarity to Pfam domain: PF01529 (DHHC zinc finger domain), Score=108.2, E-value=5e-29, N=1~cDNA EST yk282d12.5 comes from this gene [Caenorhabditis elegans]	4.9
5516	14750790	gi|14750790|ref|XP_034677.1| general transcription factor II, i, isoform 5 [Homo sapiens] ref|XP_011605.4| general transcription factor II, i, isoform 5 [Homo sapiens] ref|XP_034678.1| similar to general transcription factor II, i (H. sapiens) [Homo sapiens] ref|XP_034682.1| similar to general transcription factor II, i (H. sapiens) [Homo sapiens]	4.2
5519	3327362	gi|3327362|dbj|BAA31704.1| (AB015754) cytochrome c oxidase subunit I [Spirometra erinaceieuropaei]	5.2
5520	14149807	gi|14149807|ref|NP_115517.1| hypothetical protein DKFZp434K1421 [Homo sapiens] emb|CAB66740.1| (AL136806) hypothetical protein [Homo sapiens]	5E-53

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
5521	10567777	gi|10567777|gb|AAG18583.1|AF292395_1 (AF292395) KRP170 [Strongylocentrotus purpuratus]	8.2
5524	5931705	gi|5931705|emb|CAB56603.1| (Y18890) pol protein [Human endogenous retrovirus K]	6.2
5528	11271464	gi|11271464|pir||C82792 methionyl-tRNA synthetase XF0549 [imported] - Xylella fastidiosa (strain 9a5c) gb|AAF83359.1|AE003902_4 (AE003902) methionyl-tRNA synthetase [Xylella fastidiosa 9a5c]	6.5
5530	2193879	gi|2193879|emb|CAA54180.1| (X76785) hypothetical protein [Homo sapiens]	8.7
5531	7292567	gi|7292567|gb|AAF47967.1| (AE003484) CG2186 gene product [Drosophila melanogaster]	6.7
5532	729093	gi|729093|sp|P39881|CUT1_CANFA CCAAT DISPLACEMENT PROTEIN (HOMEOBOX PROTEIN CLOX) (CLOX-1) pir||S33121 homeotic protein CDP - dog (fragment) emb|CAA48782.1| (X69017) Clox [Canis sp.]	0.14
5534	13569850	gi|13569850|ref|NP_076357.1| RIKEN cDNA 9330127I20 [Mus musculus] gb|AAG34081.1| (AF295105) cardiac Ca2+ release channel [Mus musculus]	0.00000006
5535	14250321	gi|14250321|gb|AAH08590.1|AAH08590 (BC008590) hypothetical protein FLJ21313 [Homo sapiens]	1E-60
5536	2143962	gi|2143962|pir||I59422 rsec8 - rat (fragment) gb|AAC52265.1| (U32498) rsec8 [Rattus norvegicus]	3E-99
5539	13475196	gi|13475196|ref|NP_106760.1| transposase [Mesorhizobium loti] dbj|BAB52546.1| (AP003008) transposase [Mesorhizobium loti]	5.6
5544	13376066	gi|13376066|ref|NP_079019.1| hypothetical protein FLJ21934 [Homo sapiens] ref|XP_017673.2| hypothetical protein FLJ21934 [Homo sapiens] dbj|BAB15179.1| (AK025587) unnamed protein product [Homo sapiens]	1E-40
5545	13365831	gi|13365831|dbj|BAB39301.1| (AB056753) hypothetical protein [Macaca fascicularis]	4.7
5547	2865238	gi|2865238|gb|AAC38862.1| (U89706) DNA polymerase alpha [Urostyla grandis]	5.5
5548	14752983	gi|14752983|ref|XP_004626.3| hypothetical protein FLJ10377 [Homo sapiens]	2.5

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
5550	13489060	gi|13489060|ref|NP_109590.1| retinoic acid induced 1; hypothetical protein DKFZp434A139 [Homo sapiens] emb|CAC20423.1| (AJ271790) retinoid-acid induced protein 1 [Homo sapiens]	1E-21
5556	7512077	gi|7512077|pir||T30878 dynein heavy chain isotype 4 - sea urchin (Tripneustes gratilla) (fragment) gb|AAA63587.1| (U03973) dynein heavy chain isotype 4 [Tripneustes gratilla]	4E-27
5564	9971630	gi|9971630|dbj|BAB12582.1| (AB046525) polymerase protein [Hepatitis B virus]	9.1
5565	1072920	gi|1072920|pir||S49369 mobilization protein - Campylobacter coli plasmid pCCT1 and PCCT2 emb|CAA57597.1| (X82080) Mob [Campylobacter coli] emb|CAA57594.1| (X82079) mobilization protein [Campylobacter coli]	4.7
5568	12644030	gi|12644030|sp|Q28295|VWF_CANFA VON WILLEBRAND FACTOR PRECURSOR (VWF)	8.8
5572	9964333	gi|9964333|ref|NP_064801.1| AMV019 [Amsacta moorei entomopoxvirus] gb|AAG02725.1|AF250284_19 (AF250284) AMV019 [Amsacta moorei entomopoxvirus]	8.3
5579	10436768	gi|10436768|dbj|BAB14906.1| (AK024391) unnamed protein product [Homo sapiens]	1.2
5580	13786443	gi|13786443|gb|AAK39568.1|AC025296_3 (AC025296) hypothetical protein [Oryza sativa]	0.75
5581	13376632	gi|13376632|ref|NP_079355.1| hypothetical protein FLJ23231 [Homo sapiens] dbj|BAB15581.1| (AK026884) unnamed protein product [Homo sapiens] gb|AAH05001.1|AAH05001 (BC005001) hypothetical protein FLJ23231 [Homo sapiens]	0.58
5584	12641960	gi|12641960|gb|AAK00073.1|AF200382_1 (AF200382) cytochrome oxidase subunit I (COI) [Ceratosolen nanus]	4.9
5585	1708893	gi|1708893|sp|P51782|LYC_TRIVU LYSOZYME C PRECURSOR (1,4-BETA-N-ACETYLMURAMIDASE C) gb|AAB97109.1| (U40664) lysozyme [Trichosurus vulpecula]	2.3
5586	10047155	gi|10047155|dbj|BAB13371.1| (AB046765) KIAA1545 protein [Homo sapiens]	1.7

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
5587	7446806	gi|7446806|pir||F69791 conserved hypothetical protein yebB - Bacillus subtilis gb|AAB62312.1| (U51115) unknown protein [Bacillus subtilis] emb|CAB12456.1| (Z99107) similar to hypothetical proteins [Bacillus subtilis]	9.3
5591	400222	gi|400222|sp|P22533|MANB_CALSA BETA-MANNANASE/ENDOGLUCANASE A PRECURSOR [INCLUDES: MANNAN ENDO-1,4-BETA-MANNOSIDASE A (BETA-MANNANASE) (ENDO-1,4-MANNANASE); ENDO-1,4-BETA-GLUCANASE (CELLULASE)] pir||A48954 mannan endo-1,4-beta-mannosidase (EC 3.2.1.78) - Caldocellum saccharolyticum gb|AAA71887.1| (L01257) beta-mannanase [Caldicellulosiruptor saccharolyticus]	8.6
5593	14029388	gi|14029388|gb|AAK52669.1|AF319948_1 (AF319948) MMS19 [Drosophila melanogaster]	7.7
5595	1196482	gi|1196482|gb|AAA88209.1| (M20307) unknown protein [Plasmid P1]	5.2
5599	14762995	gi|14762995|ref|XP_044123.1| cadherin 20, type 2 [Homo sapiens]	4E-17
5600	13383732	gi|13383732|gb|AAK21107.1|AF327877_3 (AF327877) envelope polyprotein [Equine infectious anemia virus]	3.7
5611	7521539	gi|7521539|pir||A70410 processing proteinase (EC 3.4.-.-) - Aquifex aeolicus gb|AAC07272.1| (AE000732) processing protease [Aquifex aeolicus]	9.5
5612	14721452	gi|14721452|ref|XP_049513.1| 48294 [Homo sapiens]	1
5615	13512594	gi|13512594|gb|AAK28688.1| (AF078553) unknown function U3 [Ehrlichia canis]	9.1
5618	7490184	gi|7490184|pir||T37997 carboxypeptidase y - fission yeast (Schizosaccharomyces pombe) pir||T43236 carboxypeptidase C (EC 3.4.16.5) precursor [validated] fission yeast (Schizosaccharomyces pombe) emb|CAB10121.1| (Z97209) carboxypeptidase y [Schizosaccharomyces pombe] dbj|BAA25568.1| (D86560) carboxypeptidase Y [Schizosaccharomyces pombe]	0.01
5619	11119139	gi|11119139|gb|AAG30518.1| (AF308549) immunoglobulin heavy chain [Homo sapiens]	1.1

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
5622	7507209	gi|7507209|pir||T29623 hypothetical protein T05E8.3 - Caenorhabditis elegans gb|AAB52427.1| (U97014) strong similarity to the 'DEAH' subfamily of the 'DEAD' box family of helicases [Caenorhabditis elegans]	0.7
5623	7484413	gi|7484413|pir||T08026 hypothetical protein B - Chlamydomonas reinhardtii chloroplast gb|AAB05800.1| (U62943) unknown [Chlamydomonas reinhardtii]	9.3
5624	14766128	gi|14766128|ref|XP_038109.1| KIAA1683 protein [Homo sapiens] emb|CAB66801.1| (AL136867) hypothetical protein [Homo sapiens]	0.15
5629	6491915	gi|6491915|gb|AAF14073.1|AF104231_1 (AF104231) paired-homeodomain transcription factor PAX4 [Mus musculus]	2.8
5630	14149940	gi|14149940|ref|NP_115610.1| hypothetical protein FLJ23059 [Homo sapiens] dbj|BAB15536.1| (AK026712) unnamed protein product [Homo sapiens]	1E-10
5636	7500466	gi|7500466|pir||T21747 hypothetical protein F35C12.2 - Caenorhabditis elegans	3.7
5638	7490377	gi|7490377|pir||T41496 conserved hypothetical protein SPCC622.16c - fission yeast (Schizosaccharomyces pombe) emb|CAA21872.1| (AL033127) conserved hypothetical protein [Schizosaccharomyces pombe]	6.3
5642	6322907	gi|6322907|ref|NP_012980.1| heavy chain of cytoplasmic dynein; Dyn1p [Saccharomyces cerevisiae] sp|P36022|DYHC_YEAST DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) pir||S38128 dynein heavy chain, cytosolic - yeast (Saccharomyces cerevisiae) emb|CAA82132.1| (Z28279) ORF YKR054c [Saccharomyces cerevisiae]	4
5646	7594617	gi|7594617|emb|CAB88111.1| (AL078581) dJ12G14.1 (novel cyclophilin type peptidyl-prolyl cis-trans isomerase) [Homo sapiens]	8E-73
5647	14916439	gi|14916439|ref|NP_149094.1| rhophilin-like protein [Homo sapiens] gb|AAK58588.1|AF268032_1 (AF268032) rhophilin-like protein [Homo sapiens]	2E-14

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
5648	7227910	gi|7227910|sp|O77408|OAR1_LYMST OCTOPAMINE RECEPTOR 1 (OA1) gb|AAC61296.1| (U62771) octopamine receptor type 1 [Lymnaea stagnalis]	5.5
5649	13161815	gi|13161815|emb|CAC32956.1| (AJ293063) cytochrome oxidase I [Aleochara punctatella]	7.9
5651	13631750	gi|13631750|ref|XP_010294.3| arylsulfatase E precursor [Homo sapiens]	2E-12
5653	9181886	gi|9181886|gb|AAF85678.1|AF266288_4 (AF266288) C protein [Measles virus]	3.3
5654	14755042	gi|14755042|ref|XP_045122.1| KIAA1451 protein [Homo sapiens]	0.000000005
5655	9408429	gi|9408429|gb|AAF87294.1| (AF228467) unknown [Letharia vulpina]	2.4
5656	14530763	gi|14530763|emb|CAC42469.1| (AL137139) bA134O15.1 (similar to citrate lyase) [Homo sapiens]	2E-11
5661	2496882	gi|2496882|sp|Q11187|YPD8_CAEEL HYPOTHETICAL 99.0 KD PROTEIN C05D11.8 IN CHROMOSOME III gb|AAB53828.1| (U00048) C05D11.8 gene product [Caenorhabditis elegans]	4.9
5663	1276867	gi|1276867|gb|AAA97866.1| (U40233) alkane hydroxylase [Stenotrophomonas maltophilia]	8.2
5664	4867907	gi|4867907|dbj|BAA77721.1| (AB008177) hepatic nuclear factor 1-beta short form [Mus musculus]	3.8
5667	7292501	gi|7292501|gb|AAF47904.1| (AE003481) CG11345 gene product [Drosophila melanogaster]	3.9
5673	1346543	gi|1346543|sp|P49285|ML1A_CHICK MELATONIN RECEPTOR TYPE 1A (MEL-1A-R) (CKA) gb|AAA92498.1| (U31820) Mel-1a melatonin receptor [Gallus gallus]	7
5675	14731714	gi|14731714|ref|XP_028009.1| KIAA1563 protein [Homo sapiens]	4E-26
5676	9628467	gi|9628467|ref|NP_043350.1| putative [Human papillomavirus type 21] gb|AAA79398.1| (U31779) putative [Human papillomavirus type 21]	1.2
5680	13241978	gi|13241978|gb|AAK16497.1|AF329199_1 (AF329199) CocoaCrisp [Gallus gallus]	1.9
5681	11466217	gi|11466217|ref|NP_066540.1| SecY-independent transporter protein [Naegleria gruberi] gb|AAG17818.1|AF288092_43 (AF288092) SecY-independent transporter protein [Naegleria gruberi]	4.2

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
5682	10581459	gi|10581459|gb|AAG20194.1| (AE005096) enoyl-CoA hydratase; Fadl [Halobacterium sp. NRC-1]	5
5684	4903124	gi|4903124|dbj|BAA78009.1| (AB027308) nucleotide-binding protein [Plasmid R64]	3.1
5685	13242251	gi|13242251|ref|NP_077336.1| hairy and enhancer of split 1, (Drosophila) [Rattus norvegicus] sp|Q04666|HES1_RAT TRANSCRIPTION FACTOR HES-1 (HAIRY AND ENHANCER OF SPLIT 1) (HAIRY-LIKE) (RHL) pir||S36748 transcription factor HES-1 - rat dbj|BAA02682.1| (D13417) HES-1 factor [Rattus norvegicus] prf||1905315A HES-1 protein [Rattus norvegicus]	9.4
5689	9957880	gi|9957880|gb|AAG03352.1| (AY005440) 51-kDa antigen [Ehrlichia risticii]	6.9
5691	7509017	gi|7509017|pir||T33819 hypothetical protein W05F2.7 - Caenorhabditis elegans gb|AAC78217.1| (AF106582) Hypothetical protein W05F2.7 [Caenorhabditis elegans]	0.82
5692	1082343	gi|1082343|pir||S50832 atrophin-1 - human	0.05
5696	11595629	gi|11595629|emb|CAC18249.1| (AL451018) conserved hypothetical protein [Neurospora crassa]	3.6
5698	11465898	gi|11465898|ref|NP_066447.1| ATP synthase F0 subunit 6 [Ochromonas danica] gb|AAG18413.1|AF287134_38 (AF287134) ATP synthase F0 subunit 6 [Ochromonas danica]	6.6
5699	13384736	gi|13384736|ref|NP_084514.1| dynein, cytoplasmic, heavy chain 1; dynein heavy chain, retrograde transport [Mus musculus] sp|Q9JHU4|DYHC_MOUSE DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) (CYTOPLASMIC DYNEIN HEAVY CHAIN) gb|AAF91078.1| (AY004877) cytoplasmic dynein heavy chain [Mus musculus]	3E-12
5701	11431299	gi|11431299|ref|XP_007961.1| phosphorylase kinase, beta [Homo sapiens]	8.8
5704	7486830	gi|7486830|pir||T04917 hypothetical protein T10I14.190 - Arabidopsis thaliana emb|CAA16786.1| (AL021712) putative protein [Arabidopsis thaliana] emb|CAB79191.1| (AL161557) putative protein [Arabidopsis thaliana]	0.4

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
5707	7470729	gi|7470729|pir||S75327 lysostaphin - Synechocystis sp. (strain PCC 6803) dbj|BAA17241.1| (D90904) lysostaphin [Synechocystis sp. PCC 6803]	8.8
5708	7330072	gi|7330072|gb|AAF60061.1|AF210726_82 (AF210726) ORFRU4-R [Macaca mulatta rhadinovirus 26-95]	0.24
5711	14774911	gi|14774911|ref|XP_027365.1| ADP-ribosylation factor-like 6 interacting protein [Homo sapiens]	1E-11
5712	14721018	gi|14721018|ref|XP_051562.1| similar to agrin (H. sapiens) [Homo sapiens]	0.14
5716	6324014	gi|6324014|ref|NP_014084.1| F1FO ATPase assembly protein; Atp11p [Saccharomyces cerevisiae] sp|P32453|ATPS_YEAST ATP11 PROTEIN PRECURSOR pir||S51297 ATP11 protein - yeast (Saccharomyces cerevisiae) gb|AAA34447.1| (M87006) ATP11 protein [Saccharomyces cerevisiae] emb|CAA86381.1| (Z46259) ATP11 [Saccharomyces cerevisiae] emb|CAA96245.1| (Z71591) ORF YNL315c [Saccharomyces cerevisiae]	4.1
5718	12861848	gi|12861848|dbj|BAB32292.1| (AK021073) putative [Mus musculus]	0.07
5719	14744130	gi|14744130|ref|XP_045895.1| 57406 [Homo sapiens]	1.4
5722	11612206	gi|11612206|gb|AAG37299.1| (AY009937) unknown [Sinorhizobium fredii]	7.4
5723	4494967	gi|4494967|gb|AAD21389.1| (AF083501) R11 [Macaca mulatta rhadinovirus 17577] gb|AAF60041.1|AF210726_62 (AF210726) vIRF [Macaca mulatta rhadinovirus 26-95]	3.3
5727	12644379	gi|12644379|sp|Q02099|RAD3_SCHPO DNA REPAIR PROTEIN RAD3 pir||T39911 rad3 checkpoint protein - fission yeast (Schizosaccharomyces pombe) emb|CAB40165.1| (AL049558) rad3 checkpoint protein [Schizosaccharomyces pombe]	9.3
5732	7492633	gi|7492633|pir||T40241 probable guanine nucleotide exchange factor - fission yeast (Schizosaccharomyces pombe) emb|CAB58155.1| (AL121815) putative guanine nucleotide exchange factor [Schizosaccharomyces pombe]	8.2
5737	10047255	gi|10047255|dbj|BAB13416.1| (AB046810) KIAA1590 protein [Homo sapiens]	0.00000002

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
5742	2498204	gi|2498204|sp|Q05682|CALD_HUMAN CALDESMON (CDM) pir||JH0628 caldesmon - human gb|AAA58419.1| (M83216) caldesmon [Homo sapiens]	8E-23
5744	11037059	gi|11037059|ref|NP_036540.1| protein kinase C binding protein 1 [Homo sapiens] gb|AAF71262.1| (AF233453) RACK-like protein PRKCBP1 [Homo sapiens]	0.00000001
5746	14575679	gi|14575679|gb|AAK68690.1|AF156100_1 (AF156100) hemicentin [Homo sapiens]	1.9
5748	11466210	gi|11466210|ref|NP_066533.1| NADH dehydrogenase subunit 2 [Naegleria gruberi] gb|AAG17811.1|AF288092_36 (AF288092) NADH dehydrogenase subunit 2 [Naegleria gruberi]	8.2
5750	8096340	gi|8096340|dbj|BAA95898.1| (AB036737) RERE [Homo sapiens]	0.5
5751	14275752	gi|14275752|emb|CAC40032.1| (AJ310844) P-type ATPase [Hordeum vulgare]	0.53
5752	5834582	gi|5834582|emb|CAB55313.1| (AJ132948) rfg7 protein [Homo sapiens]	1.7
5754	13877921	gi|13877921|gb|AAK44038.1|AF370223_1 (AF370223) unknown protein [Arabidopsis thaliana]	4
5755	5869818	gi|5869818|emb|CAB55575.1| (AJ249395) NADH-ubiquinone oxidoreductase subunit 6 [Globodera pallida]	4.2
5756	7023033	gi|7023033|dbj|BAA91809.1| (AK001649) unnamed protein product [Homo sapiens]	e-102
5757	14729667	gi|14729667|ref|XP_029101.1| KIAA0947 protein [Homo sapiens]	0.22
5758	14726213	gi|14726213|ref|XP_010556.3| PR domain containing 16 [Homo sapiens]	0.87

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
5761	4757900	gi|4757900|ref|NP_004334.1| calreticulin precursor; Sicca syndrome antigen A (autoantigen Ro; calreticulin); autoantigen Ro [Homo sapiens] ref|XP_032020.1| calreticulin precursor [Homo sapiens] ref|XP_032023.1| calreticulin precursor [Homo sapiens] ref|XP_032022.1| calreticulin precursor [Homo sapiens] ref|XP_009055.3| calreticulin precursor [Homo sapiens] ref|XP_032021.1| calreticulin precursor [Homo sapiens] sp|P27797|CRTC_HUMAN CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60) (52 KDA RIBONUCLEOPROTEIN AUTOANTIGEN RO/SS-A) pir||A37047 calreticulin precursor - human gb|AAA51916.1| (M84739) calreticulin [Homo sapiens] gb|AAA36582.1| (M32294) Ro ribonucleoprotein autoantigen (Ro/SS-A) precursor [Homo sapiens] gb|AAB51176.1| (AD000092) calreticulin [Homo sapiens] gb|AAH02500.1|AAH02500 (BC002500) calreticulin [Homo sapiens] gb|AAH07911.1|AAH07911 (BC007911) calreticulin [Homo sapiens]	5E-16
5762	14714688	gi|14714688|gb|AAH10485.1|AAH10485 (BC010485) Unknown (protein for MGC:7224) [Mus musculus]	1.1
5765	14751380	gi|14751380|ref|XP_041291.1| cAMP response element-binding protein CRE-BPa [Homo sapiens]	5E-14
5767	2105193	gi|2105193|gb|AAB57925.1| (U86889) hypothetical protein [Molluscum contagiosum virus subtype 1]	7.8
5771	13278418	gi|13278418|gb|AAH04019.1|AAH04019 (BC004019) Similar to mesoderm specific transcript [Mus musculus]	0.94
5772	14720481	gi|14720481|ref|XP_048811.1| hypothetical protein FLJ22116 [Homo sapiens] ref|XP_048810.1| hypothetical protein FLJ22116 [Homo sapiens]	2E-23

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
5773	6321548	gi|6321548|ref|NP_011625.1| Ygr110wp [Saccharomyces cerevisiae] sp|P53264|YG2V_YEAST HYPOTHETICAL 52.0 KD PROTEIN IN CLB6-SHY1 INTERGENIC REGION pir||S64418 hypothetical protein YGR110w - yeast (Saccharomyces cerevisiae) emb|CAA97118.1| (Z72895) ORF YGR110w [Saccharomyces cerevisiae]	2.4
5776	12853842	gi|12853842|dbj|BAB29864.1| (AK015480) putative [Mus musculus]	5.6
5778	13384736	gi|13384736|ref|NP_084514.1| dynein, cytoplasmic, heavy chain 1; dynein heavy chain, retrograde transport [Mus musculus] sp|Q9JHU4|DYHC_MOUSE DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) (CYTOPLASMIC DYNEIN HEAVY CHAIN) gb|AAF91078.1| (AY004877) cytoplasmic dynein heavy chain [Mus musculus]	2E-92
5781	7498705	gi|7498705|pir||T20640 hypothetical protein F09C3.3 - Caenorhabditis elegans	9.7
5782	11356402	gi|11356402|pir||T44074 hypothetical protein [imported] - Staphylococcus aureus (fragment)	5.5
5783	10726396	gi|10726396|gb|AAF54288.2| (AE003680) CG11773 gene product [Drosophila melanogaster]	4.1
5784	11935116	gi|11935116|gb|AAG41977.1|AF311942_1 (AF311942) ethylene receptor [Carica papaya]	7.5
5787	4456467	gi|4456467|emb|CAB37294.1| (AJ011001) TM7XN1 protein [Homo sapiens]	3.8
5788	13676779	gi|13676779|gb|AAK38272.1|AF330197_1 (AF330197) Arkadia [Mus musculus]	2.2
5789	13676779	gi|13676779|gb|AAK38272.1|AF330197_1 (AF330197) Arkadia [Mus musculus]	2.3
5795	11024704	gi|11024704|ref|NP_061956.1| hypothetical protein FLJ11219 [Homo sapiens] dbj|BAA92074.1| (AK002081) unnamed protein product [Homo sapiens]	8E-23
5797	13606086	gi|13606086|gb|AAK32948.1| (U41014) Hypothetical protein C06G1.1 [Caenorhabditis elegans]	8.3
5798	10728595	gi|10728595|gb|AAF52302.2| (AE003611) CG9011 gene product [Drosophila melanogaster]	8E-21
5799	12847975	gi|12847975|dbj|BAB27780.1| (AK011690) putative [Mus musculus]	3E-44

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
5801	7243247	gi|7243247|dbj|BAA92671.1| (AB037854) KIAA1433 protein [Homo sapiens]	3E-84
5803	10728595	gi|10728595|gb|AAF52302.2| (AE003611) CG9011 gene product [Drosophila melanogaster]	8E-21
5804	1354082	gi|1354082|gb|AAB37237.1| (U47033) polyprotein [bean yellow mosaic virus]	6.8
5808	11354734	gi|11354734|pir||C82043 conserved hypothetical protein VC2703 [imported] - Vibrio cholerae (group O1 strain N16961) gb|AAF95843.1| (AE004336) conserved hypothetical protein [Vibrio cholerae]	4.9
5809	13272353	gi|13272353|gb|AAK17116.1|AF291051_13 (AF291051) transketolase [Candidatus Carsonella ruddii]	8.9
5810	10728595	gi|10728595|gb|AAF52302.2| (AE003611) CG9011 gene product [Drosophila melanogaster]	9E-21
5818	7340927	gi|7340927|dbj|BAA92999.1| (AP001550) Similar to Schizosaccharomyces pombe chromosome I cosmid c1D4; hypothetical protein &SPAC1D4_10 (Q10155) [Oryza sativa]	5.6
5821	4115911	gi|4115911|gb|AAD03423.1| (U78517) cAMP-regulated guanine nucleotide exchange factor II [Rattus norvegicus]	3E-11
5822	7498336	gi|7498336|pir||T15086 hypothetical protein E03D2.4 - Caenorhabditis elegans gb|AAB94164.1| (AF039036) Hypothetical protein E03D2.4 [Caenorhabditis elegans]	7.1
5825	7492270	gi|7492270|pir||T40528 palmitoyl-protein thioesterase precursor - fission yeast (Schizosaccharomyces pombe) emb|CAA19178.1| (AL023634) palmitoyl-protein thioesterase precursor [Schizosaccharomyces pombe]	1.2
5827	7497138	gi|7497138|pir||T30158 hypothetical protein C37A2.6 - Caenorhabditis elegans gb|AAB52451.1| (U97194) Hypothetical protein C37A2.6 [Caenorhabditis elegans]	5.4
5830	7469981	gi|7469981|pir||S74598 hypothetical protein sll1040 - Synechocystis sp. (strain PCC 6803) dbj|BAA16750.1| (D90900) ORF_ID:sll1040~unknown protein [Synechocystis sp. PCC 6803]	9.4

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
5831	10177727	gi|10177727|dbj|BAB10973.1| (AB015471) gene_id:K9B18.6~unknown protein [Arabidopsis thaliana]	2.6
5834	2231323	gi|2231323|gb|AAB61999.1| (U77045) bactinecin 6 [Ovis aries]	6.9
5838	7495511	gi|7495511|pir||T18990 hypothetical protein C06B8.4 - Caenorhabditis elegans emb|CAB03847.1| (Z81463) predicted using Genefinder~Similarity to C.elegans olfactory receptor ODR-10 (TR:Q17376), contains similarity to Pfam domain: PF01461 (7TM chemoreceptor), Score=-92.4, E-value=4.9e-10, N=1 [Caenorhabditis elegans]	0.84
5839	14722156	gi|14722156|ref|XP_001418.4| centromere protein F (350/400kD) [Homo sapiens]	2
5841	14590902	gi|14590902|ref|NP_142975.1| hypothetical protein [Pyrococcus horikoshii] pir||E71100 hypothetical protein PH1064 - Pyrococcus horikoshii dbj|BAA30163.1| (AP000004) 718aa long hypothetical protein [Pyrococcus horikoshii]	3.5
5844	10173304	gi|10173304|dbj|BAB04409.1| (AP001509) transposase (04) [Bacillus halodurans]	2.2
5845	7510388	gi|7510388|pir||T27298 hypothetical protein Y68A4A.7 - Caenorhabditis elegans emb|CAA16418.1| (AL021503) predicted using Genefinder~contains similarity to Pfam domain: PF01604 (7TM chemoreceptor), Score=-48.3, E-value=7.1e-07, N=1 [Caenorhabditis elegans]	2.9
5851	13812127	gi|13812127|ref|NP_113254.1| hypothetical protein [Guillardia theta] gb|AAK39814.1|AF165818_22 (AF165818) hypothetical protein [Guillardia theta]	0.92
5852	6016842	gi|6016842|dbj|BAA85182.1| (AB033168) nuclear protein ZAP [Mus musculus]	3.3
5854	8922744	gi|8922744|ref|NP_060730.1| hypothetical protein FLJ10891 [Homo sapiens] dbj|BAA91884.1| (AK001753) unnamed protein product [Homo sapiens]	8E-69

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
5856	118965	gi|118965|sp|P23098|DYHC_TRIGR DYNEIN BETA CHAIN, CILIARY pir||S17653 dynein beta heavy chain, ciliary - sea urchin (Tripneustes gratilla) emb|CAA42170.1| (X59603) Beta heavy chain of outer-arm axonemal dynein ATPase [Tripneustes gratilla] prf||1714372A dynein:SUBUNIT=beta heavy chain [Tripneustes gratilla]	0.0000001
5858	10640323	gi|10640323|emb|CAC12137.1| (AL445066) conserved hypothetical membrane protein [Thermoplasma acidophilum]	1.3
5859	9964574	gi|9964574|ref|NP_065042.1| AMV260 [Amsacta moorei entomopoxvirus] gb|AAG02966.1|AF250284_260 (AF250284) AMV260 [Amsacta moorei entomopoxvirus]	4
5861	5360226	gi|5360226|dbj|BAA36472.1| (AB015177) F0-ATPase subunit 6 [Beta vulgaris]	3
5868	7327641	gi|7327641|gb|AAF45040.2| (AF146609) putative modification methyltransferase [Aeromonas hydrophila]	2.8
5871	5031969	gi|5031969|ref|NP_005758.1| purinergic receptor (family A group 5) [Homo sapiens] sp|P43657|P2Y5_HUMAN P2Y PURINOCEPTOR 5 (P2Y5) (PURINERGIC RECEPTOR 5) (RB INTRON ENCODED G-PROTEIN COUPLED RECEPTOR) pir||T09508 intron 17 purinergic receptor P2Y5 - human gb|AAB62190.1| (AF000546) purinergic receptor P2Y5 [Homo sapiens]	3.2
5872	92972	gi|92972|pir||S04757 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - rat mitochondrion	9.8
5876	13540669	gi|13540669|ref|NP_110480.1| linker for activation of T cells [Rattus norvegicus] sp|O70601|LAT_RAT LINKER FOR ACTIVATION OF T CELLS (36 KDA PHOSPHO-TYROSINE ADAPTOR PROTEIN) (PP36) (P36-38) emb|CAA04577.1| (AJ001184) 36 kDa phospho-tyrosine [Rattus norvegicus]	0.4

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
5877	7510482	gi|7510482|pir||T27406 hypothetical protein Y75B8A.24 - Caenorhabditis elegans emb|CAA22108.1| (AL033514) contains similarity to Pfam domain: PF00454 (Phosphatidylinositol 3- and 4-kinases), Score=392.3, E-value=1.6e-114, N=2; PF00613 (Phosphoinositide 3-kinase family, accessory domain (PIK domain)), Score=76.1, E-value=2.4e-19, N=1~cDNA EST yk2>	0.32
5881	11284162	gi|11284162|pir||H81077 hypothetical protein NMB1490 [imported] - Neisseria meningitidis (group B strain MD58) gb|AAF41846.1| (AE002498) hypothetical protein [Neisseria meningitidis MC58]	4.2
5882	4503801	gi|4503801|ref|NP_003893.1| far upstream element-binding protein; far upstream element binding protein; FUSE-binding protein [Homo sapiens] pir||A53184 myc far upstream element-binding protein - human gb|AAA17976.1| (U05040) FUSE binding protein [Homo sapiens]	0.4
5883	9929953	gi|9929953|dbj|BAB12133.1| (AB047609) hypothetical protein [Macaca fascicularis]	9.7
5884	13631383	gi|13631383|ref|XP_010272.2| retinoblastoma-binding protein 7 [Homo sapiens] ref|XP_045112.1| retinoblastoma-binding protein 7 [Homo sapiens]	7.3
5886	7662084	gi|7662084|ref|NP_055474.1| KIAA0377 gene product [Homo sapiens] dbj|BAA20831.1| (AB002375) KIAA0377 [Homo sapiens]	2E-44
5888	4507023	gi|4507023|ref|NP_003031.1| solute carrier family 4, anion exchanger, member 2 (erythrocyte membrane protein band 3-like 1) [Homo sapiens] sp|P04920|B3A2_HUMAN ANION EXCHANGE PROTEIN 2 (NON-ERYTHROID BAND 3-LIKE PROTEIN) (BND3L) pir||S21086 anion exchange protein 2 - human emb|CAA44067.1| (X62137) anion exchange protein 2 (AE2) [Homo sapiens]	9.1

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
5892	6321764	gi|6321764|ref|NP_011840.1| Yhl023cp [Saccharomyces cerevisiae] sp|P38742|YHC3_YEAST HYPOTHETICAL 130.0 KD PROTEIN IN SNF6-SPO11 INTERGENIC REGION pir||S46837 hypothetical protein YHL023c - yeast (Saccharomyces cerevisiae) gb|AAB65076.1| (U11582) No definition line found [Saccharomyces cerevisiae]	7.4
5894	7507827	gi|7507827|pir||T16876 hypothetical protein T14E8.3 - Caenorhabditis elegans gb|AAA82386.1| (U41036) Hypothetical protein T14E8.3 [Caenorhabditis elegans]	2.4
5896	119714	gi|119714|sp|P13983|EXTN_TOBAC EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) pir||S06733 hydroxyproline-rich glycoprotein precursor - common tobacco emb|CAA32090.1| (X13885) extensin (AA 1-620) [Nicotiana tabacum]	2.4
5897	13540669	gi|13540669|ref|NP_110480.1| linker for activation of T cells [Rattus norvegicus] sp|O70601|LAT_RAT LINKER FOR ACTIVATION OF T CELLS (36 KDA PHOSPHO-TYROSINE ADAPTOR PROTEIN) (PP36) (P36-38) emb|CAA04577.1| (AJ001184) 36 kDa phospho-tyrosine [Rattus norvegicus]	0.4
5898	14787176	gi|14787176|gb|AAG54083.1| (AY017475) CSMD1 [Mus musculus]	0.5
5899	14192869	gi|14192869|gb|AAK55774.1|AC079038_8 (AC079038) Putative polyprotein [Oryza sativa]	1.9
5900	11260604	gi|11260604|pir||G82485 acetate kinase VCA0235 [imported] - Vibrio cholerae (group O1 strain N16961) gb|AAF96146.1| (AE004363) acetate kinase [Vibrio cholerae]	5.4
5914	5688864	gi|5688864|dbj|BAA82706.1| (AB030586) amino acid transporter-like protein 1 [Arabidopsis thaliana]	0.74
5915	14571551	gi|14571551|gb|AAK64511.1| (AY036902) degenerative spermatocyte-like protein RDES [Rattus norvegicus]	7.1
5917	11496539	gi|11496539|ref|NP_044549.1| ribosomal protein S3 [Toxoplasma gondii] gb|AAD41136.1|U87145_5 (U87145) ribosomal protein S3 [Toxoplasma gondii]	2.4

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
5919	12275264	gi|12275264|emb|CAC22282.1| (AJ303456) WASP interacting protein [Rattus norvegicus]	0.29
5920	7158837	gi|7158837|gb|AAF37557.1|AF214067_1 (AF214067) serine-repeat antigen protein [Plasmodium falciparum]	3.8
5922	7327641	gi|7327641|gb|AAF45040.2| (AF146609) putative modification methyltransferase [Aeromonas hydrophila]	3.2
5934	4321845	gi|4321845|gb|AAD15841.1| (AF064782) unknown [Mus musculus]	4E-59
5938	6562754	gi|6562754|emb|CAB62893.1| (AL035475) hypothetical protein, MAL4P2.52 [Plasmodium falciparum]	0.69
5939	13814462	gi|13814462|gb|AAK41504.1| (AE006741) ABC transporter, ATP binding protein [Sulfolobus solfataricus]	2.3
5941	5802786	gi|5802786|gb|AAD51779.1| (AF124511) BVES [Gallus gallus]	1.7
5943	5596342	gi|5596342|dbj|BAA82602.1| (AB026825) sALK-2 [Ephydatia fluviatilis]	7.2
5946	9802527	gi|9802527|gb|AAF99729.1|AC004557_8 (AC004557) F17L21.9 [Arabidopsis thaliana]	6.8
5949	3820854	gi|3820854|emb|CAA10852.1| (AJ222582) maturase-like protein [Euglena granulata]	4.2
5951	7476228	gi|7476228|pir||A70905 hypothetical protein Rv0174 - Mycobacterium tuberculosis (strain H37RV) emb|CAB09741.1| (Z97050) hypothetical protein Rv0174 [Mycobacterium tuberculosis]	0.46
5953	7159336	gi|7159336|gb|AAF37725.1|AF238235_1 (AF238235) diaphanous protein [Entamoeba histolytica]	0.24
5954	7294100	gi|7294100|gb|AAF49454.1| (AE003527) CG12243 gene product [Drosophila melanogaster]	4.6
5956	2689578	gi|2689578|gb|AAB91357.1| (U96421) cytochrome b [Dennyus carljonesi fosteri]	9.4
5957	11071788	gi|11071788|emb|CAC14632.1| (AL449144) hypothetical protein P214.26 [Leishmania major]	5.7

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
5958	9631305	gi|9631305|ref|NP_048116.1| ORF MSV045 hypothetical protein [Melanoplus sanguinipes entomopoxvirus] pir||T28206 hypothetical protein ORF45 - Melanoplus sanguinipes entomopoxvirus gb|AAC97618.1| (AF063866) ORF MSV045 hypothetical protein [Melanoplus sanguinipes entomopoxvirus]	3
5959	14750752	gi|14750752|ref|XP_031441.1| phosphodiesterase 8A [Homo sapiens]	0.47
5962	4996347	gi|4996347|dbj|BAA78416.1| (AB021177) complement B/C2-A2 [Cyprinus carpio]	1.7
5964	7510076	gi|7510076|pir||T31613 hypothetical protein Y50E8A.i - Caenorhabditis elegans	7.1
5965	6958206	gi|6958206|gb|AAF32493.1|AF093132_1 (AF093132) kexin-like protease KEX1 [Pneumocystis carinii f. sp. muris]	4.5
5966	13542701	gi|13542701|gb|AAH05557.1|AAH05557 (BC005557) Unknown (protein for MGC:7062) [Mus musculus]	0.00003
5967	12852967	gi|12852967|dbj|BAB29595.1| (AK014872) putative [Mus musculus]	3.2
5969	6449214	gi|6449214|gb|AAF08856.1|AF194824_1 (AF194824) NADH dehydrogenase [Aptenia cordifolia]	0.84
5971	7492532	gi|7492532|pir||T39653 probable DNA repair and recombination protein - fission yeast (Schizosaccharomyces pombe) emb|CAA21300.1| (AL031856) putative DNA repair and recombination protein [Schizosaccharomyces pombe]	8.4
5972	1171089	gi|1171089|sp|P10243|MYBA_HUMAN MYB-RELATED PROTEIN A (A-MYB) pir||S03423 transforming protein A-myb - human	2E-28
5973	4589488	gi|4589488|dbj|BAA76772.1| (AB023145) KIAA0928 protein [Homo sapiens]	9.8
5974	6686326	gi|6686326|sp|P77589|MHPT_ECOLI PUTATIVE 3-HYDROXYPHENYLPROPIONIC ACID TRANSPORTER	1.8
5976	7298382	gi|7298382|gb|AAF53607.1| (AE003655) CG15141 gene product [Drosophila melanogaster]	5.7

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
5979	7477896	gi|7477896|pir||D70595 probable ATP-dependent RNA helicase - Mycobacterium tuberculosis (strain H37RV) emb|CAB08305.1| (Z95120) rhlE [Mycobacterium tuberculosis] gb|AAK47649.1| (AE007143) ATP-dependent RNA helicase DeaD [Mycobacterium tuberculosis CDC1551]	4.7
5980	10726674	gi|10726674|gb|AAF55880.2| (AE003734) CG16791 gene product [Drosophila melanogaster]	5.5
5983	10303299	gi|10303299|emb|CAC10094.1| (AL442164) related to SEN1 protein [Neurospora crassa]	9.4
5984	14625441	gi|14625441|dbj|BAB61903.1| (AB053446) KIAA1773 protein [Homo sapiens]	2.4
5985	2496701	gi|2496701|sp|P55552|Y4LL_RHISN HYPOTHETICAL 91.8 KD PROTEIN Y4LL gb|AAB91764.1| (AE000083) Y4lL [Rhizobium sp. NGR234]	4
5988	13652830	gi|13652830|ref|XP_017068.1| 65851 [Homo sapiens] ref|XP_039450.1| similar to NONHISTONE CHROMOSOMAL PROTEIN HMG-14 (H. sapiens) [Homo sapiens]	0.00001
5989	2098719	gi|2098719|gb|AAB57675.1| (U85709) putative fimbrial-associated protein [Actinomyces naeslundii]	5.4
5990	1142588	gi|1142588|gb|AAA84740.1| (U05313) CR3 [Trypanosoma brucei]	0.02
5991	11283273	gi|11283273|pir||A81658 hypothetical protein TC0845 [imported] - Chlamydia muridarum (strain Nigg) gb|AAF39643.1| (AE002351) hypothetical protein [Chlamydia muridarum]	7.2
5992	13507856	gi|13507856|ref|NP_109805.1| ribosomal protein L20 [Mycoplasma pneumoniae] sp|P78023|RL20_MYCPN 50S RIBOSOMAL PROTEIN L20 pir||S73363 ribosomal protein L20 - Mycoplasma pneumoniae (strain ATCC 29342) gb|AAG34734.1|AE000004_3 (AE000004) ribosomal protein L20 [Mycoplasma pneumoniae]	0.84
5997	7506563	gi|7506563|pir||T24113 hypothetical protein R10D12.3 - Caenorhabditis elegans emb|CAB03243.1| (Z81109) predicted using Genefinder~similar to G-protein coupled receptor [Caenorhabditis elegans]	6.3
5998	7510771	gi|7510771|pir||T29919 hypothetical protein ZC449.5 - Caenorhabditis elegans	3.6

	Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID NO	ACCESSN	DESCRIPTION	P VALUE
6001	14755125	gi|14755125|ref|XP_006601.4| hypothetical protein FLJ10659 [Homo sapiens]	3E-96
6005	7508360	gi|7508360|pir||T25220 hypothetical protein T24B8.4 - Caenorhabditis elegans emb|CAA92756.1| (Z68338) predicted using Genefinder~contains similarity to Pfam domain: PF02205 (Wiskott Aldrich syndrome homology region 2), Score=43.6, E-value=1.5e-09, N=2~cDNA EST yk96d7.5 comes from this gene~cDNA EST yk96d7.3 comes from this gene~cDNA EST yk76d1>	1
6006	4960210	gi|4960210|gb|AAD34644.1|AF154112_1 (AF154112) transcription co-repressor Sin3 [Xenopus laevis]	7

Table 4 SEQ ID NO	SEQ NAME	CLUSTER	PROFILE NAME	DIR	SCORE
6	2102.B18.gz43_275316	558147	Ets_Cterm	for	19.58
9	2103.M06.gz43_275519	377696	protkinase	for	20.71
38	2153.K14.gz43_278937	372952	Dead_box_helic	for	172.21
39	2154.M04.gz43_279163	377696	protkinase	for	20.71
61	2165.H06.gz43_280342	393635	zf-c2h2	for	33.96
69	2166.J11.gz43_281368	377696	protkinase	for	20.71
108	2118.A09.gz43_307025	446397	bzip	for	19.15
117	2131.I13.gz43_308085	34071	wd40	for	37.45
118	2131.B14.gz43_308094	221686	protkinase	for	33.14
228	1573.F18.gz43_208848	639849	PH	for	42.77
229	1573.K19.gz43_208869	486238	protkinase	rev	45.41
415	1585.G22.gz43_210545	412416	Dead_box_helic	for	49.67
445	1587.B06.gz43_211440	446984	ANK	rev	23.12
486	1597.G06.gz43_212233	639593	defensins	rev	18.27
487	1597.J06.gz43_212236	557975	ANK	for	35.63
502	1597.F18.gz43_212424	596882	zf-c2h2	rev	18.13
700	1694.M19.gz43_214375	425923	zf-c2h2	for	32.76
847	1706.P07.gz43_216138	639901	zf-c2h2	for	19.43
877	1707.J02.gz43_216453	550237	zf-ccch	for	26.74
1511	1755.P24.gz43_223395	606129	rvt	for	37.6
1714	1790.C14.gz43_226997	727150	bzip	for	24.2
2034	1828.J19.gz43_232472	728303	zf-c2h2	rev	18.19
2038	1828.P21.gz43_232510	509678	Retvir_asp_protease	for	28.5
2054	1838.N05.gz43_233020	481614	zf-c2h2	for	18.52
2514	1888.O06.gz43_240269	451764	rvt	for	49.99
2973	1924.H18.gz43_245579	499700	7tm_1	rev	73.7
3013	1935.E18.gz43_246500	490805	ANK	rev	28.74
3140	1981.O19.gz43_248062	558949	zf-c3hc4	rev	19.16
3403	1958.N12.gz43_250647	556308	zf-c2h2	for	40.77
3524	1923.M22.gz43_252963	562603	zf-c2h2	rev	42.42
3653	1995.C03.gz43_256117	562152	zf-c2h2	rev	18.97
3689	1995.P13.gz43_256290	562989	EGF	rev	19.4
3723	1995.B24.gz43_256452	556632	zf-c2h2	rev	20.64
3814	2007.F09.gz43_257778	560652	zf-c2hc	rev	21.49
3931	2008.F18.gz43_258308	550497	bzip	for	20.27
4151	1669.G11.gz43_260853	503275	protkinase	rev	43.25
4356	1682.O17.gz43_262495	450211	bzip	rev	26.06
4373	1682.F21.gz43_262550	546740	EFhand	rev	18.72
4688	2018.K14.gz43_264760	432970	zf-c2h2	for	48.43
4979	2041.C09.gz43_266976	556632	zf-c2h2	rev	20.88
5467	2067.I20.gz43_271090	551617	7tm_1	rev	19.77
5508	2068.F14.gz43_271375	561707	7tm_1	rev	24.27
5522	2068.D17.gz43_271421	554774	tgf-beta	for	18.24
5756	2176.J17.gz43_281945	412416	Dead_box_helic	for	37.64
6001	1561.C22.gz43_314731	447072	PH	for	31.95

Table 5						
SEQ ID NO	CLUSTER	PAIR AB	CLONES A	CLONES B	RATIO PLUS	RATIO MINUS
6	558147	12,13	3	12	-1	3.87
11	402353	12,13	13	4	3.36	-1
14	884	03,04	51	20	2.49	-1
14	884	15,17	1	10	-1	9.32
14	884	27,28	15	3	5.41	-1
14	884	28,29	3	21	-1	5.62
22	427571	08,09	6	0	8.38	-1
28	6342	30,31	0	7	-1	6.29
29	387530	30,31	2	24	-1	10.79
52	24210	08,09	2	13	-1	4.65
52	24210	21,22	0	11	-1	11.18
52	24210	23,24	1	9	-1	8.91
52	24210	25,26	12	2	5.79	-1
60	1300	25,26	6	0	5.79	-1
64	376808	08,09	0	8	-1	5.72
65	6342	30,31	0	7	-1	6.29
67	24210	08,09	2	13	-1	4.65
67	24210	21,22	0	11	-1	11.18
67	24210	23,24	1	9	-1	8.91
67	24210	25,26	12	2	5.79	-1
68	24210	08,09	2	13	-1	4.65
68	24210	21,22	0	11	-1	11.18
68	24210	23,24	1	9	-1	8.91
68	24210	25,26	12	2	5.79	-1
71	185432	03,04	0	26	-1	26.65
71	185432	08,09	10	33	-1	2.36
75	418763	15,16	15	3	5.28	-1
75	418763	15,17	15	2	8.05	-1
75	418763	27,29	11	0	14.84	-1
75	418763	28,29	5	0	6.23	-1
79	649035	27,28	0	7	-1	6.46
79	649035	28,29	7	0	8.72	-1
92	186594	25,26	12	0	11.58	-1
93	218904	08,09	6	1	8.38	-1
99	535955	15,17	1	10	-1	9.32
99	535955	16,17	0	10	-1	9.85
112	48238	08,09	6	1	8.38	-1
113	226324	15,17	0	8	-1	7.45
113	226324	16,17	0	8	-1	7.88
113	226324	27,29	5	0	6.75	-1
115	62016	16,17	0	6	-1	5.91
116	48238	08,09	6	1	8.38	-1
121	20453	25,26	3	13	-1	4.49
123	37805	08,09	10	0	13.97	-1
125	48238	08,09	6	1	8.38	-1
136	120049	15,17	10	2	5.37	-1

SEQ ID NO	CLUSTER	PAIR AB	CLONES A	CLONES B	RATIO PLUS	RATIO MINUS
140	446829	27,29	78	44	2.39	-1
147	147196	28,29	16	46	-1	2.31
147	147196	30,31	8	30	-1	3.37
153	446614	16,17	7	0	7.11	-1
160	463487	15,17	8	1	8.59	-1
170	417078	15,16	8	1	8.46	-1
170	417078	15,17	8	0	8.59	-1
176	446531	16,17	0	6	-1	5.91
178	380127	28,29	9	26	-1	2.32
199	468109	15,17	6	0	6.44	-1
199	468109	27,29	6	0	8.09	-1
199	468109	28,29	7	0	8.72	-1
200	447326	15,17	6	0	6.44	-1
219	650195	15,16	6	0	6.34	-1
219	650195	15,17	6	0	6.44	-1
238	470462	15,17	7	0	7.51	-1
242	466697	12,13	6	0	6.2	-1
248	447147	27,29	9	0	12.14	-1
255	447750	12,14	9	0	9.43	-1
255	447750	27,29	9	0	12.14	-1
255	447750	28,29	5	0	6.23	-1
261	560868	27,29	6	0	8.09	-1
276	640356	15,17	10	0	10.73	-1
287	649852	15,17	6	0	6.44	-1
292	446974	28,29	5	0	6.23	-1
307	643924	15,16	6	0	6.34	-1
307	643924	15,17	6	0	6.44	-1
309	452986	15,16	8	1	8.46	-1
320	449861	16,17	74	26	2.89	-1
320	449861	27,29	1	16	-1	11.86
326	450225	15,17	11	3	3.94	-1
326	450225	27,28	1	24	-1	22.16
326	450225	28,29	24	1	29.9	-1
327	452707	30,31	7	0	7.79	-1
337	452204	15,16	9	1	9.51	-1
337	452204	16,17	1	8	-1	7.88
337	452204	23,24	3	13	-1	4.29
337	452204	27,28	0	14	-1	12.93
337	452204	28,29	14	0	17.44	-1
343	639662	15,16	7	0	7.4	-1
343	639662	15,17	7	0	7.51	-1
351	448606	15,17	5	20	-1	3.73
351	448606	27,28	0	7	-1	6.46
374	475184	25,26	6	74	-1	12.78
374	475184	27,28	114	48	2.57	-1
374	475184	27,29	114	70	2.2	-1
374	475184	30,31	5	19	-1	3.42
403	555193	15,16	6	0	6.34	-1

SEQ ID NO	CLUSTER	PAIR AB	CLONES A	CLONES B	RATIO PLUS	RATIO MINUS
417	3	01,02	5284	2168	2.25	-1
417	3	08,09	1095	631	2.43	-1
417	3	18,20	2079	463	3.84	-1
417	3	19,20	1419	463	2.29	-1
417	3	27,29	993	3994	-1	2.98
417	3	28,29	786	3994	-1	4.08
419	237288	15,16	7	0	7.4	-1
419	237288	15,17	7	0	7.51	-1
432	639459	15,17	11	0	11.81	-1
432	639459	16,17	9	0	9.14	-1
467	639480	27,28	8	0	8.66	-1
467	639480	27,29	8	0	10.79	-1
468	644242	15,16	6	0	6.34	-1
468	644242	15,17	6	0	6.44	-1
475	640747	15,17	6	0	6.44	-1
488	640356	15,17	10	0	10.73	-1
490	31112	15,17	6	0	6.44	-1
490	31112	23,24	107	9	12.01	-1
500	23961	15,16	102	44	2.45	-1
500	23961	15,17	102	40	2.74	-1
500	23961	25,26	73	169	-1	2.4
514	645538	23,24	0	6	-1	5.94
517	556	25,26	29	57	-1	2.04
517	556	27,28	34	14	2.63	-1
517	556	28,29	14	43	-1	2.47
517	556	30,31	29	105	-1	3.26
554	446371	15,16	6	0	6.34	-1
558	640221	15,17	8	0	8.59	-1
566	5201	03,04	11	2	5.37	-1
566	5201	15,16	17	4	4.49	-1
566	5201	15,17	17	1	18.25	-1
566	5201	23,24	8	1	8.08	-1
566	5201	27,28	9	0	9.75	-1
566	5201	27,29	9	0	12.14	-1
570	639480	27,28	8	0	8.66	-1
570	639480	27,29	8	0	10.79	-1
577	649717	16,17	6	0	6.09	-1
587	557401	15,17	10	2	5.37	-1
609	650204	15,17	11	0	11.81	-1
624	645073	15,16	6	0	6.34	-1
624	645073	15,17	6	0	6.44	-1
637	981	18,19	1	9	-1	7.88
637	981	27,28	55	17	3.5	-1
637	981	28,29	17	47	-1	2.22
637	981	30,31	31	224	-1	6.5
661	448450	27,28	0	7	-1	6.46
661	448450	28,29	7	0	8.72	-1
662	643804	15,16	6	0	6.34	-1

SEQ ID NO	CLUSTER	PAIR AB	CLONES A	CLONES B	RATIO PLUS	RATIO MINUS
662	643804	15,17	6	0	6.44	-1
672	607430	15,16	6	0	6.34	-1
678	466697	12,13	6	0	6.2	-1
681	462659	15,16	7	0	7.4	-1
681	462659	15,17	7	0	7.51	-1
683	24730	21,22	0	12	-1	12.2
716	638854	15,16	32	11	3.07	-1
716	638854	15,17	32	0	34.35	-1
716	638854	16,17	11	0	11.17	-1
720	643594	15,16	7	0	7.4	-1
720	643594	15,17	7	0	7.51	-1
729	644442	27,28	0	7	-1	6.46
729	644442	28,29	7	0	8.72	-1
735	447035	16,17	8	1	8.12	-1
743	380550	27,28	14	5	3.03	-1
743	380550	27,29	14	0	18.89	-1
743	380550	28,29	5	0	6.23	-1
744	645538	23,24	0	6	-1	5.94
746	650773	15,17	6	0	6.44	-1
761	650517	15,16	6	0	6.34	-1
761	650517	15,17	6	0	6.44	-1
769	640356	15,17	10	0	10.73	-1
773	450559	16,17	2	11	-1	5.42
797	644242	15,16	6	0	6.34	-1
797	644242	15,17	6	0	6.44	-1
798	644407	30,31	6	0	6.67	-1
814	649170	27,29	6	0	8.09	-1
826	447326	15,17	6	0	6.44	-1
832	400741	23,24	37	14	2.67	-1
832	400741	30,31	19	2	10.57	-1
855	647952	15,16	6	0	6.34	-1
855	647952	15,17	6	0	6.44	-1
855	647952	28,29	8	1	9.97	-1
858	455413	23,24	4	17	-1	4.21
866	645092	15,17	8	0	8.59	-1
873	204	03,04	120	318	-1	2.72
873	204	15,17	35	82	-1	2.18
873	204	27,28	41	14	3.17	-1
873	204	27,29	41	24	2.3	-1
873	204	30,31	287	56	5.7	-1
887	645900	15,17	9	0	9.66	-1
887	645900	16,17	9	0	9.14	-1
887	645900	23,24	7	0	7.07	-1
905	557852	28,29	6	0	7.48	-1
918	451709	27,28	2	31	-1	14.31
918	451709	28,29	31	3	12.87	-1
939	448358	27,28	28	15	2.02	-1
945	639480	27,28	8	0	8.66	-1

SEQ ID NO	CLUSTER	PAIR AB	CLONES A	CLONES B	RATIO PLUS	RATIO MINUS
945	639480	27,29	8	0	10.79	-1
946	1318	01,02	17	42	-1	2.68
946	1318	03,04	42	88	-1	2.15
957	451361	23,24	1	8	-1	7.92
958	449891	15,16	8	1	8.46	-1
986	418763	15,16	15	3	5.28	-1
986	418763	15,17	15	2	8.05	-1
986	418763	27,29	11	0	14.84	-1
986	418763	28,29	5	0	6.23	-1
987	619635	25,26	7	0	6.76	-1
989	451899	15,17	9	1	9.66	-1
989	451899	27,28	4	21	-1	4.85
991	560860	27,28	0	7	-1	6.46
991	560860	28,29	7	0	8.72	-1
996	452775	27,28	1	9	-1	8.31
1006	649556	28,29	6	0	7.48	-1
1007	644611	15,16	7	0	7.4	-1
1007	644611	15,17	7	0	7.51	-1
1009	470462	15,17	7	0	7.51	-1
1010	645662	23,24	4	28	-1	6.93
1011	649259	15,16	7	0	7.4	-1
1011	649259	15,17	7	0	7.51	-1
1011	649259	27,28	8	0	8.66	-1
1011	649259	27,29	8	0	10.79	-1
1034	532307	16,17	0	7	-1	6.89
1044	414739	15,17	6	19	-1	2.95
1044	414739	16,17	2	19	-1	9.35
1047	238586	30,31	9	0	10.01	-1
1068	467057	23,24	0	7	-1	6.93
1090	549786	23,24	0	8	-1	7.92
1101	649259	15,16	7	0	7.4	-1
1101	649259	15,17	7	0	7.51	-1
1101	649259	27,28	8	0	8.66	-1
1101	649259	27,29	8	0	10.79	-1
1106	468689	15,16	6	0	6.34	-1
1106	468689	15,17	6	0	6.44	-1
1112	556325	16,17	1	8	-1	7.88
1123	645530	15,16	10	2	5.28	-1
1123	645530	15,17	10	0	10.73	-1
1132	452026	15,16	38	14	2.87	-1
1132	452026	27,28	7	26	-1	3.43
1132	452026	28,29	26	2	16.2	-1
1132	452026	30,31	9	2	5.01	-1
1134	612572	15,16	6	0	6.34	-1
1147	14157	28,29	6	0	7.48	-1
1151	454906	27,28	4	18	-1	4.16
1151	454906	28,29	18	2	11.21	-1
1154	62053	25,26	10	1	9.65	-1

SEQ ID NO	CLUSTER	PAIR AB	CLONES A	CLONES B	RATIO PLUS	RATIO MINUS
1180	645900	15,17	9	0	9.66	-1
1180	645900	16,17	9	0	9.14	-1
1180	645900	23,24	7	0	7.07	-1
1185	463824	15,16	6	0	6.34	-1
1185	463824	15,17	6	0	6.44	-1
1185	463824	27,28	0	8	-1	7.39
1185	463824	28,29	8	0	9.97	-1
1193	649617	28,29	5	0	6.23	-1
1208	452738	28,29	5	0	6.23	-1
1234	647232	16,17	9	0	9.14	-1
1234	647232	28,29	6	0	7.48	-1
1237	503122	25,26	8	178	-1	23.05
1237	503122	27,29	12	2	8.09	-1
1237	503122	30,31	22	98	-1	4
1238	515350	15,16	14	0	14.8	-1
1238	515350	15,17	14	3	5.01	-1
1244	648996	15,16	6	0	6.34	-1
1244	648996	15,17	6	0	6.44	-1
1255	416624	27,29	6	0	8.09	-1
1261	449956	12,13	6	0	6.2	-1
1261	449956	16,17	10	1	10.16	-1
1261	449956	28,29	10	0	12.46	-1
1261	449956	30,31	8	1	8.9	-1
1270	380477	15,17	7	0	7.51	-1
1276	645100	15,16	7	0	7.4	-1
1276	645100	15,17	7	0	7.51	-1
1278	554581	28,29	7	0	8.72	-1
1290	650820	16,17	8	0	8.12	-1
1306	646309	16,17	6	0	6.09	-1
1315	502683	15,16	6	0	6.34	-1
1315	502683	28,29	5	0	6.23	-1
1342	463487	15,17	8	1	8.59	-1
1352	446987	15,17	10	0	10.73	-1
1354	640922	27,28	0	7	-1	6.46
1354	640922	28,29	7	0	8.72	-1
1355	561793	30,31	6	0	6.67	-1
1382	649354	15,16	6	0	6.34	-1
1382	649354	15,17	6	0	6.44	-1
1386	507050	27,29	9	0	12.14	-1
1386	507050	28,29	7	0	8.72	-1
1392	649272	16,17	8	0	8.12	-1
1412	453470	15,16	12	1	12.68	-1
1412	453470	15,17	12	1	12.88	-1
1423	419255	15,16	11	0	11.63	-1
1423	419255	15,17	11	1	11.81	-1
1424	648996	15,16	6	0	6.34	-1
1424	648996	15,17	6	0	6.44	-1
1425	451361	23,24	1	8	-1	7.92

SEQ ID NO	CLUSTER	PAIR AB	CLONES A	CLONES B	RATIO PLUS	RATIO MINUS
1426	15296	27,28	6	0	6.5	-1
1429	643327	28,29	10	0	12.46	-1
1432	452646	28,29	5	0	6.23	-1
1442	651073	15,16	7	0	7.4	-1
1442	651073	15,17	7	0	7.51	-1
1442	651073	27,28	0	9	-1	8.31
1442	651073	28,29	9	2	5.61	-1
1452	213	03,04	17	4	4.15	-1
1452	213	08,09	137	403	-1	2.1
1452	213	21,22	2	14	-1	7.12
1452	213	27,28	4	43	-1	9.93
1452	213	27,29	4	47	-1	8.71
1452	213	30,31	123	35	3.91	-1
1468	268336	15,16	8	1	8.46	-1
1478	646060	15,16	13	3	4.58	-1
1478	646060	15,17	13	0	13.95	-1
1497	639378	27,28	8	0	8.66	-1
1497	639378	27,29	8	0	10.79	-1
1507	446910	25,26	80	346	-1	4.48
1507	446910	27,29	210	38	7.46	-1
1507	446910	28,29	210	38	6.88	-1
1508	447126	15,16	19	5	4.02	-1
1508	447126	16,17	5	20	-1	3.94
1508	447126	28,29	5	0	6.23	-1
1514	479131	23,24	1	13	-1	12.87
1523	284586	15,17	8	0	8.59	-1
1523	284586	27,28	0	17	-1	15.7
1523	284586	28,29	17	0	21.18	-1
1529	449437	15,16	14	3	4.93	-1
1529	449437	16,17	3	12	-1	3.94
1529	449437	27,28	0	8	-1	7.39
1529	449437	28,29	8	0	9.97	-1
1552	449438	27,29	5	0	6.75	-1
1552	449438	28,29	9	0	11.21	-1
1561	448152	27,28	1	17	-1	15.7
1561	448152	28,29	17	2	10.59	-1
1564	479880	23,24	0	7	-1	6.93
1594	449521	27,29	7	1	9.44	-1
1602	644190	16,17	6	0	6.09	-1
1620	639991	15,17	6	0	6.44	-1
1638	594994	28,29	6	0	7.48	-1
1660	376342	15,16	0	7	-1	6.62
1662	734646	15,16	0	14	-1	13.25
1662	734646	16,17	14	0	14.22	-1
1666	460284	23,24	6	0	6.06	-1
1666	460284	27,28	6	0	6.5	-1
1685	558412	30,31	6	0	6.67	-1
1689	640158	16,17	6	0	6.09	-1

SEQ ID NO	CLUSTER	PAIR AB	CLONES A	CLONES B	RATIO PLUS	RATIO MINUS
1706	209	01,02	9	36	-1	4.34
1706	209	03,04	445	205	2.12	-1
1706	209	15,16	36	188	-1	4.94
1706	209	15,17	36	145	-1	3.75
1706	209	18,19	0	12	-1	10.5
1706	209	19,20	12	1	8.98	-1
1706	209	21,22	19	101	-1	5.4
1706	209	27,28	250	36	7.52	-1
1706	209	27,29	250	69	4.89	-1
1713	423420	30,31	12	0	13.35	-1
1717	448758	23,24	12	27	-1	2.23
1736	470462	15,17	7	0	7.51	-1
1740	729779	15,16	0	8	-1	7.57
1740	729779	16,17	8	0	8.12	-1
1758	649722	15,17	8	0	8.59	-1
1758	649722	16,17	6	0	6.09	-1
1759	562137	23,24	8	0	8.08	-1
1769	27083	16,17	11	0	11.17	-1
1769	27083	25,26	17	56	-1	3.41
1769	27083	28,29	1	14	-1	11.24
1769	27083	30,31	31	99	-1	2.87
1784	498194	27,28	0	7	-1	6.46
1784	498194	28,29	7	0	8.72	-1
1813	734646	15,16	0	14	-1	13.25
1813	734646	16,17	14	0	14.22	-1
1816	730282	15,16	0	7	-1	6.62
1816	730282	16,17	7	0	7.11	-1
1834	640116	15,16	19	4	5.02	-1
1834	640116	15,17	19	0	20.39	-1
1842	465446	25,26	26	11	2.28	-1
1879	27083	16,17	11	0	11.17	-1
1879	27083	25,26	17	56	-1	3.41
1879	27083	28,29	1	14	-1	11.24
1879	27083	30,31	31	99	-1	2.87
1880	478458	27,29	5	0	6.75	-1
1892	734622	23,24	5	17	-1	3.37
1896	381623	15,16	10	2	5.28	-1
1896	381623	15,17	10	0	10.73	-1
1898	446575	27,28	1	10	-1	9.23
1898	446575	28,29	10	1	12.46	-1
1940	649106	15,17	7	0	7.51	-1
1971	727760	27,28	0	8	-1	7.39
1971	727760	28,29	8	0	9.97	-1
1972	454087	15,16	14	3	4.93	-1
1972	454087	15,17	14	1	15.03	-1
1972	454087	25,26	4	14	-1	3.63
1978	4584	01,02	1	11	-1	11.93
1978	4584	25,26	6	0	5.79	-1

SEQ ID NO	CLUSTER	PAIR AB	CLONES A	CLONES B	RATIO PLUS	RATIO MINUS
2009	734622	23,24	5	17	-1	3.37
2027	48619	30,31	6	0	6.67	-1
2033	646309	16,17	6	0	6.09	-1
2040	447150	23,24	0	6	-1	5.94
2041	728273	15,16	0	7	-1	6.62
2041	728273	16,17	7	0	7.11	-1
2048	438663	15,16	4	16	-1	3.78
2048	438663	25,26	97	210	-1	2.24
2048	438663	27,28	48	171	-1	3.29
2048	438663	28,29	171	58	3.67	-1
2048	438663	30,31	13	30	-1	2.07
2064	128773	15,16	4	25	-1	5.91
2064	128773	16,17	25	2	12.69	-1
2064	128773	25,26	79	261	-1	3.42
2064	128773	30,31	13	33	-1	2.28
2074	504513	15,17	6	0	6.44	-1
2082	549801	28,29	8	0	9.97	-1
2083	730484	23,24	1	12	-1	11.88
2100	606076	23,24	2	22	-1	10.89
2122	732712	15,16	0	7	-1	6.62
2122	732712	16,17	7	0	7.11	-1
2132	730059	15,16	0	6	-1	5.68
2132	730059	16,17	6	0	6.09	-1
2137	451184	16,17	14	4	3.55	-1
2140	152	03,04	153	566	-1	3.79
2140	152	08,09	136	395	-1	2.08
2140	152	15,16	59	194	-1	3.11
2140	152	15,17	59	455	-1	7.18
2140	152	16,17	194	455	-1	2.31
2140	152	21,22	232	565	-1	2.48
2140	152	30,31	75	211	-1	2.53
2150	648774	15,17	6	0	6.44	-1
2157	548275	25,26	16	3	5.15	-1
2159	479572	25,26	20	53	-1	2.75
2159	479572	28,29	96	55	2.17	-1
2200	448046	15,17	0	12	-1	11.18
2200	448046	16,17	3	12	-1	3.94
2200	448046	27,28	1	9	-1	8.31
2200	448046	28,29	9	0	11.21	-1
2204	732756	28,29	6	0	7.48	-1
2215	171511	15,16	0	7	-1	6.62
2215	171511	16,17	7	0	7.11	-1
2232	203793	16,17	12	3	4.06	-1
2232	203793	25,26	12	188	-1	16.23
2232	203793	27,28	185	66	3.04	-1
2232	203793	27,29	185	100	2.5	-1
2236	725825	15,16	0	8	-1	7.57
2236	725825	16,17	8	0	8.12	-1

SEQ ID NO	CLUSTER	PAIR AB	CLONES A	CLONES B	RATIO PLUS	RATIO MINUS
2276	407723	12,13	6	0	6.2	-1
2285	411128	12,13	24	8	3.1	-1
2285	411128	13,14	8	29	-1	3.57
2285	411128	18,19	387	158	2.8	-1
2285	411128	19,20	158	634	-1	5.36
2285	411128	25,26	6272	2943	2.06	-1
2285	411128	27,29	4900	2229	2.97	-1
2285	411128	28,29	4750	2229	2.65	-1
2289	726173	15,16	0	6	-1	5.68
2289	726173	16,17	6	0	6.09	-1
2322	732712	15,16	0	7	-1	6.62
2322	732712	16,17	7	0	7.11	-1
2337	4255	08,09	28	7	5.59	-1
2338	554080	16,17	1	9	-1	8.86
2358	4244	28,29	8	28	-1	2.81
2376	737087	28,29	5	0	6.23	-1
2378	735871	23,24	0	13	-1	12.87
2388	735292	15,16	0	9	-1	8.51
2388	735292	16,17	9	0	9.14	-1
2400	732223	27,29	5	0	6.75	-1
2401	595506	15,16	0	6	-1	5.68
2405	728884	15,16	0	8	-1	7.57
2405	728884	16,17	8	0	8.12	-1
2417	453508	25,26	27	9	2.9	-1
2417	453508	27,28	9	1	9.75	-1
2442	620462	23,24	2	19	-1	9.4
2445	735028	15,16	0	6	-1	5.68
2445	735028	16,17	6	0	6.09	-1
2449	447075	27,28	3	37	-1	11.39
2449	447075	28,29	37	14	3.29	-1
2483	645139	16,17	9	0	9.14	-1
2493	401368	27,29	48	32	2.02	-1
2514	451764	16,17	16	5	3.25	-1
2519	105056	15,16	1	10	-1	9.46
2529	560868	27,29	6	0	8.09	-1
2532	1030	21,22	13	3	4.26	-1
2532	1030	27,29	21	12	2.36	-1
2532	1030	30,31	14	5	3.11	-1
2545	455581	27,28	118	49	2.61	-1
2545	455581	27,29	118	29	5.49	-1
2545	455581	28,29	49	29	2.11	-1
2573	447550	23,24	6	0	6.06	-1
2573	447550	25,26	48	197	-1	4.25
2573	447550	30,31	6	20	-1	3
2591	447003	28,29	6	0	7.48	-1
2597	649852	15,17	6	0	6.44	-1
2598	650297	15,17	6	0	6.44	-1
2609	402516	30,31	6	0	6.67	-1

SEQ ID NO	CLUSTER	PAIR AB	CLONES A	CLONES B	RATIO PLUS	RATIO MINUS
2629	405016	16,17	15	4	3.81	-1
2655	734031	27,28	0	7	-1	6.46
2655	734031	28,29	7	0	8.72	-1
2663	736595	15,16	0	6	-1	5.68
2663	736595	16,17	6	0	6.09	-1
2669	734209	15,16	0	9	-1	8.51
2669	734209	16,17	9	0	9.14	-1
2673	561632	27,29	5	0	6.75	-1
2681	530883	15,16	0	7	-1	6.62
2682	729173	15,16	0	8	-1	7.57
2682	729173	16,17	8	0	8.12	-1
2685	726786	12,13	6	0	6.2	-1
2685	726786	15,16	0	10	-1	9.46
2685	726786	16,17	10	0	10.16	-1
2685	726786	30,31	6	0	6.67	-1
2687	448770	15,17	6	0	6.44	-1
2712	726449	27,28	16	1	17.33	-1
2712	726449	27,29	16	0	21.59	-1
2718	446752	12,14	1	12	-1	11.45
2750	289328	12,13	6	0	6.2	-1
2750	289328	30,31	8	1	8.9	-1
2772	81	15,16	30	79	-1	2.49
2772	81	15,17	30	114	-1	3.54
2772	81	18,19	0	46	-1	40.25
2772	81	19,20	46	4	8.6	-1
2772	81	27,29	49	175	-1	2.65
2772	81	30,31	52	116	-1	2.01
2775	220107	15,17	9	25	-1	2.59
2775	220107	28,29	9	39	-1	3.48
2780	402024	12,13	2	12	-1	5.81
2780	402024	12,14	2	11	-1	5.25
2782	451888	27,29	79	26	4.1	-1
2782	451888	28,29	70	26	3.35	-1
2791	731467	15,16	0	6	-1	5.68
2791	731467	16,17	6	0	6.09	-1
2801	724781	28,29	10	2	6.23	-1
2807	553850	28,29	5	0	6.23	-1
2849	555103	15,17	0	7	-1	6.52
2849	555103	23,24	0	6	-1	5.94
2861	735477	15,16	0	7	-1	6.62
2861	735477	16,17	7	0	7.11	-1
2878	736014	15,16	0	6	-1	5.68
2878	736014	16,17	6	0	6.09	-1
2879	42	08,09	190	121	2.19	-1
2879	42	27,28	792	286	3	-1
2879	42	28,29	286	1257	-1	3.53
2882	42	08,09	190	121	2.19	-1
2882	42	27,28	792	286	3	-1

SEQ ID NO	CLUSTER	PAIR AB	CLONES A	CLONES B	RATIO PLUS	RATIO MINUS
2882	42	28,29	286	1257	-1	3.53
2883	736014	15,16	0	6	-1	5.68
2883	736014	16,17	6	0	6.09	-1
2885	4470	03,04	8	0	7.81	-1
2885	4470	15,16	10	24	-1	2.27
2885	4470	15,17	10	0	10.73	-1
2885	4470	16,17	24	0	24.37	-1
2885	4470	25,26	7	0	6.76	-1
2897	554703	15,17	0	9	-1	8.38
2897	554703	16,17	1	9	-1	8.86
2898	546642	15,17	10	1	10.73	-1
2898	546642	16,17	22	1	22.34	-1
2910	732300	15,16	0	7	-1	6.62
2910	732300	16,17	7	0	7.11	-1
2938	892	15,16	0	6	-1	5.68
2938	892	27,28	6	0	6.5	-1
2938	892	27,29	6	0	8.09	-1
2941	546642	15,17	10	1	10.73	-1
2941	546642	16,17	22	1	22.34	-1
2949	734582	15,16	0	6	-1	5.68
2949	734582	16,17	6	0	6.09	-1
2983	448110	15,17	2	25	-1	11.65
2983	448110	16,17	1	25	-1	24.62
2994	450027	23,24	0	6	-1	5.94
2999	1015	08,09	10	31	-1	2.22
2999	1015	12,14	62	28	2.32	-1
2999	1015	13,14	84	28	3.05	-1
2999	1015	30,31	31	6	5.75	-1
3006	402070	27,28	1	9	-1	8.31
3006	402070	28,29	9	0	11.21	-1
3015	446964	15,17	1	12	-1	11.18
3020	414739	15,17	6	19	-1	2.95
3020	414739	16,17	2	19	-1	9.35
3038	450410	16,17	0	7	-1	6.89
3044	553316	15,16	12	3	4.23	-1
3057	14573	30,31	11	3	4.08	-1
3093	503452	16,17	1	8	-1	7.88
3099	553158	16,17	1	8	-1	7.88
3113	551289	23,24	0	7	-1	6.93
3121	554581	28,29	7	0	8.72	-1
3126	447667	16,17	0	11	-1	10.83
3126	447667	27,28	22	10	2.38	-1
3126	447667	27,29	22	3	9.89	-1
3126	447667	28,29	10	3	4.15	-1
3129	551617	15,16	9	0	9.51	-1
3129	551617	16,17	0	7	-1	6.89
3145	551117	16,17	0	6	-1	5.91
3150	1093	27,28	43	20	2.33	-1

SEQ ID NO	CLUSTER	PAIR AB	CLONES A	CLONES B	RATIO PLUS	RATIO MINUS
3150	1093	30,31	5	18	-1	3.24
3151	2284	23,24	6	17	-1	2.8
3151	2284	25,26	17	4	4.1	-1
3151	2284	30,31	14	32	-1	2.05
3168	275	15,17	3	15	-1	4.66
3168	275	18,19	0	12	-1	10.5
3172	551718	15,17	0	8	-1	7.45
3192	143346	25,26	44	435	-1	10.24
3211	551553	28,29	7	0	8.72	-1
3248	556216	15,17	0	7	-1	6.52
3248	556216	16,17	0	7	-1	6.89
3291	446814	25,26	10	27	-1	2.8
3291	446814	27,29	8	1	10.79	-1
3301	550694	15,16	21	1	22.2	-1
3301	550694	15,17	21	7	3.22	-1
3307	450963	28,29	6	0	7.48	-1
3328	554764	25,26	32	0	30.89	-1
3339	550855	16,17	1	10	-1	9.85
3355	452506	15,16	8	1	8.46	-1
3355	452506	28,29	6	0	7.48	-1
3359	408130	30,31	10	0	11.12	-1
3363	549964	23,24	8	1	8.08	-1
3372	380127	28,29	9	26	-1	2.32
3378	549320	15,17	0	7	-1	6.52
3382	558103	27,28	1	11	-1	10.16
3382	558103	28,29	11	0	13.7	-1
3382	558103	30,31	6	0	6.67	-1
3383	548864	30,31	6	0	6.67	-1
3391	10397	03,04	10	0	9.76	-1
3391	10397	27,28	6	0	6.5	-1
3391	10397	27,29	6	0	8.09	-1
3393	561892	15,17	0	7	-1	6.52
3398	548965	16,17	4	14	-1	3.45
3435	549829	16,17	0	6	-1	5.91
3452	257547	23,24	29	8	3.66	-1
3452	257547	27,28	0	8	-1	7.39
3452	257547	28,29	8	0	9.97	-1
3457	450255	16,17	0	6	-1	5.91
3469	448663	28,29	5	0	6.23	-1
3474	559575	27,28	1	9	-1	8.31
3474	559575	28,29	9	0	11.21	-1
3485	4244	28,29	8	28	-1	2.81
3499	349	01,02	78	160	-1	2.22
3499	349	03,04	91	3	29.59	-1
3499	349	12,13	33	13	2.62	-1
3499	349	13,14	13	28	-1	2.12
3499	349	16,17	15	35	-1	2.3
3499	349	27,28	12	29	-1	2.23

SEQ ID NO	CLUSTER	PAIR AB	CLONES A	CLONES B	RATIO PLUS	RATIO MINUS
3512	498194	27,28	0	7	-1	6.46
3512	498194	28,29	7	0	8.72	-1
3518	453667	23,24	3	12	-1	3.96
3538	275	15,17	3	15	-1	4.66
3538	275	18,19	0	12	-1	10.5
3559	447429	27,28	0	8	-1	7.39
3559	447429	28,29	8	0	9.97	-1
3563	449956	12,13	6	0	6.2	-1
3563	449956	16,17	10	1	10.16	-1
3563	449956	28,29	10	0	12.46	-1
3563	449956	30,31	8	1	8.9	-1
3573	134392	23,24	20	2	10.1	-1
3573	134392	25,26	0	6	-1	6.22
3583	551380	16,17	4	14	-1	3.45
3600	450242	30,31	7	0	7.79	-1
3603	451361	23,24	1	8	-1	7.92
3608	402916	23,24	8	0	8.08	-1
3608	402916	27,28	22	5	4.76	-1
3608	402916	27,29	22	4	7.42	-1
3613	555502	16,17	0	9	-1	8.86
3619	461	15,16	14	39	-1	2.64
3619	461	15,17	14	34	-1	2.26
3619	461	18,19	1	10	-1	8.75
3619	461	19,20	10	0	7.48	-1
3619	461	27,29	41	124	-1	2.24
3619	461	28,29	37	124	-1	2.69
3619	461	30,31	21	119	-1	5.09
3625	450867	15,16	7	0	7.4	-1
3627	502683	15,16	6	0	6.34	-1
3627	502683	28,29	5	0	6.23	-1
3637	447405	15,17	27	83	-1	2.86
3637	447405	18,20	2	11	-1	6.43
3637	447405	19,20	0	11	-1	14.71
3637	447405	27,29	163	60	3.66	-1
3637	447405	30,31	14	36	-1	2.31
3641	560984	16,17	0	6	-1	5.91
3650	554604	15,17	0	7	-1	6.52
3662	447858	15,16	12	3	4.23	-1
3721	555830	15,16	16	2	8.46	-1
3721	555830	15,17	16	2	8.59	-1
3731	562550	16,17	0	6	-1	5.91
3736	873	15,17	6	21	-1	3.26
3736	873	27,29	15	50	-1	2.47
3736	873	28,29	17	50	-1	2.36
3736	873	30,31	14	32	-1	2.05
3744	126	15,16	103	260	-1	2.39
3744	126	15,17	103	571	-1	5.16
3744	126	16,17	260	571	-1	2.16

SEQ ID NO	CLUSTER	PAIR AB	CLONES A	CLONES B	RATIO PLUS	RATIO MINUS
3744	126	18,19	4	37	-1	8.09
3744	126	18,20	4	13	-1	3.8
3744	126	19,20	37	13	2.13	-1
3744	126	27,28	638	323	2.14	-1
3762	555103	15,17	0	7	-1	6.52
3762	555103	23,24	0	6	-1	5.94
3774	531145	28,29	6	0	7.48	-1
3782	129715	08,09	3	27	-1	6.44
3807	554764	25,26	32	0	30.89	-1
3810	556561	15,17	0	10	-1	9.32
3810	556561	16,17	1	10	-1	9.85
3823	553787	28,29	10	0	12.46	-1
3848	556759	12,13	8	1	8.26	-1
3848	556759	15,16	11	2	5.81	-1
3848	556759	16,17	2	18	-1	8.86
3848	556759	27,29	21	1	28.33	-1
3848	556759	28,29	18	1	22.43	-1
3848	556759	30,31	10	1	11.12	-1
3857	503452	16,17	1	8	-1	7.88
3861	2284	23,24	6	17	-1	2.8
3861	2284	25,26	17	4	4.1	-1
3861	2284	30,31	14	32	-1	2.05
3864	560984	16,17	0	6	-1	5.91
3873	551444	23,24	6	0	6.06	-1
3881	548858	16,17	0	11	-1	10.83
3885	411113	16,17	0	6	-1	5.91
3894	594994	28,29	6	0	7.48	-1
3904	562550	16,17	0	6	-1	5.91
3922	460445	16,17	0	6	-1	5.91
3925	931	01,02	23	59	-1	2.78
3925	931	18,19	0	9	-1	7.88
3925	931	30,31	70	195	-1	2.5
3940	388688	27,29	8	2	5.4	-1
3940	388688	28,29	17	2	10.59	-1
4009	380127	28,29	9	26	-1	2.32
4016	378459	23,24	1	9	-1	8.91
4017	550571	16,17	0	6	-1	5.91
4036	607430	15,16	6	0	6.34	-1
4039	558098	15,16	6	0	6.34	-1
4039	558098	30,31	9	1	10.01	-1
4041	557928	16,17	0	6	-1	5.91
4079	557928	16,17	0	6	-1	5.91
4100	450242	30,31	7	0	7.79	-1
4106	448450	27,28	0	7	-1	6.46
4106	448450	28,29	7	0	8.72	-1
4111	560538	16,17	0	8	-1	7.88
4115	420892	13,14	0	6	-1	5.91
4138	450883	28,29	5	0	6.23	-1

SEQ ID NO	CLUSTER	PAIR AB	CLONES A	CLONES B	RATIO PLUS	RATIO MINUS
4139	638971	15,17	8	0	8.59	-1
4149	643804	15,16	6	0	6.34	-1
4149	643804	15,17	6	0	6.44	-1
4150	97909	27,28	31	12	2.8	-1
4150	97909	28,29	12	35	-1	2.34
4150	97909	30,31	18	54	-1	2.7
4157	603857	27,29	17	3	7.64	-1
4157	603857	28,29	31	3	12.87	-1
4162	641683	15,16	8	0	8.46	-1
4162	641683	15,17	8	0	8.59	-1
4176	640889	15,17	6	0	6.44	-1
4178	643594	15,16	7	0	7.4	-1
4178	643594	15,17	7	0	7.51	-1
4195	641728	28,29	7	1	8.72	-1
4203	359500	12,13	14	4	3.61	-1
4203	359500	27,28	18	4	4.87	-1
4203	359500	28,29	4	17	-1	3.41
4203	359500	30,31	8	22	-1	2.47
4204	649558	15,16	12	3	4.23	-1
4204	649558	15,17	12	0	12.88	-1
4231	451401	15,17	9	1	9.66	-1
4234	417259	15,17	4	14	-1	3.26
4234	417259	16,17	1	14	-1	13.79
4240	453006	27,28	0	8	-1	7.39
4240	453006	28,29	8	0	9.97	-1
4247	498194	27,28	0	7	-1	6.46
4247	498194	28,29	7	0	8.72	-1
4250	556326	16,17	0	8	-1	7.88
4257	649106	15,17	7	0	7.51	-1
4264	284586	15,17	8	0	8.59	-1
4264	284586	27,28	0	17	-1	15.7
4264	284586	28,29	17	0	21.18	-1
4265	642535	27,28	0	8	-1	7.39
4265	642535	28,29	8	0	9.97	-1
4270	801	30,31	25	7	3.97	-1
4271	449956	12,13	6	0	6.2	-1
4271	449956	16,17	10	1	10.16	-1
4271	449956	28,29	10	0	12.46	-1
4271	449956	30,31	8	1	8.9	-1
4283	455113	27,29	11	3	4.95	-1
4283	455113	28,29	13	3	5.4	-1
4285	1558	03,04	25	97	-1	3.98
4287	546705	16,17	0	6	-1	5.91
4293	452212	15,16	6	0	6.34	-1
4298	37862	25,26	14	0	13.51	-1
4299	644609	15,17	7	0	7.51	-1
4311	553877	16,17	1	8	-1	7.88
4319	550562	27,28	1	9	-1	8.31

SEQ ID NO	CLUSTER	PAIR AB	CLONES A	CLONES B	RATIO PLUS	RATIO MINUS
4319	550562	28,29	9	1	11.21	-1
4320	648320	15,16	6	0	6.34	-1
4320	648320	15,17	6	0	6.44	-1
4327	27083	16,17	11	0	11.17	-1
4327	27083	25,26	17	56	-1	3.41
4327	27083	28,29	1	14	-1	11.24
4327	27083	30,31	31	99	-1	2.87
4336	453079	16,17	8	1	8.12	-1
4346	561558	28,29	6	0	7.48	-1
4349	451037	23,24	5	15	-1	2.97
4358	639232	23,24	0	6	-1	5.94
4358	639232	25,26	10	0	9.65	-1
4358	639232	30,31	9	0	10.01	-1
4361	461835	15,16	7	0	7.4	-1
4361	461835	28,29	5	0	6.23	-1
4366	1093	27,28	43	20	2.33	-1
4366	1093	30,31	5	18	-1	3.24
4371	644240	15,17	7	0	7.51	-1
4375	388688	27,29	8	2	5.4	-1
4375	388688	28,29	17	2	10.59	-1
4380	648996	15,16	6	0	6.34	-1
4380	648996	15,17	6	0	6.44	-1
4406	449836	15,17	8	1	8.59	-1
4413	640525	15,16	7	0	7.4	-1
4413	640525	15,17	7	0	7.51	-1
4417	388085	15,16	9	0	9.51	-1
4417	388085	15,17	9	0	9.66	-1
4421	448787	15,17	23	9	2.74	-1
4421	448787	16,17	22	9	2.48	-1
4435	554742	16,17	0	6	-1	5.91
4441	549640	27,28	0	7	-1	6.46
4441	549640	30,31	15	6	2.78	-1
4445	530774	15,17	5	16	-1	2.98
4446	375814	15,16	8	0	8.46	-1
4446	375814	15,17	8	1	8.59	-1
4447	446789	15,16	16	5	3.38	-1
4450	503491	16,17	6	0	6.09	-1
4452	639441	23,24	1	8	-1	7.92
4454	649035	27,28	0	7	-1	6.46
4454	649035	28,29	7	0	8.72	-1
4461	470602	15,16	12	1	12.68	-1
4461	470602	16,17	1	9	-1	8.86
4477	453708	15,17	1	19	-1	17.7
4477	453708	16,17	1	19	-1	18.71
4483	551527	15,17	0	7	-1	6.52
4503	549945	15,16	12	2	6.34	-1
4503	549945	15,17	12	2	6.44	-1
4505	391511	27,28	8	0	8.66	-1

SEQ ID NO	CLUSTER	PAIR AB	CLONES A	CLONES B	RATIO PLUS	RATIO MINUS
4515	420686	16,17	0	8	-1	7.88
4517	551995	28,29	7	0	8.72	-1
4523	451032	15,16	6	0	6.34	-1
4538	557852	28,29	6	0	7.48	-1
4542	554500	15,16	6	0	6.34	-1
4550	43642	16,17	0	6	-1	5.91
4551	595506	15,16	0	6	-1	5.68
4553	555702	15,16	11	2	5.81	-1
4556	519109	23,24	1	34	-1	33.65
4557	450829	15,17	0	8	-1	7.45
4557	450829	16,17	0	8	-1	7.88
4598	386940	27,28	0	14	-1	12.93
4598	386940	28,29	14	0	17.44	-1
4611	375380	15,17	1	9	-1	8.38
4611	375380	16,17	0	9	-1	8.86
4619	553850	28,29	5	0	6.23	-1
4627	557401	15,17	10	2	5.37	-1
4632	349744	16,17	0	6	-1	5.91
4635	449437	15,16	14	3	4.93	-1
4635	449437	16,17	3	12	-1	3.94
4635	449437	27,28	0	8	-1	7.39
4635	449437	28,29	8	0	9.97	-1
4645	562292	16,17	0	6	-1	5.91
4652	224812	16,17	31	63	-1	2
4652	224812	25,26	200	686	-1	3.55
4652	224812	27,29	84	38	2.98	-1
4652	224812	28,29	80	38	2.62	-1
4670	446739	28,29	5	0	6.23	-1
4684	247	15,17	15	44	-1	2.73
4684	247	18,19	0	15	-1	13.13
4684	247	30,31	11	51	-1	4.17
4686	491799	15,16	0	11	-1	10.41
4691	461	15,16	14	39	-1	2.64
4691	461	15,17	14	34	-1	2.26
4691	461	18,19	1	10	-1	8.75
4691	461	19,20	10	0	7.48	-1
4691	461	27,29	41	124	-1	2.24
4691	461	28,29	37	124	-1	2.69
4691	461	30,31	21	119	-1	5.09
4696	562292	16,17	0	6	-1	5.91
4702	487182	15,17	2	11	-1	5.12
4702	487182	16,17	1	11	-1	10.83
4702	487182	25,26	3	72	-1	24.87
4706	561046	16,17	0	6	-1	5.91
4746	556040	23,24	2	15	-1	7.42
4748	452822	15,16	9	23	-1	2.42
4758	455820	16,17	0	7	-1	6.89
4767	556802	28,29	8	0	9.97	-1

SEQ ID NO	CLUSTER	PAIR AB	CLONES A	CLONES B	RATIO PLUS	RATIO MINUS
4771	465446	25,26	26	11	2.28	-1
4826	452775	27,28	1	9	-1	8.31
4827	560868	27,29	6	0	8.09	-1
4835	558534	16,17	0	7	-1	6.89
4850	549591	15,17	2	24	-1	11.18
4850	549591	16,17	7	24	-1	3.38
4885	27586	12,13	7	22	-1	3.04
4885	27586	12,14	7	21	-1	2.86
4885	27586	21,22	9	0	8.85	-1
4885	27586	25,26	17	0	16.41	-1
4885	27586	30,31	24	0	26.69	-1
4888	561558	28,29	6	0	7.48	-1
4900	2435	15,17	0	8	-1	7.45
4900	2435	27,28	0	7	-1	6.46
4900	2435	28,29	7	1	8.72	-1
4907	554604	15,17	0	7	-1	6.52
4922	559057	15,17	0	7	-1	6.52
4927	553877	16,17	1	8	-1	7.88
4950	549911	16,17	0	6	-1	5.91
4959	409612	25,26	6	0	5.79	-1
4972	226324	15,17	0	8	-1	7.45
4972	226324	16,17	0	8	-1	7.88
4972	226324	27,29	5	0	6.75	-1
4986	413915	12,13	6	0	6.2	-1
4986	413915	12,14	6	0	6.29	-1
5007	2284	23,24	6	17	-1	2.8
5007	2284	25,26	17	4	4.1	-1
5007	2284	30,31	14	32	-1	2.05
5018	365634	15,16	12	2	6.34	-1
5018	365634	16,17	2	14	-1	6.89
5018	365634	25,26	10	0	9.65	-1
5026	549829	16,17	0	6	-1	5.91
5033	411113	16,17	0	6	-1	5.91
5042	1079	03,04	24	55	-1	2.35
5042	1079	28,29	16	44	-1	2:21
5047	397581	28,29	6	20	-1	2.68
5047	397581	27,29	1	20	-1	14.83
5051	23961	15,16	102	44	2.45	-1
5051	23961	15,17	102	40	2.74	-1
5051	23961	25,26	73	169	-1	2.4
5058	446900	15,17	1	11	-1	10.25
5058	446900	16,17	2	11	-1	5.42
5065	448677	15,16	11	1	11.63	-1
5067	560538	16,17	0	8	-1	7.88
5079	62458	15,16	2	14	-1	6.62
5079	62458	15,17	2	11	-1	5.12
5079	62458	25,26	20	227	-1	11.76
5079	62458	30,31	19	245	-1	11.59

SEQ ID NO	CLUSTER	PAIR AB	CLONES A	CLONES B	RATIO PLUS	RATIO MINUS
5102	556216	15,17	0	7	-1	6.52
5102	556216	16,17	0	7	-1	6.89
5117	549041	16,17	0	6	-1	5.91
5133	453004	27,28	0	8	-1	7.39
5133	453004	28,29	8	0	9.97	-1
5135	560868	27,29	6	0	8.09	-1
5147	403419	13,14	0	9	-1	8.87
5147	403419	27,29	7	0	9.44	-1
5161	559806	16,17	0	6	-1	5.91
5168	550562	27,28	1	9	-1	8.31
5168	550562	28,29	9	1	11.21	-1
5186	91178	15,17	0	7	-1	6.52
5188	561485	15,17	0	7	-1	6.52
5188	561485	16,17	0	7	-1	6.89
5195	558412	30,31	6	0	6.67	-1
5200	453846	15,17	0	11	-1	10.25
5221	562565	15,16	0	8	-1	7.57
5221	562565	27,28	11	1	11.91	-1
5221	562565	27,29	11	0	14.84	-1
5228	553705	15,16	12	0	12.68	-1
5228	553705	28,29	8	0	9.97	-1
5231	562459	16,17	2	10	-1	4.92
5231	562459	27,28	13	29	-1	2.06
5231	562459	27,29	13	1	17.54	-1
5231	562459	28,29	29	1	36.13	-1
5236	62458	15,16	2	14	-1	6.62
5236	62458	15,17	2	11	-1	5.12
5236	62458	25,26	20	227	-1	11.76
5236	62458	30,31	19	245	-1	11.59
5240	448741	28,29	6	0	7.48	-1
5249	451401	15,17	9	1	9.66	-1
5258	451802	15,17	0	9	-1	8.38
5258	451802	16,17	1	9	-1	8.86
5264	452775	27,28	1	9	-1	8.31
5268	92639	12,14	2	11	-1	5.25
5271	452500	27,28	0	15	-1	13.85
5271	452500	28,29	15	5	3.74	-1
5272	452204	15,16	9	1	9.51	-1
5272	452204	16,17	1	8	-1	7.88
5272	452204	23,24	3	13	-1	4.29
5272	452204	27,28	0	14	-1	12.93
5272	452204	28,29	14	0	17.44	-1
5273	447025	15,16	48	19	2.67	-1
5273	447025	27,28	0	8	-1	7.39
5273	447025	27,29	0	13	-1	9.64
5277	452052	15,17	8	1	8.59	-1
5277	452052	27,28	2	14	-1	6.46
5277	452052	28,29	14	0	17.44	-1

SEQ ID NO	CLUSTER	PAIR AB	CLONES A	CLONES B	RATIO PLUS	RATIO MINUS
5281	452142	15,16	1	10	-1	9.46
5281	452142	16,17	10	2	5.08	-1
5282	451994	27,28	4	17	-1	3.92
5297	4244	28,29	8	28	-1	2.81
5308	450262	21,22	0	8	-1	8.13
5308	450262	27,28	30	14	2.32	-1
5308	450262	28,29	14	46	-1	2.64
5311	452506	15,16	8	1	8.46	-1
5311	452506	28,29	6	0	7.48	-1
5313	7022	25,26	7	0	6.76	-1
5313	7022	27,28	4	16	-1	3.69
5313	7022	28,29	16	5	3.99	-1
5315	2930	01,02	3	14	-1	5.06
5315	2930	27,29	5	0	6.75	-1
5315	2930	28,29	7	0	8.72	-1
5317	454226	28,29	5	0	6.23	-1
5321	453470	15,16	12	1	12.68	-1
5321	453470	15,17	12	1	12.88	-1
5324	454050	27,28	0	7	-1	6.46
5338	454518	27,29	6	0	8.09	-1
5338	454518	28,29	6	0	7.48	-1
5350	23649	27,28	37	12	3.34	-1
5350	23649	27,29	37	0	49.92	-1
5350	23649	28,29	12	0	14.95	-1
5357	519109	23,24	1	34	-1	33.65
5360	453783	27,28	0	8	-1	7.39
5360	453783	28,29	8	0	9.97	-1
5365	454509	25,26	7	0	6.76	-1
5365	454509	27,28	6	0	6.5	-1
5366	454562	23,24	13	4	3.28	-1
5366	454562	25,26	7	0	6.76	-1
5370	453783	27,28	0	8	-1	7.39
5370	453783	28,29	8	0	9.97	-1
5373	801	30,31	25	7	3.97	-1
5374	453494	27,28	7	0	7.58	-1
5374	453494	30,31	6	0	6.67	-1
5375	453202	15,16	6	0	6.34	-1
5375	453202	16,17	0	11	-1	10.83
5381	387530	30,31	2	24	-1	10.79
5382	453846	15,17	0	11	-1	10.25
5391	551995	28,29	7	0	8.72	-1
5397	446531	16,17	0	6	-1	5.91
5401	453508	25,26	27	9	2.9	-1
5401	453508	27,28	9	1	9.75	-1
5413	560868	27,29	6	0	8.09	-1
5448	554742	16,17	0	6	-1	5.91
5467	551617	15,16	9	0	9.51	-1
5467	551617	16,17	0	7	-1	6.89

SEQ ID NO	CLUSTER	PAIR AB	CLONES A	CLONES B	RATIO PLUS	RATIO MINUS
5489	468672	15,16	6	0	6.34	-1
5489	468672	16,17	0	8	-1	7.88
5501	402836	12,13	130	63	2.13	-1
5501	402836	23,24	17	4	4.29	-1
5508	561707	27,29	6	0	8.09	-1
5508	561707	30,31	9	1	10.01	-1
5509	561180	15,16	11	2	5.81	-1
5513	562137	23,24	8	0	8.08	-1
5518	449356	15,17	7	21	-1	2.79
5518	449356	16,17	4	21	-1	5.17
5525	549511	15,17	0	7	-1	6.52
5525	549511	16,17	0	7	-1	6.89
5526	560700	16,17	0	6	-1	5.91
5535	452523	15,17	10	2	5.37	-1
5537	406092	18,19	16	2	9.14	-1
5537	406092	25,26	7	0	6.76	-1
5537	406092	27,28	1	26	-1	24.01
5537	406092	27,29	1	28	-1	20.76
5537	406092	30,31	13	4	3.61	-1
5542	235874	12,13	62	239	-1	3.73
5542	235874	12,14	62	317	-1	4.88
5542	235874	25,26	102	21	4.69	-1
5542	235874	27,28	73	16	4.94	-1
5542	235874	28,29	16	70	-1	3.51
5542	235874	30,31	119	9	14.71	-1
5550	452957	27,29	5	0	6.75	-1
5550	452957	28,29	6	0	7.48	-1
5554	455855	27,29	8	0	10.79	-1
5559	510254	15,16	17	1	17.97	-1
5559	510254	16,17	1	8	-1	7.88
5560	451812	27,29	7	1	9.44	-1
5565	450225	15,17	11	3	3.94	-1
5565	450225	27,28	1	24	-1	22.16
5565	450225	28,29	24	1	29.9	-1
5572	503122	25,26	8	178	-1	23.05
5572	503122	27,29	12	2	8.09	-1
5572	503122	30,31	22	98	-1	4
5578	446936	23,24	10	26	-1	2.57
5578	446936	25,26	17	38	-1	2.32
5578	446936	27,28	158	31	5.52	-1
5578	446936	27,29	158	27	7.89	-1
5589	453079	16,17	8	1	8.12	-1
5599	454226	28,29	5	0	6.23	-1
5600	452973	27,28	0	9	-1	8.31
5600	452973	28,29	9	2	5.61	-1
5606	452648	23,24	2	15	-1	7.42
5611	366607	27,28	1	12	-1	11.08
5611	366607	28,29	12	0	14.95	-1

SEQ ID NO	CLUSTER	PAIR AB	CLONES A	CLONES B	RATIO PLUS	RATIO MINUS
5617	521840	15,16	6	0	6.34	-1
5620	523674	28,29	5	0	6.23	-1
5624	452775	27,28	1	9	-1	8.31
5634	454460	27,28	0	13	-1	12.01
5634	454460	28,29	13	2	8.1	-1
5662	456001	28,29	10	1	12.46	-1
5665	450914	15,16	0	6	-1	5.68
5666	455855	27,29	8	0	10.79	-1
5688	400258	16,17	6	0	6.09	-1
5688	400258	27,28	7	0	7.58	-1
5697	2544	01,02	23	9	2.36	-1
5697	2544	03,04	13	30	-1	2.37
5699	402534	12,13	8	21	-1	2.54
5704	456567	28,29	5	0	6.23	-1
5710	455601	15,17	10	0	10.73	-1
5710	455601	16,17	8	0	8.12	-1
5712	402916	23,24	8	0	8.08	-1
5712	402916	27,28	22	5	4.76	-1
5712	402916	27,29	22	4	7.42	-1
5714	27586	12,13	7	22	-1	3.04
5714	27586	12,14	7	21	-1	2.86
5714	27586	21,22	9	0	8.85	-1
5714	27586	25,26	17	0	16.41	-1
5714	27586	30,31	24	0	26.69	-1
5732	407711	15,16	0	6	-1	5.68
5733	411113	16,17	0	6	-1	5.91
5742	400426	12,14	22	10	2.31	-1
5752	155374	15,16	6	0	6.34	-1
5752	155374	15,17	6	0	6.44	-1
5752	155374	27,28	27	1	29.24	-1
5752	155374	27,29	27	0	36.42	-1
5753	409612	25,26	6	0	5.79	-1
5759	1054	03,04	49	23	2.08	-1
5759	1054	12,14	54	24	2.36	-1
5759	1054	15,17	64	28	2.45	-1
5759	1054	18,20	3	19	-1	7.41
5759	1054	19,20	5	19	-1	5.08
5759	1054	27,29	64	31	2.79	-1
5759	1054	28,29	69	31	2.77	-1
5759	1054	30,31	27	15	2	-1
5761	400454	12,14	9	1	9.43	-1
5765	409589	27,29	5	0	6.75	-1
5768	20517	12,13	18	3	6.2	-1
5768	20517	13,14	3	18	-1	5.91
5769	413915	12,13	6	0	6.2	-1
5769	413915	12,14	6	0	6.29	-1
5772	401510	12,14	8	0	8.39	-1
5775	417259	15,17	4	14	-1	3.26

SEQ ID NO	CLUSTER	PAIR AB	CLONES A	CLONES B	RATIO PLUS	RATIO MINUS
5775	417259	16,17	1	14	-1	13.79
5776	20517	12,13	18	3	6.2	-1
5776	20517	13,14	3	18	-1	5.91
5778	402534	12,13	8	21	-1	2.54
5780	419255	15,16	11	0	11.63	-1
5780	419255	15,17	11	1	11.81	-1
5788	402070	27,28	1	9	-1	8.31
5788	402070	28,29	9	0	11.21	-1
5789	402070	27,28	1	9	-1	8.31
5789	402070	28,29	9	0	11.21	-1
5792	402353	12,13	13	4	3.36	-1
5794	163970	18,20	12	25	-1	2.44
5794	163970	19,20	7	25	-1	4.77
5794	163970	27,28	7	39	-1	5.15
5794	163970	28,29	39	7	6.94	-1
5794	163970	30,31	29	6	5.38	-1
5801	268336	15,16	8	1	8.46	-1
5807	20517	12,13	18	3	6.2	-1
5807	20517	13,14	3	18	-1	5.91
5822	420686	16,17	0	8	-1	7.88
5823	447579	23,24	3	13	-1	4.29
5823	447579	28,29	7	0	8.72	-1
5825	463824	15,16	6	0	6.34	-1
5825	463824	15,17	6	0	6.44	-1
5825	463824	27,28	0	8	-1	7.39
5825	463824	28,29	8	0	9.97	-1
5827	388688	27,29	8	2	5.4	-1
5827	388688	28,29	17	2	10.59	-1
5840	446964	15,17	1	12	-1	11.18
5860	403949	12,13	11	1	11.36	-1
5862	235874	12,13	62	239	-1	3.73
5862	235874	12,14	62	317	-1	4.88
5862	235874	25,26	102	21	4.69	-1
5862	235874	27,28	73	16	4.94	-1
5862	235874	28,29	16	70	-1	3.51
5862	235874	30,31	119	9	14.71	-1
5876	644342	27,29	6	0	8.09	-1
5897	644342	27,29	6	0	8.09	-1
5898	419479	23,24	2	11	-1	5.44
5906	451508	30,31	7	0	7.79	-1
5924	218416	16,17	0	6	-1	5.91
5933	463824	15,16	6	0	6.34	-1
5933	463824	15,17	6	0	6.44	-1
5933	463824	27,28	0	8	-1	7.39
5933	463824	28,29	8	0	9.97	-1
5934	389377	27,28	7	0	7.58	-1
5934	389377	30,31	10	1	11.12	-1
5943	18786	15,17	6	0	6.44	-1

SEQ ID NO	CLUSTER	PAIR AB	CLONES A	CLONES B	RATIO PLUS	RATIO MINUS
5943	18786	30,31	6	0	6.67	-1
5944	447494	15,16	26	8	3.44	-1
5966	1454	03,04	38	14	2.65	-1
5966	1454	12,13	37	15	2.55	-1
5966	1454	13,14	15	35	-1	2.3
5966	1454	25,26	12	3	3.86	-1
5966	1454	30,31	7	22	-1	2.83
5969	15296	27,28	6	0	6.5	-1
5979	446673	16,17	8	1	8.12	-1
5991	446341	28,29	6	0	7.48	-1
6002	379335	15,16	11	0	11.63	-1
6002	379335	15,17	11	0	11.81	-1
6003	228873	27,29	20	0	26.98	-1
6003	228873	28,29	14	0	17.44	-1
6004	446663	15,17	14	32	-1	2.13
6004	446663	16,17	6	32	-1	5.25
6004	446663	18,20	1	8	-1	9.36
6004	446663	19,20	0	8	-1	10.7

Table 6

Pt ID	Path ID	Grp	Anatom Loc	Size	Grade	Histo Grade	Local Invasion	Lymph Met	Lymph Met Incid	Reg Lymph Grade	Dist Met & Loc	Dist Met Grade	Comment
15	21	III	Ascending colon	4.0	T3	G2	Extending into subserosal adipose tissue	Pos	3/8	N1	Neg	MX	invasive adenocarcinoma, moderately differentiated; focal perineural invasion is seen
52	71	II	Cecum	9.0	T3	G3	Invasion through muscularis propria, subserosal involvement; ileocec. valve involvement	Neg	0/12	N0	Neg	M0	Hyperplastic polyp in appendix.
121	140	II	Sigmoid	6	T4	G2	Invasion of muscularis propria into serosa, involving submucosa of urinary bladder	Neg	0/34	N0	Neg	M0	Perineural invasion; donut anastomosis Neg. One tubulovillous and one tubular adenoma with no high grade dysplasia.
125	144	II	Cecum	6	T3	G2	Invasion through the muscularis propria into suserosal adipose tissue. Ileocecal junction.	Neg	0/19	N0	Neg	M0	patient history of metastatic melanoma
128	147	III	Transverse colon	5.0	T3	G2	Invasion of muscularis propria into percolonic fat	Pos	1/5	N1	Neg	M0	

Table 6

Pt ID	Path ID	Grp	Anatom Loc	Size	Grade	Histo Grade	Local Invasion	Lymph Met	Lymph Met Incid	Reg Lymph Grade	Dist Met & Loc	Dist Met Grade	Comment
130	149		Splenic flexure	5.5	T3		through wall and into surrounding adipose tissue	Pos	10/24	N2	Neg	M1	
133	152	II	Rectum	5.0	T3	G2	Invasion through muscularis propria into non-peritonealized pericolic tissue; gross configuration is annular.	Neg	0/9	N0	Neg	M0	Small separate tubular adenoma (0.4 cm)
141	160	IV	Cecum	5.5	T3	G2	Invasion of muscularis propria into pericolonic adipose tissue, but not through serosa. Arising from tubular adenoma.	Pos	7/21	N2	Pos - Liver	M1	Perineural invasion identified adjacent to metastatic adenocarcinoma.
156	175	III	Hepatic flexure	3.8	T3	G2	Invasion through mucsularis propria into subserosa/pericolic adipose, no serosal involvement. Gross configuration annular.	Pos	2/13	N1	Neg	M0	Separate tubolovillous and tubular adenomas

Table 6

Pt ID	Path ID	Grp	Anatom Loc	Size	Grade	Histo Grade	Local Invasion	Lymph Met	Lymph Met Incid	Reg Lymph Grade	Dist Met & Loc	Dist Met Grade	Comment
228	247	III	Rectum	5.8	T3	G2 to G3	Invasion through muscularis propria to involve subserosal, perirectoal adipose, and serosa	Pos	1/8	N1	Neg	MX	Hyperplastic polyps
264	283	II	Ascending colon	5.5	T3	G2	Invasion through muscularis propria into subserosal adipose tissue.	Neg	0/10	N0	Neg	M0	Tubulovillous adenoma with high grade dysplasia
266	285	III	Transverse colon	9	T3	G2	Invades through muscularis propria to involve pericolonic adipose, extends to serosa.	Neg	0/15	N1	Pos - Mesenteric deposit	MX	
268	287	I	Cecum	6.5	T2	G2	Invades full thickness of muscularis propria, but mesenteric adipose free of malignancy	Neg	0/12	N0	Neg	M0	
278	297	III	Rectum	4	T3	G2	Invasion into perirectal adipose tissue.	Pos	7/10	N2	Neg	M0	Descending colon polyps, no HGD or carcinoma identified..

Table 6

Pt ID	Path ID	Grp	Anatom Loc	Size	Grade	Histo Grade	Local Invasion	Lymph Met	Lymph Met Incid	Reg Lymph Grade	Dist Met & Loc	Dist Met Grade	Comment
296	315	III	Cecum	5.5	T3	G2	Invasion through muscularis propria and invades pericolic adipose tissue. Ileocecal junction.	Pos	2/12	N1	Neg	M0	Tubulovillous adenoma (2.0 cm) with no high grade dysplasia. Neg. liver biopsy.
339	358	II	Rectosigmoid	6	T3	G2	Extends into perirectal fat but does not reach serosa	Neg	0/6	N0	Neg	M0	1 hyperplastic polyp identified
341	360	II	Ascending colon	2 cm invasive	T3	G2	Invasion through muscularis propria to involve pericolonic fat. Arising from villous adenoma.	Neg	0/4	N0	Neg	MX	
356	375	II	Sigmoid	6.5	T3	G2	Through colon wall into subserosal adipose tissue. No serosal spread seen.	Neg	0/4	N0	Neg	M0	
360	412	III	Ascending colon	4.3	T3	G2	Invasion thru muscularis propria to pericolonic fat	Pos	1/5	N1	Neg	M0	Two mucosal polyps
392	444	IV	Ascending colon	2	T3	G2	Invasion through muscularis propria into subserosal adipose tissue, not serosa.	Pos	1/6	N1	Pos - Liver	M1	Tumor arising at prior ileocolic surgical anastomosis.

Table 6

Pt ID	Path ID	Grp	Anatom Loc	Size	Grade	Histo Grade	Local Invasion	Lymph Met	Lymph Met Incid	Reg Lymph Grade	Dist Met & Loc	Dist Met Grade	Comment
393	445	II	Cecum	6.0	T3	G2	Cecum, invades through muscularis propria to involve subserosal adipose tissue but not serosa.	Neg	0/21	N0	Neg	M0	
413	465	IV	Cecum	4.8	T3	G2	Invasive through muscularis to involve periserosal fat; abutting ileocecal junction.	Neg	0/7	N0	Pos - Liver	M1	rediagnosis of oophorectomy path to metastatic colon cancer.
505	383	IV		7.5	T3	G2	Invasion through muscularis propria involving pericolic adipose, serosal surface uninvolved	Pos	2/17	N1	Pos - Liver	M1	Anatomical location of primary not notated in report. Evidence of chronic colitis.
517	395	IV	Sigmoid	3	T3	G2	penetrates muscularis propria, involves pericolonic fat.	Pos	6/6	N2	Neg	M0	No mention of distant met in report

Table 6

Pt ID	Path ID	Grp	Anatom Loc	Size	Grade	Histo Grade	Local Invasion	Lymph Met	Lymph Met Incid	Reg Lymph Grade	Dist Met & Loc	Dist Met Grade	Comment
534	553	II	Ascending colon	12	T3	G3	Invasion through the muscularis propria involving pericolic fat. Serosa free of tumor.	Neg	0/8	N0	Neg	M0	Omentum with fibrosis and fat necrosis. Small bowel with acute and chronic serositis, focal abscess and adhesions.
546	565	IV	Ascending colon	5.5	T3	G2	Invasion through muscularis propria extensively through submucosal and extending to serosa.	Pos	6/12	N2	Pos - Liver	M1	
577	596	II	Cecum	11.5	T3	G2	Invasion through the bowel wall, into suberosal adipose. Serosal surface free of tumor.	Neg	0/58	N0	Neg	M0	Appendix dilated and fibrotic, but not involved by tumor

Table 6

Pt ID	Path ID	Grp	Anatom Loc	Size	Grade	Histo Grade	Local Invasion	Lymph Met	Lymph Met Incid	Reg Lymph Grade	Dist Met & Loc	Dist Met Grade	Comment
695	714	II	Cecum	14.0	T3	G2	extending through bowel wall into serosal fat	Neg	0/22	N0	Neg	MX	moderately differentiated adenocarcinoma with mucinous diferentiation (% not stated), tubular adenoma and hyperplstic polyps present,
784	803	IV	Ascending colon	3.5	T3	G3	through muscularis propria into pericolic soft tissues	Pos	5/17	N2	Pos - Liver	M1	invasive poorly differentiated adenosquamous carcinoma
786	805	IV	Descending colon	9.5	T3	G2	through muscularis propria into pericolic fat, but not at serosal surface	Neg	0/12	N0	Pos - Liver	M1	moderately differentiated invasive adenocarcinoma
787	806	II	Rectosigmoid	2.5	T3	G2-G3	Invasion of muscularis propria into soft tissue	Neg		N0	Neg	MX	Peritumoral lymphocytic response; 5 LN examined in pericolic fat, no metastatases observed.
789	808	IV	Cecum	5.0	T3	G2-G3	Extending through muscularis propria into pericolonic fat	Pos	5/10	N2	Pos - Liver	M1	Three fungating lesions examined.

Table 6

Pt ID	Path ID	Grp	Anatom Loc	Size	Grade	Histo Grade	Local Invasion	Lymph Met	Lymph Met Incid	Reg Lymph Grade	Dist Met & Loc	Dist Met Grade	Comment
790	809	IV	Rectum	6.8	T3	G1-G2	Invading through muscularis propria into perirectal fat	Pos	3/13	N1	Pos - Liver	M1	
791	810	IV	Ascending colon	5.8	T3	G3	Through the muscularis propria into pericolic fat	Pos	13/25	N2	Pos - Liver	M1	poorly differentiated invasive colonic adenocarcinoma
888	908	IV	Ascending colon	2.0	T2	G1	Into muscularis propria	Pos	3/21	N0	Pos - Liver	M1	well to moderately differentiated adenocarcinomas; this patient has tumors of the ascending colon and the sigmoid colon
889	909	IV	Cecum	4.8	T3	G2	Through muscularis propria int subserosal tissue	Pos	1/4	N1	Pos - Liver	M1	moderately differentiated adenocarcinoma
890	910	IV	Ascending colon		T3	G2	Through muscularis propria into subserosa.	Pos	11/15	N2	Pos - Liver	M1	
891	911	IV	Rectum	5.2	T3	G2	Invasion through muscularis propria into perirectal soft tissue	Pos	4/15	N2	Pos - Liver	M1	Perineural invasion present.

Table 6

Pt ID	Path ID	Grp	Anatom Loc	Size	Grade	Histo Grade	Local Invasion	Lymph Met	Lymph Met Incid	Reg Lymph Grade	Dist Met & Loc	Dist Met Grade	Comment
892	912	IV	Sigmoid	5.0	T3	G2	Invasion into pericolic sort tissue. Tumor focally invading skeletal muscle attached to colon.	Pos	1/28	N1	Pos - Liver, left and right lobe, omentum	M1	Perineural invasion present, extensive. Patient with a history of colon cancer.
893	913	IV	Transverse colon	6.0	T3	G2-G3	Through muscularis propria into pericolic fat	Pos	14/17	N2	Pos - Liver	M1	Perineural invasion focally present. Omentum mass, but resection with no tumor identified.
989	1009	IV	Sigmoid	6.0	T3	G2	Invasion through colon wall and focally involving subserosal tissue.	Pos	1/7	N1	Pos - Liver	M1	Primary adenocarcinom a arising from tubulovillous adenoma.

Table 8

SEQ ID NO	SpotID	T/N Colon >2x	T/N Colon <halfx	T/N Colon Num Ratios
6	43971	0.0	75.0	8.0
31	40453	0.0	42.9	7.0
40	40457	0.0	71.4	7.0
44	46308	0.0	50.0	8.0
50	45610	0.0	62.5	8.0
70	42816	0.0	50.0	8.0
72	44673	0.0	50.0	8.0
74	42422	0.0	37.5	8.0
77	43983	0.0	37.5	8.0
81	44679	0.0	50.0	8.0
84	42418	0.0	37.5	8.0
133	39755	0.0	42.9	7.0
139	44916	0.0	50.0	8.0
147	45618	0.0	37.5	8.0
149	44926	0.0	50.0	8.0
152	44216	0.0	37.5	8.0
153	38367	0.0	42.9	7.0
158	38357	0.0	57.1	7.0
161	41869	0.0	42.9	7.0
162	43508	0.0	37.5	8.0
164	38365	0.0	57.1	7.0
166	39069	0.0	42.9	7.0
171	39061	0.0	57.1	7.0
180	39767	0.0	42.9	7.0
184	43881	0.0	37.5	8.0
186	43873	0.0	37.5	8.0
195	39769	0.0	57.1	7.0
196	39775	0.0	57.1	7.0
197	46330	0.0	37.5	8.0
198	42471	0.0	37.5	8.0
200	41173	0.0	42.9	7.0
202	42479	0.0	50.0	8.0
216	39621	0.0	42.9	7.0
217	46007	0.0	50.0	8.0
218	46015	0.0	62.5	8.0
225	45301	0.0	37.5	8.0
228	45303	0.0	37.5	8.0
250	41033	0.0	57.1	7.0
260	41035	0.0	57.1	7.0
268	41027	0.0	42.9	7.0
274	41737	0.0	42.9	7.0
301	39647	0.0	42.9	7.0
307	38943	0.0	42.9	7.0

Table 8

SEQ ID NO	SpotID	T/N Colon >2x	T/N Colon <halfx	T/N Colon Num Ratios
309	38939	0.0	42.9	7.0
315	44939	0.0	37.5	8.0
324	42827	0.0	37.5	8.0
326	38231	0.0	42.9	7.0
334	42819	0.0	37.5	8.0
352	43521	0.0	62.5	8.0
358	45633	0.0	50.0	8.0
364	44931	0.0	50.0	8.0
365	45635	0.0	50.0	8.0
366	46345	0.0	37.5	8.0
390	44947	0.0	50.0	8.0
391	44247	0.0	50.0	8.0
403	43501	0.0	37.5	8.0
406	43489	0.0	50.0	8.0
407	44951	0.0	37.5	8.0
413	41755	0.0	42.9	7.0
420	43541	0.0	37.5	8.0
424	44953	0.0	50.0	8.0
426	46365	0.0	62.5	8.0
432	44909	0.0	50.0	8.0
435	38210	0.0	42.9	7.0
443	38928	0.0	42.9	7.0
444	44911	0.0	50.0	8.0
446	46361	0.0	50.0	8.0
450	39632	0.0	42.9	7.0
452	39620	0.0	42.9	7.0
455	46363	0.0	62.5	8.0
458	41736	0.0	57.1	7.0
464	38944	0.0	42.9	7.0
467	45605	0.0	62.5	8.0
468	45609	0.0	100.0	8.0
471	38228	0.0	57.1	7.0
472	41740	0.0	42.9	7.0
476	41032	0.0	42.9	7.0
480	39638	0.0	57.1	7.0
482	41760	0.0	42.9	7.0
490	41754	0.0	71.4	7.0
496	39980	0.0	57.1	7.0
497	46315	0.0	37.5	8.0
507	40674	0.0	42.9	7.0
509	38566	0.0	57.1	7.0
519	38590	0.0	42.9	7.0
539	42813	0.0	37.5	8.0

Table 8

SEQ ID NO	SpotID	T/N Colon >2x	T/N Colon <halfx	T/N Colon Num Ratios
554	43515	0.0	50.0	8.0
558	41400	0.0	42.9	7.0
560	40702	0.0	42.9	7.0
563	40000	0.0	42.9	7.0
573	38185	0.0	42.9	7.0
582	39587	0.0	42.9	7.0
587	44925	0.0	50.0	8.0
592	39597	0.0	57.1	7.0
593	39593	0.0	42.9	7.0
603	38893	0.0	42.9	7.0
606	42842	0.0	62.5	8.0
607	43540	0.0	50.0	8.0
611	42840	0.0	50.0	8.0
614	43548	0.0	37.5	8.0
617	43538	0.0	50.0	8.0
618	46340	0.0	37.5	8.0
644	39586	0.0	42.9	7.0
651	45656	0.0	37.5	8.0
654	44254	0.0	50.0	8.0
655	45652	0.0	37.5	8.0
666	46285	0.0	37.5	8.0
667	40290	0.0	42.9	7.0
668	40304	0.0	42.9	7.0
680	39592	0.0	42.9	7.0
682	44950	0.0	37.5	8.0
691	45571	0.0	37.5	8.0
702	45654	0.0	37.5	8.0
703	45660	0.0	37.5	8.0
705	40292	0.0	42.9	7.0
711	40294	0.0	42.9	7.0
722	46364	0.0	37.5	8.0
724	38892	0.0	42.9	7.0
733	40998	0.0	57.1	7.0
736	40996	0.0	57.1	7.0
738	41712	0.0	42.9	7.0
757	38196	0.0	42.9	7.0
773	44881	0.0	37.5	8.0
776	39610	0.0	42.9	7.0
790	41016	0.0	42.9	7.0
793	39942	0.0	42.9	7.0
795	41718	0.0	42.9	7.0
798	39938	0.0	42.9	7.0
801	46289	0.0	37.5	8.0

Table 8

SEQ ID NO	SpotID	T/N Colon >2x	T/N Colon <halfx	T/N Colon Num Ratios
804	41024	0.0	42.9	7.0
807	38536	0.0	71.4	7.0
810	39948	0.0	42.9	7.0
816	39236	0.0	71.4	7.0
818	38540	0.0	42.9	7.0
820	41720	0.0	42.9	7.0
821	41728	0.0	42.9	7.0
831	46293	0.0	37.5	8.0
843	41358	0.0	71.4	7.0
846	39954	0.0	57.1	7.0
850	41360	0.0	42.9	7.0
864	38550	0.0	42.9	7.0
866	38409	0.0	31.7	41.0
868	40652	0.0	42.9	7.0
881	42070	0.0	57.1	7.0
883	42072	0.0	57.1	7.0
884	42074	0.0	42.9	7.0
886	40658	0.0	42.9	7.0
889	41372	0.0	42.9	7.0
895	40670	0.0	42.9	7.0
905	38147	0.0	42.9	7.0
915	39563	0.0	42.9	7.0
916	38863	0.0	42.9	7.0
918	38859	0.0	42.9	7.0
937	40346	0.0	42.9	7.0
941	41046	0.0	42.9	7.0
945	45605	0.0	62.5	8.0
946	40326	0.0	71.4	7.0
948	40328	0.0	42.9	7.0
950	41032	0.0	42.9	7.0
955	40342	0.0	42.9	7.0
960	41742	0.0	42.9	7.0
962	41056	0.0	42.9	7.0
972	43215	0.0	50.0	8.0
974	43203	0.0	37.5	8.0
975	42497	0.0	37.5	8.0
981	42505	0.0	62.5	8.0
984	43209	0.0	50.0	8.0
985	38431	0.0	57.1	7.0
986	24379	0.0	36.6	41.0
989	43909	0.0	100.0	8.0
991	41667	0.0	42.9	7.0
992	40985	0.0	42.9	7.0

Table 8

SEQ ID NO	SpotID	T/N Colon >2x	T/N Colon <halfx	T/N Colon Num Ratios
996	38873	0.0	42.9	7.0
998	38875	0.0	42.9	7.0
999	40977	0.0	42.9	7.0
1001	38169	0.0	42.9	7.0
1005	40987	0.0	42.9	7.0
1006	40261	0.0	42.9	7.0
1010	39809	0.0	42.9	7.0
1015	40973	0.0	42.9	7.0
1016	39579	0.0	42.9	7.0
1018	40965	0.0	42.9	7.0
1024	40263	0.0	42.9	7.0
1026	39811	0.0	57.1	7.0
1028	40513	0.0	57.1	7.0
1031	39821	0.0	42.9	7.0
1032	38871	0.0	42.9	7.0
1038	38175	0.0	42.9	7.0
1053	40267	0.0	42.9	7.0
1054	40273	0.0	42.9	7.0
1057	40525	0.0	42.9	7.0
1064	41685	0.0	42.9	7.0
1066	40991	0.0	42.9	7.0
1067	41217	0.0	71.4	7.0
1072	39907	0.0	57.1	7.0
1076	41221	0.0	42.9	7.0
1085	42027	0.0	42.9	7.0
1106	41227	0.0	42.9	7.0
1112	41923	0.0	71.4	7.0
1114	41223	0.0	42.9	7.0
1124	38503	0.0	42.9	7.0
1130	41933	0.0	42.9	7.0
1132	40623	0.0	42.9	7.0
1135	38527	0.0	42.9	7.0
1138	39905	0.0	42.9	7.0
1141	40613	0.0	42.9	7.0
1142	40615	0.0	42.9	7.0
1146	39925	0.0	42.9	7.0
1147	41333	0.0	42.9	7.0
1152	40627	0.0	42.9	7.0
1153	41339	0.0	42.9	7.0
1157	39933	0.0	42.9	7.0
1159	40629	0.0	42.9	7.0
1166	42045	0.0	42.9	7.0
1167	39921	0.0	42.9	7.0

Table 8

SEQ ID NO	SpotID	T/N Colon >2x	T/N Colon <halfx	T/N Colon Num Ratios
1170	40637	0.0	71.4	7.0
1181	42035	0.0	42.9	7.0
1186	43931	0.0	37.5	8.0
1189	46029	0.0	37.5	8.0
1193	42523	0.0	37.5	8.0
1199	39829	0.0	42.9	7.0
1203	43923	0.0	62.5	8.0
1206	43229	0.0	50.0	8.0
1208	44629	0.0	37.5	8.0
1220	43219	0.0	50.0	8.0
1222	39835	0.0	100.0	7.0
1231	40529	0.0	100.0	7.0
1234	43921	0.0	37.5	8.0
1238	45319	0.0	50.0	8.0
1241	45313	0.0	37.5	8.0
1245	44627	0.0	37.5	8.0
1246	44631	0.0	37.5	8.0
1250	40531	0.0	42.9	7.0
1255	46035	0.0	62.5	8.0
1270	41233	0.0	85.7	7.0
1274	40537	0.0	42.9	7.0
1280	44637	0.0	37.5	8.0
1281	45335	0.0	37.5	8.0
1290	40535	0.0	57.1	7.0
1292	41241	0.0	42.9	7.0
1293	41943	0.0	42.9	7.0
1311	41947	0.0	42.9	7.0
1382	38765	0.0	57.1	7.0
1392	39467	0.0	57.1	7.0
1398	42861	0.0	62.5	8.0
1399	43559	0.0	37.5	8.0
1401	38146	0.0	37.5	8.0
1402	43553	0.0	37.5	8.0
1408	43555	0.0	42.9	7.0
1412	39463	0.0	71.4	7.0
1413	43557	0.0	42.9	7.0
1415	40175	0.0	42.9	7.0
1418	40167	0.0	42.9	7.0
1422	40260	0.0	37.5	8.0
1429	44965	0.0	37.5	8.0
1430	44969	0.0	42.9	7.0
1432	44967	0.0	42.9	7.0
1442	40165	0.0	42.9	7.0

Table 8

SEQ ID NO	SpotID	T/N Colon >2x	T/N Colon <halfx	T/N Colon Num Ratios
1446	44265	0.0	42.9	7.0
1448	38162	0.0	37.5	8.0
1450	41678	0.0	37.5	8.0
1452	40974	0.0	37.5	8.0
1454	41674	0.0	37.5	8.0
1458	46379	0.0	37.5	8.0
1463	41670	0.0	37.5	8.0
1467	42871	0.0	50.0	8.0
1472	38172	0.0	37.5	8.0
1474	44273	0.0	50.0	8.0
1475	44277	0.0	50.0	8.0
1476	43569	0.0	37.5	8.0
1483	38872	0.0	50.0	8.0
1486	43577	0.0	50.0	8.0
1492	39576	0.0	57.1	7.0
1493	44977	0.0	50.0	8.0
1501	39580	0.0	62.5	8.0
1502	45689	0.0	37.5	8.0
1503	44985	0.0	50.0	8.0
1504	45681	0.0	75.0	8.0
1507	39578	0.0	57.1	7.0
1508	40984	0.0	50.0	8.0
1510	39584	0.0	42.9	7.0
1512	40990	0.0	37.5	8.0
1514	46391	0.0	37.5	8.0
1516	41682	0.0	42.9	7.0
1526	38769	0.0	42.9	7.0
1530	44612	0.0	37.5	8.0
1532	44622	0.0	37.5	8.0
1548	39473	0.0	57.1	7.0
1550	42281	0.0	42.9	7.0
1553	45320	0.0	37.5	8.0
1554	39479	0.0	42.9	7.0
1560	42287	0.0	42.9	7.0
1561	45314	0.0	37.5	8.0
1562	45326	0.0	37.5	8.0
1567	42273	0.0	42.9	7.0
1568	43210	0.0	37.5	8.0
1573	43910	0.0	37.5	8.0
1575	42279	0.0	42.9	7.0
1584	46034	0.0	37.5	8.0
1585	43934	0.0	50.0	8.0
1586	43936	0.0	50.0	8.0

Table 8

SEQ ID NO	SpotID	T/N Colon >2x	T/N Colon <halfx	T/N Colon Num Ratios
1587	44632	0.0	50.0	8.0
1588	43222	0.0	50.0	8.0
1589	40187	0.0	42.9	7.0
1590	44626	0.0	50.0	8.0
1597	44640	0.0	50.0	8.0
1599	43232	0.0	37.5	8.0
1601	43930	0.0	37.5	8.0
1603	44628	0.0	37.5	8.0
1609	44638	0.0	37.5	8.0
1610	45332	0.0	50.0	8.0
1611	46042	0.0	37.5	8.0
1613	43228	0.0	37.5	8.0
1615	43932	0.0	37.5	8.0
1619	40183	0.0	57.1	7.0
1623	44260	0.0	37.5	8.0
1628	43562	0.0	62.5	8.0
1632	43564	0.0	37.5	8.0
1634	45666	0.0	50.0	8.0
1636	44968	0.0	37.5	8.0
1638	42852	0.0	37.5	8.0
1642	44974	0.0	50.0	8.0
1645	41587	0.0	42.9	7.0
1646	44266	0.0	37.5	8.0
1647	44268	0.0	37.5	8.0
1648	44962	0.0	37.5	8.0
1653	44972	0.0	37.5	8.0
1654	45668	0.0	50.0	8.0
1662	41593	0.0	42.9	7.0
1664	45676	0.0	50.0	8.0
1667	42866	0.0	62.5	8.0
1669	44274	0.0	37.5	8.0
1673	42874	0.0	50.0	8.0
1675	42876	0.0	37.5	8.0
1679	42289	0.0	57.1	7.0
1681	42880	0.0	37.5	8.0
1682	43580	0.0	50.0	8.0
1686	46384	0.0	37.5	8.0
1689	45682	0.0	37.5	8.0
1698	46396	0.0	50.0	8.0
1703	38406	0.0	57.1	7.0
1705	44282	0.0	37.5	8.0
1706	46400	0.0	37.5	8.0
1717	46388	0.0	37.5	8.0

Table 8

SEQ ID NO	SpotID	T/N Colon >2x	T/N Colon <halfx	T/N Colon Num Ratios
1722	38416	0.0	42.9	7.0
1727	42301	0.0	42.9	7.0
1728	44978	0.0	37.5	8.0
1729	42543	0.0	37.5	8.0
1732	42535	0.0	37.5	8.0
1733	45684	0.0	50.0	8.0
1737	44990	0.0	50.0	8.0
1738	45686	0.0	62.5	8.0
1739	46390	0.0	37.5	8.0
1740	42531	0.0	50.0	8.0
1746	43243	0.0	37.5	8.0
1747	43947	0.0	50.0	8.0
1749	46055	0.0	50.0	8.0
1753	44651	0.0	37.5	8.0
1756	45347	0.0	37.5	8.0
1757	42547	0.0	37.5	8.0
1758	39816	0.0	42.9	7.0
1760	44643	0.0	50.0	8.0
1763	42555	0.0	37.5	8.0
1764	39114	0.0	57.1	7.0
1770	43945	0.0	37.5	8.0
1771	44647	0.0	37.5	8.0
1776	45359	0.0	37.5	8.0
1777	42551	0.0	50.0	8.0
1781	46049	0.0	37.5	8.0
1785	42545	0.0	37.5	8.0
1787	43261	0.0	37.5	8.0
1788	44657	0.0	50.0	8.0
1793	43249	0.0	37.5	8.0
1794	43255	0.0	37.5	8.0
1796	43959	0.0	50.0	8.0
1797	40524	0.0	42.9	7.0
1801	40526	0.0	42.9	7.0
1808	43961	0.0	50.0	8.0
1814	44661	0.0	50.0	8.0
1816	40520	0.0	42.9	7.0
1819	46075	0.0	50.0	8.0
1821	46079	0.0	50.0	8.0
1822	45375	0.0	37.5	8.0
1823	41222	0.0	42.9	7.0
1826	45367	0.0	37.5	8.0
1827	46067	0.0	37.5	8.0
1831	41224	0.0	42.9	7.0

Table 8

SEQ ID NO	SpotID	T/N Colon >2x	T/N Colon <halfx	T/N Colon Num Ratios
1834	41230	0.0	57.1	7.0
1836	39204	0.0	42.9	7.0
1845	38504	0.0	42.9	7.0
1850	40612	0.0	42.9	7.0
1851	40616	0.0	42.9	7.0
1854	40614	0.0	42.9	7.0
1855	40624	0.0	42.9	7.0
1859	39912	0.0	42.9	7.0
1861	39918	0.0	42.9	7.0
1868	39906	0.0	42.9	7.0
1870	38528	0.0	42.9	7.0
1875	39226	0.0	42.9	7.0
1885	38514	0.0	42.9	7.0
1888	38522	0.0	42.9	7.0
1891	39230	0.0	42.9	7.0
1892	39922	0.0	42.9	7.0
1898	39924	0.0	42.9	7.0
1906	39936	0.0	42.9	7.0
1907	40626	0.0	42.9	7.0
1913	41240	0.0	57.1	7.0
1916	40225	0.0	42.9	7.0
1922	41641	0.0	42.9	7.0
1927	42036	0.0	42.9	7.0
1929	41938	0.0	42.9	7.0
1932	40235	0.0	42.9	7.0
1935	38117	0.0	42.9	7.0
1944	40929	0.0	42.9	7.0
1946	41952	0.0	42.9	7.0
1949	39527	0.0	57.1	7.0
1950	39533	0.0	42.9	7.0
1954	41944	0.0	42.9	7.0
1957	42046	0.0	42.9	7.0
1963	41342	0.0	42.9	7.0
1964	39535	0.0	42.9	7.0
1969	40544	0.0	42.9	7.0
1970	38821	0.0	42.9	7.0
1971	40231	0.0	42.9	7.0
1972	41647	0.0	42.9	7.0
1973	41344	0.0	42.9	7.0
1977	38823	0.0	42.9	7.0
1980	40943	0.0	42.9	7.0
1988	38831	0.0	42.9	7.0
1990	38127	0.0	42.9	7.0

Table 8

SEQ ID NO	SpotID	T/N Colon >2x	T/N Colon <halfx	T/N Colon Num Ratios
1992	42044	0.0	42.9	7.0
2007	40945	0.0	42.9	7.0
2008	40953	0.0	42.9	7.0
2013	38135	0.0	42.9	7.0
2015	40959	0.0	42.9	7.0
2022	40249	0.0	42.9	7.0
2034	39551	0.0	42.9	7.0
2036	40949	0.0	42.9	7.0
2038	41651	0.0	42.9	7.0
2042	38143	0.0	42.9	7.0
2043	38835	0.0	42.9	7.0
2045	38843	0.0	42.9	7.0
2060	41987	0.0	42.9	7.0
2068	40587	0.0	42.9	7.0
2072	39875	0.0	42.9	7.0
2076	40589	0.0	42.9	7.0
2077	38471	0.0	42.9	7.0
2079	38483	0.0	42.9	7.0
2081	41283	0.0	42.9	7.0
2120	39195	0.0	42.9	7.0
2121	39891	0.0	42.9	7.0
2125	39193	0.0	42.9	7.0
2130	39199	0.0	42.9	7.0
2158	40593	0.0	42.9	7.0
2163	40603	0.0	42.9	7.0
2177	42009	0.0	42.9	7.0
2185	39526	0.0	42.9	7.0
2187	39536	0.0	42.9	7.0
2193	40942	0.0	42.9	7.0
2195	38120	0.0	42.9	7.0
2199	40238	0.0	42.9	7.0
2202	40240	0.0	42.9	7.0
2204	39522	0.0	42.9	7.0
2206	39534	0.0	42.9	7.0
2208	42011	0.0	42.9	7.0
2214	42013	0.0	42.9	7.0
2224	38132	0.0	42.9	7.0
2229	40256	0.0	42.9	7.0
2235	42343	0.0	37.5	8.0
2236	43041	0.0	37.5	8.0
2237	38144	0.0	42.9	7.0
2239	39548	0.0	57.1	7.0
2243	38842	0.0	42.9	7.0

Table 8

SEQ ID NO	SpotID	T/N Colon >2x	T/N Colon <halfx	T/N Colon Num Ratios
2247	38142	0.0	42.9	7.0
2250	38138	0.0	42.9	7.0
2257	39552	0.0	57.1	7.0
2263	39544	0.0	42.9	7.0
2270	41650	0.0	42.9	7.0
2271	40952	0.0	42.9	7.0
2272	41652	0.0	42.9	7.0
2278	38470	0.0	42.9	7.0
2279	40954	0.0	42.9	7.0
2288	43753	0.0	50.0	8.0
2290	39176	0.0	57.1	7.0
2293	39874	0.0	42.9	7.0
2294	40590	0.0	42.9	7.0
2300	40592	0.0	42.9	7.0
2304	41292	0.0	42.9	7.0
2312	39180	0.0	42.9	7.0
2314	41294	0.0	42.9	7.0
2323	39192	0.0	42.9	7.0
2326	39888	0.0	42.9	7.0
2327	40584	0.0	42.9	7.0
2328	41282	0.0	42.9	7.0
2329	41990	0.0	42.9	7.0
2336	39184	0.0	42.9	7.0
2338	44459	0.0	62.5	8.0
2340	40586	0.0	42.9	7.0
2341	41992	0.0	42.9	7.0
2342	44457	0.0	37.5	8.0
2345	40580	0.0	42.9	7.0
2346	39186	0.0	85.7	7.0
2347	43747	0.0	50.0	8.0
2349	41288	0.0	42.9	7.0
2350	41986	0.0	42.9	7.0
2352	38494	0.0	71.4	7.0
2353	39188	0.0	85.7	7.0
2354	41996	0.0	42.9	7.0
2359	40608	0.0	42.9	7.0
2364	45165	0.0	50.0	8.0
2367	41312	0.0	42.9	7.0
2368	39198	0.0	42.9	7.0
2370	41306	0.0	42.9	7.0
2371	39904	0.0	57.1	7.0
2374	45163	0.0	37.5	8.0
2376	42002	0.0	42.9	7.0

Table 8

SEQ ID NO	SpotID	T/N Colon >2x	T/N Colon <halfx	T/N Colon Num Ratios
2380	41310	0.0	42.9	7.0
2383	39200	0.0	42.9	7.0
2386	42899	0.0	50.0	8.0
2388	45869	0.0	37.5	8.0
2390	42901	0.0	37.5	8.0
2393	45709	0.0	62.5	8.0
2400	42893	0.0	50.0	8.0
2404	43585	0.0	37.5	8.0
2408	43599	0.0	50.0	8.0
2412	43587	0.0	37.5	8.0
2413	44301	0.0	50.0	8.0
2414	46411	0.0	37.5	8.0
2415	42909	0.0	62.5	8.0
2422	42895	0.0	37.5	8.0
2423	44995	0.0	37.5	8.0
2424	42911	0.0	50.0	8.0
2426	45865	0.0	37.5	8.0
2429	42885	0.0	37.5	8.0
2432	42887	0.0	50.0	8.0
2434	45705	0.0	37.5	8.0
2439	42012	0.0	42.9	7.0
2442	43593	0.0	37.5	8.0
2448	42905	0.0	37.5	8.0
2449	44303	0.0	50.0	8.0
2456	45697	0.0	50.0	8.0
2468	44305	0.0	62.5	8.0
2469	43609	0.0	37.5	8.0
2471	45009	0.0	50.0	8.0
2475	44317	0.0	50.0	8.0
2476	45719	0.0	37.5	8.0
2477	43761	0.0	50.0	8.0
2478	46431	0.0	50.0	8.0
2480	44311	0.0	62.5	8.0
2483	45017	0.0	50.0	8.0
2484	46421	0.0	50.0	8.0
2485	44313	0.0	50.0	8.0
2487	45019	0.0	37.5	8.0
2489	46417	0.0	37.5	8.0
2491	46423	0.0	37.5	8.0
2496	45713	0.0	37.5	8.0
2498	46425	0.0	37.5	8.0
2500	45013	0.0	37.5	8.0
2502	44319	0.0	37.5	8.0

Table 8

SEQ ID NO	SpotID	T/N Colon >2x	T/N Colon <halfx	T/N Colon Num Ratios
2503	45723	0.0	37.5	8.0
2504	46427	0.0	37.5	8.0
2505	42534	0.0	37.5	8.0
2511	43938	0.0	37.5	8.0
2516	43950	0.0	37.5	8.0
2517	45360	0.0	37.5	8.0
2518	43944	0.0	37.5	8.0
2524	45348	0.0	37.5	8.0
2527	46052	0.0	37.5	8.0
2532	43946	0.0	37.5	8.0
2534	43236	0.0	37.5	8.0
2539	44650	0.0	37.5	8.0
2541	43242	0.0	50.0	8.0
2544	43244	0.0	50.0	8.0
2549	46056	0.0	50.0	8.0
2550	42556	0.0	37.5	8.0
2551	43262	0.0	50.0	8.0
2555	45169	0.0	37.5	8.0
2560	42550	0.0	37.5	8.0
2563	42552	0.0	37.5	8.0
2564	43966	0.0	50.0	8.0
2581	43968	0.0	37.5	8.0
2582	42554	0.0	50.0	8.0
2591	44660	0.0	37.5	8.0
2592	45362	0.0	37.5	8.0
2596	45376	0.0	62.5	8.0
2601	45364	0.0	37.5	8.0
2604	45374	0.0	37.5	8.0
2605	46066	0.0	37.5	8.0
2608	45368	0.0	37.5	8.0
2609	46078	0.0	50.0	8.0
2613	44668	0.0	50.0	8.0
2614	45370	0.0	37.5	8.0
2619	43592	0.0	37.5	8.0
2620	45875	0.0	37.5	8.0
2621	46068	0.0	75.0	8.0
2623	42882	0.0	37.5	8.0
2629	43588	0.0	37.5	8.0
2638	44296	0.0	37.5	8.0
2639	43401	0.0	50.0	8.0
2641	44298	0.0	37.5	8.0
2642	45710	0.0	50.0	8.0
2646	45008	0.0	50.0	8.0

Table 8

SEQ ID NO	SpotID	T/N Colon >2x	T/N Colon <halfx	T/N Colon Num Ratios
2647	42910	0.0	62.5	8.0
2648	43596	0.0	75.0	8.0
2649	45706	0.0	37.5	8.0
2655	46410	0.0	37.5	8.0
2658	44994	0.0	50.0	8.0
2662	45708	0.0	50.0	8.0
2666	46416	0.0	37.5	8.0
2667	42912	0.0	37.5	8.0
2671	42902	0.0	37.5	8.0
2673	44300	0.0	37.5	8.0
2676	42904	0.0	50.0	8.0
2677	43598	0.0	50.0	8.0
2686	42906	0.0	50.0	8.0
2688	42695	0.0	37.5	8.0
2689	46404	0.0	37.5	8.0
2690	42898	0.0	50.0	8.0
2694	45885	0.0	37.5	8.0
2703	42908	0.0	37.5	8.0
2704	44292	0.0	37.5	8.0
2710	46412	0.0	37.5	8.0
2711	44306	0.0	37.5	8.0
2713	43614	0.0	37.5	8.0
2715	43616	0.0	37.5	8.0
2718	43612	0.0	50.0	8.0
2726	43606	0.0	87.5	8.0
2727	43610	0.0	50.0	8.0
2729	43602	0.0	37.5	8.0
2732	45714	0.0	37.5	8.0
2733	43604	0.0	50.0	8.0
2739	45018	0.0	50.0	8.0
2755	45718	0.0	37.5	8.0
2812	46418	0.0	37.5	8.0
2885	46215	0.0	37.5	8.0
2966	45529	0.0	37.5	8.0
2983	46229	0.0	37.5	8.0
2984	45533	0.0	50.0	8.0
3006	43756	0.0	50.0	8.0
3011	43758	0.0	62.5	8.0
3082	46222	0.0	37.5	8.0
3093	46212	0.0	37.5	8.0
3129	42718	0.0	37.5	8.0
3145	42710	0.0	37.5	8.0
3176	43424	0.0	37.5	8.0

Table 8

SEQ ID NO	SpotID	T/N Colon >2x	T/N Colon <halfx	T/N Colon Num Ratios
3193	44822	0.0	37.5	8.0
3211	44818	0.0	50.0	8.0
3245	45860	0.0	50.0	8.0
3257	45858	0.0	37.5	8.0
3268	42356	0.0	37.5	8.0
3269	42364	0.0	37.5	8.0
3278	45862	0.0	37.5	8.0
3296	43064	0.0	37.5	8.0
3336	45170	0.0	37.5	8.0
3339	43768	0.0	50.0	8.0
3356	43776	0.0	50.0	8.0
3359	45176	0.0	50.0	8.0
3388	42698	0.0	50.0	8.0
3393	45184	0.0	37.5	8.0
3405	45878	0.0	37.5	8.0
3412	45884	0.0	37.5	8.0
3438	46020	0.0	37.5	8.0
3439	46032	0.0	50.0	8.0
3442	46026	0.0	37.5	8.0
3443	42516	0.0	50.0	8.0
3457	44117	0.0	50.0	8.0
3463	42719	0.0	50.0	8.0
3514	43423	0.0	50.0	8.0
3575	46233	0.0	37.5	8.0
3595	43054	0.0	50.0	8.0
3596	42352	0.0	37.5	8.0
3605	43746	0.0	50.0	8.0
3613	42366	0.0	50.0	8.0
3650	40101	0.0	42.9	7.0
3656	39407	0.0	42.9	7.0
3698	38695	0.0	42.9	7.0
3702	40107	0.0	42.9	7.0
3711	39401	0.0	42.9	7.0
3716	39405	0.0	42.9	7.0
3723	38697	0.0	42.9	7.0
3836	42213	0.0	42.9	7.0
3870	38717	0.0	42.9	7.0
3881	38719	0.0	42.9	7.0
3919	38707	0.0	42.9	7.0
3934	38713	0.0	42.9	7.0
3955	39419	0.0	42.9	7.0
4028	42274	0.0	42.9	7.0
4039	38772	0.0	42.9	7.0

Table 8

SEQ ID NO	SpotID	T/N Colon >2x	T/N Colon <halfx	T/N Colon Num Ratios
4041	42286	0.0	42.9	7.0
4045	38770	0.0	42.9	7.0
4055	42282	0.0	42.9	7.0
4059	42284	0.0	42.9	7.0
4097	38774	0.0	42.9	7.0
4124	40313	0.0	42.9	7.0
4131	45625	0.0	50.0	8.0
4137	41005	0.0	42.9	7.0
4140	38203	0.0	42.9	7.0
4145	46325	0.0	37.5	8.0
4146	39611	0.0	42.9	7.0
4147	40309	0.0	57.1	7.0
4153	45619	0.0	37.5	8.0
4163	41697	0.0	42.9	7.0
4166	38899	0.0	42.9	7.0
4170	38903	0.0	42.9	7.0
4171	41003	0.0	42.9	7.0
4173	40995	0.0	42.9	7.0
4175	46321	0.0	37.5	8.0
4177	41017	0.0	42.9	7.0
4182	42474	0.0	50.0	8.0
4195	42478	0.0	37.5	8.0
4197	41015	0.0	42.9	7.0
4212	41713	0.0	42.9	7.0
4214	42480	0.0	37.5	8.0
4217	43886	0.0	37.5	8.0
4228	43888	0.0	37.5	8.0
4240	44586	0.0	37.5	8.0
4252	43188	0.0	37.5	8.0
4254	45304	0.0	62.5	8.0
4263	45996	0.0	37.5	8.0
4275	46016	0.0	37.5	8.0
4277	43198	0.0	37.5	8.0
4279	44606	0.0	50.0	8.0
4282	42496	0.0	50.0	8.0
4285	43900	0.0	37.5	8.0
4286	44608	0.0	37.5	8.0
4288	43902	0.0	75.0	8.0
4290	46006	0.0	37.5	8.0
4293	43192	0.0	37.5	8.0
4296	42490	0.0	37.5	8.0
4299	43896	0.0	37.5	8.0
4305	42492	0.0	37.5	8.0

Table 8

SEQ ID NO	SpotID	T/N Colon >2x	T/N Colon <halfx	T/N Colon Num Ratios
4307	46008	0.0	50.0	8.0
4317	39941	0.0	42.9	7.0
4324	42053	0.0	42.9	7.0
4341	38541	0.0	42.9	7.0
4343	42055	0.0	42.9	7.0
4350	39241	0.0	42.9	7.0
4371	40647	0.0	42.9	7.0
4384	41355	0.0	42.9	7.0
4386	39261	0.0	42.9	7.0
4395	39967	0.0	42.9	7.0
4397	38559	0.0	42.9	7.0
4400	40663	0.0	42.9	7.0
4403	40669	0.0	42.9	7.0
4408	39263	0.0	42.9	7.0
4421	44930	0.0	37.5	8.0
4424	42071	0.0	42.9	7.0
4425	45638	0.0	37.5	8.0
4428	44228	0.0	37.5	8.0
4429	41371	0.0	42.9	7.0
4434	45640	0.0	50.0	8.0
4435	44163	0.0	37.5	8.0
4436	44171	0.0	37.5	8.0
4439	42818	0.0	50.0	8.0
4440	45634	0.0	50.0	8.0
4441	45644	0.0	50.0	8.0
4447	43471	0.0	37.5	8.0
4448	43536	0.0	62.5	8.0
4453	44944	0.0	37.5	8.0
4454	45646	0.0	37.5	8.0
4457	44238	0.0	37.5	8.0
4458	44936	0.0	50.0	8.0
4461	44161	0.0	37.5	8.0
4469	44938	0.0	50.0	8.0
4470	45636	0.0	50.0	8.0
4477	44804	0.0	37.5	8.0
4483	44100	0.0	50.0	8.0
4544	46230	0.0	37.5	8.0
4547	45532	0.0	37.5	8.0
4557	45526	0.0	50.0	8.0
4573	45536	0.0	37.5	8.0
4593	41535	0.0	42.9	7.0
4594	40123	0.0	57.1	7.0
4600	41525	0.0	42.9	7.0

Table 8

SEQ ID NO	SpotID	T/N Colon >2x	T/N Colon <halfx	T/N Colon Num Ratios
4611	40817	0.0	42.9	7.0
4620	40821	0.0	42.9	7.0
4629	41529	0.0	42.9	7.0
4632	40825	0.0	42.9	7.0
4645	41527	0.0	42.9	7.0
4696	41527	0.0	42.9	7.0
4718	40823	0.0	42.9	7.0
4727	38758	0.0	57.1	7.0
4729	42229	0.0	42.9	7.0
4743	38764	0.0	42.9	7.0
4754	42235	0.0	42.9	7.0
4768	42239	0.0	42.9	7.0
4835	39472	0.0	42.9	7.0
4922	40868	0.0	57.1	7.0
4938	40866	0.0	42.9	7.0
4950	41576	0.0	42.9	7.0
4978	40870	0.0	42.9	7.0
5065	39488	0.0	42.9	7.0
5117	40888	0.0	42.9	7.0
5140	40886	0.0	42.9	7.0
5150	40890	0.0	42.9	7.0
5165	41588	0.0	42.9	7.0
5186	41596	0.0	42.9	7.0
5228	42290	0.0	42.9	7.0
5252	43118	0.0	50.0	8.0
5300	43114	0.0	62.5	8.0
5341	45220	0.0	37.5	8.0
5360	44518	0.0	37.5	8.0
5539	43120	0.0	37.5	8.0
5559	43812	0.0	50.0	8.0
5596	43810	0.0	50.0	8.0
5643	45224	0.0	50.0	8.0
5649	45226	0.0	37.5	8.0
5665	45922	0.0	37.5	8.0
5671	43265	0.0	37.5	8.0
5701	42573	0.0	37.5	8.0
5724	45232	0.0	37.5	8.0
5752	41161	0.0	71.4	7.0
5763	41163	0.0	42.9	7.0
5812	44591	0.0	50.0	8.0
5815	43189	0.0	37.5	8.0
5817	45293	0.0	37.5	8.0
5818	42487	0.0	37.5	8.0

Table 8

SEQ ID NO	SpotID	T/N Colon >2x	T/N Colon <halfx	T/N Colon Num Ratios
5821	43191	0.0	37.5	8.0
5825	38917	0.0	42.9	7.0
5829	38913	0.0	42.9	7.0
5836	41875	0.0	42.9	7.0
5837	45987	0.0	37.5	8.0
5847	45289	0.0	37.5	8.0
5848	45989	0.0	50.0	8.0
5979	44537	0.0	50.0	8.0
80	44681	12.5	37.5	8.0
86	43981	12.5	50.0	8.0
78	44675	37.5	0.0	8.0
104	42428	37.5	0.0	8.0
3248	45866	37.5	0.0	8.0
1853	39216	42.9	0.0	7.0
2049	41657	42.9	0.0	7.0
5148	40188	42.9	0.0	7.0
16	44200	50.0	0.0	8.0
3619	43404	50.0	0.0	8.0
600	42108	57.1	0.0	7.0
4684	40125	57.1	0.0	7.0
1591	44634	62.5	0.0	8.0
1518	46399	71.4	0.0	7.0
1978	38827	71.4	0.0	7.0
17	44202	75.0	0.0	8.0
1975	41244	85.7	0.0	7.0
118	43970	87.5	0.0	8.0
114	43972	100.0	0.0	8.0

Table 13

CloneID	ES No	ClusterID	SequenceName
M00007960D:E09	ES 168	142842	1513.A14.gz43_300454
M00007963D:D03	ES 168	142614	1513.A15.gz43_300470
M00021925A:H07	ES 168	120049	1513.D19.gz43_300537
M00022072A:E12	ES 168	153316	1513.E14.gz43_300458
M00022135D:D06	ES 168	145815	1513.F09.gz43_300379
M00022255B:F12	ES 168	158321	1513.H09.gz43_300381
M00022445D:E12	ES 168	101499	1513.J13.gz43_300447
M00022537D:C05	ES 168	168195	1513.L10.gz43_300401
M00022622A:G01	ES 168	99011	1513.N16.gz43_300499
M00022648C:D08	ES 168	169458	1513.O03.gz43_300292
M00022710C:H03	ES 168	171073	1513.P18.gz43_300533
M00023406A:G03	ES 168	189993	1521.C14.gz43_303619
M00027018B:F01	ES 168	94539	1521.F23.gz43_303766
M00027100A:D12	ES 168	220463	1521.H05.gz43_303480
M00027103D:B05	ES 168	189073	1521.H06.gz43_303496
M00027123D:F02	ES 168	186594	1521.H13.gz43_303608
M00027126C:H05	ES 168	222818	1521.H14.gz43_303624
M00027219B:G12	ES 168	188309	1521.J06.gz43_303498
M00027287B:H10	ES 168	217042	1521.K08.gz43_303531
M00027514C:F01	ES 168	187525	1521.N10.gz43_303566
M00027517C:F08	ES 168	215366	1521.N12.gz43_303598
M00027586B:B03	ES 168	218904	1521.O13.gz43_303615
M00027587C:F02	ES 168	185056	1521.O16.gz43_303663
M00027694C:C11	ES 168	186404	1521.P20.gz43_303728
M00028061D:D10	ES 168	432159	2128.A24.gz43_277785
M00028359D:F09	ES 168	188377	2128.H15.gz43_277648
M00028627B:F12	ES 168	427799	2128.K06.gz43_277507
M00032476D:F07	ES 168	155615	2128.P17.gz43_277688
M00032477A:B02	ES 168	125604	2128.P18.gz43_277704
M00032685B:C10	ES 168	427571	2130.H13.gz43_278017
M00032686C:D10	ES 168	38494	2130.H16.gz43_278065
M00032686D:G09	ES 168	78607	2130.H18.gz43_278097
M00032695B:A01	ES 168	44615	2130.I20.gz43_278130
M00032703D:E10	ES 168	90192	2130.J18.gz43_278099
M00032732A:A03	ES 168	376753	2130.M21.gz43_278150
M00032736A:B06	ES 168	429735	2130.N02.gz43_277847
M00032738D:G11	ES 168	436888	2130.N09.gz43_277959
M00032745C:F03	ES 168	72838	2130.O05.gz43_277896
M00032766A:A10	ES 168	427907	2131.A01.gz43_307885
M00032779A:A04	ES 168	37875	2131.A19.gz43_308173
M00032780A:B09	ES 168	48238	2131.A23.gz43_308237
M00032783A:H08	ES 168	226324	2131.B04.gz43_307934
M00032786A:H04	ES 168	221686	2131.B14.gz43_308094
M00032809B:E10	ES 168	441801	2131.E06.gz43_307969

Table 13

CloneID	ES No	ClusterID	SequenceName
M00032811A:G10	ES 168	48238	2131.E12.gz43_308065
M00032857A:B02	ES 168	34071	2131.I13.gz43_308085
M00032858D:H11	ES 168	26926	2131.I19.gz43_308181
M00032859C:E04	ES 168	441874	2131.I21.gz43_308213
M00032865A:D11	ES 168	440284	2131.J16.gz43_308134
M00032872B:A02	ES 168	62016	2131.K11.gz43_308055
M00032886A:D04	ES 168	48238	2131.M02.gz43_307913
M00032914B:D09	ES 168	12481	2131.P18.gz43_308172
M00032915B:D01	ES 168	37805	2131.P19.gz43_308188
M00039047C:A05	ES 168	376044	2152.A18.gz43_278491
M00039052B:H03	ES 168	36453	2152.B14.gz43_278428
M00039069D:E12	ES 168	387530	2152.D12.gz43_278398
M00039109A:H09	ES 168	375655	2152.H10.gz43_278370
M00039121C:C06	ES 168	375415	2152.J18.gz43_278500
M00039183B:E03	ES 168	400617	2176.A09.gz43_281808
M00039184A:A08	ES 168	400047	2176.A13.gz43_281872
M00039184C:C05	ES 168	402411	2176.A16.gz43_281920
M00039214C:D12	ES 168	390563	2153.D08.gz43_278834
M00039222C:G06	ES 168	375706	2153.F03.gz43_278756
M00039240A:H08	ES 168	390017	2153.I08.gz43_278839
M00039241A:H11	ES 168	376384	2153.I11.gz43_278887
M00039244C:F10	ES 168	379046	2153.J06.gz43_278808
M00039251A:G12	ES 168	372952	2153.K14.gz43_278937
M00039274C:D12	ES 168	377596	2153.O08.gz43_278845
M00039330B:H09	ES 168	60037	2154.G05.gz43_279173
M00039336A:C07	ES 168	376044	2154.G21.gz43_279429
M00039346C:G08	ES 168	390968	2154.I18.gz43_279383
M00039363B:H10	ES 168	409330	2176.B02.gz43_281697
M00039366C:B10	ES 168	400171	2176.B12.gz43_281857
M00039366D:A02	ES 168	404736	2176.B13.gz43_281873
M00039369D:D11	ES 168	407195	2176.C02.gz43_281698
M00039371A:E01	ES 168	407443	2176.C07.gz43_281778
M00039373B:B09	ES 168	403671	2176.C12.gz43_281858
M00039375A:C09	ES 168	411124	2176.C17.gz43_281938
M00039379A:D03	ES 168	411985	2176.D02.gz43_281699
M00039404B:G11	ES 168	377696	2154.M04.gz43_279163
M00039440C:F09	ES 168	376255	2155.A24.gz43_279855
M00039451B:C06	ES 168	389425	2155.B19.gz43_279776
M00039451B:F01	ES 168	378420	2155.B21.gz43_279808
M00039457A:D07	ES 168	373973	2155.C12.gz43_279665
M00039479A:A10	ES 168	376439	2155.F16.gz43_279732
M00039479D:C06	ES 168	375510	2155.F21.gz43_279812
M00039499C:G09	ES 168	413767	2176.E09.gz43_281812
M00039502D:H03	ES 168	401675	2176.E19.gz43_281972

Table 13

CloneID	ES No	ClusterID	SequenceName
M00039503B:G05	ES 168	413621	2176.F01.gz43_281685
M00039503D:E08	ES 168	412621	2176.F02.gz43_281701
M00039504B:F05	ES 168	402941	2176.F06.gz43_281765
M00039505B:G07	ES 168	413627	2176.F13.gz43_281877
M00039507D:E03	ES 168	412483	2176.F24.gz43_282053
M00039508D:C03	ES 168	411113	2176.G03.gz43_281718
M00039514A:G03	ES 168	402392	2176.G24.gz43_282054
M00039514B:E07	ES 168	407711	2176.H02.gz43_281703
M00039516C:H06	ES 168	400633	2176.H09.gz43_281815
M00039521A:D02	ES 168	400454	2176.H20.gz43_281991
M00039521C:B01	ES 168	405932	2176.H22.gz43_282023
M00039523A:D09	ES 168	402411	2176.I04.gz43_281736
M00039525B:H03	ES 168	409612	2176.I14.gz43_281896
M00039527B:D06	ES 168	406855	2176.I19.gz43_281976
M00039530B:H07	ES 168	414355	2176.J04.gz43_281737
M00039534A:H04	ES 168	49950	2176.J13.gz43_281881
M00039534D:E07	ES 168	412416	2176.J17.gz43_281945
M00039536B:E10	ES 168	402147	2176.J20.gz43_281993
M00039536B:H03	ES 168	413997	2176.J21.gz43_282009
M00039537B:F06	ES 168	401510	2176.J24.gz43_282057
M00039562A:D10	ES 168	400428	2176.K08.gz43_281802
M00039562D:B02	ES 168	400233	2176.K10.gz43_281834
M00039562D:G01	ES 168	408986	2176.K11.gz43_281850
M00039563C:D01	ES 168	407260	2176.K13.gz43_281882
M00039564B:F08	ES 168	408306	2176.K18.gz43_281962
M00039564C:H05	ES 168	409589	2176.K21.gz43_282010
M00039565B:H09	ES 168	402287	2176.K24.gz43_282058
M00039566D:E08	ES 168	400628	2176.L06.gz43_281771
M00039568C:E05	ES 168	94771	2176.L11.gz43_281851
M00039583A:G09	ES 168	408649	2176.L24.gz43_282059
M00039586A:C03	ES 168	406499	2176.M13.gz43_281884
M00039586D:D05	ES 168	406734	2176.M17.gz43_281948
M00039588A:H12	ES 168	202308	2176.M20.gz43_281996
M00039588B:H02	ES 168	409262	2176.M21.gz43_282012
M00039588D:F10	ES 168	402049	2176.M22.gz43_282028
M00039592C:F09	ES 168	413346	2176.N07.gz43_281789
M00039592D:E01	ES 168	401005	2176.N09.gz43_281821
M00039594A:F09	ES 168	413133	2176.N14.gz43_281901
M00039599A:E08	ES 168	407964	2176.O07.gz43_281790
M00039605D:E02	ES 168	401426	2176.P01.gz43_281695
M00039606C:B07	ES 168	202308	2176.P07.gz43_281791
M00039607A:F05	ES 168	402147	2176.P09.gz43_281823
M00039610A:G11	ES 168	413915	2176.P23.gz43_282047
M00039619C:B01	ES 168	376994	2155.I16.gz43_279735

Table 13

CloneID	ES No	ClusterID	SequenceName
M00039632A:C01	ES 168	60037	2155.J03.gz43_279528
M00039664B:H10	ES 168	376839	2155.N05.gz43_279564
M00039665C:B01	ES 168	379805	2155.N15.gz43_279724
M00039674B:G11	ES 168	373680	2155.P11.gz43_279662
M00039675C:C05	ES 168	379879	2155.P22.gz43_279838
M00039679C:A02	ES 168	379279	2164.A24.gz43_280239
M00039681B:F05	ES 168	379046	2164.B15.gz43_280096
M00039698A:A06	ES 168	396785	2164.D18.gz43_280146
M00039730B:B07	ES 168	398028	2164.H18.gz43_280150
M00039734A:E06	ES 168	377772	2178.A12.gz43_282310
M00039752D:D07	ES 168	402070	2178.B16.gz43_282375
M00039753B:A11	ES 168	401748	2178.B17.gz43_282391
M00039760B:F12	ES 168	419751	2178.C15.gz43_282360
M00039760C:H07	ES 168	420504	2178.C18.gz43_282408
M00039774A:E11	ES 168	380025	2164.I10.gz43_280023
M00039778D:D05	ES 168	397167	2164.J03.gz43_279912
M00039820D:F08	ES 168	376074	2164.O24.gz43_280253
M00039823D:D09	ES 168	216179	2164.P10.gz43_280030
M00039871C:C01	ES 168	398061	2165.F09.gz43_280388
M00039883D:G06	ES 168	373905	2165.H01.gz43_280262
M00039885B:A10	ES 168	393635	2165.H06.gz43_280342
M00039893A:G12	ES 168	376808	2165.I10.gz43_280407
M00039905B:F09	ES 168	376773	2165.K01.gz43_280265
M00039977C:C05	ES 168	67549	2165.P01.gz43_280270
M00039978D:C04	ES 168	396969	2165.P07.gz43_280366
M00039986B:A11	ES 168	375655	2166.A06.gz43_281279
M00039988B:C08	ES 168	379879	2166.A11.gz43_281359
M00040001A:H02	ES 168	398831	2166.A23.gz43_281551
M00040070C:D11	ES 168	377696	2166.J11.gz43_281368
M00040076B:D01	ES 168	233814	2166.K07.gz43_281305
M00040096D:C03	ES 168	379879	2166.N07.gz43_281308
M00040113C:H09	ES 168	185432	2166.P24.gz43_281582
M00040134A:A07	ES 168	402411	2178.D07.gz43_282233
M00040141A:G10	ES 168	417259	2178.E04.gz43_282186
M00040145B:C12	ES 168	385980	2178.E21.gz43_282458
M00040160C:A04	ES 168	414821	2178.G05.gz43_282204
M00040161C:H06	ES 168	417426	2178.G11.gz43_282300
M00040161D:C03	ES 168	415527	2178.G12.gz43_282316
M00040171B:F01	ES 168	416819	2178.H19.gz43_282429
M00040171B:H03	ES 168	402353	2178.H20.gz43_282445
M00040181B:B06	ES 168	418340	2178.J12.gz43_282319
M00040181B:C05	ES 168	403837	2178.J13.gz43_282335
M00040183B:C06	ES 168	418682	2178.K02.gz43_282160
M00040183D:C08	ES 168	402534	2178.K05.gz43_282208

Table 13

CloneID	ES No	ClusterID	SequenceName
M00040188B:E05	ES 168	419255	2178.L07.gz43_282241
M00040189D:A06	ES 168	403154	2178.L12.gz43_282321
M00040190B:C02	ES 168	418482	2178.L14.gz43_282353
M00040196B:F10	ES 168	416914	2178.L20.gz43_282449
M00040197B:D05	ES 168	415950	2178.M03.gz43_282178
M00040222A:E06	ES 168	57183	2178.M22.gz43_282482
M00040222C:E06	ES 168	416370	2178.N03.gz43_282179
M00040223B:G05	ES 168	417240	2178.N07.gz43_282243
M00040227A:E07	ES 168	402070	2178.N16.gz43_282387
M00040230B:B01	ES 168	415058	2178.O07.gz43_282244
M00040233C:F09	ES 168	416762	2178.O21.gz43_282468
M00040235C:D02	ES 168	402049	2178.P04.gz43_282197
M00039747A:H06	ES 169	423884	2184.A03.gz43_282699
M00039748A:E12	ES 169	422788	2184.A05.gz43_282731
M00039749B:G05	ES 169	402298	2184.A08.gz43_282779
M00039750C:F08	ES 169	403306	2184.A17.gz43_282923
M00039762C:D11	ES 169	140224	2184.A22.gz43_283003
M00039770C:B08	ES 169	424793	2184.B21.gz43_282988
M00039947A:G06	ES 169	423202	2184.C17.gz43_282925
M00039950C:C05	ES 169	403306	2184.D01.gz43_282670
M00039958D:D05	ES 169	402049	2184.D16.gz43_282910
M00040210D:C09	ES 169	424996	2184.F12.gz43_282848
M00040248A:G09	ES 169	402941	2178.P19.gz43_282437
M00040294B:E09	ES 169	402298	2184.G24.gz43_283041
M00040297B:G04	ES 169	423214	2184.H17.gz43_282930
M00040318C:B09	ES 169	403111	2184.J04.gz43_282724
M00040319A:E03	ES 169	422542	2184.J07.gz43_282772
M00040319C:F08	ES 169	235376	2184.J10.gz43_282820
M00040319D:G10	ES 169	423534	2184.J11.gz43_282836
M00040320A:B06	ES 169	401748	2184.J12.gz43_282852
M00040322B:A08	ES 169	420958	2184.K02.gz43_282693
M00040323D:F04	ES 169	423008	2184.K13.gz43_282869
M00040328D:A03	ES 169	402298	2184.L01.gz43_282678
M00040330D:C12	ES 169	421826	2184.L10.gz43_282822
M00040338C:D05	ES 169	396509	2184.M14.gz43_282887
M00040347B:B11	ES 169	424723	2184.N13.gz43_282872
M00040363A:G07	ES 169	403837	2184.O04.gz43_282729
M00040364B:E11	ES 169	422590	2184.O07.gz43_282777
M00042341A:D08	ES 169	0	1561.A04.gz43_314441
M00042341A:H04	ES 169	0	1561.A06.gz43_314473
M00042341D:G11	ES 169	0	1561.A14.gz43_314601
M00042342A:B04	ES 169	0	1561.A15.gz43_314617
M00042342C:H03	ES 169	0	1561.A18.gz43_314665

Table 13

CloneID	ES No	ClusterID	SequenceName
M00042342D:D03	ES 169	0	1561.A20.gz43_314697
M00042343A:C05	ES 169	0	1561.A24.gz43_314761
M00042343B:D05	ES 169	0	1561.B04.gz43_314442
M00042343B:E06	ES 169	0	1561.B05.gz43_314458
M00042343B:F12	ES 169	0	1561.B06.gz43_314474
M00042343D:F08	ES 169	0	1561.B09.gz43_314522
M00042344B:F02	ES 169	0	1561.B17.gz43_314650
M00042344B:H12	ES 169	0	1561.B19.gz43_314682
M00042344D:F03	ES 169	0	1561.C01.gz43_314395
M00042345A:E04	ES 169	0	1561.C03.gz43_314427
M00042345B:A05	ES 169	0	1561.C05.gz43_314459
M00042345D:B01	ES 169	0	1561.C10.gz43_314539
M00042345D:D04	ES 169	0	1561.C12.gz43_314571
M00042521A:E10	ES 169	0	1561.C16.gz43_314635
M00042521C:F11	ES 169	0	1561.C19.gz43_314683
M00042521D:G09	ES 169	0	1561.C22.gz43_314731
M00042522A:A05	ES 169	0	1561.C24.gz43_314763
M00042522C:H10	ES 169	0	1561.D10.gz43_314540
M00042522D:A08	ES 169	0	1561.D11.gz43_314556
M00042523B:H01	ES 169	0	1561.D20.gz43_314700
M00042523C:E08	ES 169	0	1561.D23.gz43_314748
M00042523C:H04	ES 169	0	1561.E02.gz43_314413
M00042523C:H06	ES 169	0	1561.E03.gz43_314429
M00042524C:C12	ES 169	0	1561.E15.gz43_314621
M00042524D:A10	ES 169	0	1561.E17.gz43_314653
M00042524D:D06	ES 169	0	1561.E19.gz43_314685
M00042525C:H07	ES 169	0	1561.F12.gz43_314574
M00042525D:E01	ES 169	0	1561.F15.gz43_314622
M00042526A:E10	ES 169	0	1561.F17.gz43_314654
M00042526A:F11	ES 169	0	1561.F19.gz43_314686
M00042526B:C12	ES 169	0	1561.F20.gz43_314702
M00042526C:B12	ES 169	0	1561.F23.gz43_314750
M00042526D:A02	ES 169	0	1561.F24.gz43_314766
M00042526D:A05	ES 169	0	1561.G01.gz43_314399
M00042526D:A07	ES 169	0	1561.G02.gz43_314415
M00042526D:D04	ES 169	0	1561.G04.gz43_314447
M00042527B:B01	ES 169	0	1561.G11.gz43_314559
M00042527C:A10	ES 169	0	1561.G14.gz43_314607
M00042527C:F01	ES 169	0	1561.G15.gz43_314623
M00042527D:E05	ES 169	0	1561.G20.gz43_314703
M00042527D:F12	ES 169	0	1561.G23.gz43_314751
M00042528C:G06	ES 169	0	1561.H07.gz43_314496
M00042528D:D09	ES 169	0	1561.H09.gz43_314528
M00042528D:H03	ES 169	0	1561.H10.gz43_314544

Table 13

CloneID	ES No	ClusterID	SequenceName
M00042529A:B12	ES 169	0	1561.H13.gz43_314592
M00042529A:G07	ES 169	0	1561.H15.gz43_314624
M00042529B:E03	ES 169	0	1561.H19.gz43_314688
M00042529D:D07	ES 169	0	1561.I02.gz43_314417
M00042530C:H02	ES 169	0	1561.I11.gz43_314561
M00042530D:A02	ES 169	0	1561.I12.gz43_314577
M00042530D:F09	ES 169	0	1561.I14.gz43_314609
M00042530D:H12	ES 169	0	1561.I17.gz43_314657
M00042531B:D12	ES 169	0	1561.I22.gz43_314737
M00042531B:G12	ES 169	0	1561.J01.gz43_314402
M00042531D:G08	ES 169	0	1561.J05.gz43_314466
M00042532A:D08	ES 169	0	1561.J09.gz43_314530
M00042532A:H03	ES 169	0	1561.J14.gz43_314610
M00042533B:F11	ES 169	0	1561.K02.gz43_314419
M00042533C:F04	ES 169	0	1561.K05.gz43_314467
M00042533D:B05	ES 169	0	1561.K06.gz43_314483
M00042534A:G10	ES 169	0	1561.K14.gz43_314611
M00042534B:B08	ES 169	0	1561.K16.gz43_314643
M00042534B:D06	ES 169	0	1561.K17.gz43_314659
M00042534C:A09	ES 169	0	1561.K19.gz43_314691
M00042534C:G04	ES 169	0	1561.K20.gz43_314707
M00042534D:D10	ES 169	0	1561.K23.gz43_314755
M00042535B:E04	ES 169	0	1561.L03.gz43_314436
M00042536B:G08	ES 169	0	1561.L15.gz43_314628
M00042536C:A06	ES 169	0	1561.L16.gz43_314644
M00042536C:B03	ES 169	0	1561.L18.gz43_314676
M00042537A:A07	ES 169	0	1561.L22.gz43_314740
M00042537A:D12	ES 169	0	1561.M01.gz43_314405
M00042537A:G09	ES 169	0	1561.M04.gz43_314453
M00042537A:H04	ES 169	0	1561.M05.gz43_314469
M00042537B:A07	ES 169	0	1561.M06.gz43_314485
M00042537B:B05	ES 169	0	1561.M07.gz43_314501
M00042537C:D04	ES 169	0	1561.M10.gz43_314549
M00042539B:D09	ES 169	0	1561.N06.gz43_314486
M00042539C:A04	ES 169	0	1561.N07.gz43_314502
M00042539C:E05	ES 169	0	1561.N08.gz43_314518
M00042539C:H08	ES 169	0	1561.N09.gz43_314534
M00042539D:A04	ES 169	0	1561.N10.gz43_314550
M00042540A:D11	ES 169	0	1561.N13.gz43_314598
M00042540A:G11	ES 169	0	1561.N14.gz43_314614
M00042540B:B03	ES 169	0	1561.N16.gz43_314646
M00042540C:A12	ES 169	0	1561.N17.gz43_314662
M00042540D:F12	ES 169	0	1561.N23.gz43_314758
M00042540D:H02	ES 169	0	1561.N24.gz43_314774

Table 13

CloneID	ES No	ClusterID	SequenceName
M00042541A:B07	ES 169	0	1561.O04.gz43_314455
M00042541A:E06	ES 169	0	1561.O06.gz43_314487
M00042541A:G02	ES 169	0	1561.O07.gz43_314503
M00042541B:B05	ES 169	0	1561.O09.gz43_314535
M00042542A:C11	ES 169	0	1561.O18.gz43_314679
M00042542B:B01	ES 169	0	1561.O21.gz43_314727
M00042542B:C11	ES 169	0	1561.O23.gz43_314759
M00042542B:E04	ES 169	0	1561.O24.gz43_314775
M00042543B:H12	ES 169	0	1561.P18.gz43_314680
M00042543C:F06	ES 169	0	1561.P21.gz43_314728
M00042546A:D03	ES 169	446572	1562.B01.gz43_207804
M00042546D:E06	ES 169	446389	1562.B13.gz43_207996
M00042547B:D11	ES 169	446531	1562.B22.gz43_208140
M00042548B:A01	ES 169	456845	1562.C12.gz43_207981
M00042548B:G01	ES 169	462149	1562.C14.gz43_208013
M00042550A:D12	ES 169	446674	1562.D12.gz43_207982
M00042550C:H10	ES 169	446981	1562.D18.gz43_208078
M00042552C:D02	ES 169	466280	1562.E22.gz43_208143
M00042552D:A11	ES 169	464091	1562.F01.gz43_207808
M00042554A:C02	ES 169	451780	1562.F04.gz43_207856
M00042554C:E02	ES 169	467262	1562.F08.gz43_207920
M00042554C:F09	ES 169	447597	1562.F10.gz43_207952
M00042554D:C08	ES 169	465594	1562.F12.gz43_207984
M00042555A:A04	ES 169	464067	1562.F17.gz43_208064
M00042555A:A10	ES 169	447152	1562.F18.gz43_208080
M00042555B:B07	ES 169	464905	1562.F20.gz43_208112
M00042555D:G10	ES 169	469511	1562.G05.gz43_207873
M00042556A:G12	ES 169	451737	1562.G10.gz43_207953
M00042556B:D12	ES 169	466719	1562.G12.gz43_207985
M00042556B:E10	ES 169	447174	1562.G14.gz43_208017
M00042557A:D09	ES 169	455075	1562.H05.gz43_207874
M00042557D:H12	ES 169	469837	1562.H17.gz43_208066
M00042558A:D03	ES 169	447517	1562.H18.gz43_208082
M00042558A:F11	ES 169	468330	1562.H20.gz43_208114
M00042558D:B07	ES 169	447308	1562.I03.gz43_207843
M00042560B:A01	ES 169	408386	1562.J01.gz43_207812
M00042560B:G10	ES 169	456462	1562.J04.gz43_207860
M00042561B:E12	ES 169	446620	1562.J21.gz43_208132
M00042561C:E12	ES 169	446621	1562.J24.gz43_208180
M00042562C:A07	ES 169	457405	1562.K14.gz43_208021
M00042563A:F10	ES 169	446829	1562.L02.gz43_207830
M00042563C:D08	ES 169	459536	1562.L09.gz43_207942
M00042563C:E02	ES 169	446614	1562.L10.gz43_207958
M00042563D:D02	ES 169	459523	1562.L11.gz43_207974

Table 13

CloneID	ES No	ClusterID	SequenceName
M00042563D:D09	ES 169	446495	1562.L12.gz43_207990
M00042564A:F01	ES 169	461559	1562.L19.gz43_208102
M00042564B:D11	ES 169	446495	1562.L22.gz43_208150
M00042564D:F10	ES 169	456471	1562.M06.gz43_207895
M00042565A:G05	ES 169	432159	1562.M10.gz43_207959
M00042565A:H03	ES 169	463487	1562.M12.gz43_207991
M00042567C:E02	ES 169	446703	1562.N16.gz43_208056
M00042567C:E07	ES 169	460972	1562.N18.gz43_208088
M00042567D:B08	ES 169	457783	1562.N21.gz43_208136
M00042567D:E12	ES 169	460493	1562.N24.gz43_208184
M00042568C:E03	ES 169	446657	1562.O14.gz43_208025
M00042568C:E08	ES 169	460766	1562.O15.gz43_208041
M00042569B:G07	ES 169	43338	1562.P03.gz43_207850
M00042569C:B05	ES 169	447346	1562.P05.gz43_207882
M00042569D:D02	ES 169	460190	1562.P09.gz43_207946
M00042570A:E08	ES 169	460516	1562.P11.gz43_207978
M00042570B:F11	ES 169	417078	1562.P18.gz43_208090
M00042570C:B12	ES 169	457842	1562.P21.gz43_208138
M00042571C:F03	ES 169	468783	1563.A14.gz43_208395
M00042571D:D06	ES 169	467057	1563.A15.gz43_208411
M00042572B:C07	ES 169	446302	1563.A19.gz43_208475
M00042572B:E05	ES 169	460789	1563.A20.gz43_208491
M00042573A:D05	ES 169	466971	1563.B05.gz43_208252
M00042573C:D05	ES 169	456052	1563.B14.gz43_208396
M00042573D:A10	ES 169	463896	1563.B21.gz43_208508
M00042574A:F05	ES 169	446409	1563.B23.gz43_208540
M00042574B:A07	ES 169	456925	1563.B24.gz43_208556
M00042574C:A04	ES 169	456920	1563.C04.gz43_208237
M00042575A:E01	ES 170	467327	1563.C14.gz43_208397
M00042575A:E02	ES 170	451383	1563.C15.gz43_208413
M00042575B:F02	ES 170	451382	1563.C20.gz43_208493
M00042575D:A11	ES 170	464275	1563.D01.gz43_208190
M00042575D:C05	ES 170	447417	1563.D03.gz43_208222
M00042576B:D11	ES 170	459961	1563.D12.gz43_208366
M00042576D:A08	ES 170	446213	1563.D17.gz43_208446
M00042576D:F01	ES 170	446839	1563.D21.gz43_208510
M00042577A:A11	ES 170	464547	1563.D23.gz43_208542
M00042577B:D05	ES 170	467051	1563.E06.gz43_208271
M00042578A:E08	ES 170	447597	1563.E14.gz43_208399
M00042579A:B05	ES 170	446933	1563.E22.gz43_208527
M00042579B:E05	ES 170	467644	1563.F01.gz43_208192
M00042580C:A03	ES 170	463951	1563.F13.gz43_208384
M00042691A:D08	ES 170	460244	1563.F19.gz43_208480

Table 13

CloneID	ES No	ClusterID	SequenceName
M00042691A:G04	ES 170	462767	1563.F21.gz43_208512
M00042691C:A05	ES 170	456985	1563.G04.gz43_208241
M00042691D:B03	ES 170	457890	1563.G08.gz43_208305
M00042691D:F03	ES 170	446776	1563.G12.gz43_208369
M00042692A:E11	ES 170	467293	1563.G16.gz43_208433
M00042692B:F04	ES 170	44503	1563.G22.gz43_208529
M00042693B:D03	ES 170	446549	1563.H09.gz43_208322
M00042694B:G05	ES 170	446962	1563.H18.gz43_208466
M00042694C:F01	ES 170	462008	1563.H23.gz43_208546
M00042695C:F05	ES 170	461734	1563.I09.gz43_208323
M00042695D:E11	ES 170	460884	1563.I12.gz43_208371
M00042695D:H01	ES 170	463368	1563.I14.gz43_208403
M00042697B:F06	ES 170	451454	1563.J01.gz43_208196
M00042697D:A03	ES 170	447190	1563.J03.gz43_208228
M00042698A:A01	ES 170	142559	1563.J05.gz43_208260
M00042699C:H06	ES 170	453605	1563.K08.gz43_208309
M00042700B:C12	ES 170	138049	1563.K12.gz43_208373
M00042700C:F11	ES 170	468109	1563.K20.gz43_208501
M00042700D:G08	ES 170	468979	1563.K24.gz43_208565
M00042702B:B07	ES 170	447326	1563.L20.gz43_208502
M00042702B:G07	ES 170	447826	1563.L22.gz43_208534
M00042702D:H01	ES 170	469944	1563.M02.gz43_208215
M00042704A:C02	ES 170	447433	1563.M18.gz43_208471
M00042705A:B07	ES 170	465339	1563.N08.gz43_208312
M00042706C:D02	ES 170	51939	1563.O02.gz43_208217
M00042707B:G05	ES 170	450929	1563.O14.gz43_208409
M00042707C:A09	ES 170	446922	1563.O16.gz43_208441
M00042709B:G05	ES 170	468930	1564.A01.gz43_296552
M00042709C:B05	ES 170	464937	1564.A02.gz43_296568
M00042710A:G10	ES 170	462393	1564.A08.gz43_296664
M00042710B:B09	ES 170	457975	1564.A09.gz43_296680
M00042711A:F01	ES 170	389425	1564.A20.gz43_296856
M00042711B:H04	ES 170	463143	1564.B01.gz43_296553
M00042711C:H10	ES 170	447006	1564.B06.gz43_296633
M00042711D:A03	ES 170	446191	1564.B07.gz43_296649
M00042711D:G04	ES 170	462604	1564.B09.gz43_296681
M00042712A:E08	ES 170	467780	1564.B12.gz43_296729
M00042712B:C04	ES 170	447429	1564.B16.gz43_296793
M00042712C:E06	ES 170	447649	1564.B19.gz43_296841
M00042713B:C08	ES 170	465785	1564.C01.gz43_296554
M00042713B:F03	ES 170	447189	1564.C03.gz43_296586
M00042713C:A09	ES 170	446230	1564.C04.gz43_296602
M00042713C:B08	ES 170	447268	1564.C05.gz43_296618
M00042713D:C06	ES 170	465782	1564.C07.gz43_296650

Table 13

CloneID	ES No	ClusterID	SequenceName
M00042714A:G04	ES 170	456530	1564.C11.gz43_296714
M00042714A:H05	ES 170	447561	1564.C12.gz43_296730
M00042714B:C07	ES 170	447430	1564.C13.gz43_296746
M00042714B:E01	ES 170	447826	1564.C15.gz43_296778
M00042714C:C10	ES 170	465528	1564.C19.gz43_296842
M00042714C:F12	ES 170	449171	1564.C21.gz43_296874
M00042714D:E11	ES 170	452504	1564.C24.gz43_296922
M00042715D:A10	ES 170	457644	1564.D13.gz43_296747
M00042715D:E02	ES 170	446741	1564.D15.gz43_296779
M00042716A:F09	ES 170	446866	1564.D22.gz43_296891
M00042716D:G04	ES 170	462337	1564.E11.gz43_296716
M00042717B:G11	ES 170	462865	1564.E19.gz43_296844
M00042719A:H06	ES 170	452687	1564.F15.gz43_296781
M00042719C:H05	ES 170	405932	1564.F19.gz43_296845
M00042720C:E03	ES 170	461135	1564.G07.gz43_296654
M00042721A:G07	ES 170	446964	1564.G13.gz43_296750
M00042721B:A04	ES 170	446230	1564.G14.gz43_296766
M00042721D:B03	ES 170	457922	1564.G19.gz43_296846
M00042721D:D01	ES 170	450723	1564.G21.gz43_296878
M00042722A:G08	ES 170	462348	1564.H03.gz43_296591
M00042722B:D06	ES 170	460051	1564.H05.gz43_296623
M00042722D:C12	ES 170	459158	1564.H13.gz43_296751
M00042723A:D09	ES 170	446601	1564.H15.gz43_296783
M00042724A:G02	ES 170	453766	1564.I01.gz43_296560
M00042724D:B04	ES 170	446345	1564.I09.gz43_296688
M00042724D:H04	ES 170	447048	1564.I13.gz43_296752
M00042726B:E01	ES 170	446732	1564.I20.gz43_296864
M00042726D:G11	ES 170	462398	1564.J01.gz43_296561
M00042729A:F11	ES 170	461316	1564.K05.gz43_296626
M00042729A:H08	ES 170	462986	1564.K08.gz43_296674
M00042729B:F10	ES 170	461313	1564.K12.gz43_296738
M00042730D:D01	ES 170	424996	1564.L05.gz43_296627
M00042732A:A11	ES 170	453679	1564.L12.gz43_296739
M00042733C:C05	ES 170	454825	1564.M08.gz43_296676
M00042733D:G08	ES 170	450723	1564.M13.gz43_296756
M00042735A:G07	ES 170	469754	1564.M20.gz43_296868
M00042735A:G12	ES 170	469766	1564.M21.gz43_296884
M00042735B:A06	ES 170	403949	1564.M23.gz43_296916
M00042735C:G02	ES 170	420686	1564.N05.gz43_296629
M00042735D:A07	ES 170	463824	1564.N06.gz43_296645
M00042736A:F03	ES 170	447387	1564.N11.gz43_296725
M00042736B:G09	ES 170	447813	1564.N14.gz43_296773
M00042737A:A07	ES 170	463821	1564.N19.gz43_296853
M00042737B:C07	ES 170	390563	1564.O01.gz43_296566

Table 13

CloneID	ES No	ClusterID	SequenceName
M00042737B:E02	ES 170	467189	1564.O02.gz43_296582
M00042737C:C07	ES 170	446740	1564.O04.gz43_296614
M00042737C:E03	ES 170	447579	1564.O05.gz43_296630
M00042737D:D03	ES 170	466614	1564.O08.gz43_296678
M00042738D:H12	ES 170	463217	1564.O19.gz43_296854
M00042739A:C06	ES 170	446242	1564.O20.gz43_296870
M00042739A:D02	ES 170	460078	1564.O21.gz43_296886
M00042739A:G07	ES 170	446922	1564.O23.gz43_296918
M00042739B:F06	ES 170	453762	1564.P02.gz43_296583
M00042740A:A01	ES 170	457656	1564.P09.gz43_296695
M00042742B:H03	ES 170	450940	1573.A06.gz43_208651
M00042744A:D11	ES 170	466894	1573.B07.gz43_208668
M00042745B:B06	ES 170	464622	1573.C01.gz43_208573
M00042745C:E11	ES 170	452399	1573.C05.gz43_208637
M00042745D:H04	ES 170	452093	1573.C08.gz43_208685
M00042747A:G12	ES 170	469150	1573.C22.gz43_208909
M00042747D:B01	ES 170	447293	1573.D01.gz43_208574
M00042747D:C08	ES 170	447421	1573.D02.gz43_208590
M00042748D:D08	ES 170	466920	1573.D10.gz43_208718
M00042750D:E07	ES 170	447645	1573.E04.gz43_208623
M00042881C:C11	ES 170	639372	1573.E15.gz43_208799
M00042882C:F06	ES 170	642146	1573.F10.gz43_208720
M00042882C:G07	ES 170	467293	1573.F12.gz43_208752
M00042882D:C04	ES 170	645690	1573.F15.gz43_208800
M00042883A:F06	ES 170	639849	1573.F18.gz43_208848
M00042884D:E03	ES 170	648467	1573.G17.gz43_208833
M00042885A:G09	ES 170	463060	1573.G21.gz43_208897
M00042886A:H03	ES 170	650364	1573.H04.gz43_208626
M00042886C:F01	ES 170	650195	1573.H11.gz43_208738
M00042886D:E10	ES 170	645470	1573.H16.gz43_208818
M00042887D:A11	ES 170	455996	1573.H21.gz43_208898
M00042888A:F02	ES 170	650231	1573.I03.gz43_208611
M00042889D:A01	ES 170	447161	1573.J08.gz43_208692
M00042889D:A12	ES 170	464205	1573.J10.gz43_208724
M00042890C:G11	ES 170	497434	1573.K01.gz43_208581
M00042890D:D03	ES 170	556711	1573.K03.gz43_208613
M00042890D:G05	ES 170	401426	1573.K06.gz43_208661
M00042891C:H01	ES 170	486238	1573.K19.gz43_208869
M00042892C:E03	ES 170	557974	1573.L09.gz43_208710
M00042892D:C04	ES 170	641890	1573.L10.gz43_208726
M00042892D:E06	ES 170	650852	1573.L13.gz43_208774
M00042892D:H04	ES 170	452506	1573.L14.gz43_208790
M00042894B:E05	ES 170	633946	1573.M08.gz43_208695
M00042894D:G05	ES 170	651029	1573.M17.gz43_208839

Table 13

CloneID	ES No	ClusterID	SequenceName
M00042895C:C10	ES 170	453908	1573.N01.gz43_208584
M00042896A:D04	ES 170	650756	1573.N12.gz43_208760
M00042896A:E03	ES 170	452611	1573.N13.gz43_208776
M00042896A:F09	ES 170	650944	1573.N14.gz43_208792
M00042898A:H05	ES 170	447141	1573.P02.gz43_208602
M00042900B:B10	ES 170	465104	1574.A03.gz43_208987
M00042900C:H11	ES 170	470593	1574.A04.gz43_209003
M00042901A:F12	ES 170	447750	1574.A11.gz43_209115
M00042901A:H11	ES 170	389591	1574.A14.gz43_209163
M00042902B:G02	ES 170	469608	1574.B04.gz43_209004
M00042902B:H01	ES 170	470462	1574.B05.gz43_209020
M00042902C:E11	ES 170	447660	1574.B07.gz43_209052
M00042903A:E04	ES 170	467710	1574.B12.gz43_209132
M00042903B:C09	ES 170	465984	1574.B15.gz43_209180
M00042904A:B01	ES 170	447212	1574.B24.gz43_209324
M00042904A:H10	ES 170	470641	1574.C03.gz43_208989
M00042905A:A07	ES 170	447147	1574.C07.gz43_209053
M00042905B:G03	ES 170	60260	1574.C11.gz43_209117
M00042905C:G08	ES 170	447815	1574.C14.gz43_209165
M00042906A:A12	ES 170	447218	1574.C17.gz43_209213
M00042906C:A10	ES 170	451624	1574.D04.gz43_209006
M00042907A:B11	ES 170	95617	1574.D14.gz43_209166
M00042907A:F03	ES 170	447692	1574.D15.gz43_209182
M00042907D:A11	ES 170	447173	1574.E02.gz43_208975
M00042908A:B01	ES 170	642691	1574.E06.gz43_209039
M00042908B:A11	ES 170	641069	1574.E12.gz43_209135
M00042908C:A03	ES 170	649744	1574.E18.gz43_209231
M00042908C:D12	ES 170	714629	1574.E20.gz43_209263
M00042908D:G12	ES 170	647086	1574.E24.gz43_209327
M00042909B:C04	ES 170	647639	1574.F07.gz43_209056
M00042909B:H08	ES 170	650398	1574.F12.gz43_209136
M00042909C:F10	ES 170	650235	1574.F17.gz43_209216
M00042909D:B11	ES 170	650564	1574.F18.gz43_209232
M00042910C:D03	ES 170	480508	1574.G04.gz43_209009
M00042910D:A02	ES 170	466697	1574.G06.gz43_209041
M00042910D:E11	ES 170	649965	1574.G08.gz43_209073
M00042911A:A02	ES 170	649810	1574.G11.gz43_209121
M00042911A:B02	ES 170	649900	1574.G12.gz43_209137
M00042911A:D04	ES 170	641029	1574.G15.gz43_209185
M00042911A:H12	ES 170	527355	1574.G18.gz43_209233
M00042911B:F10	ES 170	648855	1574.G21.gz43_209281
M00042911B:H08	ES 170	644376	1574.G23.gz43_209313
M00042911C:D01	ES 170	562247	1574.G24.gz43_209329
M00042912A:C01	ES 170	649965	1574.H06.gz43_209042

Table 13

CloneID	ES No	ClusterID	SequenceName
M00042912B:F11	ES 171	645924	1574.H11.gz43_209122
M00042912D:H08	ES 171	645954	1574.H16.gz43_209202
M00042912D:H10	ES 171	640356	1574.H17.gz43_209218
M00042913A:D09	ES 171	452989	1574.H18.gz43_209234
M00042913B:E10	ES 171	639740	1574.H22.gz43_209298
M00042914A:B05	ES 171	639371	1574.I09.gz43_209091
M00042914A:H10	ES 171	650423	1574.I16.gz43_209203
M00042914B:H03	ES 171	467364	1574.I20.gz43_209267
M00042914D:B10	ES 171	649852	1574.I22.gz43_209299
M00042915A:E06	ES 171	482043	1574.J05.gz43_209028
M00042915A:G10	ES 171	651051	1574.J06.gz43_209044
M00042915C:E05	ES 171	639923	1574.J12.gz43_209140
M00042915D:A11	ES 171	650527	1574.J15.gz43_209188
M00042915D:D06	ES 171	642151	1574.J17.gz43_209220
M00042915D:E03	ES 171	643940	1574.J18.gz43_209236
M00054791A:G04	ES 171	646404	1574.J21.gz43_209284
M00054791B:C09	ES 171	446974	1574.J24.gz43_209332
M00054792B:A03	ES 171	648159	1574.K18.gz43_209237
M00054793C:C01	ES 171	538237	1574.L07.gz43_209062
M00054793C:D11	ES 171	413767	1574.L11.gz43_209126
M00054793D:H11	ES 171	640306	1574.L13.gz43_209158
M00054794B:F09	ES 171	284269	1574.L23.gz43_209318
M00054794C:G11	ES 171	450506	1574.M06.gz43_209047
M00054794D:D02	ES 171	474298	1574.M09.gz43_209095
M00054794D:D08	ES 171	646568	1574.M10.gz43_209111
M00054795A:A08	ES 171	640181	1574.M16.gz43_209207
M00054796B:A01	ES 171	639391	1574.N04.gz43_209016
M00054796B:C08	ES 171	641525	1574.N05.gz43_209032
M00054797C:F03	ES 171	644789	1574.N20.gz43_209272
M00054797D:F01	ES 171	472101	1574.O01.gz43_208969
M00054798B:A01	ES 171	453572	1574.O06.gz43_209049
M00054798D:A12	ES 171	641315	1574.O15.gz43_209193
M00054798D:F01	ES 171	650773	1574.O17.gz43_209225
M00054799C:G11	ES 171	641875	1574.P02.gz43_208986
M00054799D:H02	ES 171	645223	1574.P05.gz43_209034
M00054800B:C06	ES 171	639787	1574.P10.gz43_209114
M00054800B:C11	ES 171	513262	1574.P12.gz43_209146
M00054800B:E08	ES 171	474298	1574.P15.gz43_209194
M00054800D:D08	ES 171	639901	1574.P23.gz43_209322
M00054800D:F08	ES 171	513248	1575.A01.gz43_209339
M00054911A:C08	ES 171	549699	1575.A05.gz43_209403
M00054911A:G01	ES 171	559776	1575.A10.gz43_209483
M00054911A:H06	ES 171	528616	1575.A13.gz43_209531

Table 13

CloneID	ES No	ClusterID	SequenceName
M00054911B:E10	ES 171	639992	1575.A15.gz43_209563
M00054911D:D03	ES 171	41878	1575.B02.gz43_209356
M00054912A:H08	ES 171	646949	1575.B05.gz43_209404
M00054912B:C05	ES 171	589098	1575.B08.gz43_209452
M00054912C:C01	ES 171	641057	1575.B13.gz43_209532
M00054912D:F11	ES 171	182437	1575.B19.gz43_209628
M00054912D:G01	ES 171	417130	1575.B20.gz43_209644
M00054912D:G04	ES 171	640230	1575.B21.gz43_209660
M00054913A:B12	ES 171	377855	1575.B24.gz43_209708
M00054913C:G03	ES 171	451811	1575.C12.gz43_209517
M00054914C:D12	ES 171	447246	1575.D04.gz43_209390
M00054914D:G07	ES 171	467381	1575.D09.gz43_209470
M00054915A:G03	ES 171	413767	1575.D13.gz43_209534
M00054915D:B08	ES 171	452220	1575.D21.gz43_209662
M00054915D:D05	ES 171	646293	1575.D22.gz43_209678
M00054915D:E07	ES 171	468109	1575.D24.gz43_209710
M00054916A:A05	ES 171	649872	1575.E02.gz43_209359
M00054916A:E05	ES 171	639256	1575.E05.gz43_209407
M00054916A:F10	ES 171	639394	1575.E06.gz43_209423
M00054916B:E02	ES 171	648664	1575.E11.gz43_209503
M00054916C:C04	ES 171	545980	1575.E13.gz43_209535
M00054917A:F07	ES 171	473854	1575.E22.gz43_209679
M00054917B:A05	ES 171	648609	1575.E23.gz43_209695
M00054917B:F01	ES 171	649082	1575.F03.gz43_209376
M00054917C:D03	ES 171	643843	1575.F08.gz43_209456
M00054917C:F03	ES 171	648532	1575.F10.gz43_209488
M00054917D:A03	ES 171	647991	1575.F14.gz43_209552
M00054917D:A12	ES 171	644692	1575.F16.gz43_209584
M00054917D:D12	ES 171	639662	1575.F18.gz43_209616
M00054917D:E05	ES 171	639255	1575.F19.gz43_209632
M00054917D:H02	ES 171	648532	1575.F23.gz43_209696
M00054918A:D02	ES 171	649506	1575.G02.gz43_209361
M00054918A:F09	ES 171	553100	1575.G04.gz43_209393
M00054918B:H01	ES 171	449861	1575.G10.gz43_209489
M00054918B:H08	ES 171	645252	1575.G11.gz43_209505
M00054918D:C03	ES 171	456923	1575.G15.gz43_209569
M00054918D:C11	ES 171	452204	1575.G16.gz43_209585
M00054918D:G02	ES 171	645252	1575.G18.gz43_209617
M00054918D:H09	ES 171	468222	1575.G19.gz43_209633
M00054919A:H04	ES 171	452845	1575.G24.gz43_209713
M00054919C:F06	ES 171	644556	1575.H05.gz43_209410
M00054919D:H12	ES 171	642084	1575.H14.gz43_209554
M00054920A:A05	ES 171	61616	1575.H16.gz43_209586
M00054920A:B07	ES 171	554010	1575.H18.gz43_209618

Table 13

CloneID	ES No	ClusterID	SequenceName
M00054920A:C11	ES 171	564440	1575.H22.gz43_209682
M00054920B:C04	ES 171	649933	1575.I03.gz43_209379
M00054920B:C12	ES 171	500337	1575.I05.gz43_209411
M00054920C:A06	ES 171	643843	1575.I10.gz43_209491
M00054920C:D05	ES 171	452707	1575.I12.gz43_209523
M00054920C:F02	ES 171	649555	1575.I15.gz43_209571
M00055426B:B02	ES 171	452986	1575.J06.gz43_209428
M00055426C:B12	ES 171	447574	1575.J14.gz43_209556
M00055426C:C10	ES 171	649746	1575.J15.gz43_209572
M00055426D:F03	ES 171	639144	1575.J21.gz43_209668
M00055427A:F01	ES 171	643924	1575.K05.gz43_209413
M00055427A:F02	ES 171	654723	1575.K06.gz43_209429
M00055427B:E01	ES 171	41141	1575.K10.gz43_209493
M00055427B:F06	ES 171	640814	1575.K11.gz43_209509
M00055427C:A06	ES 171	504568	1575.K13.gz43_209541
M00055427C:E12	ES 171	630269	1575.K17.gz43_209605
M00055427C:F07	ES 171	650487	1575.K18.gz43_209621
M00055427C:H11	ES 171	468783	1575.K19.gz43_209637
M00055427D:E05	ES 171	456420	1575.K21.gz43_209669
M00055428A:C02	ES 171	643279	1575.L01.gz43_209350
M00055428B:H02	ES 171	645347	1575.L05.gz43_209414
M00055428C:G06	ES 171	243722	1575.L12.gz43_209526
M00055428D:G12	ES 171	611927	1575.L18.gz43_209622
M00055429A:H04	ES 171	639520	1575.L22.gz43_209686
M00055429B:B12	ES 171	467989	1575.M01.gz43_209351
M00055429B:E12	ES 171	446254	1575.M02.gz43_209367
M00055429B:G04	ES 171	639444	1575.M03.gz43_209383
M00055429B:H02	ES 171	447254	1575.M04.gz43_209399
M00055429D:G07	ES 171	584071	1575.M11.gz43_209511
M00055430B:E08	ES 171	495143	1575.M16.gz43_209591
M00055430B:H02	ES 171	560700	1575.M19.gz43_209639
M00055430C:G11	ES 171	452293	1575.M23.gz43_209703
M00055430D:F04	ES 171	650184	1575.N01.gz43_209352
M00055431A:E01	ES 171	451994	1575.N05.gz43_209416
M00055431A:H05	ES 171	645344	1575.N07.gz43_209448
M00055431B:A01	ES 171	570812	1575.N09.gz43_209480
M00055431C:H08	ES 171	639523	1575.N15.gz43_209576
M00055432A:A03	ES 171	446495	1575.N19.gz43_209640
M00055432A:D05	ES 171	639150	1575.N21.gz43_209672
M00055432B:B04	ES 171	642073	1575.N23.gz43_209704
M00055432B:H02	ES 171	641542	1575.O02.gz43_209369
M00055432C:D12	ES 171	447913	1575.O05.gz43_209417
M00055432C:F01	ES 171	645162	1575.O07.gz43_209449
M00055432D:H12	ES 171	655551	1575.O15.gz43_209577

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055433A:B07	ES 171	644371	1575.O16.gz43_209593
M00055433A:B08	ES 171	446932	1575.O17.gz43_209609
M00055433A:C02	ES 171	641925	1575.O18.gz43_209625
M00055433A:E04	ES 171	649195	1575.O22.gz43_209689
M00055433C:A11	ES 171	638758	1575.O24.gz43_209721
M00055433D:A09	ES 171	651211	1575.P02.gz43_209370
M00055433D:C07	ES 171	458734	1575.P04.gz43_209402
M00055433D:F06	ES 171	492242	1575.P06.gz43_209434
M00055434A:A03	ES 171	647109	1575.P08.gz43_209466
M00055434C:B11	ES 171	651020	1575.P18.gz43_209626
M00055434D:B06	ES 171	640369	1575.P21.gz43_209674
M00055434D:E09	ES 171	57183	1575.P22.gz43_209690
M00055435B:C09	ES 171	639829	1576.A04.gz43_209771
M00055435C:E12	ES 171	640055	1576.A08.gz43_209835
M00055435D:G11	ES 171	639287	1576.A13.gz43_209915
M00055436A:E04	ES 171	626061	1576.A15.gz43_209947
M00055436B:B06	ES 171	639711	1576.A19.gz43_210011
M00055436B:B09	ES 171	454409	1576.A20.gz43_210027
M00055437D:B06	ES 171	466092	1576.B17.gz43_209980
M00055439B:B07	ES 171	640522	1576.C21.gz43_210045
M00055439B:C10	ES 171	450199	1576.C23.gz43_210077
M00055439D:E08	ES 171	648506	1576.D11.gz43_209886
M00055440D:D02	ES 171	653616	1576.E09.gz43_209855
M00055441A:G07	ES 171	640734	1576.E16.gz43_209967
M00055441C:H06	ES 171	640230	1576.F03.gz43_209760
M00055443D:G04	ES 171	649288	1576.G13.gz43_209921
M00055444D:C05	ES 171	639750	1576.H03.gz43_209762
M00055446B:A12	ES 171	484145	1576.I05.gz43_209795
M00055446B:D08	ES 171	639928	1576.I08.gz43_209843
M00055450B:G07	ES 171	526606	1576.L08.gz43_209846
M00055451B:D08	ES 171	446439	1576.M09.gz43_209863
M00055451B:D12	ES 171	456125	1576.M10.gz43_209879
M00055451C:B08	ES 171	624440	1576.M12.gz43_209911
M00055451C:E10	ES 171	639786	1576.M14.gz43_209943
M00055453D:E12	ES 171	560791	1576.O12.gz43_209913
M00055455B:G12	ES 171	479051	1576.P24.gz43_210106
M00055456A:B03	ES 171	559369	1585.A06.gz43_210283
M00055456A:F01	ES 171	642478	1585.A10.gz43_210347
M00055456B:G08	ES 171	641645	1585.A22.gz43_210539
M00055456C:A10	ES 171	466440	1585.B02.gz43_210220
M00055456C:G04	ES 171	484126	1585.B06.gz43_210284
M00055456D:E06	ES 171	452202	1585.B13.gz43_210396
M00055456D:G04	ES 171	639932	1585.B14.gz43_210412
M00055457D:F09	ES 171	650605	1585.B23.gz43_210556

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055458B:B04	ES 171	648123	1585.C02.gz43_210221
M00055458C:G02	ES 171	643843	1585.C11.gz43_210365
M00055458D:F04	ES 171	640997	1585.C16.gz43_210445
M00055459B:A02	ES 171	641467	1585.C22.gz43_210541
M00055460A:D01	ES 171	640662	1585.D14.gz43_210414
M00055460B:G06	ES 171	598589	1585.E03.gz43_210239
M00055460C:C12	ES 171	640561	1585.E06.gz43_210287
M00055460C:D10	ES 171	592346	1585.E07.gz43_210303
M00055460C:G09	ES 171	592346	1585.E11.gz43_210367
M00055460D:B06	ES 171	641066	1585.E15.gz43_210431
M00055461A:A06	ES 171	643991	1585.E23.gz43_210559
M00055461A:H03	ES 171	447863	1585.F03.gz43_210240
M00055461C:E05	ES 171	640792	1585.F13.gz43_210400
M00055461D:C09	ES 171	607422	1585.F17.gz43_210464
M00055462A:A09	ES 171	640368	1585.F22.gz43_210544
M00055462C:A11	ES 172	640400	1585.G12.gz43_210385
M00055462C:C03	ES 172	598589	1585.G14.gz43_210417
M00055462D:H12	ES 172	412416	1585.G22.gz43_210545
M00055463A:A11	ES 172	398061	1585.G23.gz43_210561
M00055463D:G01	ES 172	544461	1585.H09.gz43_210338
M00055464B:E06	ES 172	640913	1585.H13.gz43_210402
M00055464B:E11	ES 172	556654	1585.H14.gz43_210418
M00055464B:G03	ES 172	664711	1585.H15.gz43_210434
M00055464D:A04	ES 172	661194	1585.H19.gz43_210498
M00055464D:F08	ES 172	650914	1585.H22.gz43_210546
M00055465A:C05	ES 172	651038	1585.I01.gz43_210211
M00055465D:F12	ES 172	639607	1585.I13.gz43_210403
M00055466A:C05	ES 172	549611	1585.I15.gz43_210435
M00055466C:A01	ES 172	559343	1585.I23.gz43_210563
M00055467A:A07	ES 172	555820	1585.J07.gz43_210308
M00055467D:A01	ES 172	559549	1585.J20.gz43_210516
M00055467D:C10	ES 172	51939	1585.J22.gz43_210548
M00055467D:G08	ES 172	505933	1585.J24.gz43_210580
M00055468A:A05	ES 172	646318	1585.K02.gz43_210229
M00055468C:B07	ES 172	639726	1585.K16.gz43_210453
M00055469A:D08	ES 172	640068	1585.K24.gz43_210581
M00055469B:A06	ES 172	553402	1585.L04.gz43_210262
M00055469C:F09	ES 172	645201	1585.L12.gz43_210390
M00055470C:F03	ES 172	562067	1585.M07.gz43_210311
M00055470D:F12	ES 172	640293	1585.M12.gz43_210391
M00055491A:H01	ES 172	584745	1585.M17.gz43_210471
M00055492A:D03	ES 172	639136	1585.N04.gz43_210264
M00055492A:H06	ES 172	646303	1585.N10.gz43_210360

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CloneID	ES No	ClusterID	SequenceName
M00055492C:H07	ES 172	646318	1585.N22.gz43_210552
M00055492D:B08	ES 172	474821	1585.N24.gz43_210584
M00055493C:B06	ES 172	556551	1585.O12.gz43_210393
M00055493D:B07	ES 172	555193	1585.O14.gz43_210425
M00055493D:D12	ES 172	650353	1585.O16.gz43_210457
M00055494A:A06	ES 172	645117	1585.O18.gz43_210489
M00055494C:G10	ES 172	562236	1585.P05.gz43_210282
M00055494C:G11	ES 172	558839	1585.P06.gz43_210298
M00055495A:D11	ES 172	642415	1585.P12.gz43_210394
M00055495C:F03	ES 172	237288	1585.P22.gz43_210554
M00055516B:E11	ES 172	552783	1587.A04.gz43_211407
M00055517A:D09	ES 172	650161	1587.A16.gz43_211599
M00055517C:H07	ES 172	492483	1587.B02.gz43_211376
M00055517D:D09	ES 172	446984	1587.B06.gz43_211440
M00055517D:D11	ES 172	290226	1587.B07.gz43_211456
M00055519A:C01	ES 172	558785	1587.B23.gz43_211712
M00055519A:F08	ES 172	234606	1587.C01.gz43_211361
M00055519A:H01	ES 172	644051	1587.C03.gz43_211393
M00055520B:D11	ES 172	590218	1587.D04.gz43_211410
M00055520B:E04	ES 172	481220	1587.D05.gz43_211426
M00055521C:B08	ES 172	597780	1587.E01.gz43_211363
M00055521C:B09	ES 172	638943	1587.E02.gz43_211379
M00055521C:C08	ES 172	639056	1587.E03.gz43_211395
M00055521C:D02	ES 172	559324	1587.E04.gz43_211411
M00055522C:F06	ES 172	561202	1587.F04.gz43_211412
M00055523C:F05	ES 172	551518	1587.F21.gz43_211684
M00055524B:B08	ES 172	640419	1587.G08.gz43_211477
M00055524B:D11	ES 172	648747	1587.G10.gz43_211509
M00055528A:E08	ES 172	641615	1587.J11.gz43_211528
M00055528D:B02	ES 172	645544	1587.K05.gz43_211433
M00055528D:H07	ES 172	649932	1587.K13.gz43_211561
M00055529D:D05	ES 172	643723	1587.L03.gz43_211402
M00055529D:D11	ES 172	646711	1587.L04.gz43_211418
M00055529D:G03	ES 172	555326	1587.L06.gz43_211450
M00055530A:C07	ES 172	649149	1587.L09.gz43_211498
M00055531B:D10	ES 172	639132	1587.M04.gz43_211419
M00055531B:E05	ES 172	650617	1587.M05.gz43_211435
M00055531C:C04	ES 172	644479	1587.M10.gz43_211515
M00055531D:E06	ES 172	639213	1587.M13.gz43_211563
M00055532C:G08	ES 172	639459	1587.N03.gz43_211404
M00055532D:A12	ES 172	207552	1587.N04.gz43_211420
M00055533B:B11	ES 172	641216	1587.N15.gz43_211596
M00055533D:G02	ES 172	116869	1587.O04.gz43_211421
M00055534A:E06	ES 172	194095	1587.O05.gz43_211437

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CloneID	ES No	ClusterID	SequenceName
M00055535B:A11	ES 172	639826	1587.P03.gz43_211406
M00055535C:A03	ES 172	634409	1587.P07.gz43_211470
M00055535C:E08	ES 172	640072	1587.P10.gz43_211518
M00055536B:H11	ES 172	649390	1588.A03.gz43_217281
M00055536D:D12	ES 172	447869	1588.A07.gz43_217345
M00055537C:A01	ES 172	552001	1588.A11.gz43_211923
M00055537C:A01	ES 172	552001	1588.A11.gz43_217409
M00055537C:E04	ES 172	451671	1588.A15.gz43_217473
M00055538A:C05	ES 172	419706	1588.A18.gz43_212035
M00055538B:G09	ES 172	639461	1588.A21.gz43_217569
M00055538C:E04	ES 172	642631	1588.B02.gz43_211780
M00055538D:D12	ES 172	649335	1588.B06.gz43_211844
M00055538D:D12	ES 172	649335	1588.B06.gz43_217330
M00055538D:F12	ES 172	640089	1588.B09.gz43_211892
M00055538D:H07	ES 172	648206	1588.B11.gz43_211924
M00055540D:G11	ES 172	403419	1588.C19.gz43_217539
M00055541C:D02	ES 172	643277	1588.D05.gz43_211830
M00055542B:B11	ES 172	453606	1588.D17.gz43_212022
M00055542B:B11	ES 172	453606	1588.D17.gz43_217508
M00055542C:B02	ES 172	451361	1588.D21.gz43_217572
M00055542C:D07	ES 172	639114	1588.D22.gz43_212102
M00055542C:H05	ES 172	641031	1588.E02.gz43_217269
M00055543B:A06	ES 172	568331	1588.E15.gz43_211991
M00055543C:B09	ES 172	638917	1588.E16.gz43_217493
M00055543D:H01	ES 172	452342	1588.F01.gz43_211768
M00055543D:H03	ES 172	639543	1588.F02.gz43_211784
M00055544A:A07	ES 172	473701	1588.F03.gz43_211800
M00055544C:A01	ES 172	648748	1588.F13.gz43_211960
M00055544C:B07	ES 172	562414	1588.F15.gz43_211992
M00055545A:C01	ES 172	644173	1588.F23.gz43_217606
M00055545B:A04	ES 172	562274	1588.G03.gz43_211801
M00055545B:C01	ES 172	556867	1588.G05.gz43_211833
M00055545C:D09	ES 172	639099	1588.G13.gz43_211961
M00055545D:B06	ES 172	505042	1588.G16.gz43_212009
M00055545D:C03	ES 172	642414	1588.G17.gz43_217511
M00055546B:H03	ES 172	466092	1588.H02.gz43_217272
M00055546C:B01	ES 172	562468	1588.H04.gz43_217304
M00055546C:F11	ES 172	32812	1588.H09.gz43_211898
M00055547A:H11	ES 172	649564	1588.H18.gz43_217528
M00055547B:C05	ES 172	557983	1588.H21.gz43_212090
M00055547B:G09	ES 172	648494	1588.H24.gz43_217624
M00055547C:B01	ES 172	448673	1588.I02.gz43_211787
M00055547C:B07	ES 172	650982	1588.I04.gz43_217305
M00055547D:G06	ES 172	641401	1588.I15.gz43_217481

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CloneID	ES No	ClusterID	SequenceName
M00055548A:D07	ES 172	529799	1588.I18.gz43_217529
M00055548A:F04	ES 172	449891	1588.I22.gz43_217593
M00055548B:A03	ES 172	638837	1588.J02.gz43_217274
M00055548B:C03	ES 172	646159	1588.J06.gz43_211852
M00055548B:G06	ES 172	639480	1588.J09.gz43_211900
M00055548B:G06	ES 172	639480	1588.J09.gz43_217386
M00055548C:E05	ES 172	512634	1588.J13.gz43_211964
M00055548C:G09	ES 172	639295	1588.J17.gz43_212028
M00055549A:B04	ES 172	442531	1588.J22.gz43_212108
M00055549C:E10	ES 172	639316	1588.K08.gz43_211885
M00055549C:E10	ES 172	639316	1588.K08.gz43_217371
M00055549C:F08	ES 172	453768	1588.K10.gz43_217403
M00055550A:C07	ES 172	645365	1588.K19.gz43_212061
M00055550C:E07	ES 172	450123	1588.L05.gz43_211838
M00055550C:F03	ES 172	645938	1588.L07.gz43_211870
M00055550D:D02	ES 172	457146	1588.L11.gz43_217420
M00055551A:A12	ES 172	650521	1588.L18.gz43_212046
M00055551C:C08	ES 172	551662	1588.M07.gz43_217357
M00055552C:G03	ES 172	447379	1588.M20.gz43_217565
M00055553A:D08	ES 172	406436	1588.N01.gz43_217262
M00055553A:F11	ES 172	645891	1588.N02.gz43_211792
M00055553A:F11	ES 172	645891	1588.N02.gz43_217278
M00055553A:H08	ES 172	420702	1588.N04.gz43_211824
M00055553B:D05	ES 172	554789	1588.N06.gz43_217342
M00055553B:H04	ES 172	644242	1588.N09.gz43_211904
M00055553C:D06	ES 172	644723	1588.N11.gz43_211936
M00055553C:H12	ES 172	641078	1588.N15.gz43_212000
M00055553D:C07	ES 172	640747	1588.N16.gz43_212016
M00055553D:E06	ES 172	645781	1588.N18.gz43_217534
M00055554C:B04	ES 172	644012	1588.O05.gz43_217327
M00055554D:F01	ES 172	377692	1588.O11.gz43_217423
M00055555D:B05	ES 172	639395	1588.O22.gz43_217599
M00055556A:A04	ES 172	646350	1588.P05.gz43_211842
M00055556A:E07	ES 172	649099	1588.P06.gz43_211858
M00055556A:E07	ES 172	649099	1588.P06.gz43_217344
M00055556C:H09	ES 172	701221	1588.P14.gz43_217472
M00055557A:A04	ES 172	447023	1588.P18.gz43_217536
M00055557A:C11	ES 172	639425	1588.P21.gz43_212098
M00055557B:B10	ES 172	477064	1588.P24.gz43_217632
M00055557B:F07	ES 172	509798	1597.A03.gz43_212179
M00055558B:G11	ES 172	637966	1597.A16.gz43_212387
M00055558D:C08	ES 172	460666	1597.A21.gz43_212467
M00055558D:D07	ES 172	645913	1597.A23.gz43_212499
M00055559A:D06	ES 172	469731	1597.B06.gz43_212228

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CloneID	ES No	ClusterID	SequenceName
M00055559C:D07	ES 172	555021	1597.B12.gz43_212324
M00055560D:C03	ES 172	470822	1597.C10.gz43_212293
M00055561A:F07	ES 172	647614	1597.C17.gz43_212405
M00055561B:G12	ES 172	645538	1597.C24.gz43_212517
M00055561C:C07	ES 172	639781	1597.D05.gz43_212214
M00055562B:D03	ES 172	592122	1597.D14.gz43_212358
M00055562B:H02	ES 172	475152	1597.D17.gz43_212406
M00055562C:F02	ES 172	640195	1597.D22.gz43_212486
M00055562D:B06	ES 172	639056	1597.E05.gz43_212215
M00055563A:A02	ES 172	640356	1597.E08.gz43_212263
M00055563A:C03	ES 172	647431	1597.E09.gz43_212279
M00055563A:D02	ES 172	449258	1597.E10.gz43_212295
M00055565A:C08	ES 172	454825	1597.F10.gz43_212296
M00055565A:F11	ES 172	553318	1597.F16.gz43_212392
M00055565B:F04	ES 172	596882	1597.F18.gz43_212424
M00055565D:G08	ES 172	664195	1597.G03.gz43_212185
M00055566A:E02	ES 172	639593	1597.G06.gz43_212233
M00055567A:A06	ES 172	446230	1597.G23.gz43_212505
M00055567A:A11	ES 172	647069	1597.G24.gz43_212521
M00055567B:G07	ES 172	649829	1597.H04.gz43_212202
M00055568A:B04	ES 172	556511	1597.H15.gz43_212378
M00055568A:D05	ES 172	646293	1597.H17.gz43_212410
M00055568C:F07	ES 172	638869	1597.H24.gz43_212522
M00055568C:G11	ES 172	641890	1597.I01.gz43_212155
M00055569A:C08	ES 172	643488	1597.I10.gz43_212299
M00055569A:D01	ES 172	650740	1597.I12.gz43_212331
M00055569A:F06	ES 172	644928	1597.I18.gz43_212427
M00055569B:G10	ES 172	553114	1597.I24.gz43_212523
M00055569D:C02	ES 172	557975	1597.J06.gz43_212236
M00055570B:F07	ES 172	659031	1597.J12.gz43_212332
M00055572C:E08	ES 172	447423	1597.L05.gz43_212222
M00055573A:B11	ES 172	666644	1597.L12.gz43_212334
M00055573B:D11	ES 172	589483	1597.L18.gz43_212430
M00055573B:E01	ES 172	553602	1597.L19.gz43_212446
M00055574A:D12	ES 172	642527	1597.M09.gz43_212287
M00055574A:F12	ES 172	640181	1597.M11.gz43_212319
M00055574B:D04	ES 172	557713	1597.M15.gz43_212383
M00055574B:F06	ES 172	650235	1597.M17.gz43_212415
M00055574D:B07	ES 172	649431	1597.M24.gz43_212527
M00055574D:E02	ES 173	649668	1597.N02.gz43_212176
M00055575C:B04	ES 173	45921	1597.N14.gz43_212368
M00055575D:G04	ES 173	640956	1597.N18.gz43_212432
M00055576A:D09	ES 173	650593	1597.N21.gz43_212480

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055576A:F07	ES 173	649349	1597.N23.gz43_212512
M00055576D:E09	ES 173	643162	1597.O12.gz43_212337
M00055577A:G09	ES 173	640851	1597.O20.gz43_212465
M00055577B:F05	ES 173	648483	1597.O24.gz43_212529
M00055577C:G02	ES 173	639698	1597.P05.gz43_212226
M00055578B:D05	ES 173	362177	1597.P12.gz43_212338
M00055578C:F11	ES 173	668852	1597.P22.gz43_212498
M00055578D:E11	ES 173	561602	1597.P24.gz43_212530
M00055579C:D04	ES 173	641191	1598.A07.gz43_212627
M00055579D:C11	ES 173	459521	1598.A11.gz43_212691
M00055579D:G09	ES 173	641957	1598.A13.gz43_212723
M00055580B:B08	ES 173	641425	1598.A17.gz43_212787
M00055581A:C02	ES 173	640025	1598.B02.gz43_212548
M00055581C:A01	ES 173	648580	1598.B04.gz43_212580
M00055581C:B08	ES 173	647360	1598.B05.gz43_212596
M00055582B:A06	ES 173	648159	1598.B15.gz43_212756
M00055583A:A05	ES 173	641262	1598.C05.gz43_212597
M00055583C:A01	ES 173	86311	1598.C18.gz43_212805
M00055584A:G11	ES 173	641925	1598.D06.gz43_212614
M00055584B:B01	ES 173	639070	1598.D07.gz43_212630
M00055585A:E12	ES 173	651000	1598.D21.gz43_212854
M00055585B:F01	ES 173	415538	1598.E02.gz43_212551
M00055585C:F05	ES 173	449247	1598.E06.gz43_212615
M00055586A:F05	ES 173	639116	1598.E11.gz43_212695
M00055586C:A06	ES 173	553087	1598.E21.gz43_212855
M00055586D:G07	ES 173	645707	1598.F05.gz43_212600
M00055588A:C03	ES 173	639444	1598.G05.gz43_212601
M00055588B:H11	ES 173	140909	1598.G11.gz43_212697
M00055588C:G09	ES 173	509973	1598.G15.gz43_212761
M00055589A:B06	ES 173	646914	1598.G21.gz43_212857
M00055589B:E08	ES 173	644572	1598.H03.gz43_212570
M00055589B:H02	ES 173	642008	1598.H04.gz43_212586
M00055590A:B03	ES 173	464091	1598.H11.gz43_212698
M00055590A:E01	ES 173	645264	1598.H15.gz43_212762
M00055590D:G07	ES 173	635439	1598.I11.gz43_212699
M00055591A:B08	ES 173	641472	1598.I12.gz43_212715
M00055591D:A07	ES 173	556868	1598.J04.gz43_212588
M00055591D:E08	ES 173	512521	1598.J05.gz43_212604
M00055592B:C10	ES 173	641467	1598.J12.gz43_212716
M00055593A:F08	ES 173	641838	1598.K09.gz43_212669
M00055593C:D08	ES 173	638941	1598.K14.gz43_212749
M00055594B:A01	ES 173	446371	1598.K21.gz43_212861
M00055594C:B03	ES 173	470769	1598.L04.gz43_212590
M00055594C:F11	ES 173	646590	1598.L06.gz43_212622

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055594D:F07	ES 173	455864	1598.L12.gz43_212718
M00055595C:F12	ES 173	447272	1598.M01.gz43_212543
M00055595C:G03	ES 173	478229	1598.M02.gz43_212559
M00055595D:C04	ES 173	554273	1598.M04.gz43_212591
M00055596A:C02	ES 173	144626	1598.M08.gz43_212655
M00055596A:E07	ES 173	640826	1598.M10.gz43_212687
M00055596B:D03	ES 173	458979	1598.M16.gz43_212783
M00055597B:B04	ES 173	463028	1598.N05.gz43_212608
M00055597D:B05	ES 173	641440	1598.N09.gz43_212672
M00055597D:E10	ES 173	564440	1598.N11.gz43_212704
M00055599D:C08	ES 173	640298	1598.N23.gz43_212896
M00055600A:C04	ES 173	507188	1598.O07.gz43_212641
M00055600C:C02	ES 173	647312	1598.O17.gz43_212801
M00055600D:B02	ES 173	515931	1598.O19.gz43_212833
M00055601B:D12	ES 173	640695	1598.P05.gz43_212610
M00055601B:H02	ES 173	641191	1598.P07.gz43_212642
M00055601C:C11	ES 173	553925	1598.P10.gz43_212690
M00055602A:D04	ES 173	640634	1598.P20.gz43_212850
M00055602B:B10	ES 173	201904	1599.A01.gz43_212923
M00055602B:B12	ES 173	644764	1599.A03.gz43_212955
M00055602D:G08	ES 173	643906	1599.A15.gz43_213147
M00055603D:A09	ES 173	641338	1599.B01.gz43_212924
M00055604D:E07	ES 173	643279	1599.B09.gz43_213052
M00055604D:F05	ES 173	559380	1599.B10.gz43_213068
M00055606A:B11	ES 173	554833	1599.B19.gz43_213212
M00055606A:F09	ES 173	461524	1599.B21.gz43_213244
M00055606C:F04	ES 173	641839	1599.C09.gz43_213053
M00055606D:C05	ES 173	641542	1599.C12.gz43_213101
M00055608C:E03	ES 173	641680	1599.D10.gz43_213070
M00055608C:G11	ES 173	607715	1599.D15.gz43_213150
M00055609B:D10	ES 173	460929	1599.E01.gz43_212927
M00055609B:F10	ES 173	640930	1599.E03.gz43_212959
M00055610B:E04	ES 173	454527	1599.F02.gz43_212944
M00055610D:H09	ES 173	639255	1599.F09.gz43_213056
M00055611C:E03	ES 173	551896	1599.F24.gz43_213296
M00055612A:H05	ES 173	645031	1599.G13.gz43_213121
M00055615C:E01	ES 173	640868	1599.I08.gz43_213043
M00055615D:C07	ES 173	639703	1599.I11.gz43_213091
M00055617A:H12	ES 173	641254	1599.J09.gz43_213060
M00055619A:C03	ES 173	213631	1599.K12.gz43_213109
M00055619B:H04	ES 173	639480	1599.K19.gz43_213221
M00055619C:D06	ES 173	647518	1599.K24.gz43_213301
M00055619C:F07	ES 173	640221	1599.L01.gz43_212934
M00055619D:A04	ES 173	640382	1599.L05.gz43_212998

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055620D:D05	ES 173	640416	1599.L17.gz43_213190
M00055621B:G03	ES 173	561626	1599.L23.gz43_213286
M00055623D:G05	ES 173	641069	1599.N09.gz43_213064
M00055628B:B07	ES 173	607138	1599.P21.gz43_213258
M00055629A:D08	ES 173	647266	1600.A15.gz43_213531
M00055629B:G09	ES 173	455075	1600.A22.gz43_213643
M00055630B:E09	ES 173	561180	1600.B13.gz43_213500
M00055630B:G04	ES 173	645004	1600.B15.gz43_213532
M00055632A:B11	ES 173	559423	1600.B24.gz43_213676
M00055632D:A06	ES 173	640799	1600.C10.gz43_213453
M00055633B:A08	ES 173	634012	1600.C21.gz43_213629
M00055633B:G02	ES 173	131348	1600.C24.gz43_213677
M00055633D:A02	ES 173	649717	1600.D04.gz43_213358
M00055634C:C10	ES 173	446659	1600.D21.gz43_213630
M00055634C:F09	ES 173	166041	1600.D23.gz43_213662
M00055636A:H12	ES 173	650180	1600.E24.gz43_213679
M00055637B:A01	ES 173	642361	1600.F24.gz43_213680
M00055637B:H12	ES 173	641253	1600.G05.gz43_213377
M00055638A:A10	ES 173	554335	1600.G13.gz43_213505
M00055638D:D07	ES 173	639934	1600.H02.gz43_213330
M00055638D:E09	ES 173	646695	1600.H04.gz43_213362
M00055639D:D03	ES 173	548959	1600.I01.gz43_213315
M00055639D:F08	ES 173	640956	1600.I03.gz43_213347
M00055640A:G03	ES 173	635965	1600.I07.gz43_213411
M00055640B:C01	ES 173	472129	1600.I09.gz43_213443
M00055640C:E06	ES 173	557401	1600.I12.gz43_213491
M00055640C:F05	ES 173	467381	1600.I13.gz43_213507
M00055640C:F08	ES 173	151279	1600.I14.gz43_213523
M00055641A:C12	ES 173	562000	1600.I19.gz43_213603
M00055642D:A05	ES 173	553516	1600.J23.gz43_213668
M00055643A:C01	ES 173	451615	1600.K05.gz43_213381
M00055643B:E05	ES 173	642246	1600.K11.gz43_213477
M00055643C:G10	ES 173	645261	1600.K18.gz43_213589
M00055643D:A05	ES 173	656268	1600.K20.gz43_213621
M00055643D:G11	ES 173	561069	1600.K24.gz43_213685
M00055644A:D10	ES 173	549124	1600.L02.gz43_213334
M00055644A:D12	ES 173	554722	1600.L03.gz43_213350
M00055644B:H12	ES 173	379040	1600.L07.gz43_213414
M00055645A:C07	ES 173	156097	1600.L19.gz43_213606
M00055646C:B04	ES 173	646352	1600.M13.gz43_213511
M00055647A:H10	ES 173	446621	1600.M19.gz43_213607
M00055647B:A05	ES 173	641210	1600.M20.gz43_213623
M00055647C:D02	ES 173	639886	1600.N04.gz43_213368
M00055647D:B11	ES 173	467563	1600.N11.gz43_213480

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055648B:C01	ES 173	453441	1600.N19.gz43_213608
M00055649A:H07	ES 173	640320	1600.O11.gz43_213481
M00055649C:F02	ES 173	491368	1600.O16.gz43_213561
M00055650A:B05	ES 173	553285	1600.O21.gz43_213641
M00055650C:F12	ES 173	640029	1600.P09.gz43_213450
M00055651A:D06	ES 173	638779	1600.P16.gz43_213562
M00055651A:E06	ES 173	641702	1600.P17.gz43_213578
M00055651B:F08	ES 173	458736	1600.P20.gz43_213626
M00055651C:E01	ES 173	550515	1600.P24.gz43_213690
M00055651C:F07	ES 173	643513	1669.A01.gz43_260687
M00055652A:G11	ES 173	554510	1669.A07.gz43_260783
M00055652B:B11	ES 173	618998	1669.A10.gz43_260831
M00055652B:F12	ES 173	406734	1669.A12.gz43_260863
M00055653A:G08	ES 173	649631	1669.A24.gz43_261055
M00055653B:C03	ES 173	647333	1669.B06.gz43_260768
M00055653B:E12	ES 173	86311	1669.B09.gz43_260816
M00055653B:G01	ES 173	644971	1669.B10.gz43_260832
M00055653B:G11	ES 173	640259	1669.B11.gz43_260848
M00055653D:H02	ES 173	463312	1669.B23.gz43_261040
M00055654A:B07	ES 173	462247	1669.C01.gz43_260689
M00055654B:G09	ES 173	472226	1669.C06.gz43_260769
M00055654C:A05	ES 173	641469	1669.C08.gz43_260801
M00055654C:C10	ES 173	638971	1669.C09.gz43_260817
M00055654C:D03	ES 173	556488	1669.C10.gz43_260833
M00055654D:F02	ES 173	650677	1669.C17.gz43_260945
M00055655A:A09	ES 173	642111	1669.C18.gz43_260961
M00055655B:B08	ES 173	642411	1669.C22.gz43_261025
M00055656A:E09	ES 173	643804	1669.D11.gz43_260850
M00055657A:B04	ES 173	450883	1669.E08.gz43_260803
M00055659A:A08	ES 173	648773	1669.F11.gz43_260852
M00055659C:B10	ES 173	639706	1669.F21.gz43_261012
M00055659C:D06	ES 173	639674	1669.F24.gz43_261060
M00055660A:A06	ES 173	452687	1669.G10.gz43_260837
M00055660A:C05	ES 173	503275	1669.G11.gz43_260853
M00055660A:C08	ES 173	643563	1669.G12.gz43_260869
M00055660B:H02	ES 173	589483	1669.G17.gz43_260949
M00055661B:E07	ES 173	455778	1669.H06.gz43_260774
M00055661C:E11	ES 173	658447	1669.H12.gz43_260870
M00055662B:F11	ES 173	447585	1669.I04.gz43_260743
M00055662C:C11	ES 173	523875	1669.I07.gz43_260791
M00055662C:D05	ES 173	645758	1669.I08.gz43_260807
M00055662C:D12	ES 173	641379	1669.I09.gz43_260823
M00055662C:H06	ES 173	446188	1669.I12.gz43_260871
M00055662D:A09	ES 173	639596	1669.I15.gz43_260919

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055662D:B07	ES 173	639665	1669.I17.gz43_260951
M00055662D:E05	ES 173	640018	1669.I20.gz43_260999
M00055662D:F09	ES 173	559575	1669.I21.gz43_261015
M00055663A:B02	ES 173	641091	1669.I22.gz43_261031
M00055663A:G04	ES 173	640261	1669.I24.gz43_261063
M00055663A:H10	ES 173	641658	1669.J01.gz43_260696
M00055663B:E02	ES 173	640078	1669.J04.gz43_260744
M00055663C:D05	ES 173	658271	1669.J07.gz43_260792
M00055663C:F05	ES 173	512521	1669.J08.gz43_260808
M00055663D:B05	ES 173	643909	1669.J10.gz43_260840
M00055664B:G08	ES 173	640211	1669.J16.gz43_260936
M00055665B:A12	ES 173	451906	1669.K06.gz43_260777
M00055665B:B10	ES 174	465104	1669.K07.gz43_260793
M00055665D:F11	ES 174	640179	1669.K18.gz43_260969
M00055666A:G04	ES 174	642078	1669.K23.gz43_261049
M00055666B:C03	ES 174	448484	1669.L07.gz43_260794
M00055666B:E06	ES 174	640678	1669.L11.gz43_260858
M00055666C:C11	ES 174	639804	1669.L12.gz43_260874
M00055666D:D08	ES 174	639932	1669.L16.gz43_260938
M00055667A:B12	ES 174	642332	1669.L20.gz43_261002
M00055667A:H10	ES 174	456561	1669.L23.gz43_261050
M00055667B:C08	ES 174	639752	1669.M01.gz43_260699
M00055667C:F07	ES 174	646894	1669.M10.gz43_260843
M00055667D:B01	ES 174	561894	1669.M12.gz43_260875
M00055668B:A10	ES 174	550999	1669.M19.gz43_260987
M00055668B:B07	ES 174	557401	1669.M20.gz43_261003
M00055668B:D05	ES 174	639906	1669.M21.gz43_261019
M00055668C:A04	ES 174	642068	1669.N02.gz43_260716
M00055668C:F05	ES 174	648340	1669.N05.gz43_260764
M00055668D:E11	ES 174	556750	1669.N10.gz43_260844
M00055669B:G02	ES 174	648352	1669.N18.gz43_260972
M00055669D:B08	ES 174	639743	1669.O02.gz43_260717
M00055670A:B04	ES 174	648352	1669.O07.gz43_260797
M00055670D:F02	ES 174	641683	1669.O17.gz43_260957
M00055671A:H03	ES 174	518569	1669.P01.gz43_260702
M00055671B:B02	ES 174	642230	1669.P03.gz43_260734
M00055672D:F06	ES 174	640092	1670.A08.gz43_261183
M00055673A:E09	ES 174	95617	1670.A11.gz43_261231
M00055673B:A04	ES 174	645146	1670.A16.gz43_261311
M00055673B:B08	ES 174	639469	1670.A18.gz43_261343
M00055673D:C01	ES 174	639805	1670.B07.gz43_261168
M00055674A:C11	ES 174	651088	1670.B12.gz43_261248
M00055674C:E05	ES 174	645968	1670.B21.gz43_261392

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055675A:G03	ES 174	643522	1670.C06.gz43_261153
M00055675D:E04	ES 174	650673	1670.C14.gz43_261281
M00055676B:D05	ES 174	446242	1670.C20.gz43_261377
M00055676D:H07	ES 174	426366	1670.D05.gz43_261138
M00055678C:H05	ES 174	289328	1670.D14.gz43_261282
M00055679B:E03	ES 174	642321	1670.D23.gz43_261426
M00055680B:D09	ES 174	553642	1670.E15.gz43_261299
M00055680B:H04	ES 174	647427	1670.E17.gz43_261331
M00055680C:E01	ES 174	493622	1670.E20.gz43_261379
M00055681A:F02	ES 174	416808	1670.E24.gz43_261443
M00055681D:F11	ES 174	642502	1670.F18.gz43_261348
M00055682A:B07	ES 174	637966	1670.F22.gz43_261412
M00055682C:D06	ES 174	641618	1670.G09.gz43_261205
M00055682D:G02	ES 174	641902	1670.G19.gz43_261365
M00055683B:D10	ES 174	640645	1670.H06.gz43_261158
M00055683C:A03	ES 174	557625	1670.H10.gz43_261222
M00055683C:D11	ES 174	644699	1670.H14.gz43_261286
M00055683C:H11	ES 174	553921	1670.H17.gz43_261334
M00055684B:D06	ES 174	599838	1670.I10.gz43_261223
M00055684D:A10	ES 174	506901	1670.I18.gz43_261351
M00055685A:E10	ES 174	601137	1670.I23.gz43_261431
M00055685A:F02	ES 174	647856	1670.I24.gz43_261447
M00055685A:F06	ES 174	447802	1670.J02.gz43_261096
M00055685B:E12	ES 174	645909	1670.J06.gz43_261160
M00055685D:B06	ES 174	649558	1670.J18.gz43_261352
M00055686B:D03	ES 174	641624	1670.K06.gz43_261161
M00055686D:E04	ES 174	641726	1670.K12.gz43_261257
M00055686D:E10	ES 174	641728	1670.K13.gz43_261273
M00055687C:B04	ES 174	554564	1670.K24.gz43_261449
M00055687C:B11	ES 174	649284	1670.L01.gz43_261082
M00055687C:F01	ES 174	643594	1670.L05.gz43_261146
M00055687C:F07	ES 174	639136	1670.L06.gz43_261162
M00055688A:A02	ES 174	641287	1670.L09.gz43_261210
M00055688A:E04	ES 174	649921	1670.L12.gz43_261258
M00055689B:F04	ES 174	446675	1670.M05.gz43_261147
M00055689C:B03	ES 174	634122	1670.M08.gz43_261195
M00055689C:C03	ES 174	634122	1670.M10.gz43_261227
M00055689D:G01	ES 174	567636	1670.M18.gz43_261355
M00055691A:D08	ES 174	640826	1670.M22.gz43_261419
M00055691B:E07	ES 174	640889	1670.N03.gz43_261116
M00055691C:E02	ES 174	646638	1670.N06.gz43_261164
M00055691D:B07	ES 174	642644	1670.N11.gz43_261244
M00055691D:E04	ES 174	502609	1670.N13.gz43_261276
M00055692A:E05	ES 174	561920	1670.N18.gz43_261356

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055695D:E01	ES 174	645431	1670.P12.gz43_261262
M00055699C:D02	ES 174	41141	1671.B11.gz43_261616
M00055700B:E10	ES 174	553985	1671.B23.gz43_261808
M00055701A:B04	ES 174	560546	1671.C12.gz43_261633
M00055701B:C03	ES 174	642039	1671.C17.gz43_261713
M00055702C:D01	ES 174	646028	1671.D09.gz43_261586
M00055702C:F11	ES 174	640947	1671.D10.gz43_261602
M00055702D:H10	ES 174	605761	1671.D11.gz43_261618
M00055704A:D09	ES 174	642062	1671.E08.gz43_261571
M00055704B:C04	ES 174	551415	1671.E12.gz43_261635
M00055705C:F12	ES 174	471268	1671.F17.gz43_261716
M00055705C:G01	ES 174	641876	1671.F18.gz43_261732
M00055706B:H12	ES 174	463548	1671.G10.gz43_261605
M00055707A:B07	ES 174	649429	1671.G14.gz43_261669
M00055707A:E07	ES 174	468316	1671.G17.gz43_261717
M00055707A:F11	ES 174	453006	1671.G20.gz43_261765
M00055707B:E02	ES 174	640879	1671.G22.gz43_261797
M00055709D:G10	ES 174	417259	1671.H17.gz43_261718
M00055710B:E04	ES 174	641700	1671.H22.gz43_261798
M00055711B:B08	ES 174	561422	1671.I07.gz43_261559
M00055711C:A07	ES 174	463368	1671.I11.gz43_261623
M00055711D:H12	ES 174	558890	1671.I21.gz43_261783
M00055713C:B06	ES 174	455552	1671.J08.gz43_261576
M00055713C:D11	ES 174	469688	1671.J10.gz43_261608
M00055713C:F12	ES 174	558086	1671.J11.gz43_261624
M00055713C:H01	ES 174	446933	1671.J12.gz43_261640
M00055715A:D10	ES 174	463368	1671.K08.gz43_261577
M00055715C:C11	ES 174	640534	1671.K20.gz43_261769
M00055717A:C06	ES 174	644325	1671.L10.gz43_261610
M00055717A:H01	ES 174	521888	1671.L12.gz43_261642
M00055717B:A03	ES 174	451401	1671.L14.gz43_261674
M00055717B:E04	ES 174	421826	1671.L17.gz43_261722
M00055717C:B07	ES 174	536415	1671.L23.gz43_261818
M00055718A:F01	ES 174	478192	1671.M09.gz43_261595
M00055718A:H05	ES 174	640282	1671.M10.gz43_261611
M00055718B:H11	ES 174	465589	1671.M17.gz43_261723
M00055719A:A06	ES 174	646105	1671.N09.gz43_261596
M00055719A:D11	ES 174	557710	1671.N12.gz43_261644
M00055719A:G04	ES 174	645505	1671.N17.gz43_261724
M00055719A:G12	ES 174	510195	1671.N18.gz43_261740
M00055719C:A09	ES 174	640282	1671.N23.gz43_261820
M00055720B:D06	ES 174	645344	1671.O12.gz43_261645
M00055721A:A07	ES 174	466265	1671.O22.gz43_261805
M00055721B:D08	ES 174	642288	1671.P07.gz43_261566

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055722A:B05	ES 174	492094	1671.P18.gz43_261742
M00055722A:C04	ES 174	600115	1671.P21.gz43_261790
M00055722B:A01	ES 174	498194	1672.A01.gz43_261841
M00055722B:G12	ES 174	645171	1672.A06.gz43_261921
M00055722C:E11	ES 174	650303	1672.A12.gz43_262017
M00055722C:F11	ES 174	642491	1672.A13.gz43_262033
M00055722D:A07	ES 174	641056	1672.A14.gz43_262049
M00055722D:B10	ES 174	460967	1672.A17.gz43_262097
M00055722D:E05	ES 174	544797	1672.A19.gz43_262129
M00055722D:G12	ES 174	470769	1672.A23.gz43_262193
M00055723A:B08	ES 174	556326	1672.B03.gz43_261874
M00055723A:C04	ES 174	647688	1672.B04.gz43_261890
M00055723A:F04	ES 174	649360	1672.B07.gz43_261938
M00055723B:A09	ES 174	642078	1672.B11.gz43_262002
M00055723B:C03	ES 174	642197	1672.B14.gz43_262050
M00055723B:H08	ES 174	46976	1672.B17.gz43_262098
M00055723C:A08	ES 174	648472	1672.B18.gz43_262114
M00055723C:B02	ES 174	489426	1672.B19.gz43_262130
M00055723C:F09	ES 174	503923	1672.B22.gz43_262178
M00055723D:C04	ES 174	522497	1672.C03.gz43_261875
M00055723D:E05	ES 174	649106	1672.C06.gz43_261923
M00055724A:C12	ES 174	284586	1672.C12.gz43_262019
M00055724A:E03	ES 174	645018	1672.C15.gz43_262067
M00055724A:G08	ES 174	504568	1672.C17.gz43_262099
M00055724B:D04	ES 174	467822	1672.C20.gz43_262147
M00055724B:G03	ES 174	642722	1672.C23.gz43_262195
M00055724B:H03	ES 174	557221	1672.D02.gz43_261860
M00055724D:A02	ES 174	559828	1672.D17.gz43_262100
M00055725A:F12	ES 174	641305	1672.E02.gz43_261861
M00055725A:G07	ES 174	557833	1672.E03.gz43_261877
M00055725D:B02	ES 174	522548	1672.E14.gz43_262053
M00055725D:F05	ES 174	452212	1672.E19.gz43_262133
M00055726C:F01	ES 174	645004	1672.F16.gz43_262086
M00055726D:H12	ES 174	489249	1672.F24.gz43_262214
M00055727A:G01	ES 174	507188	1672.G02.gz43_261863
M00055727B:F10	ES 174	642535	1672.G12.gz43_262023
M00055727C:B02	ES 174	559776	1672.G16.gz43_262087
M00055727D:G01	ES 174	641070	1672.H02.gz43_261864
M00055727D:H04	ES 174	639711	1672.H04.gz43_261896
M00055728B:G11	ES 174	647060	1672.H16.gz43_262088
M00055728C:B08	ES 174	455113	1672.H17.gz43_262104
M00055728D:F02	ES 174	554708	1672.H22.gz43_262184
M00055729A:B12	ES 174	672032	1672.I02.gz43_261865
M00055729B:G03	ES 174	641101	1672.I12.gz43_262025

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055729C:D11	ES 174	642315	1672.I16.gz43_262089
M00055729C:E02	ES 174	477064	1672.I17.gz43_262105
M00055729D:A06	ES 174	546705	1672.I18.gz43_262121
M00055729D:F05	ES 174	644609	1672.I21.gz43_262169
M00055731A:C03	ES 174	461583	1672.J13.gz43_262042
M00055731A:G05	ES 174	640704	1672.J17.gz43_262106
M00055731A:H07	ES 174	235397	1672.J18.gz43_262122
M00055731C:F09	ES 174	454383	1672.K06.gz43_261931
M00055731C:H07	ES 174	639458	1672.K08.gz43_261963
M00055731D:B10	ES 174	646129	1672.K11.gz43_262011
M00055731D:E12	ES 174	555681	1672.K13.gz43_262043
M00055731D:F09	ES 174	640879	1672.K15.gz43_262075
M00055732A:B04	ES 174	651085	1672.K18.gz43_262123
M00055732A:C12	ES 174	322255	1672.K19.gz43_262139
M00055732A:F09	ES 174	642557	1672.K21.gz43_262171
M00055733A:G04	ES 174	642631	1672.L11.gz43_262012
M00055733B:F11	ES 174	504501	1672.L16.gz43_262092
M00055733B:H05	ES 174	419443	1672.L17.gz43_262108
M00055733C:G02	ES 174	383609	1672.L18.gz43_262124
M00055733C:H12	ES 174	650397	1672.L20.gz43_262156
M00055733D:B11	ES 174	561968	1672.L21.gz43_262172
M00055733D:D04	ES 174	645151	1672.L23.gz43_262204
M00055733D:H01	ES 174	416377	1672.M04.gz43_261901
M00055734D:A02	ES 174	461474	1672.M16.gz43_262093
M00055734D:D01	ES 174	646609	1672.M19.gz43_262141
M00055734D:E05	ES 174	642376	1672.M21.gz43_262173
M00055734D:E10	ES 174	645165	1672.M22.gz43_262189
M00055734D:G12	ES 174	558146	1672.M23.gz43_262205
M00055735A:B05	ES 174	647669	1672.N01.gz43_261854
M00055735B:F11	ES 175	642111	1672.N10.gz43_261998
M00055735C:G08	ES 175	648667	1672.N14.gz43_262062
M00055735D:C01	ES 175	502826	1672.N18.gz43_262126
M00055735D:E10	ES 175	556336	1672.N19.gz43_262142
M00055736A:B11	ES 175	648265	1672.N23.gz43_262206
M00055736B:C08	ES 175	643897	1672.O04.gz43_261903
M00055736C:D06	ES 175	466434	1672.O09.gz43_261983
M00055736D:D11	ES 175	642263	1672.O15.gz43_262079
M00055737B:A03	ES 175	640266	1672.O20.gz43_262159
M00055738B:H11	ES 175	100821	1672.P13.gz43_262048
M00055738C:A12	ES 175	647556	1672.P14.gz43_262064
M00055738C:C02	ES 175	647906	1672.P15.gz43_262080
M00055738D:G08	ES 175	645085	1672.P20.gz43_262160
M00055739A:B02	ES 175	550049	1672.P21.gz43_262176

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055739A:B04	ES 175	608540	1672.P22.gz43_262192
M00055739A:C09	ES 175	558301	1681.A01.gz43_296936
M00055739B:B06	ES 175	468613	1681.A03.gz43_296968
M00055739B:D09	ES 175	644836	1681.A04.gz43_296984
M00055739B:H08	ES 175	568467	1681.A08.gz43_297048
M00055739C:D11	ES 175	648481	1681.A10.gz43_297080
M00055739D:B12	ES 175	644684	1681.A13.gz43_297128
M00055739D:C03	ES 175	463815	1681.A14.gz43_297144
M00055739D:E04	ES 175	644919	1681.A16.gz43_297176
M00055740A:B03	ES 175	462245	1681.A19.gz43_297224
M00055740B:C06	ES 175	643142	1681.A21.gz43_297256
M00055740B:F09	ES 175	463824	1681.A24.gz43_297304
M00055740C:A07	ES 175	648905	1681.B03.gz43_296969
M00055740C:E06	ES 175	644937	1681.B04.gz43_296985
M00055740D:G12	ES 175	150839	1681.B10.gz43_297081
M00055741A:D09	ES 175	640504	1681.B13.gz43_297129
M00055741B:B12	ES 175	640997	1681.B15.gz43_297161
M00055741C:A09	ES 175	526459	1681.B18.gz43_297209
M00055741D:H01	ES 175	548920	1681.C01.gz43_296938
M00055742B:H06	ES 175	645147	1681.C08.gz43_297050
M00055742C:A07	ES 175	640306	1681.C10.gz43_297082
M00055742C:C01	ES 175	419479	1681.C11.gz43_297098
M00055742D:H03	ES 175	413621	1681.C16.gz43_297178
M00055743B:E01	ES 175	389377	1681.C24.gz43_297306
M00055743C:C01	ES 175	508755	1681.D02.gz43_296955
M00055743C:D12	ES 175	463951	1681.D05.gz43_297003
M00055743D:D04	ES 175	649427	1681.D09.gz43_297067
M00055743D:E07	ES 175	448703	1681.D10.gz43_297083
M00055744A:B04	ES 175	642263	1681.D15.gz43_297163
M00055744B:B02	ES 175	640017	1681.D19.gz43_297227
M00055744B:C08	ES 175	218416	1681.D20.gz43_297243
M00055744C:D02	ES 175	642644	1681.E02.gz43_296956
M00055744D:A11	ES 175	447936	1681.E08.gz43_297052
M00055744D:F03	ES 175	645000	1681.E11.gz43_297100
M00055745A:H02	ES 175	453726	1681.E19.gz43_297228
M00055745B:H02	ES 175	470667	1681.E23.gz43_297292
M00055745C:A06	ES 175	468959	1681.E24.gz43_297308
M00055745C:G06	ES 175	552085	1681.F03.gz43_296973
M00055745D:F11	ES 175	556654	1681.F09.gz43_297069
M00055746A:C09	ES 175	644053	1681.F10.gz43_297085
M00055746C:F06	ES 175	587696	1681.F17.gz43_297197
M00055746C:F10	ES 175	471277	1681.F18.gz43_297213
M00055746C:G06	ES 175	644468	1681.F19.gz43_297229
M00055747C:E09	ES 175	529742	1681.G11.gz43_297102

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055748A:B03	ES 175	593343	1681.G19.gz43_297230
M00055748A:D07	ES 175	448251	1681.G21.gz43_297262
M00055748C:C07	ES 175	446925	1681.H03.gz43_296975
M00055748D:C03	ES 175	594040	1681.H09.gz43_297071
M00055749B:C10	ES 175	461917	1681.H17.gz43_297199
M00055749B:D12	ES 175	452504	1681.H18.gz43_297215
M00055749C:B03	ES 175	644105	1681.H19.gz43_297231
M00055749C:C04	ES 175	489040	1681.H20.gz43_297247
M00055749D:B07	ES 175	426366	1681.I01.gz43_296944
M00055749D:C01	ES 175	644105	1681.I02.gz43_296960
M00055749D:D06	ES 175	649356	1681.I03.gz43_296976
M00055749D:F12	ES 175	644342	1681.I04.gz43_296992
M00055750B:H01	ES 175	644510	1681.I17.gz43_297200
M00055750C:H10	ES 175	638943	1681.J01.gz43_296945
M00055750D:H06	ES 175	649763	1681.J05.gz43_297009
M00055751A:F06	ES 175	488432	1681.J09.gz43_297073
M00055752A:E10	ES 175	649702	1681.J20.gz43_297249
M00055752A:G10	ES 175	644479	1681.J23.gz43_297297
M00055752C:C06	ES 175	510724	1681.K03.gz43_296978
M00055752C:F06	ES 175	644345	1681.K05.gz43_297010
M00055752C:H07	ES 175	611927	1681.K07.gz43_297042
M00055752D:C01	ES 175	641144	1681.K09.gz43_297074
M00055752D:F01	ES 175	644342	1681.K10.gz43_297090
M00055753A:D04	ES 175	639703	1681.K16.gz43_297186
M00055753B:A02	ES 175	483042	1681.K18.gz43_297218
M00055753B:A06	ES 175	447485	1681.K19.gz43_297234
M00055753B:F10	ES 175	449438	1681.K22.gz43_297282
M00055753D:C06	ES 175	446676	1681.L03.gz43_296979
M00055754A:E04	ES 175	446355	1681.L08.gz43_297059
M00055754A:E07	ES 175	550223	1681.L09.gz43_297075
M00055754A:H06	ES 175	478833	1681.L11.gz43_297107
M00055755A:B11	ES 175	514838	1681.L18.gz43_297219
M00055755C:F12	ES 175	464171	1681.M08.gz43_297060
M00055755D:C09	ES 175	491544	1681.M09.gz43_297076
M00055756C:C03	ES 175	639750	1681.M16.gz43_297188
M00055756D:B05	ES 175	643941	1681.M20.gz43_297252
M00055756D:E05	ES 175	108479	1681.M21.gz43_297268
M00055757A:A07	ES 175	553675	1681.M24.gz43_297316
M00055757B:B07	ES 175	646552	1681.N06.gz43_297029
M00055757B:C04	ES 175	639420	1681.N07.gz43_297045
M00055757B:D06	ES 175	235194	1681.N09.gz43_297077
M00055757D:B05	ES 175	643984	1681.N18.gz43_297221
M00055758A:G02	ES 175	644461	1681.N21.gz43_297269
M00055758C:H10	ES 175	645603	1681.O01.gz43_296950

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055758D:E02	ES 175	640264	1681.O04.gz43_296998
M00055759A:B02	ES 175	492917	1681.O08.gz43_297062
M00055759A:E01	ES 175	295143	1681.O11.gz43_297110
M00055759C:C07	ES 175	453188	1681.O18.gz43_297222
M00055760A:E06	ES 175	453324	1681.O23.gz43_297302
M00055761A:E06	ES 175	451508	1681.P15.gz43_297175
M00055761B:F01	ES 175	646453	1681.P21.gz43_297271
M00055761B:F09	ES 175	641968	1681.P22.gz43_297287
M00055761D:C03	ES 175	648320	1682.A06.gz43_262305
M00055761D:H08	ES 175	488680	1682.A09.gz43_262353
M00055762B:B11	ES 175	639981	1682.A14.gz43_262433
M00055762C:B04	ES 175	643940	1682.A16.gz43_262465
M00055762C:E06	ES 175	494378	1682.A17.gz43_262481
M00055762C:H07	ES 175	466147	1682.A20.gz43_262529
M00055763A:H02	ES 175	649360	1682.B03.gz43_262258
M00055763B:D07	ES 175	550562	1682.B05.gz43_262290
M00055763B:E09	ES 175	644278	1682.B08.gz43_262338
M00055763C:A10	ES 175	462815	1682.B12.gz43_262402
M00055763C:G08	ES 175	642564	1682.B14.gz43_262434
M00055763D:B11	ES 175	562870	1682.B15.gz43_262450
M00055764A:F02	ES 175	621636	1682.B18.gz43_262498
M00055764B:F05	ES 175	462393	1682.B22.gz43_262562
M00055764C:C07	ES 175	644765	1682.B24.gz43_262594
M00055765A:A04	ES 175	524470	1682.C10.gz43_262371
M00055765A:B02	ES 175	584179	1682.C11.gz43_262387
M00055765A:C11	ES 175	642204	1682.C16.gz43_262467
M00055765A:G02	ES 175	629002	1682.C20.gz43_262531
M00055765D:E06	ES 175	642460	1682.D11.gz43_262388
M00055765D:F04	ES 175	644853	1682.D13.gz43_262420
M00055766A:A01	ES 175	462742	1682.D15.gz43_262452
M00055766A:D08	ES 175	641576	1682.D17.gz43_262484
M00055766A:E08	ES 175	639232	1682.D18.gz43_262500
M00055766A:H03	ES 175	558719	1682.D20.gz43_262532
M00055766B:B01	ES 175	447224	1682.D23.gz43_262580
M00055766B:E11	ES 175	637387	1682.E04.gz43_262277
M00055766B:H10	ES 175	642852	1682.E08.gz43_262341
M00055766C:C07	ES 175	464091	1682.E10.gz43_262373
M00055766C:C11	ES 175	448944	1682.E11.gz43_262389
M00055766C:E05	ES 175	447712	1682.E12.gz43_262405
M00055766C:G12	ES 175	451037	1682.E15.gz43_262453
M00055766D:C05	ES 175	562021	1682.E18.gz43_262501
M00055766D:D05	ES 175	50351	1682.E20.gz43_262533
M00055766D:F09	ES 175	560393	1682.E24.gz43_262597
M00055767A:D10	ES 175	634660	1682.F04.gz43_262278

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055767B:D02	ES 175	642082	1682.F11.gz43_262390
M00055767D:A12	ES 175	642082	1682.F17.gz43_262486
M00055767D:E07	ES 175	642417	1682.F20.gz43_262534
M00055767D:F04	ES 175	546740	1682.F21.gz43_262550
M00055768A:B05	ES 175	648996	1682.F24.gz43_262598
M00055768B:H12	ES 175	541499	1682.G13.gz43_262423
M00055768D:G02	ES 175	555140	1682.G22.gz43_262567
M00055770A:F01	ES 175	640997	1682.G24.gz43_262599
M00055770A:G08	ES 175	644173	1682.H02.gz43_262248
M00055770A:H11	ES 175	530238	1682.H03.gz43_262264
M00055770B:D06	ES 175	446757	1682.H06.gz43_262312
M00055770B:F06	ES 175	642474	1682.H07.gz43_262328
M00055770C:A02	ES 175	551167	1682.H08.gz43_262344
M00055770C:D01	ES 175	234606	1682.H09.gz43_262360
M00055770C:H11	ES 175	562876	1682.H12.gz43_262408
M00055770D:E10	ES 175	464510	1682.H19.gz43_262520
M00055771A:A11	ES 175	557797	1682.H22.gz43_262568
M00055771B:G05	ES 175	471268	1682.I10.gz43_262377
M00055771C:A11	ES 175	453079	1682.I12.gz43_262409
M00055771C:D09	ES 175	509410	1682.I13.gz43_262425
M00055771C:F05	ES 175	642604	1682.I15.gz43_262457
M00055772A:C10	ES 175	642036	1682.I24.gz43_262601
M00055772A:E12	ES 175	648588	1682.J01.gz43_262234
M00055772A:H08	ES 175	642791	1682.J04.gz43_262282
M00055772C:B09	ES 175	452503	1682.J08.gz43_262346
M00055772C:E11	ES 175	463951	1682.J10.gz43_262378
M00055772C:G08	ES 175	138470	1682.J12.gz43_262410
M00055772D:C10	ES 175	641563	1682.J15.gz43_262458
M00055772D:D03	ES 175	517912	1682.J16.gz43_262474
M00055772D:F10	ES 175	450553	1682.J18.gz43_262506
M00055772D:F11	ES 175	642558	1682.J19.gz43_262522
M00055772D:H04	ES 175	466971	1682.J20.gz43_262538
M00055773A:F05	ES 175	644451	1682.J22.gz43_262570
M00055773B:A07	ES 175	644914	1682.J24.gz43_262602
M00055773C:C09	ES 175	446163	1682.K04.gz43_262283
M00055773C:D12	ES 175	650272	1682.K05.gz43_262299
M00055773C:H12	ES 175	454540	1682.K06.gz43_262315
M00055773D:G11	ES 175	642637	1682.K09.gz43_262363
M00055774A:D04	ES 175	449975	1682.K14.gz43_262443
M00055774B:F07	ES 175	647940	1682.K18.gz43_262507
M00055774B:H01	ES 175	641185	1682.K20.gz43_262539
M00055774C:D09	ES 175	640617	1682.K22.gz43_262571
M00055774D:A05	ES 175	642417	1682.L02.gz43_262252

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055774D:B07	ES 176	553380	1682.L03.gz43_262268
M00055774D:E02	ES 176	458979	1682.L06.gz43_262316
M00055775A:G09	ES 176	101499	1682.L12.gz43_262412
M00055775B:A06	ES 176	447206	1682.L16.gz43_262476
M00055775B:G02	ES 176	644240	1682.L20.gz43_262540
M00055775B:G04	ES 176	559662	1682.L21.gz43_262556
M00055775C:B02	ES 176	645327	1682.L24.gz43_262604
M00055775C:B10	ES 176	553877	1682.M02.gz43_262253
M00055775C:D08	ES 176	642265	1682.M03.gz43_262269
M00055775C:E10	ES 176	641056	1682.M04.gz43_262285
M00055778A:E09	ES 176	621635	1682.M16.gz43_262477
M00055778A:F09	ES 176	461835	1682.M18.gz43_262509
M00055778A:F12	ES 176	642564	1682.M19.gz43_262525
M00055778A:G02	ES 176	509027	1682.M20.gz43_262541
M00055778B:C03	ES 176	645036	1682.M22.gz43_262573
M00055778B:E01	ES 176	458425	1682.M24.gz43_262605
M00055778C:D09	ES 176	494767	1682.N06.gz43_262318
M00055778D:A03	ES 176	642095	1682.N11.gz43_262398
M00055778D:C03	ES 176	639829	1682.N12.gz43_262414
M00055779A:B06	ES 176	642166	1682.N15.gz43_262462
M00055779A:H05	ES 176	480035	1682.N20.gz43_262542
M00055779B:F06	ES 176	556476	1682.N24.gz43_262606
M00055780A:C04	ES 176	89082	1682.O13.gz43_262431
M00055780A:C06	ES 176	561558	1682.O14.gz43_262447
M00055780A:E01	ES 176	650451	1682.O15.gz43_262463
M00055780A:E03	ES 176	642491	1682.O16.gz43_262479
M00055780A:E11	ES 176	450211	1682.O17.gz43_262495
M00055780A:F07	ES 176	641496	1682.O18.gz43_262511
M00055780A:G04	ES 176	453090	1682.O20.gz43_262543
M00055780C:E02	ES 176	641174	1682.P06.gz43_262320
M00055780C:E10	ES 176	502614	1682.P07.gz43_262336
M00055780D:D09	ES 176	642332	1682.P12.gz43_262416
M00055780D:F08	ES 176	453091	1682.P13.gz43_262432
M00055781A:B04	ES 176	642147	1682.P19.gz43_262528
M00055782B:C08	ES 176	643230	1683.A19.gz43_262897
M00055782C:H01	ES 176	459064	1683.B06.gz43_262690
M00055782D:H01	ES 176	649883	1683.B11.gz43_262770
M00055783A:C06	ES 176	642184	1683.B14.gz43_262818
M00055783A:F03	ES 176	644486	1683.B18.gz43_262882
M00055783B:A04	ES 176	523590	1683.B20.gz43_262914
M00055783C:A05	ES 176	506285	1683.C01.gz43_262611
M00055783D:B02	ES 176	497971	1683.C05.gz43_262675
M00055784A:B07	ES 176	140909	1683.C12.gz43_262787
M00055784A:D05	ES 176	456626	1683.C16.gz43_262851

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055784A:G10	ES 176	450384	1683.C19.gz43_262899
M00055784C:H02	ES 176	675768	1683.D03.gz43_262644
M00055784D:E03	ES 176	457847	1683.D05.gz43_262676
M00055785A:H08	ES 176	549434	1683.D09.gz43_262740
M00055785B:B06	ES 176	650076	1683.D12.gz43_262788
M00055785D:C06	ES 176	672601	1683.E01.gz43_262613
M00055786D:E10	ES 176	461990	1683.E19.gz43_262901
M00055787B:E02	ES 176	541209	1683.F03.gz43_262646
M00055787B:F10	ES 176	648905	1683.F04.gz43_262662
M00055787C:D09	ES 176	643350	1683.F10.gz43_262758
M00055787C:E12	ES 176	449836	1683.F12.gz43_262790
M00055787D:B07	ES 176	642318	1683.F16.gz43_262854
M00055789C:C12	ES 176	640799	1683.G23.gz43_262967
M00055789C:F10	ES 176	463290	1683.H01.gz43_262616
M00055789D:B04	ES 176	642146	1683.H03.gz43_262648
M00055789D:C06	ES 176	621635	1683.H04.gz43_262664
M00055790B:A08	ES 176	638962	1683.H14.gz43_262824
M00055790B:D05	ES 176	553546	1683.H18.gz43_262888
M00055790C:C02	ES 176	415950	1683.H22.gz43_262952
M00055790D:G10	ES 176	467306	1683.I04.gz43_262665
M00055791B:E02	ES 176	510545	1683.I11.gz43_262777
M00055791C:A02	ES 176	396191	1683.I15.gz43_262841
M00055792B:D08	ES 176	396149	1683.J14.gz43_262826
M00055793A:H09	ES 176	554117	1683.K06.gz43_262699
M00055793B:B06	ES 176	641919	1683.K08.gz43_262731
M00055794A:D08	ES 176	605761	1683.L08.gz43_262732
M00055794B:F04	ES 176	561718	1683.L17.gz43_262876
M00055794C:D10	ES 176	457396	1683.L21.gz43_262940
M00055795A:F09	ES 176	446595	1683.M09.gz43_262749
M00055795A:F12	ES 176	454485	1683.M10.gz43_262765
M00055795B:F09	ES 176	641700	1683.M15.gz43_262845
M00055795C:B10	ES 176	388085	1683.M20.gz43_262925
M00055795D:E09	ES 176	645508	1683.N05.gz43_262686
M00055795D:F08	ES 176	450218	1683.N06.gz43_262702
M00055795D:H08	ES 176	77144	1683.N11.gz43_262782
M00055796A:A08	ES 176	437580	1683.N15.gz43_262846
M00055796B:G05	ES 176	644047	1683.O05.gz43_262687
M00055796C:E11	ES 176	647639	1683.O10.gz43_262767
M00055796D:E06	ES 176	553979	1683.O16.gz43_262863
M00055796D:E10	ES 176	640525	1683.O17.gz43_262879
M00055797B:A11	ES 176	417617	1683.O23.gz43_262975
M00055797B:B04	ES 176	639807	1683.O24.gz43_262991
M00055797C:F08	ES 176	517224	1683.P09.gz43_262752
M00055798B:D12	ES 176	418340	1684.A04.gz43_263041

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055798B:F02	ES 176	644915	1684.A05.gz43_263057
M00055798B:G04	ES 176	645560	1684.A06.gz43_263073
M00055798D:A10	ES 176	455028	1684.A10.gz43_263137
M00055798D:H10	ES 176	483726	1684.A13.gz43_263185
M00055799B:G02	ES 176	674574	1684.A23.gz43_263345
M00055799C:D09	ES 176	645700	1684.A24.gz43_263361
M00055799D:F11	ES 176	640334	1684.B06.gz43_263074
M00055800A:F01	ES 176	462247	1684.B14.gz43_263202
M00055800A:F02	ES 176	490414	1684.B15.gz43_263218
M00055800C:E11	ES 176	640537	1684.B22.gz43_263330
M00055800D:B03	ES 176	462249	1684.C04.gz43_263043
M00055801D:E06	ES 176	564382	1684.C23.gz43_263347
M00055802A:C03	ES 176	494767	1684.D06.gz43_263076
M00055802B:H03	ES 176	486134	1684.D17.gz43_263252
M00055802C:E12	ES 176	643991	1684.D22.gz43_263332
M00055803A:C06	ES 176	513238	1684.E06.gz43_263077
M00055803A:F03	ES 176	455405	1684.E10.gz43_263141
M00055803A:G08	ES 176	642653	1684.E11.gz43_263157
M00055803B:A11	ES 176	530774	1684.E13.gz43_263189
M00055803B:E10	ES 176	557344	1684.E18.gz43_263269
M00055804B:C02	ES 176	639194	1684.F18.gz43_263270
M00055804D:F02	ES 176	463821	1684.G01.gz43_262999
M00055805A:A02	ES 176	640222	1684.G05.gz43_263063
M00055805A:C11	ES 176	641059	1684.G06.gz43_263079
M00055805B:C08	ES 176	642198	1684.G12.gz43_263175
M00055805C:D10	ES 176	630259	1684.G17.gz43_263255
M00055805D:C11	ES 176	640617	1684.G21.gz43_263319
M00055805D:H01	ES 176	529325	1684.G23.gz43_263351
M00055806B:B10	ES 176	644314	1684.H08.gz43_263112
M00055806B:D04	ES 176	464040	1684.H10.gz43_263144
M00055806C:D07	ES 176	496051	1684.H13.gz43_263192
M00055806C:E09	ES 176	375814	1684.H14.gz43_263208
M00055806C:G01	ES 176	549616	1684.H17.gz43_263256
M00055806D:H03	ES 176	450252	1684.H23.gz43_263352
M00055806D:H06	ES 176	640520	1684.H24.gz43_263368
M00055807A:B10	ES 176	32812	1684.I03.gz43_263033
M00055807B:F05	ES 176	520320	1684.I12.gz43_263177
M00055807B:G10	ES 176	446789	1684.I14.gz43_263209
M00055807C:F05	ES 176	639441	1684.I17.gz43_263257
M00055807D:C04	ES 176	470602	1684.I21.gz43_263321
M00055808A:C06	ES 176	450741	1684.J05.gz43_263066
M00055808B:A04	ES 176	650782	1684.J08.gz43_263114
M00055808B:H07	ES 176	210839	1684.J14.gz43_263210
M00055808D:C12	ES 176	460517	1684.J20.gz43_263306

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055808D:F09	ES 176	520320	1684.J24.gz43_263370
M00055809A:B10	ES 176	550370	1684.K05.gz43_263067
M00055809C:D01	ES 176	644901	1684.K17.gz43_263259
M00055809C:E11	ES 176	454772	1684.K19.gz43_263291
M00055809C:H10	ES 176	640479	1684.K22.gz43_263339
M00055810A:H03	ES 176	413277	1684.L06.gz43_263084
M00055810D:G04	ES 176	649995	1684.L19.gz43_263292
M00055811B:A03	ES 176	455665	1684.L23.gz43_263356
M00055811C:A01	ES 176	517327	1684.M01.gz43_263005
M00055811C:D12	ES 176	645015	1684.M03.gz43_263037
M00055811D:C02	ES 176	650231	1684.M07.gz43_263101
M00055811D:C12	ES 176	554742	1684.M09.gz43_263133
M00055811D:E01	ES 176	452828	1684.M10.gz43_263149
M00055812A:E01	ES 176	503491	1684.M15.gz43_263229
M00055812B:F03	ES 176	466016	1684.M19.gz43_263293
M00055812C:B07	ES 176	648752	1684.M24.gz43_263373
M00055812D:E03	ES 176	550604	1684.N09.gz43_263134
M00055813A:D10	ES 176	644147	1684.N12.gz43_263182
M00055813C:E03	ES 176	551683	1684.N17.gz43_263262
M00055813D:B12	ES 176	494271	1684.N19.gz43_263294
M00055814A:F02	ES 176	528134	1684.O01.gz43_263007
M00055814C:C07	ES 176	647336	1684.O11.gz43_263167
M00055815A:H12	ES 176	642850	1684.O24.gz43_263375
M00055815C:B03	ES 176	642099	1684.P04.gz43_263056
M00055815C:G05	ES 176	648221	1684.P08.gz43_263120
M00055815D:A11	ES 176	642962	1684.P09.gz43_263136
M00055815D:B02	ES 176	447015	1684.P10.gz43_263152
M00055815D:B03	ES 176	549640	1684.P11.gz43_263168
M00055816A:C04	ES 176	649035	1684.P17.gz43_263264
M00055816B:B07	ES 176	564854	1684.P23.gz43_263360
M00055816D:A10	ES 176	363172	1693.A07.gz43_213787
M00055816D:B11	ES 176	492242	1693.A09.gz43_213819
M00055816D:E10	ES 176	452863	1693.A13.gz43_213883
M00055817A:E05	ES 176	643397	1693.A17.gz43_213947
M00055817A:H07	ES 176	648580	1693.A19.gz43_213979
M00055817B:C04	ES 176	449542	1693.A23.gz43_214043
M00055818B:H03	ES 176	638837	1693.C10.gz43_213837
M00055819A:A06	ES 176	475624	1693.C23.gz43_214045
M00055819A:B10	ES 176	559854	1693.D01.gz43_213694
M00055822C:D09	ES 176	451966	1693.F18.gz43_213968
M00055823B:F02	ES 176	674526	1693.G08.gz43_213809
M00055825B:C11	ES 176	645155	1693.H03.gz43_213730
M00055825B:E03	ES 176	650204	1693.H04.gz43_213746
M00055825B:F09	ES 176	643054	1693.H06.gz43_213778

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055825D:A03	ES 176	642962	1693.H13.gz43_213890
M00055825D:D11	ES 176	551681	1693.H20.gz43_214002
M00055826A:G04	ES 176	640464	1693.I06.gz43_213779
M00055826B:G07	ES 176	645746	1693.I13.gz43_213891
M00055826C:G06	ES 176	650487	1693.I19.gz43_213987
M00055827A:A12	ES 176	650579	1693.J01.gz43_213700
M00055827D:A01	ES 176	455716	1693.J19.gz43_213988
M00055827D:C02	ES 176	556286	1693.J22.gz43_214036
M00055827D:G11	ES 176	583915	1693.K03.gz43_213733
M00055828A:H10	ES 176	647425	1693.K07.gz43_213797
M00055828B:E10	ES 176	517280	1693.K10.gz43_213845
M00055829C:A07	ES 176	648567	1693.L02.gz43_213718
M00055829D:H10	ES 176	645146	1693.L15.gz43_213926
M00055830A:G10	ES 176	645073	1693.L17.gz43_213958
M00055830C:H10	ES 176	451134	1693.M06.gz43_213783
M00055831A:C06	ES 176	644781	1693.M15.gz43_213927
M00055831B:C04	ES 177	517237	1693.M23.gz43_214055
M00055832A:A08	ES 177	481864	1693.N08.gz43_213816
M00055832C:H09	ES 177	648328	1693.N19.gz43_213992
M00055833D:F11	ES 177	650912	1693.O14.gz43_213913
M00055834B:C11	ES 177	557741	1693.O20.gz43_214009
M00055835C:F08	ES 177	642054	1693.P21.gz43_214026
M00055836A:B12	ES 177	645149	1694.A05.gz43_214139
M00055836C:D01	ES 177	452735	1694.A10.gz43_214219
M00055837A:B08	ES 177	447597	1694.A15.gz43_214299
M00055837A:D09	ES 177	644210	1694.A16.gz43_214315
M00055837A:F02	ES 177	489249	1694.A18.gz43_214347
M00055837A:H08	ES 177	645289	1694.A19.gz43_214363
M00055837B:E07	ES 177	644987	1694.A23.gz43_214427
M00055837D:D08	ES 177	642253	1694.B09.gz43_214204
M00055837D:G10	ES 177	504944	1694.B11.gz43_214236
M00055838A:A03	ES 177	643800	1694.B12.gz43_214252
M00055838A:B02	ES 177	448450	1694.B13.gz43_214268
M00055838B:D06	ES 177	467901	1694.B15.gz43_214300
M00055838B:G12	ES 177	644417	1694.B16.gz43_214316
M00055838B:H04	ES 177	644494	1694.B17.gz43_214332
M00055838C:A08	ES 177	447002	1694.B18.gz43_214348
M00055838C:B08	ES 177	643948	1694.B19.gz43_214364
M00055839B:A10	ES 177	643804	1694.C13.gz43_214269
M00055839B:C07	ES 177	648039	1694.C15.gz43_214301
M00055839B:E07	ES 177	558890	1694.C18.gz43_214349
M00055839B:H09	ES 177	537586	1694.C19.gz43_214365
M00055839C:B11	ES 177	467521	1694.C22.gz43_214413

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055839C:D06	ES 177	645948	1694.C23.gz43_214429
M00055840A:G06	ES 177	553145	1694.D08.gz43_214190
M00055840B:B02	ES 177	522869	1694.D11.gz43_214238
M00055840C:D06	ES 177	640618	1694.D17.gz43_214334
M00055840C:H06	ES 177	644548	1694.D18.gz43_214350
M00055840D:B03	ES 177	643977	1694.D20.gz43_214382
M00055841B:F09	ES 177	485237	1694.E09.gz43_214207
M00055841B:H03	ES 177	503546	1694.E10.gz43_214223
M00055841C:A03	ES 177	643843	1694.E12.gz43_214255
M00055841C:D05	ES 177	607430	1694.E15.gz43_214303
M00055841C:D11	ES 177	599759	1694.E17.gz43_214335
M00055841C:H04	ES 177	140648	1694.E20.gz43_214383
M00055841D:C11	ES 177	650528	1694.E21.gz43_214399
M00055842B:A04	ES 177	642079	1694.F05.gz43_214144
M00055842B:D04	ES 177	644063	1694.F09.gz43_214208
M00055842C:A11	ES 177	644548	1694.F11.gz43_214240
M00055842C:C03	ES 177	506901	1694.F12.gz43_214256
M00055842D:C02	ES 177	645505	1694.F15.gz43_214304
M00055842D:D07	ES 177	643809	1694.F17.gz43_214336
M00055842D:F07	ES 177	462557	1694.F19.gz43_214368
M00055843B:D10	ES 177	644212	1694.G04.gz43_214129
M00055843D:H01	ES 177	472119	1694.G15.gz43_214305
M00055844A:D03	ES 177	643825	1694.G18.gz43_214353
M00055844A:D07	ES 177	647577	1694.G19.gz43_214369
M00055844A:F11	ES 177	649068	1694.G20.gz43_214385
M00055844B:C12	ES 177	644075	1694.G24.gz43_214449
M00055844C:F01	ES 177	645290	1694.H06.gz43_214162
M00055844D:E11	ES 177	456728	1694.H10.gz43_214226
M00055844D:E12	ES 177	644314	1694.H11.gz43_214242
M00055844D:H09	ES 177	466697	1694.H16.gz43_214322
M00055845A:C03	ES 177	643999	1694.H19.gz43_214370
M00055845A:H10	ES 177	644569	1694.H21.gz43_214402
M00055845C:A11	ES 177	647448	1694.I05.gz43_214147
M00055845C:C12	ES 177	468222	1694.I08.gz43_214195
M00055845C:E02	ES 177	646420	1694.I10.gz43_214227
M00055845C:E05	ES 177	525456	1694.I11.gz43_214243
M00055845D:G11	ES 177	650276	1694.I16.gz43_214323
M00055846A:D07	ES 177	181364	1694.I18.gz43_214355
M00055846B:B12	ES 177	419751	1694.I23.gz43_214435
M00055846B:C12	ES 177	542282	1694.I24.gz43_214451
M00055846B:F11	ES 177	647191	1694.J01.gz43_214084
M00055846D:G08	ES 177	647383	1694.J12.gz43_214260
M00055846D:G09	ES 177	645681	1694.J13.gz43_214276
M00055846D:G11	ES 177	640171	1694.J14.gz43_214292

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055847B:G12	ES 177	651131	1694.J19.gz43_214372
M00055847C:A11	ES 177	646459	1694.J21.gz43_214404
M00055847C:C01	ES 177	646810	1694.J22.gz43_214420
M00055847C:H09	ES 177	452976	1694.J24.gz43_214452
M00055848A:E07	ES 177	645681	1694.K06.gz43_214165
M00055848B:C03	ES 177	647383	1694.K13.gz43_214277
M00055848C:A02	ES 177	645197	1694.K15.gz43_214309
M00055848C:G07	ES 177	558981	1694.K17.gz43_214341
M00055848C:H06	ES 177	646248	1694.K19.gz43_214373
M00055849C:G07	ES 177	547841	1694.L06.gz43_214166
M00055849D:B04	ES 177	450949	1694.L08.gz43_214198
M00055849D:H09	ES 177	469511	1694.L13.gz43_214278
M00055850C:D01	ES 177	608873	1694.L21.gz43_214406
M00055850C:G05	ES 177	647318	1694.L22.gz43_214422
M00055851A:C03	ES 177	466265	1694.M06.gz43_214167
M00055851A:C09	ES 177	649842	1694.M07.gz43_214183
M00055851A:G11	ES 177	97507	1694.M12.gz43_214263
M00055851A:H10	ES 177	647522	1694.M14.gz43_214295
M00055851B:B09	ES 177	562229	1694.M16.gz43_214327
M00055851B:G02	ES 177	639295	1694.M18.gz43_214359
M00055851B:G10	ES 177	425923	1694.M19.gz43_214375
M00055851C:F12	ES 177	643594	1694.M23.gz43_214439
M00055851C:H05	ES 177	472801	1694.M24.gz43_214455
M00055852A:C12	ES 177	639341	1694.N09.gz43_214216
M00055852B:F10	ES 177	562813	1694.N12.gz43_214264
M00055852B:G09	ES 177	642293	1694.N14.gz43_214296
M00055852B:H04	ES 177	457661	1694.N16.gz43_214328
M00055852D:B11	ES 177	644708	1694.N20.gz43_214392
M00055852D:G12	ES 177	649611	1694.N21.gz43_214408
M00055853B:H06	ES 177	647578	1694.O04.gz43_214137
M00055853C:C12	ES 177	603388	1694.O08.gz43_214201
M00055853C:H03	ES 177	647577	1694.O10.gz43_214233
M00055853D:A07	ES 177	650492	1694.O11.gz43_214249
M00055853D:B04	ES 177	643130	1694.O13.gz43_214281
M00055853D:C07	ES 177	650217	1694.O15.gz43_214313
M00055854A:B07	ES 177	592122	1694.O17.gz43_214345
M00055854A:D01	ES 177	639510	1694.O19.gz43_214377
M00055854A:E03	ES 177	645145	1694.O21.gz43_214409
M00055854A:E04	ES 177	638854	1694.O22.gz43_214425
M00055854C:C07	ES 177	549624	1694.P04.gz43_214138
M00055854C:E03	ES 177	570939	1694.P05.gz43_214154
M00055854C:H11	ES 177	471364	1694.P09.gz43_214218
M00055855A:B11	ES 177	404816	1694.P14.gz43_214298
M00055855A:G05	ES 177	462659	1694.P16.gz43_214330

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055855B:B11	ES 177	643909	1694.P20.gz43_214394
M00055855B:D12	ES 177	465576	1694.P21.gz43_214410
M00055855C:F11	ES 177	603388	1694.P23.gz43_214442
M00055855D:D12	ES 177	509027	1695.A04.gz43_214911
M00055855D:G08	ES 177	644442	1695.A07.gz43_214959
M00055856A:C06	ES 177	564854	1695.A08.gz43_214975
M00055856A:D12	ES 177	644149	1695.A09.gz43_214991
M00055856C:F07	ES 177	550267	1695.A20.gz43_215167
M00055857C:D09	ES 177	646372	1695.B08.gz43_214976
M00055858A:G07	ES 177	642070	1695.B24.gz43_215232
M00055860D:E04	ES 177	596882	1695.D05.gz43_214930
M00055861B:F04	ES 177	645848	1695.D08.gz43_214978
M00055861C:G03	ES 177	645538	1695.D13.gz43_215058
M00055862A:C01	ES 177	140224	1695.D21.gz43_215186
M00055862D:B02	ES 177	640147	1695.E09.gz43_214995
M00055862D:D06	ES 177	449500	1695.E11.gz43_215027
M00055863B:C07	ES 177	644030	1695.E20.gz43_215171
M00055863D:D09	ES 177	644047	1695.F07.gz43_214964
M00055864A:C09	ES 177	644047	1695.F13.gz43_215060
M00055864A:E11	ES 177	650773	1695.F14.gz43_215076
M00055864B:C09	ES 177	561877	1695.F18.gz43_215140
M00055865C:G11	ES 177	649660	1695.G23.gz43_215221
M00055865C:H06	ES 177	650517	1695.G24.gz43_215237
M00055866A:G10	ES 177	397399	1695.H07.gz43_214966
M00055866C:G09	ES 177	644435	1695.H17.gz43_215126
M00055866C:H06	ES 177	644410	1695.H18.gz43_215142
M00055867A:B02	ES 177	645288	1695.H23.gz43_215222
M00055868B:B04	ES 177	649436	1695.I16.gz43_215111
M00055868C:F02	ES 177	562059	1695.I24.gz43_215239
M00055868D:D08	ES 177	469437	1695.J05.gz43_214936
M00055869C:G06	ES 177	449936	1695.J14.gz43_215080
M00055869D:A07	ES 177	642411	1695.J16.gz43_215112
M00055870B:D04	ES 177	649846	1695.J24.gz43_215240
M00055871A:H06	ES 177	524261	1695.K09.gz43_215001
M00055871B:B03	ES 177	648819	1695.K11.gz43_215033
M00055871C:C07	ES 177	643099	1695.K21.gz43_215193
M00055871C:C10	ES 177	644801	1695.K22.gz43_215209
M00055872A:C08	ES 177	644755	1695.L11.gz43_215034
M00055872A:D08	ES 177	644830	1695.L12.gz43_215050
M00055872A:E05	ES 177	505858	1695.L13.gz43_215066
M00055872A:E11	ES 177	640534	1695.L15.gz43_215098
M00055872D:D12	ES 177	447035	1695.M08.gz43_214987
M00055873A:E03	ES 177	643451	1695.M16.gz43_215115
M00055873D:E04	ES 177	643488	1695.N10.gz43_215020

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055874A:F06	ES 177	645497	1695.N18.gz43_215148
M00055875A:G05	ES 177	554646	1695.O14.gz43_215085
M00055875B:E09	ES 177	646633	1695.P03.gz43_214910
M00055875C:C07	ES 177	516512	1695.P11.gz43_215038
M00055875D:A07	ES 177	640136	1695.P20.gz43_215182
M00055875D:D01	ES 177	643333	1695.P22.gz43_215214
M00055875D:H10	ES 177	650179	1696.A01.gz43_215247
M00055877A:H04	ES 177	645638	1696.A07.gz43_215343
M00055877B:B05	ES 177	484991	1696.A09.gz43_215375
M00055877D:C05	ES 177	643233	1696.A21.gz43_215567
M00055878C:C02	ES 177	593715	1696.B16.gz43_215488
M00055879A:D04	ES 177	643934	1696.C11.gz43_215409
M00055879A:G03	ES 177	450001	1696.C12.gz43_215425
M00055880B:A04	ES 177	642911	1696.D03.gz43_215282
M00055880B:A06	ES 177	447807	1696.D04.gz43_215298
M00055880C:F07	ES 177	645215	1696.D15.gz43_215474
M00055881A:A08	ES 177	447221	1696.E05.gz43_215315
M00055881A:E10	ES 177	479868	1696.E12.gz43_215427
M00055881A:G07	ES 177	446225	1696.E13.gz43_215443
M00055881D:A02	ES 177	648063	1696.E22.gz43_215587
M00055882C:A06	ES 177	450559	1696.F14.gz43_215460
M00055882D:B02	ES 177	640400	1696.F21.gz43_215572
M00055883A:C02	ES 177	179760	1696.G05.gz43_215317
M00055883A:C10	ES 177	459274	1696.G06.gz43_215333
M00055883A:H01	ES 177	643745	1696.G11.gz43_215413
M00055883D:B06	ES 177	644468	1696.G21.gz43_215573
M00055884B:F10	ES 177	451670	1696.H17.gz43_215510
M00055884B:H07	ES 177	552628	1696.H18.gz43_215526
M00055884C:B07	ES 177	643046	1696.H21.gz43_215574
M00055884D:F07	ES 177	345761	1696.I06.gz43_215335
M00055885A:D05	ES 177	558222	1696.I11.gz43_215415
M00055885B:A11	ES 177	555172	1696.I15.gz43_215479
M00055885B:B04	ES 178	586992	1696.I16.gz43_215495
M00055885C:B07	ES 178	552201	1696.J01.gz43_215256
M00055886A:B06	ES 178	643126	1696.J12.gz43_215432
M00055886D:E11	ES 178	557792	1696.K11.gz43_215417
M00055887A:F07	ES 178	644099	1696.K18.gz43_215529
M00055887D:C11	ES 178	643248	1696.L14.gz43_215466
M00055888C:F07	ES 178	639256	1696.M04.gz43_215307
M00055888C:G09	ES 178	640356	1696.M06.gz43_215339
M00055889B:E12	ES 178	570248	1696.M23.gz43_215611
M00055890A:A06	ES 178	464171	1696.N11.gz43_215420
M00055890A:D01	ES 178	549114	1696.N14.gz43_215468

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055890A:G12	ES 178	649068	1696.N21.gz43_215580
M00055890A:H11	ES 178	643724	1696.N23.gz43_215612
M00055891B:F09	ES 178	643513	1696.P02.gz43_215278
M00055892A:F04	ES 178	649027	1696.P23.gz43_215614
M00055892B:D02	ES 178	643366	1696.P24.gz43_215630
M00055893B:C05	ES 178	650476	1705.A11.gz43_215791
M00055894A:H08	ES 178	374340	1705.A22.gz43_215967
M00055894B:E09	ES 178	394373	1705.B03.gz43_215664
M00055896A:G01	ES 178	648576	1705.B11.gz43_215792
M00055896B:C06	ES 178	643948	1705.B14.gz43_215840
M00055896B:H04	ES 178	640762	1705.B18.gz43_215904
M00055896C:H10	ES 178	553951	1705.B23.gz43_215984
M00055896D:G10	ES 178	557361	1705.C03.gz43_215665
M00055898B:E07	ES 178	485237	1705.C11.gz43_215793
M00055899A:B03	ES 178	645844	1705.C18.gz43_215905
M00055899C:H01	ES 178	474577	1705.D05.gz43_215698
M00055900A:F08	ES 178	644390	1705.D16.gz43_215874
M00055900B:E12	ES 178	446728	1705.D20.gz43_215938
M00055900D:D03	ES 178	526575	1705.E01.gz43_215635
M00055901B:A02	ES 178	647522	1705.E10.gz43_215779
M00055901C:A01	ES 178	553720	1705.E16.gz43_215875
M00055901C:C10	ES 178	641087	1705.E18.gz43_215907
M00055901C:D04	ES 178	642940	1705.E19.gz43_215923
M00055902A:H11	ES 178	643513	1705.F06.gz43_215716
M00055902D:A07	ES 178	557947	1705.F14.gz43_215844
M00055902D:H10	ES 178	482163	1705.F18.gz43_215908
M00055903B:C10	ES 178	644063	1705.F24.gz43_216004
M00055903B:E05	ES 178	554166	1705.G03.gz43_215669
M00055904B:B01	ES 178	643914	1705.G12.gz43_215813
M00055904C:A07	ES 178	643809	1705.G15.gz43_215861
M00055904D:A06	ES 178	643808	1705.G18.gz43_215909
M00055905A:F11	ES 178	644354	1705.G24.gz43_216005
M00055905B:H01	ES 178	639194	1705.H06.gz43_215718
M00055905D:B06	ES 178	605596	1705.H13.gz43_215830
M00055905D:H02	ES 178	550242	1705.H17.gz43_215894
M00055906C:F03	ES 178	641562	1705.H23.gz43_215990
M00055906D:G03	ES 178	454720	1705.I06.gz43_215719
M00055907D:D06	ES 178	449994	1705.J06.gz43_215720
M00055908D:F09	ES 178	644364	1705.K04.gz43_215689
M00055909B:B12	ES 178	638869	1705.K10.gz43_215785
M00055909B:G10	ES 178	643089	1705.K16.gz43_215881
M00055909C:E08	ES 178	447326	1705.K20.gz43_215945
M00055909C:G09	ES 178	645781	1705.K21.gz43_215961
M00055909D:A09	ES 178	638919	1705.K22.gz43_215977

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055909D:E01	ES 178	89082	1705.K24.gz43_216009
M00055910B:B11	ES 178	642985	1705.L11.gz43_215802
M00055910B:H12	ES 178	639240	1705.L16.gz43_215882
M00055910C:G01	ES 178	468147	1705.L19.gz43_215930
M00055910C:G04	ES 178	685001	1705.L20.gz43_215946
M00055910D:A03	ES 178	643825	1705.L21.gz43_215962
M00055911B:E06	ES 178	644242	1705.M05.gz43_215707
M00055912A:F08	ES 178	557675	1705.M16.gz43_215883
M00055912B:E05	ES 178	648237	1705.M20.gz43_215947
M00055912C:C08	ES 178	640756	1705.M22.gz43_215979
M00055912D:F04	ES 178	644407	1705.N05.gz43_215708
M00055913A:G07	ES 178	649312	1705.N12.gz43_215820
M00055913B:D05	ES 178	644190	1705.N17.gz43_215900
M00055914A:A03	ES 178	449737	1705.O02.gz43_215661
M00055914C:D12	ES 178	643300	1705.O09.gz43_215773
M00055914C:G01	ES 178	644108	1705.O11.gz43_215805
M00055914C:G11	ES 178	641645	1705.O12.gz43_215821
M00055914D:A08	ES 178	564134	1705.O13.gz43_215837
M00055914D:G06	ES 178	553587	1705.O16.gz43_215885
M00055915A:A06	ES 178	639413	1705.O17.gz43_215901
M00055915B:D08	ES 178	447212	1705.O21.gz43_215965
M00055915C:B09	ES 178	643991	1705.O24.gz43_216013
M00055915D:A07	ES 178	640178	1705.P05.gz43_215710
M00055916A:E12	ES 178	644236	1705.P12.gz43_215822
M00055916B:C02	ES 178	649170	1705.P15.gz43_215870
M00055917B:D02	ES 178	642911	1706.A08.gz43_216139
M00055917C:F04	ES 178	549994	1706.A13.gz43_216219
M00055917D:E07	ES 178	644301	1706.A16.gz43_216267
M00055918A:F10	ES 178	645028	1706.A20.gz43_216331
M00055918B:B07	ES 178	643936	1706.A24.gz43_216395
M00055918B:B10	ES 178	459881	1706.B01.gz43_216028
M00055918B:F10	ES 178	557175	1706.B03.gz43_216060
M00055918C:C04	ES 178	651131	1706.B05.gz43_216092
M00055918C:E02	ES 178	642166	1706.B07.gz43_216124
M00055919A:A06	ES 178	647952	1706.B12.gz43_216204
M00055919B:H11	ES 178	562021	1706.B19.gz43_216316
M00055919D:H07	ES 178	644554	1706.C01.gz43_216029
M00055920A:H10	ES 178	640977	1706.C05.gz43_216093
M00055920B:F02	ES 178	644410	1706.C09.gz43_216157
M00055921A:E06	ES 178	188079	1706.C21.gz43_216349
M00055922A:F05	ES 178	465576	1706.D13.gz43_216222
M00055922A:G07	ES 178	650900	1706.D15.gz43_216254
M00055922B:A06	ES 178	447426	1706.D17.gz43_216286
M00055922B:G09	ES 178	649085	1706.D21.gz43_216350

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055922D:G10	ES 178	419009	1706.E06.gz43_216111
M00055923B:C07	ES 178	643170	1706.E10.gz43_216175
M00055924B:D02	ES 178	643627	1706.E22.gz43_216367
M00055924B:E12	ES 178	464129	1706.F01.gz43_216032
M00055924C:A09	ES 178	641484	1706.F03.gz43_216064
M00055925A:C04	ES 178	450840	1706.F11.gz43_216192
M00055925B:D09	ES 178	639154	1706.F20.gz43_216336
M00055925B:D10	ES 178	643332	1706.F21.gz43_216352
M00055926B:A05	ES 178	447123	1706.G12.gz43_216209
M00055926C:A11	ES 178	207552	1706.G18.gz43_216305
M00055927B:D06	ES 178	642308	1706.H05.gz43_216098
M00055927D:E11	ES 178	643239	1706.H10.gz43_216178
M00055928A:C06	ES 178	639038	1706.H15.gz43_216258
M00055928A:E11	ES 178	610893	1706.H17.gz43_216290
M00055928B:E11	ES 178	643383	1706.H21.gz43_216354
M00055929A:C11	ES 178	649954	1706.I14.gz43_216243
M00055929B:E01	ES 178	462089	1706.I17.gz43_216291
M00055929D:F09	ES 178	649954	1706.I24.gz43_216403
M00055930A:G04	ES 178	644629	1706.J05.gz43_216100
M00055930C:D03	ES 178	650938	1706.J09.gz43_216164
M00055930C:F06	ES 178	639596	1706.J10.gz43_216180
M00055930C:H05	ES 178	556925	1706.J15.gz43_216260
M00055930D:B05	ES 178	447520	1706.J16.gz43_216276
M00055930D:B09	ES 178	613626	1706.J17.gz43_216292
M00055930D:F05	ES 178	513211	1706.J21.gz43_216356
M00055933A:E05	ES 178	638808	1706.L07.gz43_216134
M00055933B:B11	ES 178	605114	1706.L10.gz43_216182
M00055933B:G01	ES 178	650245	1706.L11.gz43_216198
M00055934C:E06	ES 178	446795	1706.M06.gz43_216119
M00055934D:H09	ES 178	650470	1706.M12.gz43_216215
M00055935B:H06	ES 178	479604	1706.M20.gz43_216343
M00055935C:E03	ES 178	640672	1706.M23.gz43_216391
M00055936C:B05	ES 178	646596	1706.N07.gz43_216136
M00055936C:D03	ES 178	648379	1706.N08.gz43_216152
M00055936D:F03	ES 178	456920	1706.N11.gz43_216200
M00055937A:F07	ES 178	645092	1706.N17.gz43_216296
M00055937C:C08	ES 178	641716	1706.N21.gz43_216360
M00055939A:B12	ES 178	644732	1706.P02.gz43_216058
M00055939B:A11	ES 178	639901	1706.P07.gz43_216138
M00055939D:D07	ES 178	559905	1706.P13.gz43_216234
M00055940B:A08	ES 178	649873	1706.P19.gz43_216330
M00055941B:A04	ES 178	524546	1707.A12.gz43_216604
M00055942B:H10	ES 178	646317	1707.B04.gz43_216477
M00055942D:A01	ES 178	648782	1707.B12.gz43_216605

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055942D:E05	ES 178	645809	1707.B16.gz43_216669
M00055943B:E01	ES 178	447805	1707.B24.gz43_216797
M00055945C:C02	ES 178	648588	1707.D13.gz43_216623
M00055945C:D09	ES 178	648555	1707.D14.gz43_216639
M00055945D:D01	ES 178	461363	1707.D17.gz43_216687
M00055945D:E08	ES 178	644720	1707.D18.gz43_216703
M00055947C:E09	ES 178	393599	1707.E20.gz43_216736
M00055949A:E09	ES 178	499693	1707.F02.gz43_216449
M00055949D:B07	ES 178	649549	1707.F06.gz43_216513
M00055951B:A07	ES 178	644983	1707.G03.gz43_216466
M00055952C:E08	ES 178	650935	1707.G21.gz43_216754
M00055953D:B08	ES 178	642105	1707.H10.gz43_216579
M00055954C:G07	ES 178	531529	1707.H19.gz43_216723
M00055954D:B04	ES 178	561777	1707.H22.gz43_216771
M00055955B:C06	ES 178	460245	1707.I08.gz43_216548
M00055955C:H05	ES 178	650370	1707.I14.gz43_216644
M00055956D:B01	ES 178	550237	1707.J02.gz43_216453
M00055956D:C11	ES 178	447224	1707.J04.gz43_216485
M00055957B:F11	ES 178	452316	1707.J14.gz43_216645
M00055957C:F05	ES 178	644568	1707.J18.gz43_216709
M00055958C:E03	ES 178	643968	1707.K05.gz43_216502
M00055958D:F02	ES 178	647185	1707.K10.gz43_216582
M00055961D:F06	ES 178	647312	1707.L18.gz43_216711
M00055963B:C02	ES 178	555210	1707.L22.gz43_216775
M00055965A:G06	ES 178	642653	1707.M24.gz43_216808
M00055965D:G01	ES 178	472101	1707.N12.gz43_216617
M00055966B:H09	ES 178	646190	1707.N18.gz43_216713
M00055966C:D03	ES 178	645508	1707.N20.gz43_216745
M00055967A:F11	ES 178	513619	1707.O07.gz43_216538
M00055967A:G01	ES 178	646061	1707.O08.gz43_216554
M00055967B:B12	ES 178	645273	1707.O09.gz43_216570
M00055967B:F07	ES 178	645900	1707.O13.gz43_216634
M00055967D:C05	ES 178	383609	1707.O23.gz43_216794
M00055968D:E03	ES 178	643162	1707.P18.gz43_216715
M00055969A:F02	ES 178	694643	1707.P24.gz43_216811
M00055969B:B05	ES 178	640672	1708.A04.gz43_216860
M00055969D:B08	ES 178	645289	1708.A11.gz43_216972
M00055969D:F08	ES 178	642955	1708.A12.gz43_216988
M00055970C:A05	ES 178	647058	1708.A21.gz43_217132
M00055970D:F09	ES 178	645894	1708.B10.gz43_216957
M00055971B:A11	ES 178	649082	1708.B14.gz43_217021
M00055972C:C09	ES 178	557852	1708.C06.gz43_216894
M00055972C:F02	ES 178	558052	1708.C07.gz43_216910
M00055973C:F10	ES 178	647211	1708.C24.gz43_217182

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055973D:H11	ES 178	452762	1708.D08.gz43_216927
M00055974D:B01	ES 178	645264	1708.D18.gz43_217087
M00055976A:D04	ES 178	645926	1708.E22.gz43_217152
M00055976B:F01	ES 178	647280	1708.F05.gz43_216881
M00055977A:G09	ES 178	647333	1708.F19.gz43_217105
M00055977B:F06	ES 179	643723	1708.F21.gz43_217137
M00055978A:H03	ES 179	642058	1708.G11.gz43_216978
M00055978B:F01	ES 179	484355	1708.G16.gz43_217058
M00055979B:G07	ES 179	640092	1708.H12.gz43_216995
M00055979C:B07	ES 179	640204	1708.H15.gz43_217043
M00055980A:H06	ES 179	647539	1708.H23.gz43_217171
M00055980B:B07	ES 179	647924	1708.I01.gz43_216820
M00055980C:G12	ES 179	644354	1708.I08.gz43_216932
M00055981D:B07	ES 179	650513	1708.J07.gz43_216917
M00055982A:G06	ES 179	646013	1708.J17.gz43_217077
M00055982C:A12	ES 179	650018	1708.J24.gz43_217189
M00055982C:H01	ES 179	644226	1708.K04.gz43_216870
M00055983C:C09	ES 179	451709	1708.K14.gz43_217030
M00055983D:A09	ES 179	477790	1708.K18.gz43_217094
M00055984A:F05	ES 179	645848	1708.K24.gz43_217190
M00055984D:E04	ES 179	645746	1708.L08.gz43_216935
M00055985A:B06	ES 179	645288	1708.L10.gz43_216967
M00055985B:C02	ES 179	645427	1708.L13.gz43_217015
M00055985B:G12	ES 179	646126	1708.L16.gz43_217063
M00055985D:E09	ES 179	641484	1708.M02.gz43_216840
M00055986A:F05	ES 179	647539	1708.M09.gz43_216952
M00055987B:F07	ES 179	465209	1708.N06.gz43_216905
M00055988A:A12	ES 179	640179	1708.N15.gz43_217049
M00055988A:E05	ES 179	639359	1708.N21.gz43_217145
M00055989A:C09	ES 179	560349	1708.O11.gz43_216986
M00055990A:F07	ES 179	645920	1708.P01.gz43_216827
M00055990D:B02	ES 179	558452	1708.P12.gz43_217003
M00055990D:G09	ES 179	582549	1708.P15.gz43_217051
M00055991A:D10	ES 179	649309	1708.P18.gz43_217099
M00055991A:H09	ES 179	450123	1708.P20.gz43_217131
M00055991C:H11	ES 179	646212	1708.P24.gz43_217195
M00055992A:D08	ES 179	645662	1717.A08.gz43_218513
M00055993A:E02	ES 179	643288	1717.A19.gz43_218689
M00055993D:F12	ES 179	649556	1717.B06.gz43_218482
M00055994A:G04	ES 179	603388	1717.B11.gz43_218562
M00055994B:B12	ES 179	651119	1717.B15.gz43_218626
M00055994C:E06	ES 179	642887	1717.B23.gz43_218754
M00055994C:F05	ES 179	639377	1717.B24.gz43_218770

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055995A:G09	ES 179	643808	1717.C14.gz43_218611
M00055995B:A02	ES 179	477521	1717.C15.gz43_218627
M00055995C:F05	ES 179	650534	1717.C20.gz43_218707
M00055996A:C10	ES 179	466277	1717.D02.gz43_218420
M00055996B:H04	ES 179	466271	1717.D08.gz43_218516
M00055996C:A02	ES 179	650018	1717.D09.gz43_218532
M00055996C:A08	ES 179	640645	1717.D10.gz43_218548
M00055996D:D07	ES 179	558856	1717.D13.gz43_218596
M00055996D:G02	ES 179	587106	1717.D15.gz43_218628
M00055997A:B08	ES 179	642000	1717.D19.gz43_218692
M00055997A:C08	ES 179	634365	1717.D20.gz43_218708
M00055997A:F04	ES 179	552846	1717.D23.gz43_218756
M00055997D:A11	ES 179	541214	1717.E11.gz43_218565
M00055998A:F06	ES 179	644990	1717.E20.gz43_218709
M00055998B:A04	ES 179	644612	1717.E22.gz43_218741
M00055998B:D06	ES 179	560860	1717.F01.gz43_218406
M00055998B:G03	ES 179	402100	1717.F03.gz43_218438
M00055998C:D04	ES 179	513888	1717.F05.gz43_218470
M00055998D:G05	ES 179	645076	1717.F18.gz43_218678
M00055999A:A04	ES 179	478025	1717.F19.gz43_218694
M00055999A:B07	ES 179	207530	1717.F20.gz43_218710
M00055999A:H10	ES 179	646387	1717.F22.gz43_218742
M00055999C:A01	ES 179	642881	1717.G04.gz43_218455
M00055999D:C05	ES 179	549889	1717.G12.gz43_218583
M00055999D:H04	ES 179	644210	1717.G17.gz43_218663
M00056000A:B02	ES 179	447822	1717.G19.gz43_218695
M00056000A:E11	ES 179	647443	1717.G22.gz43_218743
M00056000C:D09	ES 179	649259	1717.H08.gz43_218520
M00056001C:E09	ES 179	562221	1717.H20.gz43_218712
M00056001C:F07	ES 179	447556	1717.H21.gz43_218728
M00056001D:B06	ES 179	641736	1717.I03.gz43_218441
M00056001D:G12	ES 179	643971	1717.I05.gz43_218473
M00056002A:A03	ES 179	644611	1717.I06.gz43_218489
M00056002A:H06	ES 179	559400	1717.I09.gz43_218537
M00056002D:E09	ES 179	419443	1717.I15.gz43_218633
M00056003A:A08	ES 179	449261	1717.I17.gz43_218665
M00056003A:B07	ES 179	641580	1717.I19.gz43_218697
M00056003A:C01	ES 179	645197	1717.I20.gz43_218713
M00056003B:E11	ES 179	618670	1717.J02.gz43_218426
M00056003B:G11	ES 179	464498	1717.J03.gz43_218442
M00056003C:C09	ES 179	644824	1717.J05.gz43_218474
M00056003C:H10	ES 179	645162	1717.J07.gz43_218506
M00056004A:E12	ES 179	451469	1717.J13.gz43_218602
M00056004B:F04	ES 179	643498	1717.J17.gz43_218666

Table 13

CloneID	ES No	ClusterID	SequenceName
M00056004D:F03	ES 179	452775	1717.K03.gz43_218443
M00056004D:F12	ES 179	444454	1717.K04.gz43_218459
M00056005B:H08	ES 179	641167	1717.K20.gz43_218715
M00056005C:F11	ES 179	561836	1717.L03.gz43_218444
M00056005D:C04	ES 179	470462	1717.L07.gz43_218508
M00056005D:F12	ES 179	362177	1717.L10.gz43_218556
M00056006A:E04	ES 179	643440	1717.L15.gz43_218636
M00056006A:G09	ES 179	532307	1717.L18.gz43_218684
M00056006B:A10	ES 179	637977	1717.L19.gz43_218700
M00056006B:B05	ES 179	592941	1717.L20.gz43_218716
M00056006B:C12	ES 179	411885	1717.L24.gz43_218780
M00056006D:C06	ES 179	643239	1717.M06.gz43_218493
M00056006D:D05	ES 179	639940	1717.M07.gz43_218509
M00056006D:E03	ES 179	643477	1717.M10.gz43_218557
M00056006D:F05	ES 179	651083	1717.M11.gz43_218573
M00056007A:B02	ES 179	555736	1717.M16.gz43_218653
M00056007A:G07	ES 179	647194	1717.M22.gz43_218749
M00056007B:C10	ES 179	449713	1717.M24.gz43_218781
M00056007B:E08	ES 179	649701	1717.N03.gz43_218446
M00056007C:A03	ES 179	448418	1717.N05.gz43_218478
M00056007D:F07	ES 179	644022	1717.N13.gz43_218606
M00056007D:H12	ES 179	262760	1717.N14.gz43_218622
M00056008A:H03	ES 179	675319	1717.N17.gz43_218670
M00056008B:E04	ES 179	641283	1717.N21.gz43_218734
M00056008B:G01	ES 179	456627	1717.N24.gz43_218782
M00056008B:G05	ES 179	447802	1717.O02.gz43_218431
M00056008C:D04	ES 179	639178	1717.O04.gz43_218463
M00056008C:D08	ES 179	644030	1717.O05.gz43_218479
M00056008D:D02	ES 179	644612	1717.O13.gz43_218607
M00056008D:D03	ES 179	642260	1717.O14.gz43_218623
M00056009A:H08	ES 179	557895	1717.O18.gz43_218687
M00056009C:F09	ES 179	649860	1717.O23.gz43_218767
M00056009D:A02	ES 179	646143	1717.O24.gz43_218783
M00056009D:C12	ES 179	640709	1717.P01.gz43_218416
M00056010A:E05	ES 179	644972	1717.P05.gz43_218480
M00056011A:C11	ES 179	644949	1717.P13.gz43_218608
M00056011B:A06	ES 179	517274	1717.P17.gz43_218672
M00056011B:E10	ES 179	489426	1717.P19.gz43_218704
M00056011C:D04	ES 179	555172	1717.P22.gz43_218752
M00056013A:C09	ES 179	538808	1718.B12.gz43_218965
M00056013D:D07	ES 179	640181	1718.B21.gz43_219109
M00056016C:F11	ES 179	643744	1718.D04.gz43_218839
M00056016D:E02	ES 179	644967	1718.D07.gz43_218887
M00056017A:B08	ES 179	643975	1718.D09.gz43_218919

Table 13

CloneID	ES No	ClusterID	SequenceName
M00056019B:A01	ES 179	643510	1718.F02.gz43_218809
M00056020B:C09	ES 179	650348	1718.F23.gz43_219145
M00056020C:H03	ES 179	650391	1718.G06.gz43_218874
M00056020D:D03	ES 179	545509	1718.G08.gz43_218906
M00056021A:H06	ES 179	557344	1718.G17.gz43_219050
M00056021C:H08	ES 179	639629	1718.H03.gz43_218827
M00056023D:D08	ES 179	650749	1718.I21.gz43_219116
M00056026B:H01	ES 179	644982	1718.K18.gz43_219070
M00056028D:F06	ES 179	645883	1718.M11.gz43_218960
M00056029B:H03	ES 179	467057	1718.M20.gz43_219104
M00056029D:D08	ES 179	447659	1718.N06.gz43_218881
M00056031D:E06	ES 179	495942	1718.O14.gz43_219010
M00056032B:H08	ES 179	397399	1718.P04.gz43_218851
M00056033A:C11	ES 179	425455	1718.P13.gz43_218995
M00056033C:H09	ES 179	451993	1718.P24.gz43_219171
M00056033D:F06	ES 179	645973	1719.A03.gz43_219204
M00056033D:G07	ES 179	642198	1719.A04.gz43_219220
M00056034A:G10	ES 179	646048	1719.A10.gz43_219316
M00056034C:D07	ES 179	452325	1719.A17.gz43_219428
M00056034C:H09	ES 179	648390	1719.A21.gz43_219492
M00056034D:E09	ES 179	640559	1719.A23.gz43_219524
M00056035B:A04	ES 179	550376	1719.B03.gz43_219205
M00056035B:D11	ES 179	566745	1719.B06.gz43_219253
M00056035B:E10	ES 179	549786	1719.B07.gz43_219269
M00056035C:H11	ES 179	452504	1719.B15.gz43_219397
M00056035D:C08	ES 179	447645	1719.B17.gz43_219429
M00056035D:G10	ES 179	467597	1719.B21.gz43_219493
M00056036B:B01	ES 179	648045	1719.C01.gz43_219174
M00056036B:F02	ES 179	408428	1719.C05.gz43_219238
M00056036D:B06	ES 179	468689	1719.C14.gz43_219382
M00056036D:D01	ES 179	452729	1719.C15.gz43_219398
M00056036D:F05	ES 179	644054	1719.C17.gz43_219430
M00056037A:D11	ES 179	645530	1719.C20.gz43_219478
M00056037A:E10	ES 179	645707	1719.C22.gz43_219510
M00056037B:G02	ES 179	646088	1719.D03.gz43_219207
M00056037C:D06	ES 179	476077	1719.D09.gz43_219303
M00056037C:G11	ES 179	638912	1719.D10.gz43_219319
M00056038B:G08	ES 179	481614	1719.D15.gz43_219399
M00056038D:F03	ES 179	468330	1719.D21.gz43_219495
M00056039A:A02	ES 179	550365	1719.D23.gz43_219527
M00056039A:F04	ES 179	647976	1719.E01.gz43_219176
M00056039B:C03	ES 179	649293	1719.E04.gz43_219224
M00056039C:D05	ES 179	453804	1719.E08.gz43_219288
M00056039C:G05	ES 179	645973	1719.E11.gz43_219336

Table 13

CloneID	ES No	ClusterID	SequenceName
M00056039C:H01	ES 179	642852	1719.E12.gz43_219352
M00056040A:E09	ES 179	647144	1719.E15.gz43_219400
M00056040C:A03	ES 179	649118	1719.E20.gz43_219480
M00056040C:B03	ES 179	454438	1719.E21.gz43_219496
M00056040C:C12	ES 179	646687	1719.E22.gz43_219512
M00056041A:C07	ES 179	479722	1719.F05.gz43_219241
M00056041B:F03	ES 179	644817	1719.F10.gz43_219321
M00056042B:A03	ES 179	558432	1719.F23.gz43_219529
M00056042B:B05	ES 179	483266	1719.F24.gz43_219545
M00056043A:A09	ES 179	460727	1719.G13.gz43_219370
M00056043A:H12	ES 179	556325	1719.G16.gz43_219418
M00056043B:E03	ES 179	643897	1719.G19.gz43_219466
M00056043C:G03	ES 179	490898	1719.G24.gz43_219546
M00056043D:E03	ES 179	641193	1719.H04.gz43_219227
M00056044B:A01	ES 179	236965	1719.H12.gz43_219355
M00056044C:C01	ES 179	649900	1719.H15.gz43_219403
M00056044D:B04	ES 179	646579	1719.H19.gz43_219467
M00056044D:F01	ES 179	588502	1719.H22.gz43_219515
M00056044D:G07	ES 179	458683	1719.H24.gz43_219547
M00056045A:D03	ES 179	557676	1719.I01.gz43_219180
M00056045C:C09	ES 179	449814	1719.I10.gz43_219324
M00056045D:C09	ES 180	402476	1719.I21.gz43_219500
M00056045D:E06	ES 180	462293	1719.I23.gz43_219532
M00056046A:B04	ES 180	644738	1719.J02.gz43_219197
M00056046A:B12	ES 180	461517	1719.J04.gz43_219229
M00056046A:D12	ES 180	559550	1719.J06.gz43_219261
M00056046A:G08	ES 180	452102	1719.J07.gz43_219277
M00056046D:C11	ES 180	645070	1719.K04.gz43_219230
M00056047A:E09	ES 180	650348	1719.K09.gz43_219310
M00056047B:D11	ES 180	639711	1719.K17.gz43_219438
M00056047C:E03	ES 180	639255	1719.K22.gz43_219518
M00056047C:E08	ES 180	454844	1719.K23.gz43_219534
M00056047D:G10	ES 180	557853	1719.L06.gz43_219263
M00056048A:D12	ES 180	644894	1719.L09.gz43_219311
M00056048B:E01	ES 180	451544	1719.L12.gz43_219359
M00056048D:B09	ES 180	456840	1719.L19.gz43_219471
M00056049A:C11	ES 180	612572	1719.L22.gz43_219519
M00056049B:E11	ES 180	645942	1719.M04.gz43_219232
M00056049C:A08	ES 180	642184	1719.M06.gz43_219264
M00056049C:H04	ES 180	643748	1719.M11.gz43_219344
M00056049C:H07	ES 180	554070	1719.M12.gz43_219360
M00056049D:D03	ES 180	645431	1719.M16.gz43_219424
M00056049D:E01	ES 180	641715	1719.M17.gz43_219440

Table 13

CloneID	ES No	ClusterID	SequenceName
M00056050A:B05	ES 180	644686	1719.M19.gz43_219472
M00056050A:D02	ES 180	558439	1719.M21.gz43_219504
M00056050C:A09	ES 180	644639	1719.N01.gz43_219185
M00056050D:F04	ES 180	406734	1719.N07.gz43_219281
M00056051A:C03	ES 180	649259	1719.N11.gz43_219345
M00056051A:H11	ES 180	528616	1719.N12.gz43_219361
M00056051B:B03	ES 180	645375	1719.N15.gz43_219409
M00056051C:C09	ES 180	595066	1719.N21.gz43_219505
M00056051C:H09	ES 180	587106	1719.N23.gz43_219537
M00056051D:A07	ES 180	640603	1719.N24.gz43_219553
M00056051D:H02	ES 180	645151	1719.O05.gz43_219250
M00056052A:A11	ES 180	649429	1719.O06.gz43_219266
M00056052A:C07	ES 180	644819	1719.O07.gz43_219282
M00056052C:G07	ES 180	647038	1719.O16.gz43_219426
M00056052D:G01	ES 180	641786	1719.O22.gz43_219522
M00056053A:F01	ES 180	506920	1719.P03.gz43_219219
M00056053C:B04	ES 180	645814	1719.P08.gz43_219299
M00056053C:E04	ES 180	232093	1719.P10.gz43_219331
M00056053D:D07	ES 180	497101	1719.P15.gz43_219411
M00056054A:B06	ES 180	644692	1719.P17.gz43_219443
M00056054A:D09	ES 180	465589	1719.P18.gz43_219459
M00056054A:E03	ES 180	467255	1719.P19.gz43_219475
M00056054A:G07	ES 180	647306	1719.P22.gz43_219523
M00056054B:G05	ES 180	645049	1720.A02.gz43_219572
M00056054B:H11	ES 180	648013	1720.A03.gz43_219588
M00056054C:C09	ES 180	558494	1720.A04.gz43_219604
M00056054C:E12	ES 180	454906	1720.A06.gz43_219636
M00056055A:E04	ES 180	447676	1720.A14.gz43_219764
M00056055B:B06	ES 180	640818	1720.A18.gz43_219828
M00056057B:D01	ES 180	466795	1720.C02.gz43_219574
M00056057B:E12	ES 180	644927	1720.C04.gz43_219606
M00056057C:B02	ES 180	648688	1720.C05.gz43_219622
M00056057C:D06	ES 180	456059	1720.C08.gz43_219670
M00056057C:E01	ES 180	447635	1720.C09.gz43_219686
M00056057C:E12	ES 180	644928	1720.C12.gz43_219734
M00056057D:E11	ES 180	641469	1720.C15.gz43_219782
M00056058A:B07	ES 180	558154	1720.C16.gz43_219798
M00056058A:F08	ES 180	467780	1720.C19.gz43_219846
M00056058B:H09	ES 180	452630	1720.C22.gz43_219894
M00056059A:A02	ES 180	644597	1720.D06.gz43_219639
M00056059A:B01	ES 180	649054	1720.D08.gz43_219671
M00056059B:D10	ES 180	473007	1720.D11.gz43_219719
M00056060C:C06	ES 180	448627	1720.E04.gz43_219608
M00056060D:H11	ES 180	642166	1720.E10.gz43_219704

Table 13

CloneID	ES No	ClusterID	SequenceName
M00056061A:E05	ES 180	644916	1720.E12.gz43_219736
M00056061B:A03	ES 180	641801	1720.E13.gz43_219752
M00056062D:D08	ES 180	446415	1720.F20.gz43_219865
M00056062D:F12	ES 180	643510	1720.G01.gz43_219562
M00056063C:F10	ES 180	375577	1720.G15.gz43_219786
M00056063C:G11	ES 180	650549	1720.G16.gz43_219802
M00056065B:A02	ES 180	641253	1720.H06.gz43_219643
M00056065D:C11	ES 180	643381	1720.H16.gz43_219803
M00056066A:D03	ES 180	553923	1720.H20.gz43_219867
M00056066B:H04	ES 180	14157	1720.I02.gz43_219580
M00056066D:G04	ES 180	461351	1720.I16.gz43_219804
M00056067A:A12	ES 180	455716	1720.I18.gz43_219836
M00056067B:D08	ES 180	645900	1720.I21.gz43_219884
M00056068D:A06	ES 180	644822	1720.J18.gz43_219837
M00056068D:E06	ES 180	641253	1720.J22.gz43_219901
M00056069A:F01	ES 180	460047	1720.K06.gz43_219646
M00056069A:F06	ES 180	644225	1720.K08.gz43_219678
M00056069B:E04	ES 180	645076	1720.K14.gz43_219774
M00056070C:B09	ES 180	644701	1720.L12.gz43_219743
M00056072B:C06	ES 180	551181	1720.M11.gz43_219728
M00056072D:E08	ES 180	649364	1720.M21.gz43_219888
M00056073B:H11	ES 180	636654	1720.N08.gz43_219681
M00056074B:D12	ES 180	643348	1720.N23.gz43_219921
M00056074B:E11	ES 180	641135	1720.O02.gz43_219586
M00056074C:H08	ES 180	487567	1720.O12.gz43_219746
M00056074C:H09	ES 180	651108	1720.O13.gz43_219762
M00056077B:E03	ES 180	448485	1729.A06.gz43_217713
M00056077C:H02	ES 180	646696	1729.A12.gz43_217809
M00056078A:D07	ES 180	479868	1729.A20.gz43_217937
M00056078B:G02	ES 180	650900	1729.B04.gz43_217682
M00056079A:B01	ES 180	613722	1729.B18.gz43_217906
M00056080C:D04	ES 180	464778	1729.C22.gz43_217971
M00056081A:C05	ES 180	649149	1729.D04.gz43_217684
M00056081B:F09	ES 180	640891	1729.D12.gz43_217812
M00056082A:E12	ES 180	560054	1729.E11.gz43_217797
M00056082B:G07	ES 180	570939	1729.E15.gz43_217861
M00056083D:D11	ES 180	647437	1729.F16.gz43_217878
M00056084C:D11	ES 180	649202	1729.G03.gz43_217671
M00056087B:G12	ES 180	644715	1729.H12.gz43_217816
M00056087D:E04	ES 180	446243	1729.H22.gz43_217976
M00056087D:G07	ES 180	649520	1729.H24.gz43_218008
M00056089D:A09	ES 180	454176	1729.J05.gz43_217706
M00056089D:E07	ES 180	649356	1729.J08.gz43_217754
M00056091A:E04	ES 180	644054	1729.K04.gz43_217691

Table 13

CloneID	ES No	ClusterID	SequenceName
M00056091C:C06	ES 180	644712	1729.K11.gz43_217803
M00056091C:D09	ES 180	645050	1729.K13.gz43_217835
M00056091C:H03	ES 180	464267	1729.K15.gz43_217867
M00056091D:C12	ES 180	645409	1729.K17.gz43_217899
M00056091D:E10	ES 180	649328	1729.K20.gz43_217947
M00056092B:D10	ES 180	535436	1729.L02.gz43_217660
M00056092C:E12	ES 180	710155	1729.L08.gz43_217756
M00056093A:B12	ES 180	650547	1729.L16.gz43_217884
M00056093A:F08	ES 180	418763	1729.L18.gz43_217916
M00056093B:D03	ES 180	645131	1729.L20.gz43_217948
M00056095A:C02	ES 180	644543	1729.M22.gz43_217981
M00056095B:A07	ES 180	643440	1729.N06.gz43_217726
M00056095C:E02	ES 180	644965	1729.N12.gz43_217822
M00056095C:G07	ES 180	649514	1729.N14.gz43_217854
M00056097B:C04	ES 180	649082	1729.P04.gz43_217696
M00056097B:G01	ES 180	649570	1729.P06.gz43_217728
M00056098B:C04	ES 180	649054	1729.P16.gz43_217888
M00056098D:A08	ES 180	597647	1729.P22.gz43_217984
M00056120C:H04	ES 180	648654	1731.A01.gz43_219940
M00056120D:F01	ES 180	644037	1731.A02.gz43_219956
M00056121A:E05	ES 180	464990	1731.A09.gz43_220068
M00056121D:A12	ES 180	642204	1731.A19.gz43_220228
M00056121D:C11	ES 180	648013	1731.A20.gz43_220244
M00056122A:A05	ES 180	503122	1731.A22.gz43_220276
M00056122A:B05	ES 180	589098	1731.A23.gz43_220292
M00056122A:D02	ES 180	648076	1731.A24.gz43_220308
M00056122B:A07	ES 180	639555	1731.B04.gz43_219989
M00056122B:G01	ES 180	648109	1731.B07.gz43_220037
M00056122B:G09	ES 180	627515	1731.B08.gz43_220053
M00056122C:H12	ES 180	460190	1731.B12.gz43_220117
M00056122D:B07	ES 180	557419	1731.B13.gz43_220133
M00056122D:F10	ES 180	646917	1731.B17.gz43_220197
M00056123B:F02	ES 180	531461	1731.B23.gz43_220293
M00056123B:G05	ES 180	648547	1731.C01.gz43_219942
M00056123D:A07	ES 180	627341	1731.C05.gz43_220006
M00056124B:C12	ES 180	477555	1731.C14.gz43_220150
M00056124D:F06	ES 180	515350	1731.C22.gz43_220278
M00056124D:G03	ES 180	455808	1731.C23.gz43_220294
M00056125B:F01	ES 180	465127	1731.D04.gz43_219991
M00056127A:A10	ES 180	422242	1731.D07.gz43_220039
M00056127A:H03	ES 180	644928	1731.D11.gz43_220103
M00056127B:E11	ES 180	638934	1731.D13.gz43_220135
M00056127C:C02	ES 180	639774	1731.D15.gz43_220167
M00056127C:C06	ES 180	649095	1731.D16.gz43_220183

Table 13

CloneID	ES No	ClusterID	SequenceName
M00056127D:G10	ES 180	643510	1731.D23.gz43_220295
M00056128B:A07	ES 180	456985	1731.E07.gz43_220040
M00056128B:D03	ES 180	452941	1731.E08.gz43_220056
M00056128C:B11	ES 180	646584	1731.E11.gz43_220104
M00056128C:F02	ES 180	647248	1731.E14.gz43_220152
M00056129A:G01	ES 180	647431	1731.E21.gz43_220264
M00056129C:F09	ES 180	476380	1731.F03.gz43_219977
M00056130B:E11	ES 180	646785	1731.F13.gz43_220137
M00056130C:C12	ES 180	649299	1731.F15.gz43_220169
M00056130C:F08	ES 180	647290	1731.F16.gz43_220185
M00056130D:E06	ES 180	556336	1731.F22.gz43_220281
M00056131A:E09	ES 180	453726	1731.G05.gz43_220010
M00056131B:E01	ES 180	562378	1731.G12.gz43_220122
M00056131C:H03	ES 180	649735	1731.G16.gz43_220186
M00056131D:B02	ES 180	503628	1731.G19.gz43_220234
M00056132B:C12	ES 180	635354	1731.H02.gz43_219963
M00056132C:F04	ES 180	557026	1731.H06.gz43_220027
M00056133B:F01	ES 180	642936	1731.H18.gz43_220219
M00056133D:D09	ES 180	463824	1731.I01.gz43_219948
M00056134A:D04	ES 180	640695	1731.I07.gz43_220044
M00056134B:B10	ES 180	640737	1731.I10.gz43_220092
M00056134C:C06	ES 180	470006	1731.I14.gz43_220156
M00056134D:B07	ES 180	708175	1731.I21.gz43_220268
M00056134D:F02	ES 180	649482	1731.I24.gz43_220316
M00056134D:G07	ES 180	711493	1731.J02.gz43_219965
M00056134D:G11	ES 180	649617	1731.J03.gz43_219981
M00056135B:E03	ES 180	459521	1731.J10.gz43_220093
M00056135C:C05	ES 180	646039	1731.J16.gz43_220189
M00056135C:C08	ES 180	642650	1731.J17.gz43_220205
M00056135C:H06	ES 180	557867	1731.J19.gz43_220237
M00056136A:B11	ES 180	648996	1731.J23.gz43_220301
M00056136D:B08	ES 180	641957	1731.K06.gz43_220030
M00056137B:F07	ES 180	648311	1731.K14.gz43_220158
M00056137B:F11	ES 180	478393	1731.K15.gz43_220174
M00056137C:A01	ES 180	642275	1731.K17.gz43_220206
M00056137C:E01	ES 180	639395	1731.K19.gz43_220238
M00056137C:G02	ES 180	645367	1731.K20.gz43_220254
M00056137D:H05	ES 181	648742	1731.L02.gz43_219967
M00056138A:B11	ES 181	458938	1731.L04.gz43_219999
M00056138B:F05	ES 181	549691	1731.L10.gz43_220095
M00056138D:G08	ES 181	651015	1731.L17.gz43_220207
M00056139A:D12	ES 181	647232	1731.L20.gz43_220255
M00056139D:E05	ES 181	648341	1731.M08.gz43_220064

Table 13

CloneID	ES No	ClusterID	SequenceName
M00056139D:H04	ES 181	514838	1731.M10.gz43_220096
M00056140A:A07	ES 181	450049	1731.M11.gz43_220112
M00056140A:F12	ES 181	646581	1731.M16.gz43_220192
M00056140B:G06	ES 181	649557	1731.M22.gz43_220288
M00056140C:E04	ES 181	648721	1731.N01.gz43_219953
M00056140D:G07	ES 181	649278	1731.N07.gz43_220049
M00056141C:C10	ES 181	650745	1731.N13.gz43_220145
M00056141C:H01	ES 181	470667	1731.N16.gz43_220193
M00056141C:H07	ES 181	644686	1731.N17.gz43_220209
M00056141D:D09	ES 181	562755	1731.N22.gz43_220289
M00056141D:E08	ES 181	446164	1731.N23.gz43_220305
M00056142A:F03	ES 181	648481	1731.O01.gz43_219954
M00056142B:D02	ES 181	650076	1731.O06.gz43_220034
M00056142C:A09	ES 181	452738	1731.O10.gz43_220098
M00056143A:H08	ES 181	419114	1731.O23.gz43_220306
M00056144B:C01	ES 181	558377	1731.P07.gz43_220051
M00056144D:C05	ES 181	647949	1731.P12.gz43_220131
M00056146A:A09	ES 181	550714	1732.A05.gz43_220388
M00056146A:H09	ES 181	648667	1732.A12.gz43_220500
M00056146B:E05	ES 181	640634	1732.A14.gz43_220532
M00056146D:D04	ES 181	488592	1732.A20.gz43_220628
M00056149C:A02	ES 181	465734	1732.C11.gz43_220486
M00056149C:B01	ES 181	459012	1732.C12.gz43_220502
M00056149C:E10	ES 181	650877	1732.C16.gz43_220566
M00056149D:F06	ES 181	639485	1732.C22.gz43_220662
M00056150A:E04	ES 181	650820	1732.C24.gz43_220694
M00056151A:E07	ES 181	463513	1732.D16.gz43_220567
M00056152A:B11	ES 181	605761	1732.E11.gz43_220488
M00056152A:D07	ES 181	461135	1732.E13.gz43_220520
M00056152C:G08	ES 181	651075	1732.E20.gz43_220632
M00056153A:G04	ES 181	644221	1732.F07.gz43_220425
M00056153A:H07	ES 181	644801	1732.F09.gz43_220457
M00056153B:F11	ES 181	449882	1732.F16.gz43_220569
M00056154B:D02	ES 181	649443	1732.G08.gz43_220442
M00056154B:F11	ES 181	650249	1732.G10.gz43_220474
M00056155A:G09	ES 181	640162	1732.G24.gz43_220698
M00056155B:A02	ES 181	646323	1732.H01.gz43_220331
M00056157A:B11	ES 181	416624	1732.I08.gz43_220444
M00056157B:A08	ES 181	642244	1732.I12.gz43_220508
M00056157B:H06	ES 181	446184	1732.I14.gz43_220540
M00056157C:E10	ES 181	554581	1732.I19.gz43_220620
M00056157D:C02	ES 181	648930	1732.I21.gz43_220652
M00056157D:H08	ES 181	646596	1732.I23.gz43_220684
M00056158C:D11	ES 181	649482	1732.J05.gz43_220397

Table 13

CloneID	ES No	ClusterID	SequenceName
M00056158C:F09	ES 181	650987	1732.J06.gz43_220413
M00056159A:A08	ES 181	644856	1732.J14.gz43_220541
M00056159A:E03	ES 181	650909	1732.J16.gz43_220573
M00056159B:E06	ES 181	648774	1732.J21.gz43_220653
M00056159C:C11	ES 181	459260	1732.J23.gz43_220685
M00056160B:D06	ES 181	414821	1732.K09.gz43_220462
M00056160C:F12	ES 181	463966	1732.K15.gz43_220558
M00056160C:G01	ES 181	645100	1732.K16.gz43_220574
M00056160D:C06	ES 181	649991	1732.K20.gz43_220638
M00056161C:G06	ES 181	650348	1732.L12.gz43_220511
M00056161C:H10	ES 181	468262	1732.L13.gz43_220527
M00056162A:B06	ES 181	467972	1732.L19.gz43_220623
M00056162A:C09	ES 181	649947	1732.L20.gz43_220639
M00056162A:E09	ES 181	555634	1732.L21.gz43_220655
M00056162A:F01	ES 181	634409	1732.L23.gz43_220687
M00056162A:G09	ES 181	584499	1732.L24.gz43_220703
M00056162C:F02	ES 181	647412	1732.M07.gz43_220432
M00056162D:A01	ES 181	649782	1732.M11.gz43_220496
M00056162D:D03	ES 181	650116	1732.M13.gz43_220528
M00056162D:D06	ES 181	380477	1732.M14.gz43_220544
M00056163A:B10	ES 181	649883	1732.M17.gz43_220592
M00056164A:H03	ES 181	224092	1732.N20.gz43_220641
M00056165C:B11	ES 181	650534	1732.O13.gz43_220530
M00056165D:D09	ES 181	649578	1732.O15.gz43_220562
M00056167C:H06	ES 181	414006	1732.P18.gz43_220611
M00056168A:C06	ES 181	558915	1741.A01.gz43_220708
M00056168C:A05	ES 181	649795	1741.A09.gz43_220836
M00056169B:C02	ES 181	458683	1741.A21.gz43_221028
M00056169C:F07	ES 181	458085	1741.B05.gz43_220773
M00056169D:A03	ES 181	555771	1741.B08.gz43_220821
M00056169D:D05	ES 181	648777	1741.B12.gz43_220885
M00056169D:H05	ES 181	650800	1741.B16.gz43_220949
M00056170B:B09	ES 181	642256	1741.B24.gz43_221077
M00056170B:C04	ES 181	602324	1741.C01.gz43_220710
M00056170C:C09	ES 181	394772	1741.C06.gz43_220790
M00056171A:H01	ES 181	646173	1741.C20.gz43_221014
M00056171C:A08	ES 181	650063	1741.D02.gz43_220727
M00056172A:H06	ES 181	561747	1741.D14.gz43_220919
M00056172B:A12	ES 181	648855	1741.D15.gz43_220935
M00056173D:C05	ES 181	646699	1741.E07.gz43_220808
M00056174B:D02	ES 181	646915	1741.E14.gz43_220920
M00056174B:E02	ES 181	647086	1741.E16.gz43_220952
M00056174B:E04	ES 181	640285	1741.E17.gz43_220968
M00056174B:H11	ES 181	557010	1741.E20.gz43_221016

Table 13

CloneID	ES No	ClusterID	SequenceName
M00056174C:F06	ES 181	479997	1741.E24.gz43_221080
M00056174C:H09	ES 181	648063	1741.F04.gz43_220761
M00056175A:A06	ES 181	453768	1741.F10.gz43_220857
M00056175A:C04	ES 181	649136	1741.F11.gz43_220873
M00056175C:A10	ES 181	645288	1741.F19.gz43_221001
M00056175C:B11	ES 181	650146	1741.F20.gz43_221017
M00056175D:A06	ES 181	648820	1741.F24.gz43_221081
M00056175D:E05	ES 181	649299	1741.G03.gz43_220746
M00056176A:D06	ES 181	593173	1741.G07.gz43_220810
M00056176B:B05	ES 181	457272	1741.G10.gz43_220858
M00056176B:E10	ES 181	446289	1741.G12.gz43_220890
M00056176C:B11	ES 181	648865	1741.G14.gz43_220922
M00056177A:C10	ES 181	140459	1741.G19.gz43_221002
M00056177A:D12	ES 181	499690	1741.G20.gz43_221018
M00056177A:H01	ES 181	610986	1741.G23.gz43_221066
M00056177C:E08	ES 181	639996	1741.H06.gz43_220795
M00056178B:A07	ES 181	642557	1741.H14.gz43_220923
M00056178B:A11	ES 181	638730	1741.H15.gz43_220939
M00056178B:H08	ES 181	459923	1741.H17.gz43_220971
M00056178C:C02	ES 181	464778	1741.H18.gz43_220987
M00056178C:E12	ES 181	584745	1741.H20.gz43_221019
M00056178C:F02	ES 181	640922	1741.H21.gz43_221035
M00056179A:D12	ES 181	379805	1741.I08.gz43_220828
M00056179B:H12	ES 181	639886	1741.I14.gz43_220924
M00056180B:A06	ES 181	644053	1741.I23.gz43_221068
M00056180B:D05	ES 181	492982	1741.J02.gz43_220733
M00056180B:F11	ES 181	641193	1741.J04.gz43_220765
M00056180D:E06	ES 181	378694	1741.J10.gz43_220861
M00056180D:F05	ES 181	449452	1741.J12.gz43_220893
M00056180D:G07	ES 181	183842	1741.J14.gz43_220925
M00056181A:B05	ES 181	471836	1741.J16.gz43_220957
M00056181A:E07	ES 181	452729	1741.J17.gz43_220973
M00056181B:B02	ES 181	640514	1741.J19.gz43_221005
M00056181B:D06	ES 181	645521	1741.J20.gz43_221021
M00056181B:E11	ES 181	561793	1741.J21.gz43_221037
M00056181C:D02	ES 181	645578	1741.J22.gz43_221053
M00056182A:B04	ES 181	557353	1741.K02.gz43_220734
M00056182A:G11	ES 181	643206	1741.K07.gz43_220814
M00056182B:G12	ES 181	460506	1741.K09.gz43_220846
M00056182C:F08	ES 181	469409	1741.K14.gz43_220926
M00056182D:A07	ES 181	641525	1741.K15.gz43_220942
M00056183A:B09	ES 181	459974	1741.K19.gz43_221006
M00056183B:G11	ES 181	561856	1741.L04.gz43_220767
M00056183C:F01	ES 181	710362	1741.L08.gz43_220831

Table 13

CloneID	ES No	ClusterID	SequenceName
M00056183C:F11	ES 181	642840	1741.L09.gz43_220847
M00056184A:B11	ES 181	649702	1741.L14.gz43_220927
M00056184B:D08	ES 181	463487	1741.L18.gz43_220991
M00056184B:H08	ES 181	446987	1741.L20.gz43_221023
M00056184C:A09	ES 181	647688	1741.L22.gz43_221055
M00056184C:C03	ES 181	650975	1741.L24.gz43_221087
M00056184C:C07	ES 181	559349	1741.M01.gz43_220720
M00056184C:E08	ES 181	642631	1741.M04.gz43_220768
M00056184C:H03	ES 181	646309	1741.M07.gz43_220816
M00056184D:D06	ES 181	555655	1741.M11.gz43_220880
M00056185B:B06	ES 181	639132	1741.M23.gz43_221072
M00056185D:C01	ES 181	553023	1741.N07.gz43_220817
M00056185D:C06	ES 181	649085	1741.N08.gz43_220833
M00056185D:D06	ES 181	502683	1741.N09.gz43_220849
M00056185D:G07	ES 181	649577	1741.N12.gz43_220897
M00056186A:B09	ES 181	646581	1741.N14.gz43_220929
M00056186B:C03	ES 181	648491	1741.N20.gz43_221025
M00056186B:H09	ES 181	644801	1741.N24.gz43_221089
M00056186D:G05	ES 181	649705	1741.O07.gz43_220818
M00056187B:H02	ES 181	644819	1741.O12.gz43_220898
M00056188A:E05	ES 181	641945	1741.O21.gz43_221042
M00056188B:D04	ES 181	642164	1741.P01.gz43_220723
M00056188B:E07	ES 181	648344	1741.P04.gz43_220771
M00056188B:E12	ES 181	639520	1741.P05.gz43_220787
M00056188C:D02	ES 181	650188	1741.P08.gz43_220835
M00056188C:G06	ES 181	640443	1741.P11.gz43_220883
M00056188C:H04	ES 181	648665	1741.P12.gz43_220899
M00056189A:H09	ES 181	562152	1741.P18.gz43_220995
M00056189B:A01	ES 181	465594	1741.P19.gz43_221011
M00056191A:H04	ES 181	646499	1742.B04.gz43_221141
M00056191B:E08	ES 181	453762	1742.B08.gz43_221205
M00056192A:D01	ES 181	645560	1742.B19.gz43_221381
M00056195C:F12	ES 181	644916	1742.E06.gz43_221176
M00056195D:D07	ES 181	649402	1742.E12.gz43_221272
M00056196C:B03	ES 181	397363	1742.F03.gz43_221129
M00056196C:G12	ES 181	648590	1742.F09.gz43_221225
M00056197C:H01	ES 181	640101	1742.F20.gz43_221401
M00056198A:B05	ES 181	637387	1742.G01.gz43_221098
M00056200D:D05	ES 181	452066	1742.H21.gz43_221419
M00056201C:C03	ES 181	640913	1742.I08.gz43_221212
M00056203D:F05	ES 181	463168	1742.J03.gz43_221133
M00056203D:H03	ES 181	570939	1742.J04.gz43_221149
M00056204A:B08	ES 181	456920	1742.J05.gz43_221165
M00056204A:C04	ES 181	647991	1742.J07.gz43_221197

Table 13

CloneID	ES No	ClusterID	SequenceName
M00056204C:H12	ES 181	648754	1742.J18.gz43_221373
M00056205D:E06	ES 181	645802	1742.K12.gz43_221278
M00056205D:G04	ES 181	650756	1742.K15.gz43_221326
M00056206B:A10	ES 181	645177	1742.K19.gz43_221390
M00056206D:E06	ES 181	639158	1742.L03.gz43_221135
M00056206D:F07	ES 181	463545	1742.L04.gz43_221151
M00056207C:B04	ES 181	446621	1742.L17.gz43_221359
M00056208B:C10	ES 181	172843	1742.M03.gz43_221136
M00056208C:A10	ES 181	559955	1742.M06.gz43_221184
M00056208D:A12	ES 181	645223	1742.M11.gz43_221264
M00042346A:B04	ES 182	448412	1766.A01.gz43_224099
M00042346B:D12	ES 182	448491	1766.A05.gz43_224163
M00042346C:G12	ES 182	448892	1766.A09.gz43_224227
M00042432D:G02	ES 182	485237	1766.E01.gz43_224103
M00042433C:H05	ES 182	477797	1766.E13.gz43_224295
M00042434B:F04	ES 182	450334	1766.E20.gz43_224407
M00042437B:A11	ES 182	479131	1766.G01.gz43_224105
M00042438C:H11	ES 182	451183	1766.G20.gz43_224409
M00042439A:D09	ES 182	481457	1766.H03.gz43_224138
M00042461C:E09	ES 182	483219	1766.I13.gz43_224299
M00042462A:F12	ES 182	450212	1766.I19.gz43_224395
M00042464A:F06	ES 182	451793	1766.J21.gz43_224428
M00042464C:B06	ES 182	448098	1766.K04.gz43_224157
M00042470B:H11	ES 182	447377	1766.M22.gz43_224447
M00042515B:A10	ES 182	449104	1767.A01.gz43_224483
M00042515D:B11	ES 182	449215	1767.A04.gz43_224531
M00042515D:G01	ES 182	451982	1767.A05.gz43_224547
M00056209B:D02	ES 182	507050	1742.M19.gz43_221392
M00056210B:C11	ES 182	470801	1742.N09.gz43_221233
M00056210B:E03	ES 182	649354	1742.N12.gz43_221281
M00056210D:H05	ES 182	457539	1742.N15.gz43_221329
M00056211A:C08	ES 182	648036	1742.N18.gz43_221377
M00056212C:C09	ES 182	642118	1742.P01.gz43_221107
M00056213C:C01	ES 182	646275	1742.P19.gz43_221395
M00056213C:G11	ES 182	466418	1742.P24.gz43_221475
M00056214B:H03	ES 182	638807	1743.A08.gz43_221588
M00056214C:A04	ES 182	499517	1743.A10.gz43_221620
M00056214D:F05	ES 182	650975	1743.A16.gz43_221716
M00056216B:H09	ES 182	648953	1743.B17.gz43_221733
M00056217A:H11	ES 182	648155	1743.C04.gz43_221526
M00056217B:A06	ES 182	650487	1743.C05.gz43_221542
M00056217B:G03	ES 182	562359	1743.C09.gz43_221606
M00056217C:B12	ES 182	602324	1743.C10.gz43_221622

Table 13

CloneID	ES No	ClusterID	SequenceName
M00056217D:B07	ES 182	562625	1743.C16.gz43_221718
M00056218A:G11	ES 182	448780	1743.C22.gz43_221814
M00056218C:C02	ES 182	648351	1743.D05.gz43_221543
M00056218D:H06	ES 182	411603	1743.D14.gz43_221687
M00056220A:H04	ES 182	644916	1743.E16.gz43_221720
M00056220B:F11	ES 182	722253	1743.F01.gz43_221481
M00056222A:E05	ES 182	570052	1743.G11.gz43_221642
M00056222D:C06	ES 182	574166	1743.G18.gz43_221754
M00056223A:B11	ES 182	648989	1743.G23.gz43_221834
M00056223A:C03	ES 182	442347	1743.G24.gz43_221850
M00056223A:D10	ES 182	574166	1743.H01.gz43_221483
M00056223A:H07	ES 182	649709	1743.H03.gz43_221515
M00056223C:C07	ES 182	408428	1743.H11.gz43_221643
M00056224B:F01	ES 182	645549	1743.H17.gz43_221739
M00056224D:E08	ES 182	453470	1743.H23.gz43_221835
M00056225A:D08	ES 182	556635	1743.I01.gz43_221484
M00056225B:A11	ES 182	618670	1743.I06.gz43_221564
M00056227C:A01	ES 182	648777	1743.J20.gz43_221789
M00056227D:A02	ES 182	578718	1743.K04.gz43_221534
M00056228A:A02	ES 182	447892	1743.K09.gz43_221614
M00056228C:B04	ES 182	465536	1743.K24.gz43_221854
M00056229C:F05	ES 182	33738	1743.L16.gz43_221727
M00056231B:E01	ES 182	649351	1743.M11.gz43_221648
M00056232B:A11	ES 182	451487	1743.M21.gz43_221808
M00056232B:C04	ES 182	649030	1743.M23.gz43_221840
M00056232C:E06	ES 182	649272	1743.N04.gz43_221537
M00056232D:C08	ES 182	502413	1743.N09.gz43_221617
M00056235A:C12	ES 182	648816	1743.O22.gz43_221826
M00056236A:G12	ES 182	706245	1743.P07.gz43_221587
M00056236B:B03	ES 182	636876	1743.P09.gz43_221619
M00056237B:D04	ES 182	703978	1744.A06.gz43_221940
M00056237C:C05	ES 182	470292	1744.A10.gz43_222004
M00056238A:A03	ES 182	707483	1744.A19.gz43_222148
M00056238C:C11	ES 182	649042	1744.B08.gz43_221973
M00056239A:D06	ES 182	648159	1744.B14.gz43_222069
M00056240B:F08	ES 182	649396	1744.C10.gz43_222006
M00056240D:H07	ES 182	447272	1744.C15.gz43_222086
M00056242D:A02	ES 182	648989	1744.E04.gz43_221912
M00056243C:G10	ES 182	651073	1744.E22.gz43_222200
M00056244A:A01	ES 182	650463	1744.F03.gz43_221897
M00056244A:B01	ES 182	650549	1744.F04.gz43_221913
M00056245A:D11	ES 182	650463	1744.F24.gz43_222233
M00056246A:E01	ES 182	637387	1744.G17.gz43_222122
M00056246C:G07	ES 182	419255	1744.H08.gz43_221979

Table 13

CloneID	ES No	ClusterID	SequenceName
M00056246D:A07	ES 182	549178	1744.H09.gz43_221995
M00056247A:D02	ES 182	162981	1744.H17.gz43_222123
M00056247A:F07	ES 182	457221	1744.H18.gz43_222139
M00056247B:C11	ES 182	650018	1744.H21.gz43_222187
M00056249A:F11	ES 182	650919	1744.I24.gz43_222236
M00056249A:H07	ES 182	645872	1744.J02.gz43_221885
M00056249B:C02	ES 182	506719	1744.J03.gz43_221901
M00056249C:E06	ES 182	650860	1744.J10.gz43_222013
M00056250C:A08	ES 182	408961	1744.K04.gz43_221918
M00056250C:D05	ES 182	650661	1744.K07.gz43_221966
M00056251B:A12	ES 182	643327	1744.K14.gz43_222078
M00056251B:B07	ES 182	452646	1744.K15.gz43_222094
M00056251C:H04	ES 182	586794	1744.K24.gz43_222238
M00056253A:F12	ES 182	648996	1744.M08.gz43_221984
M00056253B:H04	ES 182	639119	1744.M14.gz43_222080
M00056253C:C04	ES 182	703217	1744.M18.gz43_222144
M00056253D:G04	ES 182	641874	1744.M23.gz43_222224
M00056254A:F04	ES 182	651051	1744.N02.gz43_221889
M00056254D:C04	ES 182	451361	1744.N09.gz43_222001
M00056255B:F09	ES 182	559324	1744.N18.gz43_222145
M00056255C:C04	ES 182	645472	1744.N20.gz43_222177
M00056256A:C02	ES 182	645271	1744.O01.gz43_221874
M00056256C:D12	ES 182	643944	1744.O17.gz43_222130
M00056258A:A11	ES 182	464091	1744.P19.gz43_222163
M00056258A:E10	ES 182	610269	1744.P23.gz43_222227
M00056258C:D07	ES 182	633594	1753.A05.gz43_222308
M00056258D:H06	ES 182	648590	1753.A12.gz43_222420
M00056259A:E08	ES 182	555021	1753.A17.gz43_222500
M00056259C:E03	ES 182	459914	1753.A24.gz43_222612
M00056260C:E11	ES 182	460245	1753.B14.gz43_222453
M00056260C:F08	ES 182	552839	1753.B17.gz43_222501
M00056261A:F12	ES 182	645271	1753.C03.gz43_222278
M00056262A:B07	ES 182	647897	1753.C18.gz43_222518
M00056262B:B08	ES 182	403111	1753.C23.gz43_222598
M00056262D:B11	ES 182	446572	1753.D04.gz43_222295
M00056262D:G08	ES 182	648534	1753.D06.gz43_222327
M00056263A:D08	ES 182	649262	1753.D10.gz43_222391
M00056263B:E10	ES 182	486452	1753.D17.gz43_222503
M00056264A:G05	ES 182	650679	1753.E03.gz43_222280
M00056264B:C03	ES 182	648063	1753.E06.gz43_222328
M00056265A:E01	ES 182	646609	1753.E15.gz43_222472
M00056267D:B09	ES 182	562173	1753.G15.gz43_222474
M00056268D:G07	ES 182	639520	1753.H12.gz43_222427
M00056269D:H01	ES 182	639003	1753.I03.gz43_222284

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CloneID	ES No	ClusterID	SequenceName
M00056270A:B09	ES 182	647828	1753.I06.gz43_222332
M00056270B:F02	ES 182	557857	1753.I12.gz43_222428
M00056271A:G04	ES 182	466894	1753.I24.gz43_222620
M00056271C:C06	ES 182	528162	1753.J04.gz43_222301
M00056272D:C03	ES 182	642812	1753.J22.gz43_222589
M00056273A:A07	ES 182	642200	1753.K02.gz43_222270
M00056274D:E08	ES 182	476380	1753.L06.gz43_222335
M00056276A:D05	ES 182	580179	1753.M10.gz43_222400
M00056276A:F05	ES 182	648442	1753.M14.gz43_222464
M00056276D:B12	ES 182	507066	1753.M17.gz43_222512
M00056277B:G05	ES 182	648609	1753.N05.gz43_222321
M00056279B:G06	ES 182	649592	1753.O18.gz43_222530
M00056280B:E09	ES 182	649349	1753.P13.gz43_222451
M00056280D:C06	ES 182	509202	1753.P23.gz43_222611
M00056284C:A11	ES 182	556497	1754.C23.gz43_222982
M00056285B:B01	ES 182	647839	1754.D07.gz43_222727
M00056286A:A12	ES 182	644829	1754.D20.gz43_222935
M00056286B:A04	ES 182	559857	1754.D24.gz43_222999
M00056286C:H08	ES 182	554276	1754.E10.gz43_222776
M00056287C:H08	ES 182	647462	1754.E21.gz43_222952
M00056288A:E12	ES 182	446732	1754.E23.gz43_222984
M00056288D:D03	ES 182	647759	1754.F11.gz43_222793
M00056289B:E05	ES 182	555998	1754.F20.gz43_222937
M00056289B:F09	ES 182	648524	1754.F21.gz43_222953
M00056291B:G01	ES 182	646060	1754.H12.gz43_222811
M00056291C:C11	ES 182	598471	1754.H19.gz43_222923
M00056292D:C06	ES 182	644862	1754.I07.gz43_222732
M00056293B:F02	ES 182	449882	1754.I19.gz43_222924
M00056294B:G06	ES 182	419801	1754.J20.gz43_222941
M00056295C:F12	ES 182	492587	1754.K07.gz43_222734
M00056296A:A07	ES 182	646387	1754.K12.gz43_222814
M00056297D:B10	ES 182	467709	1754.L23.gz43_222991
M00056298A:H02	ES 182	651057	1754.M07.gz43_222736
M00056298B:F10	ES 182	639804	1754.M12.gz43_222816
M00056298D:G01	ES 182	462865	1754.M22.gz43_222976
M00056299C:F06	ES 182	643984	1754.N10.gz43_222785
M00056299D:A02	ES 182	462986	1754.N12.gz43_222817
M00056300A:E06	ES 182	485480	1754.N22.gz43_222977
M00056300B:A11	ES 182	651115	1754.N24.gz43_223009
M00056301C:H08	ES 182	645844	1754.O22.gz43_222978
M00056302D:E12	ES 182	644836	1754.P22.gz43_222979
M00056303A:B03	ES 182	462398	1754.P23.gz43_222995
M00056304A:H04	ES 182	467364	1755.A17.gz43_223268
M00056304B:C05	ES 182	648683	1755.A18.gz43_223284

Table 13

CloneID	ES No	ClusterID	SequenceName
M00056304C:C03	ES 182	645073	1755.A23.gz43_223364
M00056305A:A02	ES 182	524261	1755.B06.gz43_223093
M00056305B:F09	ES 182	644880	1755.B14.gz43_223221
M00056305D:C05	ES 182	463595	1755.B20.gz43_223317
M00056305D:E08	ES 182	641681	1755.B22.gz43_223349
M00056307A:F07	ES 182	644660	1755.D05.gz43_223079
M00056307D:G02	ES 182	642145	1755.D17.gz43_223271
M00056308A:C01	ES 182	650639	1755.D20.gz43_223319
M00056308C:C12	ES 182	469802	1755.E12.gz43_223192
M00056310A:C10	ES 182	557052	1755.E15.gz43_223240
M00056310B:E06	ES 182	649514	1755.E22.gz43_223352
M00056311C:G06	ES 182	558879	1755.G04.gz43_223066
M00056313A:B06	ES 182	44503	1755.H16.gz43_223259
M00056319A:A11	ES 182	635062	1755.I11.gz43_223180
M00056320C:E08	ES 182	556444	1755.K06.gz43_223102
M00056320D:F07	ES 182	642260	1755.K10.gz43_223166
M00056323A:C09	ES 182	647951	1755.K13.gz43_223214
M00056323A:G03	ES 182	569195	1755.K15.gz43_223246
M00056323A:H05	ES 182	550403	1755.K16.gz43_223262
M00056326C:G07	ES 182	639378	1755.M08.gz43_223136
M00056328B:E07	ES 182	444222	1755.M16.gz43_223264
M00056328D:B01	ES 182	447126	1755.M19.gz43_223312
M00056329C:B09	ES 182	647248	1755.N05.gz43_223089
M00056330B:C02	ES 182	452075	1755.N14.gz43_223233
M00056333A:E09	ES 182	460929	1755.O09.gz43_223154
M00056333C:D08	ES 182	446520	1755.O23.gz43_223378
M00056338B:B08	ES 182	606129	1755.P24.gz43_223395
M00042751B:C07	ES 183	179760	1767.A07.gz43_224579
M00042751D:D03	ES 183	449215	1767.A14.gz43_224691
M00042751D:F09	ES 183	484355	1767.A16.gz43_224723
M00042751D:G06	ES 183	485431	1767.A18.gz43_224755
M00042751D:G09	ES 183	485441	1767.A19.gz43_224771
M00042752A:B04	ES 183	449275	1767.A20.gz43_224787
M00042753B:C08	ES 183	480960	1767.B13.gz43_224676
M00042753C:G12	ES 183	485183	1767.B19.gz43_224772
M00042753D:A12	ES 183	479061	1767.B20.gz43_224788
M00042753D:H11	ES 183	449746	1767.B23.gz43_224836
M00042754B:G02	ES 183	485512	1767.C02.gz43_224501
M00042755A:D09	ES 183	481614	1767.C06.gz43_224565
M00042755A:H04	ES 183	485880	1767.C10.gz43_224629
M00042755B:D01	ES 183	481594	1767.C12.gz43_224661
M00042755B:D09	ES 183	449399	1767.C13.gz43_224677
M00042755B:H04	ES 183	485882	1767.C16.gz43_224725

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CloneID	ES No	ClusterID	SequenceName
M00042755B:H11	ES 183	485907	1767.C17.gz43_224741
M00042755C:A10	ES 183	452104	1767.C19.gz43_224773
M00042756B:B01	ES 183	284586	1767.D03.gz43_224518
M00042757A:H07	ES 183	449076	1767.D15.gz43_224710
M00042758B:C06	ES 183	448325	1767.D23.gz43_224838
M00042758B:G04	ES 183	476876	1767.D24.gz43_224854
M00042760A:G12	ES 183	477098	1767.E15.gz43_224711
M00042760B:E12	ES 183	453024	1767.E18.gz43_224759
M00042760C:F10	ES 183	476438	1767.E22.gz43_224823
M00042761B:C11	ES 183	473592	1767.F04.gz43_224536
M00042761B:E05	ES 183	475562	1767.F08.gz43_224600
M00042761C:G11	ES 183	477521	1767.F12.gz43_224664
M00042761D:D12	ES 183	474580	1767.F17.gz43_224744
M00042762A:G02	ES 183	455143	1767.F22.gz43_224824
M00042763B:A03	ES 183	470801	1767.G09.gz43_224617
M00042764A:F12	ES 183	448801	1767.G22.gz43_224825
M00042764B:B10	ES 183	453606	1767.H01.gz43_224490
M00042764B:G10	ES 183	448865	1767.H04.gz43_224538
M00042764C:B10	ES 183	448251	1767.H05.gz43_224554
M00042766A:D07	ES 183	128749	1767.I04.gz43_224539
M00042766B:G11	ES 183	484633	1767.I08.gz43_224603
M00042766D:C05	ES 183	450551	1767.I14.gz43_224699
M00042767A:B10	ES 183	479880	1767.I18.gz43_224763
M00042767B:E10	ES 183	482868	1767.I21.gz43_224811
M00042767B:G04	ES 183	484964	1767.I22.gz43_224827
M00042767B:G09	ES 183	484987	1767.I23.gz43_224843
M00042767D:D02	ES 183	449437	1767.J05.gz43_224556
M00042768A:H09	ES 183	486452	1767.J09.gz43_224620
M00042768B:F02	ES 183	456513	1767.J11.gz43_224652
M00042768C:E06	ES 183	482486	1767.J15.gz43_224716
M00042769B:E12	ES 183	482876	1767.K05.gz43_224557
M00042769C:B01	ES 183	479851	1767.K08.gz43_224605
M00042769C:B06	ES 183	479868	1767.K09.gz43_224621
M00042770A:D02	ES 183	449438	1767.K15.gz43_224717
M00042771B:G05	ES 183	485073	1767.L12.gz43_224670
M00042771D:F02	ES 183	449592	1767.L16.gz43_224734
M00042772C:C12	ES 183	447218	1767.L20.gz43_224798
M00042773A:G07	ES 183	485086	1767.M02.gz43_224511
M00042773A:H11	ES 183	449689	1767.M03.gz43_224527
M00042773B:H08	ES 183	486547	1767.M06.gz43_224575
M00042774B:C01	ES 183	481057	1767.M14.gz43_224703
M00042774C:B09	ES 183	449261	1767.M16.gz43_224735
M00042775B:C09	ES 183	480703	1767.N04.gz43_224544
M00042776D:D01	ES 183	448152	1767.N17.gz43_224752

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CloneID	ES No	ClusterID	SequenceName
M00042776D:G10	ES 183	477399	1767.N18.gz43_224768
M00042777A:B10	ES 183	472119	1767.N20.gz43_224800
M00042777B:B05	ES 183	472101	1767.O02.gz43_224513
M00042777B:H02	ES 183	449015	1767.O03.gz43_224529
M00042778A:C04	ES 183	473433	1767.O11.gz43_224657
M00042778A:G07	ES 183	477387	1767.O12.gz43_224673
M00042778B:B07	ES 183	448260	1767.O15.gz43_224721
M00042778D:F11	ES 183	475797	1767.O23.gz43_224849
M00042779A:B04	ES 183	472425	1767.O24.gz43_224865
M00042779D:D04	ES 183	453385	1767.P15.gz43_224722
M00042779D:E06	ES 183	474823	1767.P17.gz43_224754
M00042780A:H05	ES 183	477757	1767.P24.gz43_224866
M00042809D:C12	ES 183	649735	1777.A23.gz43_252199
M00042809D:G09	ES 183	557375	1777.B01.gz43_251848
M00042811A:A01	ES 183	500896	1777.B23.gz43_252200
M00042811C:B06	ES 183	537506	1777.C03.gz43_251881
M00042812B:C01	ES 183	456793	1777.C11.gz43_252009
M00042815C:C02	ES 183	448340	1777.E11.gz43_252011
M00042815C:F10	ES 183	448793	1777.E13.gz43_252043
M00042816A:C09	ES 183	735534	1777.E17.gz43_252107
M00042816A:G04	ES 183	639163	1777.E21.gz43_252171
M00042816B:C08	ES 183	545162	1777.F03.gz43_251884
M00042817C:B04	ES 183	727517	1777.G05.gz43_251917
M00042819C:H02	ES 183	449718	1777.H14.gz43_252062
M00042821C:H06	ES 183	485653	1777.I17.gz43_252111
M00042824A:C02	ES 183	52034	1777.K05.gz43_251921
M00042825A:B05	ES 183	449258	1777.K17.gz43_252113
M00042828D:B11	ES 183	472400	1777.M09.gz43_251987
M00042831A:F12	ES 183	484207	1777.N18.gz43_252132
M00042831D:G06	ES 183	484669	1777.O01.gz43_251861
M00042833C:G05	ES 183	485020	1777.O18.gz43_252133
M00042835D:C04	ES 183	450883	1777.P19.gz43_252150
M00042836A:B12	ES 183	480227	1777.P24.gz43_252230
M00042836D:C07	ES 183	449291	1778.A11.gz43_225411
M00042838A:E02	ES 183	475111	1778.B02.gz43_225268
M00042839B:F05	ES 183	475942	1778.B23.gz43_225604
M00042839D:F02	ES 183	476256	1778.C07.gz43_225349
M00042840B:F08	ES 183	452202	1778.C12.gz43_225429
M00042840C:B12	ES 183	447517	1778.C14.gz43_225461
M00042841B:H05	ES 183	450673	1778.C18.gz43_225525
M00042841D:G10	ES 183	446657	1778.C23.gz43_225605
M00042842A:B04	ES 183	472307	1778.C24.gz43_225621
M00042842A:B12	ES 183	448233	1778.D01.gz43_225254
M00042842C:H11	ES 183	477555	1778.D12.gz43_225430

Table 13

CloneID	ES No	ClusterID	SequenceName
M00042843A:E07	ES 183	474597	1778.D18.gz43_225526
M00042843B:F05	ES 183	453856	1778.D22.gz43_225590
M00042844A:D02	ES 183	447983	1778.E07.gz43_225351
M00042844C:B03	ES 183	448230	1778.E12.gz43_225431
M00042844C:C12	ES 183	448383	1778.E14.gz43_225463
M00042844D:H02	ES 183	477593	1778.E18.gz43_225527
M00042845A:B05	ES 183	448104	1778.E19.gz43_225543
M00042845C:A09	ES 183	447983	1778.F03.gz43_225288
M00042846C:D09	ES 183	639991	1778.F23.gz43_225608
M00042847A:F04	ES 183	727875	1778.G10.gz43_225401
M00042848D:G12	ES 183	448029	1778.H06.gz43_225338
M00042849B:G06	ES 183	485029	1778.H12.gz43_225434
M00042850A:B11	ES 183	404603	1778.H20.gz43_225562
M00042850C:C10	ES 183	646583	1778.I06.gz43_225339
M00042851A:B08	ES 183	449273	1778.I11.gz43_225419
M00042851A:E11	ES 183	483274	1778.I12.gz43_225435
M00042851D:B08	ES 183	452990	1778.I18.gz43_225531
M00042852B:C06	ES 183	480900	1778.J04.gz43_225308
M00042852D:G07	ES 183	485480	1778.J10.gz43_225404
M00042853A:G03	ES 183	644190	1778.J12.gz43_225436
M00042854A:B11	ES 183	551811	1778.K04.gz43_225309
M00042854A:D05	ES 183	725641	1778.K07.gz43_225357
M00042854B:F05	ES 183	725266	1778.K12.gz43_225437
M00042854D:A05	ES 183	482071	1778.K16.gz43_225501
M00042855B:H06	ES 183	485841	1778.L05.gz43_225326
M00042855C:G11	ES 183	484789	1778.L08.gz43_225374
M00042855D:A12	ES 183	449110	1778.L09.gz43_225390
M00042855D:B12	ES 183	480005	1778.L12.gz43_225438
M00042855D:D06	ES 183	456737	1778.L14.gz43_225470
M00042857C:G04	ES 183	449652	1778.M11.gz43_225423
M00042857C:G05	ES 183	484841	1778.M12.gz43_225439
M00042858A:A08	ES 183	479084	1778.M14.gz43_225471
M00042859B:D06	ES 183	449403	1778.N02.gz43_225280
M00042859D:D12	ES 183	481664	1778.N11.gz43_225424
M00042860A:C01	ES 183	480641	1778.N12.gz43_225440
M00042860A:H04	ES 183	485924	1778.N16.gz43_225504
M00042860C:E02	ES 183	483066	1778.N23.gz43_225616
M00042860D:F02	ES 183	449604	1778.O02.gz43_225281
M00042860D:F05	ES 183	484091	1778.O03.gz43_225297
M00042860D:H10	ES 183	449751	1778.O06.gz43_225345
M00042861A:F04	ES 183	451368	1778.O09.gz43_225393
M00042861C:C03	ES 183	481319	1778.O13.gz43_225457
M00042861C:F07	ES 183	484468	1778.O15.gz43_225489
M00042861D:D09	ES 183	449407	1778.O18.gz43_225537

Table 13

CloneID	ES No	ClusterID	SequenceName
M00042862A:C01	ES 183	480640	1778.O23.gz43_225617
M00042862C:E02	ES 183	449521	1778.P09.gz43_225394
M00056352D:B04	ES 183	559486	1780.A05.gz43_226083
M00056352D:H02	ES 183	594994	1780.A10.gz43_226163
M00056353C:E12	ES 183	736210	1780.B04.gz43_226068
M00056353D:D10	ES 183	731925	1780.B11.gz43_226180
M00056355A:C10	ES 183	463966	1780.C10.gz43_226165
M00056355B:D02	ES 183	557029	1780.C16.gz43_226261
M00056355C:A05	ES 183	553951	1780.C18.gz43_226293
M00056355D:A05	ES 183	727129	1780.D07.gz43_226118
M00056355D:B08	ES 183	468467	1780.D09.gz43_226150
M00056355D:G04	ES 183	727235	1780.D11.gz43_226182
M00056356C:H07	ES 183	732150	1780.E02.gz43_226039
M00056357A:C08	ES 183	551167	1780.E10.gz43_226167
M00056357C:C06	ES 183	724039	1780.E23.gz43_226375
M00056358A:A10	ES 183	723859	1780.F10.gz43_226168
M00056358A:G05	ES 183	734150	1780.F12.gz43_226200
M00056358D:A06	ES 183	465697	1780.F22.gz43_226360
M00056359A:C08	ES 183	623978	1780.G05.gz43_226089
M00056359A:F06	ES 183	416326	1780.G06.gz43_226105
M00056360A:D11	ES 183	561719	1780.H08.gz43_226138
M00056360B:D09	ES 183	528981	1780.H12.gz43_226202
M00056360C:A03	ES 183	723869	1780.H14.gz43_226234
M00056360C:B01	ES 183	480005	1780.H15.gz43_226250
M00056360D:H10	ES 183	732144	1780.H23.gz43_226378
M00056361A:C01	ES 183	733806	1780.I01.gz43_226027
M00056361A:H06	ES 183	600856	1780.I05.gz43_226091
M00056361B:E02	ES 183	471646	1780.I10.gz43_226171
M00056361C:C06	ES 183	135364	1780.I12.gz43_226203
M00056362C:C02	ES 183	511606	1780.J12.gz43_226204
M00056363A:C06	ES 183	724907	1780.K02.gz43_226045
M00056363A:E10	ES 183	364334	1780.K05.gz43_226093
M00056363C:C12	ES 183	552891	1780.K14.gz43_226237
M00056363D:H03	ES 183	728774	1780.K22.gz43_226365
M00056364A:B04	ES 183	724792	1780.L02.gz43_226046
M00056364C:B01	ES 183	503862	1780.L08.gz43_226142
M00056364C:H08	ES 183	588959	1780.L15.gz43_226254
M00056364D:C05	ES 183	553244	1780.L17.gz43_226286
M00056365B:G10	ES 183	480924	1780.M11.gz43_226191
M00056366B:A11	ES 183	449242	1780.N05.gz43_226096
M00056367C:D06	ES 183	560859	1780.O07.gz43_226129
M00056367C:H05	ES 183	642558	1780.O12.gz43_226209
M00056368A:C11	ES 183	456535	1780.O20.gz43_226337
M00056368B:H09	ES 183	661194	1780.P05.gz43_226098

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CloneID	ES No	ClusterID	SequenceName
M00056368C:E07	ES 184	482831	1780.P07.gz43_226130
M00056368D:D03	ES 184	517298	1780.P11.gz43_226194
M00056368D:G05	ES 184	730301	1780.P14.gz43_226242
M00056369A:G06	ES 184	728389	1780.P22.gz43_226370
M00056369B:E03	ES 184	736001	1789.A03.gz43_226435
M00056370B:C10	ES 184	734646	1789.B02.gz43_226420
M00056370B:E07	ES 184	568484	1789.B04.gz43_226452
M00056370C:F01	ES 184	503625	1789.B08.gz43_226516
M00056370D:C06	ES 184	735649	1789.B11.gz43_226564
M00056371D:F07	ES 184	734943	1789.C12.gz43_226581
M00056372C:C06	ES 184	725389	1789.D04.gz43_226454
M00056373D:G01	ES 184	725381	1789.E09.gz43_226535
M00056374C:G08	ES 184	487079	1789.F03.gz43_226440
M00056375A:D11	ES 184	734348	1789.F11.gz43_226568
M00056375D:D12	ES 184	724257	1789.G01.gz43_226409
M00056376A:C10	ES 184	649411	1789.G09.gz43_226537
M00056377A:C01	ES 184	460284	1789.H03.gz43_226442
M00056377C:A01	ES 184	724694	1789.H12.gz43_226586
M00056377D:F08	ES 184	725274	1789.I03.gz43_226443
M00056378C:E10	ES 184	729993	1789.I09.gz43_226539
M00056382A:A12	ES 184	723972	1789.J12.gz43_226588
M00056382C:B11	ES 184	503491	1789.K03.gz43_226445
M00056382C:F11	ES 184	731542	1789.K05.gz43_226477
M00056383B:F08	ES 184	725321	1789.L04.gz43_226462
M00056383B:G08	ES 184	725448	1789.L06.gz43_226494
M00056383C:E07	ES 184	549790	1789.L07.gz43_226510
M00056384C:H04	ES 184	474346	1789.M01.gz43_226415
M00056384D:A04	ES 184	186372	1789.M02.gz43_226431
M00056385A:A07	ES 184	727523	1789.M10.gz43_226559
M00056386A:F08	ES 184	726636	1789.N01.gz43_226416
M00056386A:F09	ES 184	724388	1789.N02.gz43_226432
M00056386A:G01	ES 184	553035	1789.N03.gz43_226448
M00056386B:A07	ES 184	452806	1789.N06.gz43_226496
M00056386B:A11	ES 184	730660	1789.N07.gz43_226512
M00056386B:D07	ES 184	459918	1789.N10.gz43_226560
M00056386B:E09	ES 184	623408	1789.N12.gz43_226592
M00056387C:D01	ES 184	558412	1789.O11.gz43_226577
M00056388B:A05	ES 184	475682	1789.P01.gz43_226418
M00056388B:B03	ES 184	724009	1789.P03.gz43_226450
M00056389B:H03	ES 184	729637	1790.A10.gz43_226931
M00056389D:F01	ES 184	495712	1790.A17.gz43_227043
M00056390B:E10	ES 184	725165	1790.B08.gz43_226900
M00056390C:B08	ES 184	556769	1790.B11.gz43_226948

Table 13

CloneID	ES No	ClusterID	SequenceName
M00056390C:C04	ES 184	724914	1790.B12.gz43_226964
M00056391C:H12	ES 184	727150	1790.C14.gz43_226997
M00056391D:E06	ES 184	457508	1790.C18.gz43_227061
M00056392A:D11	ES 184	477296	1790.C19.gz43_227077
M00056392A:F06	ES 184	448817	1790.C20.gz43_227093
M00056392D:C05	ES 184	426297	1790.D07.gz43_226886
M00056392D:H02	ES 184	729111	1790.D08.gz43_226902
M00056393A:F01	ES 184	549480	1790.D11.gz43_226950
M00056393A:G06	ES 184	614463	1790.D12.gz43_226966
M00056393D:A09	ES 184	558794	1790.D21.gz43_227110
M00056393D:C12	ES 184	118514	1790.D24.gz43_227158
M00056394B:C11	ES 184	503173	1790.E14.gz43_226999
M00056394B:G05	ES 184	725454	1790.E19.gz43_227079
M00056394C:D07	ES 184	640158	1790.F01.gz43_226792
M00056395C:H03	ES 184	523364	1790.F23.gz43_227144
M00056395D:B01	ES 184	732821	1790.F24.gz43_227160
M00056396A:D03	ES 184	733563	1790.G08.gz43_226905
M00056396A:G10	ES 184	474981	1790.G12.gz43_226969
M00056396B:E10	ES 184	642985	1790.G16.gz43_227033
M00056396D:H01	ES 184	484934	1790.H05.gz43_226858
M00056397C:A09	ES 184	515038	1790.H17.gz43_227050
M00056398A:B10	ES 184	724851	1790.I11.gz43_226955
M00056398C:B09	ES 184	735396	1790.I24.gz43_227163
M00056398C:D10	ES 184	725095	1790.J02.gz43_226812
M00056399B:G09	ES 184	448758	1790.J15.gz43_227020
M00056399D:C11	ES 184	656268	1790.K04.gz43_226845
M00056400A:D08	ES 184	726494	1790.K10.gz43_226941
M00056400A:G10	ES 184	725451	1790.K16.gz43_227037
M00056400C:B11	ES 184	447222	1790.K24.gz43_227165
M00056400C:G04	ES 184	479851	1790.L03.gz43_226830
M00056401A:F09	ES 184	729950	1790.L12.gz43_226974
M00056401B:B01	ES 184	735234	1790.L15.gz43_227022
M00056402B:D07	ES 184	641576	1790.M06.gz43_226879
M00056402C:B09	ES 184	649591	1790.M07.gz43_226895
M00056402C:E10	ES 184	483008	1790.M09.gz43_226927
M00056402D:A01	ES 184	724714	1790.M10.gz43_226943
M00056402D:B07	ES 184	197839	1790.M11.gz43_226959
M00056403A:E09	ES 184	417549	1790.M18.gz43_227071
M00056403B:D09	ES 184	468467	1790.M23.gz43_227151
M00056403B:G12	ES 184	729779	1790.M24.gz43_227167
M00056403C:F02	ES 184	481077	1790.N03.gz43_226832
M00056403C:F03	ES 184	724411	1790.N04.gz43_226848
M00056403C:F12	ES 184	640261	1790.N05.gz43_226864
M00056404A:G03	ES 184	640756	1790.N12.gz43_226976

Table 13

CloneID	ES No	ClusterID	SequenceName
M00056404B:B06	ES 184	188309	1790.N14.gz43_227008
M00056404C:C12	ES 184	733643	1790.N22.gz43_227136
M00056404D:G03	ES 184	562769	1790.O02.gz43_226817
M00056405C:C12	ES 184	724078	1790.O11.gz43_226961
M00056405C:H04	ES 184	449228	1790.O13.gz43_226993
M00056405D:E05	ES 184	730948	1790.O17.gz43_227057
M00056406A:C02	ES 184	726411	1790.O20.gz43_227105
M00056406A:E01	ES 184	728454	1790.O23.gz43_227153
M00056406B:C05	ES 184	456577	1790.P03.gz43_226834
M00056406C:D09	ES 184	543323	1790.P10.gz43_226946
M00056406C:F12	ES 184	423420	1790.P13.gz43_226994
M00056407A:D10	ES 184	483147	1790.P15.gz43_227026
M00056407A:G03	ES 184	729809	1790.P16.gz43_227042
M00056409A:C03	ES 184	641687	1790.P21.gz43_227122
M00056409A:D03	ES 184	470462	1790.P23.gz43_227154
M00056409A:D06	ES 184	727633	1790.P24.gz43_227170
M00056409B:C12	ES 184	729784	1791.A03.gz43_227203
M00056409B:E07	ES 184	734253	1791.A05.gz43_227235
M00056409C:B04	ES 184	711493	1791.A06.gz43_227251
M00056410A:A04	ES 184	640744	1791.A19.gz43_227459
M00056410B:A09	ES 184	641383	1791.A23.gz43_227523
M00056410D:H03	ES 184	49703	1791.B14.gz43_227380
M00056411A:H06	ES 184	558049	1791.B17.gz43_227428
M00056411B:D01	ES 184	703978	1791.B19.gz43_227460
M00056412B:B08	ES 184	724773	1791.C22.gz43_227509
M00056413B:D07	ES 184	642637	1791.D18.gz43_227446
M00056413C:B06	ES 184	723951	1791.D24.gz43_227542
M00056414C:H08	ES 184	729899	1791.E18.gz43_227447
M00056415A:D03	ES 184	475797	1791.F01.gz43_227176
M00056415B:B10	ES 184	402471	1791.F03.gz43_227208
M00056416B:B11	ES 184	648170	1791.G01.gz43_227177
M00056416B:C09	ES 184	456544	1791.G02.gz43_227193
M00056416B:H01	ES 184	727090	1791.G04.gz43_227225
M00056416D:C08	ES 184	729199	1791.G12.gz43_227353
M00056416D:D12	ES 184	435349	1791.G13.gz43_227369
M00056416D:H10	ES 184	728986	1791.G18.gz43_227449
M00056417A:E08	ES 184	733484	1791.G23.gz43_227529
M00056417B:D05	ES 184	642170	1791.H05.gz43_227242
M00056417C:G10	ES 184	725408	1791.H14.gz43_227386
M00056417D:G09	ES 184	725407	1791.H20.gz43_227482
M00056418A:G01	ES 184	729579	1791.H24.gz43_227546
M00056418A:G09	ES 184	472684	1791.I01.gz43_227179
M00056419A:F08	ES 184	542957	1791.J07.gz43_227276
M00056419D:D02	ES 184	728440	1791.J24.gz43_227548

Table 13

CloneID	ES No	ClusterID	SequenceName
M00056419D:G04	ES 184	453762	1791.K03.gz43_227213
M00056420A:C01	ES 184	560957	1791.K04.gz43_227229
M00056420A:C12	ES 184	128749	1791.K05.gz43_227245
M00056420A:E09	ES 184	643646	1791.K07.gz43_227277
M00056420A:G11	ES 184	731390	1791.K10.gz43_227325
M00056420B:G05	ES 184	480377	1791.K12.gz43_227357
M00056420C:E08	ES 184	736507	1791.K21.gz43_227501
M00056420D:A09	ES 184	562581	1791.K23.gz43_227533
M00056421A:F12	ES 184	646146	1791.L05.gz43_227246
M00056421C:E06	ES 184	562137	1791.L11.gz43_227342
M00056421C:E12	ES 184	730178	1791.L12.gz43_227358
M00056421C:H01	ES 184	500253	1791.L14.gz43_227390
M00056422A:C12	ES 184	737019	1791.L22.gz43_227518
M00056422A:F07	ES 184	498194	1791.L24.gz43_227550
M00056422B:A08	ES 184	511149	1791.M03.gz43_227215
M00056422B:C12	ES 184	727845	1791.M04.gz43_227231
M00056422C:B10	ES 184	474965	1791.M15.gz43_227407
M00056422D:D10	ES 184	732987	1791.M22.gz43_227519
M00056423B:A12	ES 184	650437	1791.N06.gz43_227264
M00056423C:G05	ES 184	644723	1791.N14.gz43_227392
M00056423C:H03	ES 184	651053	1791.N15.gz43_227408
M00056423D:B06	ES 184	724024	1791.N17.gz43_227440
M00056423D:F10	ES 184	288134	1791.N24.gz43_227552
M00056423D:H07	ES 184	477718	1791.O02.gz43_227201
M00056424A:F05	ES 184	733490	1791.O08.gz43_227297
M00056424A:F12	ES 184	649722	1791.O09.gz43_227313
M00056424B:A11	ES 184	736893	1791.O13.gz43_227377
M00056424C:B10	ES 184	725408	1791.O19.gz43_227473
M00056424C:F02	ES 184	555359	1791.O21.gz43_227505
M00056424C:H04	ES 184	437450	1791.O24.gz43_227553
M00056424D:C08	ES 184	736632	1791.P05.gz43_227250
M00056424D:C12	ES 184	674574	1791.P06.gz43_227266
M00056425B:B02	ES 184	723963	1791.P13.gz43_227378
M00056425D:D08	ES 184	724220	1791.P22.gz43_227522
M00056425D:H01	ES 184	726768	1791.P23.gz43_227538
M00056426B:G12	ES 184	731158	1792.A09.gz43_227695
M00056426C:G05	ES 184	452981	1792.A11.gz43_227727
M00056427C:E06	ES 184	732827	1792.A21.gz43_227887
M00056428A:F10	ES 184	592186	1792.B09.gz43_227696
M00056428B:B01	ES 184	710362	1792.B11.gz43_227728
M00056429D:E02	ES 184	480005	1792.C11.gz43_227729
M00056432A:A01	ES 184	556115	1792.D06.gz43_227650
M00056432A:C08	ES 184	472073	1792.D08.gz43_227682
M00056433B:A09	ES 184	724400	1792.E03.gz43_227603

Table 13

CloneID	ES No	ClusterID	SequenceName
M00056433D:A09	ES 184	554398	1792.E12.gz43_227747
M00056433D:D08	ES 184	570928	1792.E14.gz43_227779
M00056434C:B01	ES 184	734287	1792.F06.gz43_227652
M00056435B:E06	ES 184	455972	1792.F20.gz43_227876
M00056435C:D04	ES 184	492089	1792.F22.gz43_227908
M00056476C:E05	ES 184	725238	1792.G10.gz43_227717
M00056476D:H11	ES 184	647375	1792.G16.gz43_227813
M00056477A:B11	ES 184	736751	1792.G17.gz43_227829
M00056477C:G09	ES 184	725454	1792.H12.gz43_227750
M00056478C:H01	ES 184	725584	1792.I07.gz43_227671
M00056478D:G02	ES 184	729584	1792.I12.gz43_227751
M00056479C:E04	ES 184	645476	1792.J05.gz43_227640
M00056480B:D06	ES 184	482461	1792.K02.gz43_227593
M00056481A:F02	ES 184	734646	1792.K19.gz43_227865
M00056482B:B11	ES 184	481594	1792.L18.gz43_227850
M00056482B:C09	ES 184	453713	1792.L20.gz43_227882
M00056482B:H02	ES 184	466795	1792.L22.gz43_227914
M00056483A:F10	ES 185	452618	1792.M09.gz43_227707
M00056483B:E04	ES 185	724183	1792.M13.gz43_227771
M00056483B:F04	ES 185	724390	1792.M14.gz43_227787
M00056483C:D06	ES 185	724183	1792.M20.gz43_227883
M00056483D:F06	ES 185	730282	1792.M24.gz43_227947
M00056484B:E11	ES 185	725210	1792.N12.gz43_227756
M00056484D:D01	ES 185	675299	1792.N18.gz43_227852
M00056484D:G08	ES 185	650940	1792.N21.gz43_227900
M00056485B:D11	ES 185	451404	1792.O04.gz43_227629
M00056486A:C12	ES 185	477296	1792.O16.gz43_227821
M00056486B:G02	ES 185	553983	1792.P01.gz43_227582
M00056486C:F04	ES 185	717743	1792.P05.gz43_227646
M00056486D:A12	ES 185	725006	1792.P07.gz43_227678
M00056486D:F04	ES 185	727948	1792.P10.gz43_227726
M00056487A:C10	ES 185	471931	1792.P11.gz43_227742
M00056487A:D01	ES 185	462687	1792.P12.gz43_227758
M00056487A:F05	ES 185	725348	1792.P17.gz43_227838
M00056487C:E03	ES 185	731820	1801.A04.gz43_227999
M00056487C:E04	ES 185	449291	1801.A05.gz43_228015
M00056488B:E04	ES 185	462266	1801.B03.gz43_227984
M00056488B:G10	ES 185	725434	1801.B05.gz43_228016
M00056488B:H04	ES 185	429191	1801.B06.gz43_228032
M00056491B:B09	ES 185	733006	1801.D01.gz43_227954
M00056491B:E02	ES 185	447785	1801.D02.gz43_227970
M00056491B:G05	ES 185	472485	1801.D04.gz43_228002
M00056491B:G08	ES 185	446191	1801.D05.gz43_228018

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CloneID	ES No	ClusterID	SequenceName
M00056492B:D06	ES 185	446928	1801.E04.gz43_228003
M00056495A:A07	ES 185	447658	1801.G03.gz43_227989
M00056495A:C02	ES 185	460690	1801.G05.gz43_228021
M00056496D:B12	ES 185	733151	1801.I01.gz43_227959
M00056496D:G03	ES 185	649202	1801.I05.gz43_228023
M00056497C:D05	ES 185	734261	1801.J01.gz43_227960
M00056497C:E01	ES 185	523753	1801.J02.gz43_227976
M00056497D:C11	ES 185	611604	1801.J05.gz43_228024
M00056498D:C01	ES 185	514142	1801.K01.gz43_227961
M00056499A:A04	ES 185	635951	1801.K03.gz43_227993
M00056499A:B10	ES 185	447002	1801.K05.gz43_228025
M00056500A:G12	ES 185	635951	1801.L05.gz43_228026
M00056501B:B09	ES 185	471232	1801.M01.gz43_227963
M00056501B:C07	ES 185	451383	1801.M02.gz43_227979
M00056503B:G11	ES 185	640116	1801.O06.gz43_228045
M00056504B:B01	ES 185	732598	1801.P04.gz43_228014
M00056504B:C03	ES 185	736665	1801.P05.gz43_228030
M00056567A:H06	ES 185	727410	1813.A13.gz43_229679
M00056568C:D02	ES 185	454560	1813.B14.gz43_229696
M00056570A:D09	ES 185	548893	1813.C22.gz43_229825
M00056572A:A04	ES 185	736194	1813.E06.gz43_229571
M00056572C:E03	ES 185	458186	1813.E22.gz43_229827
M00056573C:B09	ES 185	554557	1813.F20.gz43_229796
M00056576A:A04	ES 185	734043	1813.H05.gz43_229558
M00056576A:E01	ES 185	475757	1813.H08.gz43_229606
M00056576C:G01	ES 185	513540	1813.H22.gz43_229830
M00056577A:F10	ES 185	508210	1813.I06.gz43_229575
M00056577D:F08	ES 185	733664	1813.I20.gz43_229799
M00056578A:B05	ES 185	725759	1813.I22.gz43_229831
M00056578D:A02	ES 185	729281	1813.J10.gz43_229640
M00056581D:A08	ES 185	465446	1813.L13.gz43_229690
M00056583C:A05	ES 185	511351	1813.M13.gz43_229691
M00056584C:A06	ES 185	733970	1813.N10.gz43_229644
M00056585C:C08	ES 185	727260	1813.O07.gz43_229597
M00056586B:D10	ES 185	461062	1813.O24.gz43_229869
M00056631D:F06	ES 185	730897	1816.A24.gz43_231007
M00056632C:E03	ES 185	736325	1816.B20.gz43_230944
M00056632C:H08	ES 185	726494	1816.B22.gz43_230976
M00056632D:E02	ES 185	727944	1816.B24.gz43_231008
M00056633D:E05	ES 185	726104	1816.C19.gz43_230929
M00056634A:C06	ES 185	736778	1816.C21.gz43_230961
M00056634A:G11	ES 185	726448	1816.C23.gz43_230993
M00056636C:H05	ES 185	482868	1816.E19.gz43_230931
M00056636D:F03	ES 185	559684	1816.E21.gz43_230963

Table 13

CloneID	ES No	ClusterID	SequenceName
M00056637A:C08	ES 185	647808	1816.E24.gz43_231011
M00056639A:E07	ES 185	500233	1816.G20.gz43_230949
M00056639A:F11	ES 185	419711	1816.G22.gz43_230981
M00056639A:H12	ES 185	215249	1816.G23.gz43_230997
M00056640C:C01	ES 185	196279	1816.H21.gz43_230966
M00056641C:G09	ES 185	727332	1816.I19.gz43_230935
M00056642D:C05	ES 185	726818	1816.J20.gz43_230952
M00056644C:B03	ES 185	727078	1816.K19.gz43_230937
M00056645D:E06	ES 185	727108	1816.L19.gz43_230938
M00056645D:E08	ES 185	727110	1816.L20.gz43_230954
M00056645D:G01	ES 185	659700	1816.L22.gz43_230986
M00056646A:B01	ES 185	733375	1816.L24.gz43_231018
M00056646D:E03	ES 185	724083	1816.M20.gz43_230955
M00056646D:F07	ES 185	735392	1816.M22.gz43_230987
M00056647A:F06	ES 185	730596	1816.M24.gz43_231019
M00056648A:H05	ES 185	481930	1816.N19.gz43_230940
M00056648B:C08	ES 185	724565	1816.N20.gz43_230956
M00056648B:E09	ES 185	735322	1816.N23.gz43_231004
M00056650A:E01	ES 185	207530	1816.O20.gz43_230957
M00056650B:C11	ES 185	727175	1816.O23.gz43_231005
M00056651B:E12	ES 185	731966	1816.P23.gz43_231006
M00056652B:E09	ES 185	728936	1825.A14.gz43_231231
M00056653D:E07	ES 185	462409	1825.B19.gz43_231312
M00056653D:F07	ES 185	730570	1825.B21.gz43_231344
M00056654A:A07	ES 185	736415	1825.B24.gz43_231392
M00056656A:E01	ES 185	727108	1825.D21.gz43_231346
M00056657A:F06	ES 185	477718	1825.E16.gz43_231267
M00056657C:B04	ES 185	554713	1825.E20.gz43_231331
M00056658A:E11	ES 185	484987	1825.F14.gz43_231236
M00056658B:C03	ES 185	552927	1825.F16.gz43_231268
M00056658C:B12	ES 185	463741	1825.F22.gz43_231364
M00056660B:B06	ES 185	646504	1825.H19.gz43_231318
M00056660B:G12	ES 185	562984	1825.H21.gz43_231350
M00056660C:A06	ES 185	729732	1825.H22.gz43_231366
M00056661D:D06	ES 185	447074	1825.I21.gz43_231351
M00056663A:B02	ES 185	719620	1825.J16.gz43_231272
M00056663A:H09	ES 185	729675	1825.J20.gz43_231336
M00056664A:F09	ES 185	537451	1825.K17.gz43_231289
M00056664D:H06	ES 185	448104	1825.L19.gz43_231322
M00056665A:G08	ES 185	727343	1825.L23.gz43_231386
M00056666A:C04	ES 185	481592	1825.M14.gz43_231243
M00056666A:D09	ES 185	726953	1825.M16.gz43_231275
M00056666A:D10	ES 185	650973	1825.M17.gz43_231291
M00056667A:A12	ES 185	725607	1825.N13.gz43_231228

Table 13

CloneID	ES No	ClusterID	SequenceName
M00056667B:E04	ES 185	725381	1825.N17.gz43_231292
M00056667C:H01	ES 185	476477	1825.N21.gz43_231356
M00056667D:E05	ES 185	732351	1825.N22.gz43_231372
M00056668D:E03	ES 185	735605	1825.O14.gz43_231245
M00056669B:E10	ES 185	554597	1825.O24.gz43_231405
M00056670A:G02	ES 185	45934	1825.P13.gz43_231230
M00056670B:A12	ES 185	734184	1825.P14.gz43_231246
M00056670B:G05	ES 185	478458	1825.P17.gz43_231294
M00056672A:E05	ES 185	723914	1826.A13.gz43_231599
M00056672D:B08	ES 185	726722	1826.A21.gz43_231727
M00056672D:E04	ES 185	546121	1826.A23.gz43_231759
M00056674D:E09	ES 185	734622	1826.C14.gz43_231617
M00056675A:C02	ES 185	446575	1826.C18.gz43_231681
M00056675A:G02	ES 185	513156	1826.C23.gz43_231761
M00056676B:G12	ES 185	641777	1826.D16.gz43_231650
M00056676C:B04	ES 185	725899	1826.D18.gz43_231682
M00056678A:B02	ES 185	482722	1826.E13.gz43_231603
M00056678A:H05	ES 185	43352	1826.E16.gz43_231651
M00056678B:E11	ES 185	734828	1826.E17.gz43_231667
M00056678B:H02	ES 185	736246	1826.E20.gz43_231715
M00056678B:H06	ES 185	725266	1826.E21.gz43_231731
M00056678C:A12	ES 185	730664	1826.E22.gz43_231747
M00056679C:F11	ES 185	736194	1826.F22.gz43_231748
M00056681A:E06	ES 185	729387	1826.G22.gz43_231749
M00056681B:A11	ES 185	728791	1826.G24.gz43_231781
M00056682A:F05	ES 185	447489	1826.H17.gz43_231670
M00056683B:H04	ES 185	645925	1826.I14.gz43_231623
M00056683C:H10	ES 185	644445	1826.I17.gz43_231671
M00056683C:H11	ES 185	728659	1826.I18.gz43_231687
M00056684B:B12	ES 185	559610	1826.I24.gz43_231783
M00056685A:H11	ES 185	517274	1826.J17.gz43_231672
M00056685B:G04	ES 185	473238	1826.J20.gz43_231720
M00056685C:G07	ES 185	729205	1826.J24.gz43_231784
M00056686D:D07	ES 185	733789	1826.K18.gz43_231689
M00056686D:E04	ES 185	730829	1826.K20.gz43_231721
M00056689B:F03	ES 185	492094	1826.M19.gz43_231707
M00056689C:F05	ES 185	729413	1826.M24.gz43_231787
M00056692A:A05	ES 185	492629	1826.O21.gz43_231741
M00056693B:D07	ES 185	727965	1827.A02.gz43_231807
M00056693B:D11	ES 185	580601	1827.A04.gz43_231839
M00056693B:H03	ES 185	573733	1827.A09.gz43_231919
M00056693C:D12	ES 185	727968	1827.A13.gz43_231983
M00056693C:G06	ES 185	617813	1827.A14.gz43_231999
M00056693D:B02	ES 185	425396	1827.A15.gz43_232015

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CloneID	ES No	ClusterID	SequenceName
M00056693D:E12	ES 185	475942	1827.A18.gz43_232063
M00056694A:C05	ES 185	553483	1827.A22.gz43_232127
M00056694A:G02	ES 185	479997	1827.B02.gz43_231808
M00056694A:G03	ES 185	693869	1827.B03.gz43_231824
M00056694A:G11	ES 185	493830	1827.B04.gz43_231840
M00056694B:H10	ES 185	730375	1827.B08.gz43_231904
M00056695A:H09	ES 185	449701	1827.B21.gz43_232112
M00056695C:C04	ES 185	561301	1827.C01.gz43_231793
M00056695C:H08	ES 185	540618	1827.C06.gz43_231873
M00056695D:E05	ES 185	472837	1827.C10.gz43_231937
M00056695D:F01	ES 185	735974	1827.C11.gz43_231953
M00056696A:G12	ES 185	650542	1827.C16.gz43_232033
M00056696B:B03	ES 185	727506	1827.C17.gz43_232049
M00056696B:H01	ES 185	551096	1827.C24.gz43_232161
M00056697A:D02	ES 185	588059	1827.D11.gz43_231954
M00056697A:G03	ES 185	395596	1827.D13.gz43_231986
M00056697A:H10	ES 185	725084	1827.D16.gz43_232034
M00056697C:D11	ES 185	727845	1827.D21.gz43_232114
M00056697C:H10	ES 185	728556	1827.E01.gz43_231795
M00056697D:B09	ES 185	724714	1827.E04.gz43_231843
M00056697D:C09	ES 185	501030	1827.E06.gz43_231875
M00056697D:C12	ES 185	462687	1827.E07.gz43_231891
M00056698A:A07	ES 185	530656	1827.E10.gz43_231939
M00056698B:E10	ES 185	540618	1827.E17.gz43_232051
M00056698D:E11	ES 185	737109	1827.F04.gz43_231844
M00056698D:G09	ES 185	477366	1827.F06.gz43_231876
M00056699A:C07	ES 185	454844	1827.F10.gz43_231940
M00056699A:D08	ES 185	452662	1827.F11.gz43_231956
M00056699A:E08	ES 185	672032	1827.F12.gz43_231972
M00056699B:A05	ES 185	730266	1827.F15.gz43_232020
M00056699B:G04	ES 185	641072	1827.F21.gz43_232116
M00056699C:C02	ES 185	727649	1827.F24.gz43_232164
M00056699C:F09	ES 185	728196	1827.G02.gz43_231813
M00056699C:G11	ES 185	395604	1827.G04.gz43_231845
M00056699D:C09	ES 186	567122	1827.G07.gz43_231893
M00056700A:F12	ES 186	728300	1827.G14.gz43_232005
M00056700A:G05	ES 186	446607	1827.G16.gz43_232037
M00056700B:D02	ES 186	727151	1827.G17.gz43_232053
M00056700D:H07	ES 186	732770	1827.H10.gz43_231942
M00056701A:A02	ES 186	496084	1827.H12.gz43_231974
M00056701A:G09	ES 186	734264	1827.H16.gz43_232038
M00056701B:D02	ES 186	631056	1827.H18.gz43_232070
M00056701B:D06	ES 186	724489	1827.H19.gz43_232086

Table 13

CloneID	ES No	ClusterID	SequenceName
M00056701C:F08	ES 186	728196	1827.H24.gz43_232166
M00056701C:G09	ES 186	640458	1827.I01.gz43_231799
M00056701D:C03	ES 186	644354	1827.I02.gz43_231815
M00056701D:D04	ES 186	727948	1827.I06.gz43_231879
M00056701D:G03	ES 186	553140	1827.I07.gz43_231895
M00056701D:G07	ES 186	724059	1827.I08.gz43_231911
M00056701D:H12	ES 186	550454	1827.I09.gz43_231927
M00056702C:A10	ES 186	735676	1827.I17.gz43_232055
M00056702C:H02	ES 186	448698	1827.I23.gz43_232151
M00056702D:G03	ES 186	735834	1827.J04.gz43_231848
M00056703A:G01	ES 186	651050	1827.J09.gz43_231928
M00056703B:A04	ES 186	447624	1827.J13.gz43_231992
M00056703B:D07	ES 186	560678	1827.J16.gz43_232040
M00056703C:F04	ES 186	650136	1827.K01.gz43_231801
M00056703D:F08	ES 186	649927	1827.K06.gz43_231881
M00056704A:B05	ES 186	403671	1827.K08.gz43_231913
M00056704A:H08	ES 186	728552	1827.K13.gz43_231993
M00056704B:C02	ES 186	727760	1827.K14.gz43_232009
M00056704C:C10	ES 186	451183	1827.K18.gz43_232073
M00056704D:H10	ES 186	288801	1827.L01.gz43_231802
M00056705A:B12	ES 186	553805	1827.L03.gz43_231834
M00056705A:D02	ES 186	726852	1827.L04.gz43_231850
M00056705B:A12	ES 186	728768	1827.L09.gz43_231930
M00056705B:D10	ES 186	83388	1827.L10.gz43_231946
M00056706A:B03	ES 186	528981	1827.L24.gz43_232170
M00056706A:B05	ES 186	648777	1827.M01.gz43_231803
M00056706A:E09	ES 186	419465	1827.M02.gz43_231819
M00056706B:C02	ES 186	449752	1827.M06.gz43_231883
M00056706B:C07	ES 186	736100	1827.M07.gz43_231899
M00056706B:D04	ES 186	595181	1827.M08.gz43_231915
M00056706C:A07	ES 186	584693	1827.M10.gz43_231947
M00056706C:B12	ES 186	728898	1827.M11.gz43_231963
M00056706C:D05	ES 186	733064	1827.M13.gz43_231995
M00056706C:G01	ES 186	551450	1827.M18.gz43_232075
M00056707A:G11	ES 186	626791	1827.N03.gz43_231836
M00056707B:E02	ES 186	649106	1827.N06.gz43_231884
M00056707B:F06	ES 186	736276	1827.N09.gz43_231932
M00056707C:B04	ES 186	427486	1827.N12.gz43_231980
M00056707C:E01	ES 186	552430	1827.N15.gz43_232028
M00056707C:E03	ES 186	730639	1827.N16.gz43_232044
M00056707C:F10	ES 186	728768	1827.N17.gz43_232060
M00056708B:B09	ES 186	736579	1827.O12.gz43_231981
M00056708B:D03	ES 186	607202	1827.O13.gz43_231997
M00056708B:F06	ES 186	733040	1827.O18.gz43_232077

Table 13

CloneID	ES No	ClusterID	SequenceName
M00056708C:F06	ES 186	449629	1827.P01.gz43_231806
M00056708C:F11	ES 186	558317	1827.P02.gz43_231822
M00056708D:B03	ES 186	728892	1827.P05.gz43_231870
M00056708D:D10	ES 186	730463	1827.P06.gz43_231886
M00056708D:H06	ES 186	473433	1827.P13.gz43_231998
M00056709A:A05	ES 186	454087	1827.P14.gz43_232014
M00056709A:H11	ES 186	259218	1827.P18.gz43_232078
M00056709C:F06	ES 186	729428	1828.A01.gz43_232175
M00056709D:D05	ES 186	584179	1828.A05.gz43_232239
M00056709D:E12	ES 186	455297	1828.A08.gz43_232287
M00056710B:F05	ES 186	728273	1828.A23.gz43_232527
M00056710B:G12	ES 186	724006	1828.B03.gz43_232208
M00056710D:A02	ES 186	475797	1828.B09.gz43_232304
M00056710D:C05	ES 186	707609	1828.B10.gz43_232320
M00056710D:H04	ES 186	727491	1828.B14.gz43_232384
M00056711A:A09	ES 186	641287	1828.B15.gz43_232400
M00056711B:B04	ES 186	485020	1828.B18.gz43_232448
M00056711C:F10	ES 186	736551	1828.C01.gz43_232177
M00056712B:B11	ES 186	728897	1828.C19.gz43_232465
M00056712B:F02	ES 186	734453	1828.C23.gz43_232529
M00056713A:B09	ES 186	461990	1828.D13.gz43_232370
M00056713A:F05	ES 186	48619	1828.D15.gz43_232402
M00056713B:B05	ES 186	727410	1828.D17.gz43_232434
M00056713C:A10	ES 186	732006	1828.D23.gz43_232530
M00056714A:A10	ES 186	734086	1828.E11.gz43_232339
M00056714A:B02	ES 186	735047	1828.E13.gz43_232371
M00056714A:B09	ES 186	728929	1828.E15.gz43_232403
M00056714A:E12	ES 186	448217	1828.E19.gz43_232467
M00056714A:H06	ES 186	728445	1828.E22.gz43_232515
M00056714B:B06	ES 186	728966	1828.E24.gz43_232547
M00056714B:C12	ES 186	724050	1828.F01.gz43_232180
M00056714D:A11	ES 186	729813	1828.F11.gz43_232340
M00056714D:E08	ES 186	505858	1828.F12.gz43_232356
M00056714D:H07	ES 186	448217	1828.F14.gz43_232388
M00056715C:B07	ES 186	558544	1828.G05.gz43_232245
M00056716B:F12	ES 186	728182	1828.H02.gz43_232198
M00056716C:B06	ES 186	630516	1828.H04.gz43_232230
M00056718A:F10	ES 186	728925	1828.I09.gz43_232311
M00056718A:H05	ES 186	728528	1828.I11.gz43_232343
M00056718B:C02	ES 186	451972	1828.I15.gz43_232407
M00056718C:B01	ES 186	646309	1828.I19.gz43_232471
M00056718D:D12	ES 186	449585	1828.I23.gz43_232535
M00056719B:D02	ES 186	727946	1828.J09.gz43_232312
M00056719B:G04	ES 186	732770	1828.J11.gz43_232344

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CloneID	ES No	ClusterID	SequenceName
M00056719C:B10	ES 186	486363	1828.J18.gz43_232456
M00056719C:F06	ES 186	728303	1828.J19.gz43_232472
M00056720B:D05	ES 186	730233	1828.K06.gz43_232265
M00056721A:C07	ES 186	727749	1828.K13.gz43_232377
M00056721B:D03	ES 186	728002	1828.K19.gz43_232473
M00056721C:E05	ES 186	732351	1828.L01.gz43_232186
M00056721C:H01	ES 186	555763	1828.L03.gz43_232218
M00056721D:D01	ES 186	734622	1828.L07.gz43_232282
M00056721D:F12	ES 186	728178	1828.L10.gz43_232330
M00056722A:E10	ES 186	598746	1828.L13.gz43_232378
M00056722A:F08	ES 186	485899	1828.L14.gz43_232394
M00056722B:E09	ES 186	732242	1828.L19.gz43_232474
M00056722C:C09	ES 186	730627	1828.M01.gz43_232187
M00056722C:D11	ES 186	727878	1828.M02.gz43_232203
M00056723C:C09	ES 186	462687	1828.N02.gz43_232204
M00056723C:E01	ES 186	553294	1828.N05.gz43_232252
M00056723C:G03	ES 186	734990	1828.N08.gz43_232300
M00056724B:E11	ES 186	473640	1828.N20.gz43_232492
M00056724B:G03	ES 186	447150	1828.N22.gz43_232524
M00056724C:H11	ES 186	726576	1828.O05.gz43_232253
M00056725A:E02	ES 186	728061	1828.O13.gz43_232381
M00056725C:A03	ES 186	727480	1828.O21.gz43_232509
M00056725C:H06	ES 186	728627	1828.P03.gz43_232222
M00056726A:C12	ES 186	735362	1828.P07.gz43_232286
M00056726A:F08	ES 186	449210	1828.P08.gz43_232302
M00056726B:H06	ES 186	447634	1828.P10.gz43_232334
M00056726D:B05	ES 186	692627	1828.P17.gz43_232446
M00056726D:G08	ES 186	509678	1828.P21.gz43_232510
M00056746D:D06	ES 186	729206	1838.B03.gz43_232976
M00056746D:E09	ES 186	458940	1838.B05.gz43_233008
M00056747D:A03	ES 186	529356	1838.C01.gz43_232945
M00056750B:H03	ES 186	735464	1838.E03.gz43_232979
M00056753A:G01	ES 186	552613	1838.G02.gz43_232965
M00056753B:B09	ES 186	728936	1838.G06.gz43_233029
M00056755B:E07	ES 186	728464	1838.I05.gz43_233015
M00056756C:D06	ES 186	736035	1838.J03.gz43_232984
M00056756C:E10	ES 186	646713	1838.J04.gz43_233000
M00056758C:B08	ES 186	730178	1838.K05.gz43_233017
M00056759C:C04	ES 186	736210	1838.L03.gz43_232986
M00056762B:D06	ES 186	481614	1838.N05.gz43_233020
M00056763B:G04	ES 186	697527	1838.O06.gz43_233037
M00056764C:A02	ES 186	551693	1838.P01.gz43_232958
M00056766D:G09	ES 186	728454	1839.A01.gz43_233327
M00056767A:F02	ES 186	730858	1839.A07.gz43_233423

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CloneID	ES No	ClusterID	SequenceName
M00056767A:F12	ES 186	711325	1839.A08.gz43_233439
M00056767B:C01	ES 186	727737	1839.A11.gz43_233487
M00056767B:G08	ES 186	736686	1839.A13.gz43_233519
M00056767C:A09	ES 186	549801	1839.A14.gz43_233535
M00056768A:C03	ES 186	730607	1839.A17.gz43_233583
M00056768A:C10	ES 186	728487	1839.A18.gz43_233599
M00056768B:F07	ES 186	730253	1839.A21.gz43_233647
M00056768D:A09	ES 186	736773	1839.B03.gz43_233360
M00056769C:C03	ES 186	504513	1839.B09.gz43_233456
M00056770C:A07	ES 186	641968	1839.B15.gz43_233552
M00056771A:F03	ES 186	732345	1839.B23.gz43_233680
M00056771B:F03	ES 186	552432	1839.C06.gz43_233409
M00056771C:G06	ES 186	640382	1839.C13.gz43_233521
M00056771D:D10	ES 186	726229	1839.C18.gz43_233601
M00056772A:C08	ES 186	691229	1839.C22.gz43_233665
M00056772A:D03	ES 186	726699	1839.C23.gz43_233681
M00056773A:A04	ES 186	735071	1839.D18.gz43_233602
M00056773A:C04	ES 186	735872	1839.D21.gz43_233650
M00056773A:G10	ES 186	727366	1839.D22.gz43_233666
M00056773B:G12	ES 186	711797	1839.E03.gz43_233363
M00056773C:C09	ES 186	510596	1839.E05.gz43_233395
M00056773C:F12	ES 186	135593	1839.E08.gz43_233443
M00056774B:G06	ES 186	726825	1839.E19.gz43_233619
M00056774C:G03	ES 186	728350	1839.E22.gz43_233667
M00056774D:B02	ES 186	631038	1839.E24.gz43_233699
M00056774D:F06	ES 186	734724	1839.F04.gz43_233380
M00056775A:A05	ES 186	727436	1839.F05.gz43_233396
M00056775B:H07	ES 186	477053	1839.F12.gz43_233508
M00056776A:G04	ES 186	728464	1839.G06.gz43_233413
M00056776D:B02	ES 186	523868	1839.G18.gz43_233605
M00056776D:H03	ES 186	642079	1839.G22.gz43_233669
M00056777A:A03	ES 186	730029	1839.G23.gz43_233685
M00056777D:D04	ES 186	730484	1839.H14.gz43_233542
M00056778C:G08	ES 186	609459	1839.H24.gz43_233702
M00056780B:E06	ES 186	724183	1839.J04.gz43_233384
M00056780B:H04	ES 186	493193	1839.J09.gz43_233464
M00056780C:H12	ES 186	647991	1839.J14.gz43_233544
M00056780D:G05	ES 186	727216	1839.J19.gz43_233624
M00056780D:H10	ES 186	724722	1839.J22.gz43_233672
M00056781A:C05	ES 186	513156	1839.J23.gz43_233688
M00056781A:D02	ES 186	482788	1839.J24.gz43_233704
M00056781A:E06	ES 186	730505	1839.K02.gz43_233353
M00056781B:C03	ES 186	733744	1839.K07.gz43_233433
M00056781B:C05	ES 186	639178	1839.K08.gz43_233449

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CloneID	ES No	ClusterID	SequenceName
M00056781B:E01	ES 186	728133	1839.K09.gz43_233465
M00056781B:F05	ES 186	727005	1839.K10.gz43_233481
M00056782B:G05	ES 186	449010	1839.L06.gz43_233418
M00056782B:H11	ES 186	643522	1839.L07.gz43_233434
M00056782D:F02	ES 186	483549	1839.L13.gz43_233530
M00056782D:F08	ES 186	490393	1839.L14.gz43_233546
M00056782D:F10	ES 186	726261	1839.L15.gz43_233562
M00056783A:C08	ES 187	577305	1839.L18.gz43_233610
M00056783B:B01	ES 187	47461	1839.L19.gz43_233626
M00056783C:D01	ES 187	591449	1839.M01.gz43_233339
M00056783C:E03	ES 187	730352	1839.M04.gz43_233387
M00056783D:A02	ES 187	460023	1839.M06.gz43_233419
M00056783D:B07	ES 187	556458	1839.M07.gz43_233435
M00056784B:A01	ES 187	733891	1839.M15.gz43_233563
M00056784B:C02	ES 187	730296	1839.M16.gz43_233579
M00056784B:D06	ES 187	733149	1839.M17.gz43_233595
M00056784C:C06	ES 187	725784	1839.M22.gz43_233675
M00056784D:C06	ES 187	675768	1839.N01.gz43_233340
M00056784D:G10	ES 187	726344	1839.N03.gz43_233372
M00056785A:C12	ES 187	646688	1839.N05.gz43_233404
M00056785A:G06	ES 187	228118	1839.N07.gz43_233436
M00056785B:B07	ES 187	730845	1839.N12.gz43_233516
M00056785C:B09	ES 187	643968	1839.N14.gz43_233548
M00056785D:C09	ES 187	550780	1839.N19.gz43_233628
M00056785D:G07	ES 187	730592	1839.N24.gz43_233708
M00056786D:A03	ES 187	730022	1839.O15.gz43_233565
M00056787B:C07	ES 187	577305	1839.P01.gz43_233342
M00056787C:B04	ES 187	724383	1839.P08.gz43_233454
M00056787C:G01	ES 187	726384	1839.P12.gz43_233518
M00056788A:D06	ES 187	606076	1839.P21.gz43_233662
M00056871C:D05	ES 187	735801	1852.A13.gz43_235742
M00056873A:H06	ES 187	735412	1852.B17.gz43_235807
M00056873B:C09	ES 187	726408	1852.B19.gz43_235839
M00056874C:D05	ES 187	730059	1852.C19.gz43_235840
M00056875D:C04	ES 187	729981	1852.D16.gz43_235793
M00056875D:E09	ES 187	727602	1852.D18.gz43_235825
M00056875D:H12	ES 187	733040	1852.D21.gz43_235873
M00056876A:C08	ES 187	724187	1852.D23.gz43_235905
M00056876A:E02	ES 187	730152	1852.D24.gz43_235921
M00056876C:B02	ES 187	481641	1852.E14.gz43_235762
M00056876C:G10	ES 187	732837	1852.E16.gz43_235794
M00056877B:H09	ES 187	488349	1852.F14.gz43_235763
M00056877C:D11	ES 187	727975	1852.F15.gz43_235779

Table 13

CloneID	ES No	ClusterID	SequenceName
M00056877C:G12	ES 187	655327	1852.F19.gz43_235843
M00056877C:H03	ES 187	730441	1852.F20.gz43_235859
M00056879A:D12	ES 187	732752	1852.G13.gz43_235748
M00056879B:H11	ES 187	730336	1852.G24.gz43_235924
M00056879D:D01	ES 187	472704	1852.H13.gz43_235749
M00056881A:A10	ES 187	649299	1852.I13.gz43_235750
M00056881A:C02	ES 187	735096	1852.I14.gz43_235766
M00056881A:H02	ES 187	639950	1852.I16.gz43_235798
M00056881B:G04	ES 187	730301	1852.I22.gz43_235894
M00056882B:E12	ES 187	594434	1852.J14.gz43_235767
M00056882D:A06	ES 187	471931	1852.J22.gz43_235895
M00056883D:A07	ES 187	732712	1852.K15.gz43_235784
M00056883D:F07	ES 187	732872	1852.K21.gz43_235880
M00056884C:H08	ES 187	550673	1852.L14.gz43_235769
M00056884C:H11	ES 187	472307	1852.L15.gz43_235785
M00056884D:C07	ES 187	724517	1852.L16.gz43_235801
M00056884D:D06	ES 187	561396	1852.L18.gz43_235833
M00056885A:D12	ES 187	730106	1852.L23.gz43_235913
M00056885D:D01	ES 187	644843	1852.M17.gz43_235818
M00056886A:A09	ES 187	732872	1852.M19.gz43_235850
M00056886A:C11	ES 187	735326	1852.M21.gz43_235882
M00056886B:B10	ES 187	650944	1852.N13.gz43_235755
M00056886B:C05	ES 187	735672	1852.N14.gz43_235771
M00056886B:H02	ES 187	724223	1852.N17.gz43_235819
M00056886C:D02	ES 187	473512	1852.N19.gz43_235851
M00056886C:D11	ES 187	451184	1852.N20.gz43_235867
M00056887A:E01	ES 187	729087	1852.N23.gz43_235915
M00056887D:H01	ES 187	730195	1852.O17.gz43_235820
M00056888A:H04	ES 187	649030	1852.O24.gz43_235932
M00056890A:D05	ES 187	450963	1861.A06.gz43_236014
M00056891A:G11	ES 187	732315	1861.A24.gz43_236302
M00056891C:H08	ES 187	730393	1861.B08.gz43_236047
M00056892B:C09	ES 187	479572	1861.B18.gz43_236207
M00056893B:G12	ES 187	724773	1861.C16.gz43_236176
M00056893C:A02	ES 187	728640	1861.C17.gz43_236192
M00056895B:F12	ES 187	727596	1861.E03.gz43_235970
M00056895C:E11	ES 187	494393	1861.E07.gz43_236034
M00056895D:G01	ES 187	725258	1861.E14.gz43_236146
M00056896A:C01	ES 187	735834	1861.E18.gz43_236210
M00056898C:B06	ES 187	676221	1861.G10.gz43_236084
M00056898D:D11	ES 187	730760	1861.G17.gz43_236196
M00056898D:H09	ES 187	729060	1861.G20.gz43_236244
M00056899A:A11	ES 187	732676	1861.G22.gz43_236276
M00056899B:D02	ES 187	732244	1861.H04.gz43_235989

Table 13

CloneID	ES No	ClusterID	SequenceName
M00056899D:B06	ES 187	448368	1861.H12.gz43_236117
M00056900B:D01	ES 187	656667	1861.H21.gz43_236261
M00056900B:F07	ES 187	730296	1861.H24.gz43_236309
M00056900C:B12	ES 187	562345	1861.I04.gz43_235990
M00056901B:C03	ES 187	730608	1861.I16.gz43_236182
M00056902A:G12	ES 187	557525	1861.J14.gz43_236151
M00056902D:H09	ES 187	489001	1861.K12.gz43_236120
M00056903A:C08	ES 187	642897	1861.K16.gz43_236184
M00056903A:F03	ES 187	733425	1861.K18.gz43_236216
M00056903B:D09	ES 187	453001	1861.K24.gz43_236312
M00056905A:H04	ES 187	732486	1861.M12.gz43_236122
M00056906D:D11	ES 187	639223	1861.N10.gz43_236091
M00056908B:D02	ES 187	548275	1861.N16.gz43_236187
M00056908D:A11	ES 187	725451	1861.N24.gz43_236315
M00056909B:E11	ES 187	648774	1861.O11.gz43_236108
M00056910A:G05	ES 187	551602	1861.P02.gz43_235965
M00056910B:F01	ES 187	472226	1861.P04.gz43_235997
M00056911B:A01	ES 187	732653	1861.P19.gz43_236237
M00056934A:A12	ES 187	729809	1863.A01.gz43_236702
M00056934A:E07	ES 187	446820	1863.A03.gz43_236734
M00056934C:C04	ES 187	492893	1863.A08.gz43_236814
M00056934C:G09	ES 187	555478	1863.A10.gz43_236846
M00056935A:C02	ES 187	731355	1863.A18.gz43_236974
M00056935A:F04	ES 187	735484	1863.A21.gz43_237022
M00056935C:G08	ES 187	726825	1863.B11.gz43_236863
M00056936C:C06	ES 187	524706	1863.B24.gz43_237071
M00056936C:E04	ES 187	730851	1863.C01.gz43_236704
M00056936C:F11	ES 187	77737	1863.C02.gz43_236720
M00056937C:H08	ES 187	485880	1863.C24.gz43_237072
M00056938A:H09	ES 187	451624	1863.D08.gz43_236817
M00056938B:C06	ES 187	725638	1863.D11.gz43_236865
M00056938B:C09	ES 187	733144	1863.D12.gz43_236881
M00056938B:H08	ES 187	731216	1863.D15.gz43_236929
M00056938C:F10	ES 187	735306	1863.D20.gz43_237009
M00056939A:C01	ES 187	734151	1863.E03.gz43_236738
M00056939B:E05	ES 187	642528	1863.E12.gz43_236882
M00056939B:E10	ES 187	735477	1863.E13.gz43_236898
M00056939D:B02	ES 187	171511	1863.E21.gz43_237026
M00056940B:B11	ES 187	732886	1863.F12.gz43_236883
M00056940B:G07	ES 187	730564	1863.F14.gz43_236915
M00056940C:E05	ES 187	730815	1863.F17.gz43_236963
M00056941B:B02	ES 187	616541	1863.G10.gz43_236852
M00056941B:G08	ES 187	730375	1863.G18.gz43_236980
M00056941C:F07	ES 187	732491	1863.G21.gz43_237028

Table 13

CloneID	ES No	ClusterID	SequenceName
M00056941D:A05	ES 187	730452	1863.G24.gz43_237076
M00056941D:D07	ES 187	727596	1863.H01.gz43_236709
M00056941D:G05	ES 187	456183	1863.H03.gz43_236741
M00056941D:H01	ES 187	724162	1863.H04.gz43_236757
M00056942B:F04	ES 187	485183	1863.H09.gz43_236837
M00056942C:A12	ES 187	724286	1863.H12.gz43_236885
M00056942C:B12	ES 187	731162	1863.H14.gz43_236917
M00056942C:C06	ES 187	733151	1863.H15.gz43_236933
M00056942C:F11	ES 187	732756	1863.H17.gz43_236965
M00056942D:D03	ES 187	727517	1863.H20.gz43_237013
M00056942D:D07	ES 187	728076	1863.H21.gz43_237029
M00056942D:D11	ES 187	511351	1863.H22.gz43_237045
M00056943A:B04	ES 187	734629	1863.I03.gz43_236742
M00056943A:F01	ES 187	729691	1863.I05.gz43_236774
M00056943C:A01	ES 187	468015	1863.I17.gz43_236966
M00056943D:B02	ES 187	729316	1863.I20.gz43_237014
M00056943D:H08	ES 187	731125	1863.I22.gz43_237046
M00056944A:D09	ES 187	733623	1863.J03.gz43_236743
M00056944B:C02	ES 187	448233	1863.J04.gz43_236759
M00056944C:B03	ES 187	735994	1863.J12.gz43_236887
M00056944D:A06	ES 187	733081	1863.J17.gz43_236967
M00056945A:B11	ES 187	651088	1863.K04.gz43_236760
M00056945A:F02	ES 187	646314	1863.K06.gz43_236792
M00056945C:A11	ES 187	724401	1863.K12.gz43_236888
M00056946A:F07	ES 187	736293	1863.L01.gz43_236713
M00056946A:G06	ES 187	638983	1863.L02.gz43_236729
M00056946C:B08	ES 187	552416	1863.L08.gz43_236825
M00056946D:G09	ES 187	555484	1863.L17.gz43_236969
M00056947A:C05	ES 187	551441	1863.L20.gz43_237017
M00056947C:B04	ES 187	736001	1863.M02.gz43_236730
M00056947D:F09	ES 187	736349	1863.M08.gz43_236826
M00056948A:D09	ES 187	736129	1863.M12.gz43_236890
M00056948B:B03	ES 187	449061	1863.M15.gz43_236938
M00056948B:D04	ES 187	600347	1863.M17.gz43_236970
M00056948B:G05	ES 187	467803	1863.M18.gz43_236986
M00056948B:H06	ES 187	490903	1863.M19.gz43_237002
M00056948C:F03	ES 187	733910	1863.N01.gz43_236715
M00056948D:A11	ES 187	733856	1863.N03.gz43_236747
M00056949A:A04	ES 187	500239	1863.N05.gz43_236779
M00056949D:D11	ES 187	461486	1863.O02.gz43_236732
M00056950A:F01	ES 187	685968	1863.O08.gz43_236828
M00056950A:H03	ES 187	410487	1863.O10.gz43_236860
M00056950B:F03	ES 187	560252	1863.O16.gz43_236956
M00056950D:F12	ES 187	731196	1863.P02.gz43_236733

Table 13

CloneID	ES No	ClusterID	SequenceName
M00056950D:H09	ES 187	727480	1863.P03.gz43_236749
M00056951B:B06	ES 187	488447	1863.P11.gz43_236877
M00056951B:F09	ES 187	448046	1863.P13.gz43_236909
M00056951C:A04	ES 187	735818	1863.P17.gz43_236973
M00056953B:F05	ES 187	516522	1864.B04.gz43_237135
M00056954C:C04	ES 187	556141	1864.C07.gz43_237184
M00056957B:F10	ES 187	553000	1864.E18.gz43_237362
M00056959C:B10	ES 187	642781	1864.G12.gz43_237268
M00056961C:C07	ES 187	736197	1864.I03.gz43_237126
M00056961D:G02	ES 187	656070	1864.I09.gz43_237222
M00056962D:F09	ES 187	736289	1864.I17.gz43_237350
M00056968C:C06	ES 187	731089	1864.M04.gz43_237146
M00056969A:B07	ES 187	731947	1864.M14.gz43_237306
M00056969A:C07	ES 187	448712	1864.M16.gz43_237338
M00056975A:H11	ES 187	728249	1873.A13.gz43_237662
M00056975B:E04	ES 187	735440	1873.A16.gz43_237710
M00056975C:F09	ES 187	477399	1873.A18.gz43_237742
M00056976C:F05	ES 187	734561	1873.B20.gz43_237775
M00056977A:C02	ES 187	733563	1873.C04.gz43_237520
M00056977A:H10	ES 187	482461	1873.C12.gz43_237648
M00056977B:B06	ES 187	613029	1873.C13.gz43_237664
M00056978A:A03	ES 187	734936	1873.D08.gz43_237585
M00056978A:H04	ES 187	730089	1873.D11.gz43_237633
M00056978B:G02	ES 187	641658	1873.D16.gz43_237713
M00056978D:A01	ES 188	733778	1873.D24.gz43_237841
M00056978D:B07	ES 188	735123	1873.E02.gz43_237490
M00056979B:D03	ES 188	731607	1873.E08.gz43_237586
M00056979B:E03	ES 188	725321	1873.E09.gz43_237602
M00056979C:D11	ES 188	648034	1873.E12.gz43_237650
M00056980A:H06	ES 188	732438	1873.F04.gz43_237523
M00056980D:E07	ES 188	727151	1873.F20.gz43_237779
M00056981D:H02	ES 188	732535	1873.G14.gz43_237684
M00056982D:B12	ES 188	724411	1873.H02.gz43_237493
M00056983D:C12	ES 188	650919	1873.H18.gz43_237749
M00056985A:D06	ES 188	729623	1873.I12.gz43_237654
M00056985A:G07	ES 188	552254	1873.I14.gz43_237686
M00056985B:G03	ES 188	557488	1873.I18.gz43_237750
M00056985C:C06	ES 188	731453	1873.I20.gz43_237782
M00056986A:E09	ES 188	732213	1873.J06.gz43_237559
M00056987A:C02	ES 188	731592	1873.J24.gz43_237847
M00056987C:D08	ES 188	555423	1873.K04.gz43_237528
M00056987D:A09	ES 188	731302	1873.K10.gz43_237624
M00056988A:B09	ES 188	723895	1873.K17.gz43_237736

Table 13

CloneID	ES No	ClusterID	SequenceName
M00056988A:F06	ES 188	642649	1873.K20.gz43_237784
M00056988B:A06	ES 188	731358	1873.K22.gz43_237816
M00056988C:D05	ES 188	703978	1873.L04.gz43_237529
M00056988D:F05	ES 188	732113	1873.L10.gz43_237625
M00056989C:H09	ES 188	639934	1873.M03.gz43_237514
M00056989D:A07	ES 188	731476	1873.M05.gz43_237546
M00056989D:F07	ES 188	728013	1873.M10.gz43_237626
M00056989D:H11	ES 188	731317	1873.M12.gz43_237658
M00056990B:B03	ES 188	729795	1873.M18.gz43_237754
M00056990B:H07	ES 188	642288	1873.M20.gz43_237786
M00056990C:E09	ES 188	735395	1873.N02.gz43_237499
M00056990D:C11	ES 188	725825	1873.N06.gz43_237563
M00056991C:H11	ES 188	406931	1873.N18.gz43_237755
M00056992A:E01	ES 188	471883	1873.N22.gz43_237819
M00056993A:B02	ES 188	550973	1873.O12.gz43_237660
M00056993A:B08	ES 188	731542	1873.O13.gz43_237676
M00056993D:C05	ES 188	662617	1873.P02.gz43_237501
M00056993D:F05	ES 188	732114	1873.P05.gz43_237549
M00056994B:H05	ES 188	736401	1873.P18.gz43_237757
M00056994C:B04	ES 188	572426	1873.P20.gz43_237789
M00056994C:C01	ES 188	483676	1873.P22.gz43_237821
M00056995C:H06	ES 188	631251	1874.A15.gz43_238078
M00056995D:C11	ES 188	731686	1874.A19.gz43_238142
M00056996D:A02	ES 188	731317	1874.B08.gz43_237967
M00056997A:H05	ES 188	550016	1874.B18.gz43_238127
M00056997B:C11	ES 188	559053	1874.B20.gz43_238159
M00056997D:B04	ES 188	737083	1874.C06.gz43_237936
M00056998C:B10	ES 188	456236	1874.D01.gz43_237857
M00056998D:H08	ES 188	726408	1874.D08.gz43_237969
M00056999A:G12	ES 188	734708	1874.D12.gz43_238033
M00056999B:D07	ES 188	726696	1874.D16.gz43_238097
M00057000A:A05	ES 188	733932	1874.E03.gz43_237890
M00057001D:F02	ES 188	448202	1874.F16.gz43_238099
M00057003D:F02	ES 188	734629	1874.H16.gz43_238101
M00057004B:D05	ES 188	497233	1874.H21.gz43_238181
M00057006A:G10	ES 188	730662	1874.J17.gz43_238119
M00057007B:G02	ES 188	561993	1874.K16.gz43_238104
M00057007C:A06	ES 188	736413	1874.K17.gz43_238120
M00057009C:B02	ES 188	732792	1874.N01.gz43_237867
M00057011C:H03	ES 188	724810	1874.P07.gz43_237965
M00057011D:F12	ES 188	733836	1874.P13.gz43_238061
M00057012A:D12	ES 188	556637	1874.P17.gz43_238125
M00057012D:G03	ES 188	732441	1875.A03.gz43_238270
M00057012D:G04	ES 188	733571	1875.A04.gz43_238286

Table 13

CloneID	ES No	ClusterID	SequenceName
M00057013B:H07	ES 188	481581	1875.A10.gz43_238382
M00057013C:E09	ES 188	726208	1875.A13.gz43_238430
M00057013C:H01	ES 188	733756	1875.A15.gz43_238462
M00057013D:E03	ES 188	558132	1875.A17.gz43_238494
M00057014A:B11	ES 188	512377	1875.A22.gz43_238574
M00057014B:A02	ES 188	556019	1875.B02.gz43_238255
M00057014B:B01	ES 188	478448	1875.B03.gz43_238271
M00057014B:B06	ES 188	451351	1875.B04.gz43_238287
M00057014C:C08	ES 188	728852	1875.B07.gz43_238335
M00057014C:E01	ES 188	733354	1875.B12.gz43_238415
M00057014C:E03	ES 188	730828	1875.B13.gz43_238431
M00057014D:E05	ES 188	619265	1875.B19.gz43_238527
M00057014D:G10	ES 188	733664	1875.B22.gz43_238575
M00057014D:H01	ES 188	557164	1875.B23.gz43_238591
M00057015A:E02	ES 188	732047	1875.C05.gz43_238304
M00057015A:G06	ES 188	487183	1875.C07.gz43_238336
M00057015A:H12	ES 188	732550	1875.C10.gz43_238384
M00057015B:E01	ES 188	484023	1875.C15.gz43_238464
M00057016A:B04	ES 188	734074	1875.C21.gz43_238560
M00057016A:G01	ES 188	494450	1875.C23.gz43_238592
M00057016B:A09	ES 188	733723	1875.D03.gz43_238273
M00057016B:C01	ES 188	554620	1875.D04.gz43_238289
M00057016B:E06	ES 188	734392	1875.D08.gz43_238353
M00057016B:H08	ES 188	474009	1875.D09.gz43_238369
M00057016C:B05	ES 188	733970	1875.D11.gz43_238401
M00057016C:E04	ES 188	731838	1875.D14.gz43_238449
M00057016C:E11	ES 188	689424	1875.D15.gz43_238465
M00057016D:B07	ES 188	703298	1875.D17.gz43_238497
M00057016D:H03	ES 188	640904	1875.D22.gz43_238577
M00057017A:A07	ES 188	452065	1875.D23.gz43_238593
M00057017A:F11	ES 188	570573	1875.E04.gz43_238290
M00057017A:G04	ES 188	538582	1875.E06.gz43_238322
M00057017C:E03	ES 188	559096	1875.E15.gz43_238466
M00057018A:C05	ES 188	734177	1875.E21.gz43_238562
M00057018C:F02	ES 188	732119	1875.F02.gz43_238259
M00057018D:B10	ES 188	734091	1875.F05.gz43_238307
M00057018D:E05	ES 188	557896	1875.F08.gz43_238355
M00057019A:G04	ES 188	626791	1875.F12.gz43_238419
M00057019C:C08	ES 188	455148	1875.F15.gz43_238467
M00057019C:E03	ES 188	558134	1875.F16.gz43_238483
M00057019D:C02	ES 188	649074	1875.F19.gz43_238531
M00057020A:F09	ES 188	639427	1875.F23.gz43_238595
M00057020D:A05	ES 188	483919	1875.G07.gz43_238340
M00057021B:B07	ES 188	477797	1875.G18.gz43_238516

Table 13

CloneID	ES No	ClusterID	SequenceName
M00057021D:F10	ES 188	212768	1875.G24.gz43_238612
M00057022B:A04	ES 188	729731	1875.H09.gz43_238373
M00057022B:F03	ES 188	639629	1875.H11.gz43_238405
M00057022B:H04	ES 188	559699	1875.H12.gz43_238421
M00057022C:D12	ES 188	726476	1875.H14.gz43_238453
M00057022D:E10	ES 188	554693	1875.H23.gz43_238597
M00057023A:H09	ES 188	726173	1875.I03.gz43_238278
M00057023D:D05	ES 188	390968	1875.I13.gz43_238438
M00057023D:D08	ES 188	466920	1875.I14.gz43_238454
M00057023D:E11	ES 188	616985	1875.I15.gz43_238470
M00057024A:D08	ES 188	727761	1875.I21.gz43_238566
M00057024B:A03	ES 188	735021	1875.I23.gz43_238598
M00057024B:A11	ES 188	726044	1875.I24.gz43_238614
M00057024B:F07	ES 188	733625	1875.J01.gz43_238247
M00057024C:A01	ES 188	670124	1875.J04.gz43_238295
M00057024C:G08	ES 188	551485	1875.J06.gz43_238327
M00057024D:D12	ES 188	735396	1875.J10.gz43_238391
M00057024D:H11	ES 188	728797	1875.J15.gz43_238471
M00057025C:A08	ES 188	724296	1875.K02.gz43_238264
M00057025C:D11	ES 188	655312	1875.K04.gz43_238296
M00057026C:H11	ES 188	733673	1875.K21.gz43_238568
M00057026D:A05	ES 188	732598	1875.K23.gz43_238600
M00057027B:B11	ES 188	651049	1875.L07.gz43_238345
M00057027B:E04	ES 188	89082	1875.L08.gz43_238361
M00057027B:F06	ES 188	731577	1875.L11.gz43_238409
M00057027D:A12	ES 188	432159	1875.L18.gz43_238521
M00057027D:D07	ES 188	733209	1875.L21.gz43_238569
M00057027D:G03	ES 188	728791	1875.L24.gz43_238617
M00057028B:B11	ES 188	730296	1875.M11.gz43_238410
M00057028D:D09	ES 188	554080	1875.M19.gz43_238538
M00057029A:C08	ES 188	495241	1875.M23.gz43_238602
M00057029B:G10	ES 188	735412	1875.N07.gz43_238347
M00057029D:A06	ES 188	732712	1875.N14.gz43_238459
M00057029D:F01	ES 188	733479	1875.N15.gz43_238475
M00057030B:B03	ES 188	425203	1875.N22.gz43_238587
M00057030B:F01	ES 188	735989	1875.N23.gz43_238603
M00057030C:A05	ES 188	562769	1875.N24.gz43_238619
M00057030C:B03	ES 188	461486	1875.O01.gz43_238252
M00057031A:G09	ES 188	594013	1875.O12.gz43_238428
M00057031A:H02	ES 188	471522	1875.O13.gz43_238444
M00057031B:A01	ES 188	561338	1875.O14.gz43_238460
M00057032A:C01	ES 188	512863	1875.P08.gz43_238365
M00057032A:F12	ES 188	642693	1875.P10.gz43_238397
M00057032D:A04	ES 188	736385	1875.P18.gz43_238525

Table 13

CloneID	ES No	ClusterID	SequenceName
M00057033A:D08	ES 188	479208	1875.P24.gz43_238621
M00057033C:B03	ES 188	468296	1876.A08.gz43_238734
M00057033D:F10	ES 188	456469	1876.A16.gz43_238862
M00057034B:B01	ES 188	735972	1876.A23.gz43_238974
M00057034C:A11	ES 188	735221	1876.A24.gz43_238990
M00057034C:G12	ES 188	736385	1876.B05.gz43_238687
M00057035C:E10	ES 188	452833	1876.C03.gz43_238656
M00057036A:C07	ES 188	557967	1876.C14.gz43_238832
M00057036B:G08	ES 188	483959	1876.C18.gz43_238896
M00057036D:B01	ES 188	729813	1876.C24.gz43_238992
M00057036D:E09	ES 188	554734	1876.D06.gz43_238705
M00057037D:E08	ES 188	727411	1876.D24.gz43_238993
M00057038A:H07	ES 188	473026	1876.E04.gz43_238674
M00057038C:B06	ES 188	728353	1876.E07.gz43_238722
M00057038C:G08	ES 188	454819	1876.E09.gz43_238754
M00057038D:A12	ES 188	735815	1876.E11.gz43_238786
M00057040B:F01	ES 188	483101	1876.F12.gz43_238803
M00057040D:H04	ES 188	736855	1876.F18.gz43_238899
M00057041D:B11	ES 188	546632	1876.G12.gz43_238804
M00057041D:C08	ES 188	492627	1876.G13.gz43_238820
M00057042B:A10	ES 188	727321	1876.G22.gz43_238964
M00057042D:E06	ES 188	736881	1876.H06.gz43_238709
M00057042D:G02	ES 188	733772	1876.H08.gz43_238741
M00057043A:G07	ES 188	732315	1876.H12.gz43_238805
M00057043C:H11	ES 188	638857	1876.H22.gz43_238965
M00057044C:B05	ES 188	735871	1876.I16.gz43_238870
M00057045A:C04	ES 188	734466	1876.J05.gz43_238695
M00057045D:D08	ES 188	645803	1876.J20.gz43_238935
M00057046A:F02	ES 188	732159	1876.K03.gz43_238664
M00057046A:G05	ES 188	668731	1876.K05.gz43_238696
M00057046C:E05	ES 188	732042	1876.K14.gz43_238840
M00057047C:C07	ES 188	725024	1876.L11.gz43_238793
M00057047D:E01	ES 188	643933	1876.L20.gz43_238937
M00057047D:H04	ES 188	735054	1876.L23.gz43_238985
M00057048C:E04	ES 188	481293	1876.M10.gz43_238778
M00057048C:H11	ES 188	558573	1876.M12.gz43_238810
M00057048D:H10	ES 188	732562	1876.M20.gz43_238938
M00057049D:F12	ES 188	732246	1876.N07.gz43_238731
M00057050B:F06	ES 188	737087	1876.N14.gz43_238843
M00057051B:E09	ES 188	466920	1876.O06.gz43_238716
M00057051D:F07	ES 188	732242	1876.O23.gz43_238988
M00057052D:A07	ES 189	708175	1876.P18.gz43_238909
M00057053A:A02	ES 189	645262	1885.A03.gz43_239038

Table 13

CloneID	ES No	ClusterID	SequenceName
M00057053A:D11	ES 189	446616	1885.A06.gz43_239086
M00057053C:B10	ES 189	732872	1885.A12.gz43_239182
M00057053C:G04	ES 189	733623	1885.A15.gz43_239230
M00057053D:D01	ES 189	677769	1885.A16.gz43_239246
M00057054A:B12	ES 189	729502	1885.A18.gz43_239278
M00057054A:D01	ES 189	736113	1885.A19.gz43_239294
M00057055B:D07	ES 189	726380	1885.B16.gz43_239247
M00057055B:E10	ES 189	730472	1885.B17.gz43_239263
M00057055B:F05	ES 189	567005	1885.B19.gz43_239295
M00057055C:F01	ES 189	729981	1885.C02.gz43_239024
M00057055C:H07	ES 189	728445	1885.C06.gz43_239088
M00057055D:D11	ES 189	725991	1885.C07.gz43_239104
M00057055D:F05	ES 189	733417	1885.C08.gz43_239120
M00057056B:C06	ES 189	134501	1885.C16.gz43_239248
M00057056B:D05	ES 189	455884	1885.C17.gz43_239264
M00057056B:D11	ES 189	731830	1885.C18.gz43_239280
M00057056B:E09	ES 189	735423	1885.C19.gz43_239296
M00057056B:F01	ES 189	735423	1885.C21.gz43_239328
M00057056C:G03	ES 189	734241	1885.D02.gz43_239025
M00057056D:F11	ES 189	732223	1885.D06.gz43_239089
M00057057A:G01	ES 189	654723	1885.D10.gz43_239153
M00057057B:E06	ES 189	422590	1885.D13.gz43_239201
M00057057B:E07	ES 189	471982	1885.D14.gz43_239217
M00057057B:G03	ES 189	736318	1885.D15.gz43_239233
M00057058D:F09	ES 189	647427	1885.E06.gz43_239090
M00057058D:G08	ES 189	451233	1885.E07.gz43_239106
M00057059A:B04	ES 189	731449	1885.E10.gz43_239154
M00057059B:F03	ES 189	597542	1885.E15.gz43_239234
M00057059C:A04	ES 189	614455	1885.E16.gz43_239250
M00057059C:E10	ES 189	502168	1885.E19.gz43_239298
M00057059C:H02	ES 189	620462	1885.E20.gz43_239314
M00057059D:A09	ES 189	476947	1885.E21.gz43_239330
M00057059D:H09	ES 189	735292	1885.F02.gz43_239027
M00057060A:C10	ES 189	473742	1885.F04.gz43_239059
M00057060B:D07	ES 189	552641	1885.F09.gz43_239139
M00057060B:E06	ES 189	449473	1885.F10.gz43_239155
M00057060C:D05	ES 189	731844	1885.F16.gz43_239251
M00057060D:C09	ES 189	450551	1885.F20.gz43_239315
M00057061A:F09	ES 189	735216	1885.F24.gz43_239379
M00057061A:H10	ES 189	641848	1885.G01.gz43_239012
M00057061B:F01	ES 189	449015	1885.G02.gz43_239028
M00057061B:F05	ES 189	594013	1885.G03.gz43_239044
M00057061B:H02	ES 189	733573	1885.G04.gz43_239060
M00057061C:D04	ES 189	595506	1885.G06.gz43_239092

Table 13

CloneID	ES No	ClusterID	SequenceName
M00057061D:D03	ES 189	736156	1885.G09.gz43_239140
M00057061D:F05	ES 189	452623	1885.G10.gz43_239156
M00057062B:H04	ES 189	447075	1885.G22.gz43_239348
M00057062D:D04	ES 189	723853	1885.H01.gz43_239013
M00057063A:C08	ES 189	728884	1885.H07.gz43_239109
M00057063B:F06	ES 189	736285	1885.H14.gz43_239221
M00057063C:C04	ES 189	736023	1885.H17.gz43_239269
M00057064B:H10	ES 189	481366	1885.I04.gz43_239062
M00057064C:F11	ES 189	541793	1885.I07.gz43_239110
M00057064D:C09	ES 189	402180	1885.I10.gz43_239158
M00057064D:G09	ES 189	729717	1885.I12.gz43_239190
M00057065B:D12	ES 189	723919	1885.I19.gz43_239302
M00057065C:B07	ES 189	420958	1885.I21.gz43_239334
M00057066A:A09	ES 189	422242	1885.J13.gz43_239207
M00057066B:A04	ES 189	727130	1885.J20.gz43_239319
M00057066C:B02	ES 189	572273	1885.J24.gz43_239383
M00057066D:B03	ES 189	558549	1885.K03.gz43_239048
M00057066D:E01	ES 189	627515	1885.K06.gz43_239096
M00057067B:C11	ES 189	550637	1885.K11.gz43_239176
M00057067B:H04	ES 189	449996	1885.K15.gz43_239240
M00057067C:D04	ES 189	736146	1885.K17.gz43_239272
M00057067C:H09	ES 189	730128	1885.K19.gz43_239304
M00057067D:F03	ES 189	472704	1885.K23.gz43_239368
M00057067D:H06	ES 189	726699	1885.L02.gz43_239033
M00057068A:C10	ES 189	736093	1885.L03.gz43_239049
M00057068A:E07	ES 189	73846	1885.L04.gz43_239065
M00057068A:F05	ES 189	559656	1885.L05.gz43_239081
M00057068A:F07	ES 189	730528	1885.L06.gz43_239097
M00057068A:G05	ES 189	736415	1885.L08.gz43_239129
M00057068D:B03	ES 189	724773	1885.L20.gz43_239321
M00057068D:C09	ES 189	455248	1885.L22.gz43_239353
M00057068D:E05	ES 189	736210	1885.L24.gz43_239385
M00057068D:F04	ES 189	554854	1885.M01.gz43_239018
M00057069A:F09	ES 189	560581	1885.M09.gz43_239146
M00057069A:H08	ES 189	732072	1885.M10.gz43_239162
M00057069B:A08	ES 189	453508	1885.M11.gz43_239178
M00057069B:D07	ES 189	656268	1885.M13.gz43_239210
M00057069B:E07	ES 189	465470	1885.M15.gz43_239242
M00057069D:H09	ES 189	730697	1885.N02.gz43_239035
M00057070A:B07	ES 189	556385	1885.N04.gz43_239067
M00057070C:H10	ES 189	706245	1885.N18.gz43_239291
M00057070D:B08	ES 189	735028	1885.N20.gz43_239323
M00057070D:G03	ES 189	649349	1885.N23.gz43_239371
M00057071A:A10	ES 189	731262	1885.O01.gz43_239020

Table 13

CloneID	ES No	ClusterID	SequenceName
M00057071A:B04	ES 189	624133	1885.O02.gz43_239036
M00057071C:G10	ES 189	469852	1885.O15.gz43_239244
M00057071D:E01	ES 189	447758	1885.O21.gz43_239340
M00057071D:G01	ES 189	732351	1885.O22.gz43_239356
M00057072A:C06	ES 189	456530	1885.P02.gz43_239037
M00057072A:G04	ES 189	448727	1885.P04.gz43_239069
M00057072B:E02	ES 189	422687	1885.P08.gz43_239133
M00057072C:A03	ES 189	452224	1885.P10.gz43_239165
M00057072C:A09	ES 189	735283	1885.P12.gz43_239197
M00057072C:C02	ES 189	734787	1885.P14.gz43_239229
M00057072C:H01	ES 189	631526	1885.P18.gz43_239293
M00057073A:B12	ES 189	620159	1885.P22.gz43_239357
M00057073D:H05	ES 189	732487	1886.A18.gz43_239662
M00057077A:A07	ES 189	630291	1886.C24.gz43_239760
M00057077B:B06	ES 189	639629	1886.D03.gz43_239425
M00057077B:D02	ES 189	726786	1886.D06.gz43_239473
M00057078A:E06	ES 189	450563	1886.D19.gz43_239681
M00057079A:F05	ES 189	556212	1886.E23.gz43_239746
M00057082C:G03	ES 189	368965	1886.H07.gz43_239493
M00057087B:A07	ES 189	733910	1886.L03.gz43_239433
M00057087B:G10	ES 189	727461	1886.L05.gz43_239465
M00057087D:B04	ES 189	734059	1886.L13.gz43_239593
M00057088B:E02	ES 189	731358	1886.M02.gz43_239418
M00057089B:D01	ES 189	538582	1886.M20.gz43_239706
M00057089D:E03	ES 189	731966	1886.M24.gz43_239770
M00057090A:B02	ES 189	473588	1886.N04.gz43_239451
M00057090A:C03	ES 189	727407	1886.N05.gz43_239467
M00057091D:F11	ES 189	732131	1886.O22.gz43_239740
M00057092A:H02	ES 189	729446	1886.P06.gz43_239485
M00057092C:A05	ES 189	419465	1886.P15.gz43_239629
M00057092C:B10	ES 189	729792	1886.P16.gz43_239645
M00057093C:A02	ES 189	553898	1887.A08.gz43_239903
M00057093C:E01	ES 189	736634	1887.A11.gz43_239951
M00057093D:A11	ES 189	557606	1887.A17.gz43_240047
M00057094B:D07	ES 189	533689	1887.B05.gz43_239856
M00057095A:F11	ES 189	735113	1887.B21.gz43_240112
M00057095B:G03	ES 189	732873	1887.C02.gz43_239809
M00057096B:C05	ES 189	477387	1887.C20.gz43_240097
M00057096B:E06	ES 189	730697	1887.C23.gz43_240145
M00057096C:B08	ES 189	731477	1887.D04.gz43_239842
M00057096D:H05	ES 189	457842	1887.D11.gz43_239954
M00057097B:E02	ES 189	729222	1887.D20.gz43_240098
M00057098A:A04	ES 189	560885	1887.E11.gz43_239955
M00057099A:C04	ES 189	644354	1887.F09.gz43_239924

Table 13

CloneID	ES No	ClusterID	SequenceName
M00057099A:H12	ES 189	645139	1887.F10.gz43_239940
M00057099B:A06	ES 189	654475	1887.F11.gz43_239956
M00057099B:D02	ES 189	733148	1887.F15.gz43_240020
M00057099B:H11	ES 189	630655	1887.F18.gz43_240068
M00057099C:A06	ES 189	733972	1887.F20.gz43_240100
M00057099D:D11	ES 189	732550	1887.G02.gz43_239813
M00057100C:F02	ES 189	735584	1887.G18.gz43_240069
M00057100C:F03	ES 189	559361	1887.G19.gz43_240085
M00057100D:B06	ES 189	736409	1887.H02.gz43_239814
M00057100D:E09	ES 189	735515	1887.H05.gz43_239862
M00057102A:F12	ES 189	485441	1887.I04.gz43_239847
M00057102B:E12	ES 189	543772	1887.I12.gz43_239975
M00057102D:C11	ES 189	452276	1887.I17.gz43_240055
M00057103A:F11	ES 189	650920	1887.I21.gz43_240119
M00057103A:G01	ES 189	737031	1887.I22.gz43_240135
M00057104A:H06	ES 189	448325	1887.J19.gz43_240088
M00057104D:A02	ES 189	731697	1887.K09.gz43_239929
M00057105C:C06	ES 189	516799	1887.L07.gz43_239898
M00057105C:G02	ES 189	734344	1887.L12.gz43_239978
M00057105D:C10	ES 189	733209	1887.L14.gz43_240010
M00057106A:H04	ES 189	678846	1887.M06.gz43_239883
M00057108B:A12	ES 189	693869	1887.N12.gz43_239980
M00057109A:B02	ES 189	729992	1887.O06.gz43_239885
M00057109A:F11	ES 189	732885	1887.O10.gz43_239949
M00057109A:H09	ES 189	733348	1887.O12.gz43_239981
M00057109C:D10	ES 189	732312	1887.O19.gz43_240093
M00057110A:A03	ES 189	729560	1887.O24.gz43_240173
M00057110A:E12	ES 189	651121	1887.P02.gz43_239822
M00057110C:A04	ES 189	638908	1887.P06.gz43_239886
M00057110C:B09	ES 189	736009	1887.P08.gz43_239918
M00057110D:E12	ES 189	736220	1887.P17.gz43_240062
M00057112A:C12	ES 189	415825	1888.A01.gz43_240175
M00057112D:G08	ES 189	724952	1888.A18.gz43_240447
M00057113A:A08	ES 189	733171	1888.A20.gz43_240479
M00057113B:F03	ES 189	551624	1888.A23.gz43_240527
M00057114C:E07	ES 189	735018	1888.B20.gz43_240480
M00057114C:F08	ES 189	728479	1888.B21.gz43_240496
M00057115B:G06	ES 189	734737	1888.C18.gz43_240449
M00057115C:B11	ES 189	643517	1888.C19.gz43_240465
M00057115D:C10	ES 189	733225	1888.D01.gz43_240178
M00057115D:D06	ES 189	732113	1888.D02.gz43_240194
M00057115D:F06	ES 189	602673	1888.D05.gz43_240242
M00057116A:B06	ES 189	732896	1888.D07.gz43_240274
M00057116C:H09	ES 189	732476	1888.D23.gz43_240530

Table 13

CloneID	ES No	ClusterID	SequenceName
M00057116D:B10	ES 189	474108	1888.D24.gz43_240546
M00057117D:H06	ES 189	733802	1888.E21.gz43_240499
M00057118B:B04	ES 189	602012	1888.F02.gz43_240196
M00057118B:E10	ES 189	553264	1888.F06.gz43_240260
M00057120A:D01	ES 189	555655	1888.G06.gz43_240261
M00057120B:E08	ES 189	730565	1888.G11.gz43_240341
M00057120C:B09	ES 189	453733	1888.G12.gz43_240357
M00057120C:F08	ES 189	609459	1888.G14.gz43_240389
M00057121B:H10	ES 189	553338	1888.H09.gz43_240310
M00057121C:E08	ES 189	552783	1888.H12.gz43_240358
M00057122A:A07	ES 189	639923	1888.H17.gz43_240438
M00057122A:C04	ES 189	647374	1888.H18.gz43_240454
M00057122A:C11	ES 189	733006	1888.H19.gz43_240470
M00057122B:F04	ES 189	656263	1888.H23.gz43_240534
M00057122C:H08	ES 190	418482	1888.I06.gz43_240263
M00057122D:A01	ES 190	733365	1888.I07.gz43_240279
M00057123A:F09	ES 190	732937	1888.I12.gz43_240359
M00057123A:H09	ES 190	729299	1888.I15.gz43_240407
M00057123C:D03	ES 190	569256	1888.I18.gz43_240455
M00057123D:F07	ES 190	734606	1888.I22.gz43_240519
M00057124A:G08	ES 190	736539	1888.J04.gz43_240232
M00057125A:A07	ES 190	726575	1888.J21.gz43_240504
M00057125A:A12	ES 190	449770	1888.J22.gz43_240520
M00057125A:F07	ES 190	727142	1888.J24.gz43_240552
M00057125C:B11	ES 190	736534	1888.K06.gz43_240265
M00057125C:E02	ES 190	730122	1888.K10.gz43_240329
M00057125D:B02	ES 190	542490	1888.K12.gz43_240361
M00057125D:B09	ES 190	729519	1888.K13.gz43_240377
M00057126C:C05	ES 190	662617	1888.K23.gz43_240537
M00057126D:A04	ES 190	568632	1888.L03.gz43_240218
M00057127A:E10	ES 190	553087	1888.L12.gz43_240362
M00057127A:H10	ES 190	735959	1888.L15.gz43_240410
M00057127B:D10	ES 190	454961	1888.L18.gz43_240458
M00057127C:F03	ES 190	447692	1888.L24.gz43_240554
M00057128A:B04	ES 190	556867	1888.M08.gz43_240299
M00057128C:H02	ES 190	735514	1888.M24.gz43_240555
M00057129D:D07	ES 190	440284	1888.N24.gz43_240556
M00057129D:F03	ES 190	451764	1888.O06.gz43_240269
M00057130A:A02	ES 190	736548	1888.O08.gz43_240301
M00057130A:A11	ES 190	288535	1888.O10.gz43_240333
M00057130A:D10	ES 190	736810	1888.O14.gz43_240397
M00057131D:D02	ES 190	726176	1888.P17.gz43_240446
M00057131D:D07	ES 190	735131	1888.P18.gz43_240462

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CloneID	ES No	ClusterID	SequenceName
M00057132B:H05	ES 190	639644	1897.A02.gz43_240575
M00057132C:C04	ES 190	733951	1897.A04.gz43_240607
M00057133A:B07	ES 190	550227	1897.A15.gz43_240783
M00057133C:B02	ES 190	536225	1897.B05.gz43_240624
M00057134B:D06	ES 190	472068	1897.C03.gz43_240593
M00057135A:B02	ES 190	735989	1897.C23.gz43_240913
M00057135A:H03	ES 190	732544	1897.D01.gz43_240562
M00057135D:D01	ES 190	731476	1897.D12.gz43_240738
M00057136A:F01	ES 190	726810	1897.D18.gz43_240834
M00057136B:F06	ES 190	514142	1897.D21.gz43_240882
M00057137A:C01	ES 190	562008	1897.E02.gz43_240579
M00057137A:H12	ES 190	225960	1897.E06.gz43_240643
M00057137B:C07	ES 190	640662	1897.E12.gz43_240739
M00057138A:F02	ES 190	736288	1897.F05.gz43_240628
M00057138B:B02	ES 190	642273	1897.F09.gz43_240692
M00057138B:H02	ES 190	543772	1897.F12.gz43_240740
M00057138C:D06	ES 190	723853	1897.F15.gz43_240788
M00057138D:F03	ES 190	736318	1897.F18.gz43_240836
M00057138D:F10	ES 190	726440	1897.F19.gz43_240852
M00057139A:B10	ES 190	489001	1897.F23.gz43_240916
M00057139A:G08	ES 190	568031	1897.G02.gz43_240581
M00057139A:G12	ES 190	492691	1897.G04.gz43_240613
M00057139D:G07	ES 190	731317	1897.G19.gz43_240853
M00057140B:H01	ES 190	655327	1897.H08.gz43_240678
M00057140D:B03	ES 190	500758	1897.H15.gz43_240790
M00057140D:F02	ES 190	567005	1897.H17.gz43_240822
M00057141A:D09	ES 190	732965	1897.H20.gz43_240870
M00057141A:G06	ES 190	462779	1897.H23.gz43_240918
M00057142A:H07	ES 190	449035	1897.I18.gz43_240839
M00057142B:F06	ES 190	559004	1897.I22.gz43_240903
M00057144B:B07	ES 190	735087	1897.K12.gz43_240745
M00057144B:D04	ES 190	658271	1897.K13.gz43_240761
M00057144B:F10	ES 190	591449	1897.K16.gz43_240809
M00057144B:H10	ES 190	523171	1897.K17.gz43_240825
M00057144C:A02	ES 190	486076	1897.K18.gz43_240841
M00057144C:G04	ES 190	567122	1897.K23.gz43_240921
M00057144C:G08	ES 190	470684	1897.K24.gz43_240937
M00057144D:D03	ES 190	555960	1897.L02.gz43_240586
M00057145B:B07	ES 190	735131	1897.L12.gz43_240746
M00057145B:E06	ES 190	642570	1897.L14.gz43_240778
M00057145C:H03	ES 190	448202	1897.L22.gz43_240906
M00057145D:E01	ES 190	462779	1897.M02.gz43_240587
M00057146A:H05	ES 190	735801	1897.M12.gz43_240747
M00057146B:C06	ES 190	735283	1897.M13.gz43_240763

Table 13

CloneID	ES No	ClusterID	SequenceName
M00057146B:H12	ES 190	397515	1897.M17.gz43_240827
M00057146D:F05	ES 190	549461	1897.M24.gz43_240939
M00057147A:B07	ES 190	728413	1897.N03.gz43_240604
M00057147A:E11	ES 190	642936	1897.N06.gz43_240652
M00057147A:H07	ES 190	735729	1897.N08.gz43_240684
M00057147C:B01	ES 190	457846	1897.N12.gz43_240748
M00057147C:G01	ES 190	730190	1897.N14.gz43_240780
M00057147D:H09	ES 190	718314	1897.N22.gz43_240908
M00057148B:G07	ES 190	621226	1897.O05.gz43_240637
M00057148C:B02	ES 190	549285	1897.O09.gz43_240701
M00057148C:C09	ES 190	736318	1897.O12.gz43_240749
M00057149A:A04	ES 190	729843	1897.O18.gz43_240845
M00057149B:B07	ES 190	519378	1897.P03.gz43_240606
M00057149B:B08	ES 190	448212	1897.P04.gz43_240622
M00057149C:H01	ES 190	735756	1897.P11.gz43_240734
M00057150D:C04	ES 190	447003	1898.A03.gz43_242227
M00057150D:F08	ES 190	450724	1898.A05.gz43_242259
M00057151A:B04	ES 190	650297	1898.A06.gz43_242275
M00057152B:H02	ES 190	480307	1898.B05.gz43_242260
M00057152C:C10	ES 190	640603	1898.B10.gz43_242340
M00057152C:C12	ES 190	527789	1898.B12.gz43_242372
M00057153B:A04	ES 190	734484	1898.B22.gz43_242532
M00057153B:D02	ES 190	734808	1898.B24.gz43_242564
M00057153B:G07	ES 190	596809	1898.C02.gz43_242213
M00057153D:H01	ES 190	551654	1898.C15.gz43_242421
M00057154C:F04	ES 190	456816	1898.C21.gz43_242517
M00057154D:H07	ES 190	400314	1898.C23.gz43_242549
M00057155A:E11	ES 190	730661	1898.D04.gz43_242246
M00057155A:G11	ES 190	730341	1898.D07.gz43_242294
M00057155A:H07	ES 190	640563	1898.D08.gz43_242310
M00057155C:B07	ES 190	735993	1898.D12.gz43_242374
M00057155C:G04	ES 190	558477	1898.D15.gz43_242422
M00057155C:H07	ES 190	448510	1898.D16.gz43_242438
M00057155D:E12	ES 190	480142	1898.D22.gz43_242534
M00057156B:D10	ES 190	491933	1898.E06.gz43_242279
M00057156C:E08	ES 190	552972	1898.E10.gz43_242343
M00057156D:F02	ES 190	734928	1898.E17.gz43_242455
M00057157D:H08	ES 190	727608	1898.F05.gz43_242264
M00057158B:C02	ES 190	736030	1898.F10.gz43_242344
M00057158C:C10	ES 190	727976	1898.F17.gz43_242456
M00057158C:G05	ES 190	736790	1898.F19.gz43_242488
M00057159C:E11	ES 190	736228	1898.G11.gz43_242361
M00057160A:C02	ES 190	567122	1898.G16.gz43_242441
M00057160A:F11	ES 190	736940	1898.G18.gz43_242473

Table 13

CloneID	ES No	ClusterID	SequenceName
M00057160B:G08	ES 190	454073	1898.G22.gz43_242537
M00057160D:A11	ES 190	461316	1898.H04.gz43_242250
M00057161B:D02	ES 190	402516	1898.H12.gz43_242378
M00057161B:E07	ES 190	735756	1898.H14.gz43_242410
M00057161B:F04	ES 190	448381	1898.H16.gz43_242442
M00057161D:H08	ES 190	730377	1898.I06.gz43_242283
M00057162B:E10	ES 190	728353	1898.I15.gz43_242427
M00057162C:C01	ES 190	735633	1898.I21.gz43_242523
M00057163A:D11	ES 190	483529	1898.J08.gz43_242316
M00057163A:E09	ES 190	607351	1898.J09.gz43_242332
M00057163C:D06	ES 190	736288	1898.J16.gz43_242444
M00057165C:E01	ES 190	736878	1898.L21.gz43_242526
M00057165C:E08	ES 190	599714	1898.L22.gz43_242542
M00057165C:F05	ES 190	723915	1898.L23.gz43_242558
M00057165D:H05	ES 190	648820	1898.M11.gz43_242367
M00057166B:B07	ES 190	736634	1898.M15.gz43_242431
M00057166B:F05	ES 190	448563	1898.M20.gz43_242511
M00057166B:G06	ES 190	737042	1898.M22.gz43_242543
M00057166C:A10	ES 190	449529	1898.N03.gz43_242240
M00057167A:D08	ES 190	726448	1898.N13.gz43_242400
M00057167C:A05	ES 190	732253	1898.N22.gz43_242544
M00057168B:D02	ES 190	583625	1898.O12.gz43_242385
M00057168C:D03	ES 190	737006	1898.O23.gz43_242561
M00057169A:F05	ES 190	649852	1898.P05.gz43_242274
M00057169A:F06	ES 190	733552	1898.P06.gz43_242290
M00057169C:H10	ES 190	737006	1898.P15.gz43_242434
M00057169C:H12	ES 190	734794	1898.P16.gz43_242450
M00057170A:D06	ES 190	733972	1899.A01.gz43_242579
M00057170A:D11	ES 190	471887	1898.P24.gz43_242578
M00057170A:H04	ES 190	730220	1899.A06.gz43_242659
M00057170B:G01	ES 190	734724	1899.A11.gz43_242739
M00057170C:C01	ES 190	725691	1899.A14.gz43_242787
M00057170D:B08	ES 190	480623	1899.A23.gz43_242931
M00057172A:B02	ES 190	723985	1899.B19.gz43_242868
M00057172A:B04	ES 190	549128	1899.B20.gz43_242884
M00057172A:H06	ES 190	639507	1899.B22.gz43_242916
M00057172D:F08	ES 190	473238	1899.C09.gz43_242709
M00057173A:C07	ES 190	528404	1899.C11.gz43_242741
M00057173C:C07	ES 190	535866	1899.C21.gz43_242901
M00057173D:B12	ES 190	562453	1899.D02.gz43_242598
M00057173D:C07	ES 190	729039	1899.D03.gz43_242614
M00057173D:E04	ES 190	422590	1899.D04.gz43_242630
M00057174B:C06	ES 190	734209	1899.D11.gz43_242742
M00057174B:C11	ES 190	561632	1899.D13.gz43_242774

Table 13

CloneID	ES No	ClusterID	SequenceName
M00057174B:F11	ES 190	421794	1899.D15.gz43_242806
M00057174B:G03	ES 190	734744	1899.D16.gz43_242822
M00057174B:G12	ES 190	448770	1899.D17.gz43_242838
M00057174C:G07	ES 190	648221	1899.D21.gz43_242902
M00057175B:G12	ES 190	732625	1899.E08.gz43_242695
M00057175C:D02	ES 190	731370	1899.E13.gz43_242775
M00057175C:F01	ES 190	451812	1899.E16.gz43_242823
M00057175D:A12	ES 190	532904	1899.E17.gz43_242839
M00057175D:E12	ES 190	451383	1899.E22.gz43_242919
M00057176A:A04	ES 190	734692	1899.F01.gz43_242584
M00057176A:C02	ES 190	735235	1899.F03.gz43_242616
M00057176A:H10	ES 190	735764	1899.F07.gz43_242680
M00057176A:H12	ES 190	462986	1899.F08.gz43_242696
M00057176B:B07	ES 190	639779	1899.F11.gz43_242744
M00057176B:F10	ES 190	735605	1899.F16.gz43_242824
M00057176C:H08	ES 190	573733	1899.F19.gz43_242872
M00057176D:A03	ES 190	625988	1899.F20.gz43_242888
M00057177C:D07	ES 190	625988	1899.G12.gz43_242761
M00057177C:G11	ES 190	480142	1899.G13.gz43_242777
M00057177C:H04	ES 190	732429	1899.G15.gz43_242809
M00057177D:G05	ES 190	734726	1899.G22.gz43_242921
M00057179C:B05	ES 190	449548	1899.H05.gz43_242650
M00057179C:G10	ES 190	482512	1899.H08.gz43_242698
M00057179D:B09	ES 190	494423	1899.H09.gz43_242714
M00057180A:H11	ES 190	530883	1899.H15.gz43_242810
M00057180B:C06	ES 190	718314	1899.H18.gz43_242858
M00057180B:D01	ES 190	475872	1899.H19.gz43_242874
M00057180B:F05	ES 190	736280	1899.H21.gz43_242906
M00057180B:G06	ES 190	674526	1899.H23.gz43_242938
M00057180B:H05	ES 190	550588	1899.H24.gz43_242954
M00057180C:F09	ES 190	736309	1899.I06.gz43_242667
M00057180D:C10	ES 191	735789	1899.I09.gz43_242715
M00057180D:G06	ES 191	488447	1899.I11.gz43_242747
M00057181C:D10	ES 191	554221	1899.J01.gz43_242588
M00057181C:G07	ES 191	560183	1899.J03.gz43_242620
M00057181D:C09	ES 191	735801	1899.J07.gz43_242684
M00057181D:H07	ES 191	452243	1899.J11.gz43_242748
M00057182A:H07	ES 191	737116	1899.J18.gz43_242860
M00057182B:D09	ES 191	736773	1899.J22.gz43_242924
M00057182C:C03	ES 191	642936	1899.K04.gz43_242637
M00057182C:C11	ES 191	373615	1899.K06.gz43_242669
M00057182D:A08	ES 191	477098	1899.K07.gz43_242685
M00057182D:B11	ES 191	736595	1899.K09.gz43_242717

Table 13

CloneID	ES No	ClusterID	SequenceName
M00057186A:B03	ES 191	732244	1899.K14.gz43_242797
M00057186A:E12	ES 191	560568	1899.K17.gz43_242845
M00057186B:E07	ES 191	636748	1899.K22.gz43_242925
M00057189A:A08	ES 191	735871	1899.L05.gz43_242654
M00057189C:G11	ES 191	736354	1899.L20.gz43_242894
M00057189D:B08	ES 191	733623	1899.L22.gz43_242926
M00057189D:G08	ES 191	554683	1899.M02.gz43_242607
M00057191A:H09	ES 191	734031	1899.M07.gz43_242687
M00057191B:C06	ES 191	735514	1899.M09.gz43_242719
M00057191C:D02	ES 191	727523	1899.M14.gz43_242799
M00057191D:B08	ES 191	463402	1899.M17.gz43_242847
M00057191D:G10	ES 191	734928	1899.M22.gz43_242927
M00057192A:B04	ES 191	730805	1899.M23.gz43_242943
M00057192A:D05	ES 191	724061	1899.M24.gz43_242959
M00057192A:D12	ES 191	735426	1899.N01.gz43_242592
M00057192A:F01	ES 191	474346	1899.N02.gz43_242608
M00057192A:H05	ES 191	730106	1899.N04.gz43_242640
M00057192B:D10	ES 191	419711	1899.N07.gz43_242688
M00057192C:B11	ES 191	730899	1899.N10.gz43_242736
M00057192D:C10	ES 191	734724	1899.N13.gz43_242784
M00057192D:G02	ES 191	726786	1899.N16.gz43_242832
M00057192D:G04	ES 191	736402	1899.N17.gz43_242848
M00057193B:C11	ES 191	156329	1899.N21.gz43_242912
M00057193C:F11	ES 191	640635	1899.O06.gz43_242673
M00057193D:F06	ES 191	630516	1899.O09.gz43_242721
M00057194A:B07	ES 191	734061	1899.O11.gz43_242753
M00057194A:C06	ES 191	736049	1899.O13.gz43_242785
M00057194A:F01	ES 191	725089	1899.O16.gz43_242833
M00057194A:H01	ES 191	724061	1899.O18.gz43_242865
M00057194B:E05	ES 191	721768	1899.O21.gz43_242913
M00057194B:H08	ES 191	728061	1899.O24.gz43_242961
M00057194C:A03	ES 191	454812	1899.P01.gz43_242594
M00057194C:F02	ES 191	736861	1899.P05.gz43_242658
M00057194C:F10	ES 191	390968	1899.P07.gz43_242690
M00057194D:C12	ES 191	552055	1899.P10.gz43_242738
M00057196A:E03	ES 191	729173	1899.P15.gz43_242818
M00057196B:H10	ES 191	516729	1899.P17.gz43_242850
M00057197D:H10	ES 191	735797	1900.A14.gz43_243171
M00057198B:C02	ES 191	161489	1900.A20.gz43_243267
M00057199B:B06	ES 191	516729	1900.B08.gz43_243076
M00057199C:H08	ES 191	483061	1900.B12.gz43_243140
M00057200B:D04	ES 191	532904	1900.B22.gz43_243300
M00057200D:E03	ES 191	730308	1900.C04.gz43_243013
M00057201A:H03	ES 191	725905	1900.C12.gz43_243141

Table 13

CloneID	ES No	ClusterID	SequenceName
M00057201B:H10	ES 191	494423	1900.C20.gz43_243269
M00057202A:D05	ES 191	446752	1900.D06.gz43_243046
M00057203B:F08	ES 191	552457	1900.E02.gz43_242983
M00057203C:A09	ES 191	734993	1900.E04.gz43_243015
M00057203D:A09	ES 191	689424	1900.E08.gz43_243079
M00057204A:F11	ES 191	736276	1900.E15.gz43_243191
M00057204C:G06	ES 191	561626	1900.E24.gz43_243335
M00057205D:G06	ES 191	734226	1900.F20.gz43_243272
M00057206A:C06	ES 191	640350	1900.G01.gz43_242969
M00057207A:A07	ES 191	736500	1900.G20.gz43_243273
M00057207B:F06	ES 191	562320	1900.H04.gz43_243018
M00057208B:H08	ES 191	731531	1900.I08.gz43_243083
M00057208C:E12	ES 191	732771	1900.I14.gz43_243179
M00057210A:C12	ES 191	726449	1900.K01.gz43_242973
M00057210C:D09	ES 191	736778	1900.K08.gz43_243085
M00057210C:G07	ES 191	730109	1900.K12.gz43_243149
M00057211A:D01	ES 191	733272	1900.K20.gz43_243277
M00057211B:A08	ES 191	648379	1900.K22.gz43_243309
M00057211B:C09	ES 191	653616	1900.K24.gz43_243341
M00057211B:G01	ES 191	559754	1900.L04.gz43_243022
M00057211C:C06	ES 191	736738	1900.L06.gz43_243054
M00057211C:F05	ES 191	451176	1900.L09.gz43_243102
M00057212B:D05	ES 191	450284	1900.L23.gz43_243326
M00057213C:D06	ES 191	648757	1900.M12.gz43_243151
M00057214A:B05	ES 191	736497	1900.M19.gz43_243263
M00057214B:B12	ES 191	649490	1900.M22.gz43_243311
M00057216C:D12	ES 191	194769	1900.N22.gz43_243312
M00057216D:D05	ES 191	556656	1900.O04.gz43_243025
M00057216D:E12	ES 191	642985	1900.O06.gz43_243057
M00057216D:F10	ES 191	639395	1900.O07.gz43_243073
M00057217A:A12	ES 191	724638	1900.O10.gz43_243121
M00057217B:F12	ES 191	449078	1900.O19.gz43_243265
M00057217D:A06	ES 191	712120	1900.P10.gz43_243122
M00057218C:F10	ES 191	454129	1909.A04.gz43_243395
M00057219A:D05	ES 191	726251	1909.A09.gz43_243475
M00057219A:D07	ES 191	733151	1909.A10.gz43_243491
M00057219A:E11	ES 191	733309	1909.A12.gz43_243523
M00057219A:H11	ES 191	736988	1909.A13.gz43_243539
M00057219B:B10	ES 191	591979	1909.A14.gz43_243555
M00057219B:C06	ES 191	474869	1909.A15.gz43_243571
M00057219D:C02	ES 191	737010	1909.A23.gz43_243699
M00057219D:G11	ES 191	380310	1909.B03.gz43_243380
M00057219D:H04	ES 191	733868	1909.B04.gz43_243396
M00057220A:C06	ES 191	472811	1909.B08.gz43_243460

Table 13

CloneID	ES No	ClusterID	SequenceName
M00057220A:D09	ES 191	642631	1909.B09.gz43_243476
M00057220B:A06	ES 191	613067	1909.B13.gz43_243540
M00057220B:G01	ES 191	476866	1909.B17.gz43_243604
M00057220B:G10	ES 191	735622	1909.B18.gz43_243620
M00057220C:A08	ES 191	556852	1909.B20.gz43_243652
M00057220C:F08	ES 191	735514	1909.B23.gz43_243700
M00057220D:E06	ES 191	465697	1909.C03.gz43_243381
M00057220D:F02	ES 191	735510	1909.C04.gz43_243397
M00057220D:F06	ES 191	736076	1909.C05.gz43_243413
M00057221A:E10	ES 191	453587	1909.C10.gz43_243493
M00057221B:B01	ES 191	631111	1909.C12.gz43_243525
M00057221B:E11	ES 191	735306	1909.C15.gz43_243573
M00057221C:E07	ES 191	553850	1909.C22.gz43_243685
M00057221C:F02	ES 191	418682	1909.C23.gz43_243701
M00057222B:A06	ES 191	398061	1909.D05.gz43_243414
M00057222D:C10	ES 191	735514	1909.D11.gz43_243510
M00057223A:F06	ES 191	732899	1909.D17.gz43_243606
M00057223B:A07	ES 191	734609	1909.D21.gz43_243670
M00057223B:B04	ES 191	736894	1909.D22.gz43_243686
M00057223B:G01	ES 191	726892	1909.E03.gz43_243383
M00057223C:A01	ES 191	549578	1909.E05.gz43_243415
M00057223C:B01	ES 191	727255	1909.E06.gz43_243431
M00057223D:H03	ES 191	736738	1909.E13.gz43_243543
M00057224A:D07	ES 191	454355	1909.E16.gz43_243591
M00057224B:H02	ES 191	727558	1909.E24.gz43_243719
M00057224C:B02	ES 191	475562	1909.F02.gz43_243368
M00057225A:C08	ES 191	550121	1909.F10.gz43_243496
M00057225A:E03	ES 191	602673	1909.F11.gz43_243512
M00057225C:F09	ES 191	734562	1909.F23.gz43_243704
M00057225C:H07	ES 191	734828	1909.G01.gz43_243353
M00057225D:E01	ES 191	734690	1909.G05.gz43_243417
M00057226A:B04	ES 191	646552	1909.G13.gz43_243545
M00057226A:E09	ES 191	374125	1909.G16.gz43_243593
M00057226C:A09	ES 191	734915	1909.G23.gz43_243705
M00057226C:E05	ES 191	427113	1909.H01.gz43_243354
M00057226C:F05	ES 191	175524	1909.H02.gz43_243370
M00057226C:F12	ES 191	642940	1909.H04.gz43_243402
M00057226C:H10	ES 191	648140	1909.H08.gz43_243466
M00057226D:B03	ES 191	735050	1909.H10.gz43_243498
M00057226D:C10	ES 191	735172	1909.H11.gz43_243514
M00057227B:A05	ES 191	732159	1909.H20.gz43_243658
M00057227B:D12	ES 191	560399	1909.H23.gz43_243706
M00057227B:H04	ES 191	607202	1909.H24.gz43_243722
M00057229A:B03	ES 191	632499	1909.I06.gz43_243435

Table 13

CloneID	ES No	ClusterID	SequenceName
M00057229B:F11	ES 191	647815	1909.I11.gz43_243515
M00057229B:G11	ES 191	650599	1909.I12.gz43_243531
M00057230B:B07	ES 191	616985	1909.I21.gz43_243675
M00057230B:F10	ES 191	641510	1909.I24.gz43_243723
M00057230C:C05	ES 191	723959	1909.J03.gz43_243388
M00057230C:G12	ES 191	598087	1909.J09.gz43_243484
M00057230D:C05	ES 191	456224	1909.J12.gz43_243532
M00057231A:D04	ES 191	733149	1909.J17.gz43_243612
M00057231A:G04	ES 191	405546	1909.J22.gz43_243692
M00057231B:A01	ES 191	561877	1909.K01.gz43_243357
M00057231C:B04	ES 191	735749	1909.K02.gz43_243373
M00057231C:E06	ES 191	737010	1909.K06.gz43_243437
M00057231C:F12	ES 191	398061	1909.K09.gz43_243485
M00057231C:G04	ES 191	735140	1909.K10.gz43_243501
M00057231D:A04	ES 191	639565	1909.K14.gz43_243565
M00057231D:A05	ES 191	732736	1909.K15.gz43_243581
M00057231D:F10	ES 191	486051	1909.K22.gz43_243693
M00057232B:G02	ES 191	728121	1909.L06.gz43_243438
M00057232D:B03	ES 191	555336	1909.L12.gz43_243534
M00057232D:B05	ES 191	735131	1909.L13.gz43_243550
M00057233A:C04	ES 191	724417	1909.L15.gz43_243582
M00057233B:G04	ES 191	454563	1909.M01.gz43_243359
M00057233D:G12	ES 191	463513	1909.M09.gz43_243487
M00057234B:F06	ES 191	727532	1909.M18.gz43_243631
M00057234C:D11	ES 191	664711	1909.M23.gz43_243711
M00057234D:A12	ES 191	733874	1909.N03.gz43_243392
M00057234D:C09	ES 191	726760	1909.N04.gz43_243408
M00057234D:E04	ES 191	601051	1909.N05.gz43_243424
M00057235B:A07	ES 191	731467	1909.N14.gz43_243568
M00057235C:C08	ES 191	734151	1909.N21.gz43_243680
M00057235C:F03	ES 191	734553	1909.N22.gz43_243696
M00057235D:A05	ES 191	733160	1909.O01.gz43_243361
M00057235D:C03	ES 191	417822	1909.O03.gz43_243393
M00057236A:F08	ES 191	450340	1909.O10.gz43_243505
M00057236B:D11	ES 191	725120	1909.O13.gz43_243553
M00057236C:C07	ES 191	453132	1909.O19.gz43_243649
M00057236D:H09	ES 191	625810	1909.P01.gz43_243362
M00057237B:D10	ES 191	735817	1909.P10.gz43_243506
M00057237D:C11	ES 191	724781	1909.P19.gz43_243650
M00057237D:D09	ES 191	473578	1909.P22.gz43_243698
M00057238A:D07	ES 191	641680	1910.A03.gz43_243763
M00057238B:F05	ES 191	551437	1910.A09.gz43_243859
M00057239B:F05	ES 191	647704	1910.B07.gz43_243828
M00057239C:E05	ES 191	734466	1910.B10.gz43_243876

Table 13

CloneID	ES No	ClusterID	SequenceName
M00057239C:G07	ES 191	729125	1910.B13.gz43_243924
M00057239D:D01	ES 191	456753	1910.B16.gz43_243972
M00057240A:F03	ES 191	730028	1910.C01.gz43_243733
M00057240B:C01	ES 191	730046	1910.C06.gz43_243813
M00042351A:H03	ES 192	499660	1923.A02.gz43_252631
M00042351C:G01	ES 192	498777	1923.A05.gz43_252679
M00042351C:G11	ES 192	452094	1923.A06.gz43_252695
M00042351D:D02	ES 192	496446	1923.A09.gz43_252743
M00042351D:F08	ES 192	451429	1923.A10.gz43_252759
M00057240C:A06	ES 192	733855	1910.C13.gz43_243925
M00057241B:B04	ES 192	734094	1910.D01.gz43_243734
M00057241D:C04	ES 192	734226	1910.D08.gz43_243846
M00057241D:G01	ES 192	733945	1910.D14.gz43_243942
M00057242A:H11	ES 192	734808	1910.D19.gz43_244022
M00057242B:F07	ES 192	735477	1910.D21.gz43_244054
M00057242C:G12	ES 192	611604	1910.E01.gz43_243735
M00057242D:C07	ES 192	650067	1910.E06.gz43_243815
M00057242D:F10	ES 192	453454	1910.E09.gz43_243863
M00057243A:H03	ES 192	457846	1910.E15.gz43_243959
M00057243C:D01	ES 192	733552	1910.F02.gz43_243752
M00057243C:H11	ES 192	734884	1910.F06.gz43_243816
M00057244C:D08	ES 192	481273	1910.F22.gz43_244072
M00057244C:E06	ES 192	455821	1910.F24.gz43_244104
M00057245A:F03	ES 192	555641	1910.G07.gz43_243833
M00057245B:A08	ES 192	43349	1910.G10.gz43_243881
M00057245B:E02	ES 192	484964	1910.G12.gz43_243913
M00057245D:G02	ES 192	476455	1910.G20.gz43_244041
M00057246A:G11	ES 192	558617	1910.H01.gz43_243738
M00057246C:B12	ES 192	733991	1910.H12.gz43_243914
M00057246D:G09	ES 192	563313	1910.H18.gz43_244010
M00057247C:B11	ES 192	734849	1910.I03.gz43_243771
M00057247C:C11	ES 192	732859	1910.I04.gz43_243787
M00057247C:F10	ES 192	550730	1910.I06.gz43_243819
M00057247D:D10	ES 192	734371	1910.I10.gz43_243883
M00057248A:H10	ES 192	734894	1910.I21.gz43_244059
M00057248B:D11	ES 192	733144	1910.J01.gz43_243740
M00057248C:B08	ES 192	733989	1910.J06.gz43_243820
M00057249A:B05	ES 192	733055	1910.J12.gz43_243916
M00057249A:C06	ES 192	555103	1910.J14.gz43_243948
M00057249C:C07	ES 192	473588	1910.J21.gz43_244060
M00057249D:G03	ES 192	639779	1910.K05.gz43_243805
M00057249D:H09	ES 192	449042	1910.K06.gz43_243821
M00057250B:A03	ES 192	731392	1910.K11.gz43_243901

Table 13

CloneID	ES No	ClusterID	SequenceName
M00057250B:D04	ES 192	726011	1910.K14.gz43_243949
M00057250C:G02	ES 192	735665	1910.K21.gz43_244061
M00057251A:F02	ES 192	514838	1910.L03.gz43_243774
M00057252A:D10	ES 192	731125	1910.L19.gz43_244030
M00057252B:E04	ES 192	647242	1910.M01.gz43_243743
M00057252C:D08	ES 192	732978	1910.M08.gz43_243855
M00057252D:B10	ES 192	639494	1910.M09.gz43_243871
M00057252D:D04	ES 192	585976	1910.M12.gz43_243919
M00057253A:C05	ES 192	731238	1910.M17.gz43_243999
M00057253A:H10	ES 192	735754	1910.M20.gz43_244047
M00057253B:C06	ES 192	725095	1910.M22.gz43_244079
M00057253C:A06	ES 192	729428	1910.N02.gz43_243760
M00057253C:D11	ES 192	735403	1910.N03.gz43_243776
M00057254A:E12	ES 192	477555	1910.N12.gz43_243920
M00057254A:G07	ES 192	557353	1910.N14.gz43_243952
M00057254B:D04	ES 192	552598	1910.N18.gz43_244016
M00057255C:A07	ES 192	558332	1910.O17.gz43_244001
M00057255C:C10	ES 192	732962	1910.O18.gz43_244017
M00057255D:E02	ES 192	449537	1910.O24.gz43_244113
M00057256B:A05	ES 192	661194	1910.P09.gz43_243874
M00057256D:A11	ES 192	649390	1910.P17.gz43_244002
M00057257A:H10	ES 192	726081	1910.P23.gz43_244098
M00057257B:C11	ES 192	514697	1910.P24.gz43_244114
M00057258C:C09	ES 192	731516	1911.A24.gz43_244483
M00057259D:D11	ES 192	420504	1911.B23.gz43_244468
M00057260A:E05	ES 192	630348	1911.C02.gz43_244133
M00057260A:E11	ES 192	728756	1911.C03.gz43_244149
M00057260C:A04	ES 192	734928	1911.C12.gz43_244293
M00057262B:C03	ES 192	482145	1911.D07.gz43_244214
M00057265C:F03	ES 192	725951	1911.D24.gz43_244486
M00057265D:B12	ES 192	735071	1911.E04.gz43_244167
M00057266C:G12	ES 192	554703	1911.E24.gz43_244487
M00057266D:B12	ES 192	733570	1911.F02.gz43_244136
M00057267A:H04	ES 192	731457	1911.F10.gz43_244264
M00057267C:B12	ES 192	650552	1911.F17.gz43_244376
M00057267C:G09	ES 192	735687	1911.F23.gz43_244472
M00057268A:H05	ES 192	640158	1911.G17.gz43_244377
M00057268B:B03	ES 192	652782	1911.G18.gz43_244393
M00057268D:E04	ES 192	446247	1911.H05.gz43_244186
M00057269C:E01	ES 192	725784	1911.H18.gz43_244394
M00057269C:H06	ES 192	732213	1911.H22.gz43_244458
M00057269D:F02	ES 192	586794	1911.I01.gz43_244123
M00057271A:E04	ES 192	480723	1911.J02.gz43_244140
M00057271B:D09	ES 192	450199	1911.J06.gz43_244204

Table 13

CloneID	ES No	ClusterID	SequenceName
M00057272C:D08	ES 192	728790	1911.J23.gz43_244476
M00057273A:C08	ES 192	630655	1911.K04.gz43_244173
M00057273B:A12	ES 192	735834	1911.K10.gz43_244269
M00057273C:F07	ES 192	736294	1911.K14.gz43_244333
M00057273C:F11	ES 192	482985	1911.K15.gz43_244349
M00057273D:A06	ES 192	729321	1911.K19.gz43_244413
M00057273D:B06	ES 192	474691	1911.K20.gz43_244429
M00057274B:C05	ES 192	735249	1911.L06.gz43_244206
M00057274C:G01	ES 192	735676	1911.L13.gz43_244318
M00057275A:G02	ES 192	456011	1911.L21.gz43_244446
M00057275B:A12	ES 192	546642	1911.L24.gz43_244494
M00057275B:B02	ES 192	648710	1911.M01.gz43_244127
M00057277B:C09	ES 192	736014	1911.M11.gz43_244287
M00057277B:E10	ES 192	642142	1911.M12.gz43_244303
M00057279A:G02	ES 192	736014	1911.N04.gz43_244176
M00057280C:B08	ES 192	734849	1911.O01.gz43_244129
M00057281A:D08	ES 192	450692	1911.O11.gz43_244289
M00057281A:H02	ES 192	456065	1911.O12.gz43_244305
M00057283A:E06	ES 192	736860	1911.P04.gz43_244178
M00057283B:D09	ES 192	736860	1911.P10.gz43_244274
M00057283D:B12	ES 192	734131	1911.P23.gz43_244482
M00057283D:D04	ES 192	552249	1911.P24.gz43_244498
M00057287A:H06	ES 192	730187	1912.B21.gz43_244820
M00057287C:B12	ES 192	734546	1912.C01.gz43_244501
M00057290B:A02	ES 192	728768	1912.D08.gz43_244614
M00057290D:G03	ES 192	558045	1912.D16.gz43_244742
M00057291B:D08	ES 192	732300	1912.D24.gz43_244870
M00057291B:H08	ES 192	730189	1912.E03.gz43_244535
M00057292A:B08	ES 192	639427	1912.E19.gz43_244791
M00057292C:C09	ES 192	731910	1912.F03.gz43_244536
M00057293A:H03	ES 192	737109	1912.F12.gz43_244680
M00057293B:H04	ES 192	733856	1912.F16.gz43_244744
M00057299C:A08	ES 192	420402	1912.H10.gz43_244650
M00057299D:E04	ES 192	424672	1912.H15.gz43_244730
M00057300A:A08	ES 192	736449	1912.H17.gz43_244762
M00057300A:B06	ES 192	148201	1912.H18.gz43_244778
M00057301A:A08	ES 192	726430	1912.I11.gz43_244667
M00057302C:D04	ES 192	726874	1912.J18.gz43_244780
M00057305B:B10	ES 192	648738	1912.L05.gz43_244574
M00057309B:E10	ES 192	481930	1912.N06.gz43_244592
M00057314A:A10	ES 192	465528	1921.A01.gz43_244883
M00057314B:H06	ES 192	737114	1921.A07.gz43_244979
M00057314D:E09	ES 192	726692	1921.A16.gz43_245123
M00057314D:F04	ES 192	734894	1921.A17.gz43_245139

Table 13

CloneID	ES No	ClusterID	SequenceName
M00057315D:C06	ES 192	736733	1921.B06.gz43_244964
M00057316A:A08	ES 192	736551	1921.B10.gz43_245028
M00057316A:B04	ES 192	552623	1921.B11.gz43_245044
M00057316A:D09	ES 192	727093	1921.B12.gz43_245060
M00057316C:A06	ES 192	457092	1921.B20.gz43_245188
M00057316D:D02	ES 192	640341	1921.C04.gz43_244933
M00057316D:G04	ES 192	734412	1921.C06.gz43_244965
M00057318A:B02	ES 192	550085	1921.C08.gz43_244997
M00057318B:H05	ES 192	730997	1921.C17.gz43_245141
M00057318C:C12	ES 192	480377	1921.C20.gz43_245189
M00057318C:G04	ES 192	655312	1921.C22.gz43_245221
M00057319D:E06	ES 192	556430	1921.D15.gz43_245110
M00057320A:C03	ES 192	641312	1921.D21.gz43_245206
M00057320A:G08	ES 192	470199	1921.E02.gz43_244903
M00057320B:H03	ES 192	710362	1921.E05.gz43_244951
M00057320D:C02	ES 192	447705	1921.E11.gz43_245047
M00057323A:F01	ES 192	51616	1921.E18.gz43_245159
M00057323B:G04	ES 192	729125	1921.F03.gz43_244920
M00057323B:H08	ES 192	77737	1921.F04.gz43_244936
M00057323D:E10	ES 192	473225	1921.F16.gz43_245128
M00057324A:A09	ES 192	567078	1921.F18.gz43_245160
M00057324A:C08	ES 192	727231	1921.F19.gz43_245176
M00057324B:A06	ES 192	513306	1921.F23.gz43_245240
M00057324B:E04	ES 192	735469	1921.G04.gz43_244937
M00057324C:G05	ES 192	731748	1921.G11.gz43_245049
M00057324D:E10	ES 192	727013	1921.G13.gz43_245081
M00057324D:H03	ES 192	548635	1921.G14.gz43_245097
M00057325B:B09	ES 192	557693	1921.G17.gz43_245145
M00057325B:D06	ES 192	643005	1921.G18.gz43_245161
M00057325B:H04	ES 192	557451	1921.G24.gz43_245257
M00057325C:F03	ES 192	484974	1921.H03.gz43_244922
M00057326A:E11	ES 192	734522	1921.H10.gz43_245034
M00057326D:B10	ES 192	735054	1921.H18.gz43_245162
M00057328A:F02	ES 192	733723	1921.H21.gz43_245210
M00057328A:F10	ES 192	697006	1921.H22.gz43_245226
M00057328C:F11	ES 192	732969	1921.I06.gz43_244971
M00057328D:G02	ES 192	556490	1921.I10.gz43_245035
M00057331C:E10	ES 192	557177	1921.I21.gz43_245211
M00057331C:F10	ES 192	452936	1921.I22.gz43_245227
M00057331D:D08	ES 192	549552	1921.J01.gz43_244892
M00057332A:C06	ES 192	635849	1921.J06.gz43_244972
M00057332C:F12	ES 192	726692	1921.J14.gz43_245100
M00057333A:D08	ES 192	733464	1921.J19.gz43_245180
M00057333B:F03	ES 192	541793	1921.J24.gz43_245260

Table 13

CloneID	ES No	ClusterID	SequenceName
M00057334A:C12	ES 192	726406	1921.K16.gz43_245133
M00057334B:F01	ES 192	734582	1921.K21.gz43_245213
M00057334D:A12	ES 192	735425	1921.L04.gz43_244942
M00057334D:E03	ES 192	732114	1921.L07.gz43_244990
M00057336B:E01	ES 192	727018	1921.L13.gz43_245086
M00057336D:F07	ES 192	448431	1921.L21.gz43_245214
M00057337A:A06	ES 192	727132	1921.L22.gz43_245230
M00057337A:A11	ES 192	482722	1921.L23.gz43_245246
M00057337C:G12	ES 192	554647	1921.M10.gz43_245039
M00057337C:H07	ES 192	496909	1921.M13.gz43_245087
M00057337D:F06	ES 192	614455	1921.M16.gz43_245135
M00057338B:D08	ES 192	643909	1921.M24.gz43_245263
M00057338C:H01	ES 192	466697	1921.N05.gz43_244960
M00057339A:E08	ES 192	551607	1921.N12.gz43_245072
M00057339B:C04	ES 192	477688	1921.N17.gz43_245152
M00057339D:C01	ES 192	448250	1921.O04.gz43_244945
M00057339D:H09	ES 192	733146	1921.O06.gz43_244977
M00057341D:B09	ES 192	482788	1921.P08.gz43_245010
M00057343D:B10	ES 192	481273	1921.P17.gz43_245154
M00057344A:G07	ES 192	642986	1921.P24.gz43_245266
M00042351D:H05	ES 193	451429	1923.A11.gz43_252775
M00042352A:G05	ES 193	451518	1923.A14.gz43_252823
M00042352A:G09	ES 193	456672	1923.A15.gz43_252839
M00042352B:F03	ES 193	498194	1923.A19.gz43_252903
M00042352B:F10	ES 193	451430	1923.A20.gz43_252919
M00042352C:G01	ES 193	451302	1923.A23.gz43_252967
M00042352D:A11	ES 193	450902	1923.A24.gz43_252983
M00042352D:F11	ES 193	498504	1923.B01.gz43_252616
M00042353B:A11	ES 193	493575	1923.B05.gz43_252680
M00042353B:B02	ES 193	494378	1923.B06.gz43_252696
M00042353D:B08	ES 193	494393	1923.B13.gz43_252808
M00042353D:C06	ES 193	451043	1923.B14.gz43_252824
M00042354B:A07	ES 193	450823	1923.B17.gz43_252872
M00042354C:F04	ES 193	451126	1923.B19.gz43_252904
M00042355A:A12	ES 193	494133	1923.B22.gz43_252952
M00042355A:C03	ES 193	451126	1923.B23.gz43_252968
M00042355A:H09	ES 193	424723	1923.C01.gz43_252617
M00042355B:A05	ES 193	450875	1923.C02.gz43_252633
M00042355B:B07	ES 193	451009	1923.C03.gz43_252649
M00042355B:E10	ES 193	497400	1923.C04.gz43_252665
M00042355C:F02	ES 193	451383	1923.C05.gz43_252681
M00042355C:G09	ES 193	451470	1923.C07.gz43_252713
M00042442A:A12	ES 193	494130	1923.C23.gz43_252969

Table 13

CloneID	ES No	ClusterID	SequenceName
M00042442A:G04	ES 193	499178	1923.C24.gz43_252985
M00042442B:A07	ES 193	448936	1923.D02.gz43_252634
M00042443B:D03	ES 193	451176	1923.D11.gz43_252778
M00042443D:E01	ES 193	497101	1923.D15.gz43_252842
M00042444A:C10	ES 193	446263	1923.D17.gz43_252874
M00042444A:D04	ES 193	451212	1923.D18.gz43_252890
M00042444A:H06	ES 193	499779	1923.D19.gz43_252906
M00042444C:E02	ES 193	451124	1923.E01.gz43_252619
M00042445A:B04	ES 193	487745	1923.E06.gz43_252699
M00042445C:A08	ES 193	451544	1923.E10.gz43_252763
M00042446B:G02	ES 193	450507	1923.E19.gz43_252907
M00042446D:F04	ES 193	450507	1923.E24.gz43_252987
M00042447C:H10	ES 193	448663	1923.F06.gz43_252700
M00042447D:E04	ES 193	450302	1923.F08.gz43_252732
M00042447D:G10	ES 193	492110	1923.F09.gz43_252748
M00042448B:B02	ES 193	450926	1923.F12.gz43_252796
M00042448B:C04	ES 193	451049	1923.F13.gz43_252812
M00042448C:B07	ES 193	494423	1923.F18.gz43_252892
M00042448C:C09	ES 193	451054	1923.F20.gz43_252924
M00042449A:H10	ES 193	448556	1923.F24.gz43_252988
M00042449C:D10	ES 193	450219	1923.G02.gz43_252637
M00042449D:C06	ES 193	452094	1923.G04.gz43_252669
M00042449D:H11	ES 193	450765	1923.G06.gz43_252701
M00042450A:B01	ES 193	450912	1923.G07.gz43_252717
M00042450A:D02	ES 193	495941	1923.G09.gz43_252749
M00042450C:B09	ES 193	494362	1923.G18.gz43_252893
M00042451D:H10	ES 193	451618	1923.H04.gz43_252670
M00042452C:A09	ES 193	486912	1923.H10.gz43_252766
M00042452C:C10	ES 193	449974	1923.H11.gz43_252782
M00042452D:C04	ES 193	488680	1923.H15.gz43_252846
M00042452D:G06	ES 193	492094	1923.H17.gz43_252878
M00042453A:D12	ES 193	450166	1923.H20.gz43_252926
M00042453C:D12	ES 193	451518	1923.I03.gz43_252655
M00042454A:F02	ES 193	450400	1923.I12.gz43_252799
M00042454D:H10	ES 193	450723	1923.I19.gz43_252911
M00042455A:C06	ES 193	488859	1923.I20.gz43_252927
M00042455A:G12	ES 193	492304	1923.I22.gz43_252959
M00042455B:D05	ES 193	454575	1923.I24.gz43_252991
M00042455B:G09	ES 193	492292	1923.J02.gz43_252640
M00042455C:D11	ES 193	450255	1923.J03.gz43_252656
M00042455C:E04	ES 193	490890	1923.J04.gz43_252672
M00042455D:H08	ES 193	446621	1923.J09.gz43_252752
M00042456A:C08	ES 193	456492	1923.J10.gz43_252768
M00042456A:F08	ES 193	450425	1923.J12.gz43_252800

Table 13

CloneID	ES No	ClusterID	SequenceName
M00042456C:H07	ES 193	492981	1923.J19.gz43_252912
M00042456D:B06	ES 193	453667	1923.J20.gz43_252928
M00042456D:D07	ES 193	100821	1923.J22.gz43_252960
M00042457D:D02	ES 193	489426	1923.K07.gz43_252721
M00042458B:B08	ES 193	59512	1923.K11.gz43_252785
M00042458B:G05	ES 193	558729	1923.K13.gz43_252817
M00042458C:C07	ES 193	562353	1923.K14.gz43_252833
M00042458C:D08	ES 193	395968	1923.K16.gz43_252865
M00042458C:E06	ES 193	552581	1923.K17.gz43_252881
M00042458D:E06	ES 193	562588	1923.K20.gz43_252929
M00042459A:E04	ES 193	562587	1923.K23.gz43_252977
M00042459B:F03	ES 193	556916	1923.L05.gz43_252690
M00042459B:F12	ES 193	468729	1923.L06.gz43_252706
M00042459C:B11	ES 193	562274	1923.L09.gz43_252754
M00042459C:E06	ES 193	562627	1923.L12.gz43_252802
M00042459C:G02	ES 193	526733	1923.L13.gz43_252818
M00042459D:B07	ES 193	552236	1923.L15.gz43_252850
M00042459D:E03	ES 193	560420	1923.L18.gz43_252898
M00042459D:G04	ES 193	527679	1923.L20.gz43_252930
M00042460B:C06	ES 193	374282	1923.L24.gz43_252994
M00042460B:D10	ES 193	556804	1923.M03.gz43_252659
M00042460B:G12	ES 193	559575	1923.M08.gz43_252739
M00042460C:A02	ES 193	550362	1923.M11.gz43_252787
M00042460C:B02	ES 193	452232	1923.M14.gz43_252835
M00042460C:G08	ES 193	562603	1923.M22.gz43_252963
M00042460C:H10	ES 193	562543	1923.M23.gz43_252979
M00042460D:H06	ES 193	551755	1923.N05.gz43_252692
M00042516A:A06	ES 193	455439	1923.N08.gz43_252740
M00042516A:A10	ES 193	562115	1923.N09.gz43_252756
M00042516A:C08	ES 193	562060	1923.N10.gz43_252772
M00042516B:E03	ES 193	558559	1923.N13.gz43_252820
M00042516C:C04	ES 193	562399	1923.N18.gz43_252900
M00042516D:B11	ES 193	562275	1923.N22.gz43_252964
M00042516D:C01	ES 193	562398	1923.N23.gz43_252980
M00042516D:H08	ES 193	553312	1923.O01.gz43_252629
M00042516D:H09	ES 193	638444	1923.O02.gz43_252645
M00042517C:B04	ES 193	495074	1923.O05.gz43_252693
M00042517D:A12	ES 193	494300	1923.O09.gz43_252757
M00042517D:G04	ES 193	211273	1923.O11.gz43_252789
M00042518D:A08	ES 193	487522	1923.O18.gz43_252901
M00042519D:F09	ES 193	456024	1923.P02.gz43_252646
M00042519D:H07	ES 193	492982	1923.P04.gz43_252678
M00042520A:F09	ES 193	452833	1923.P10.gz43_252774
M00042520C:E12	ES 193	449104	1923.P16.gz43_252870

Table 13

CloneID	ES No	ClusterID	SequenceName
M00043296A:E08	ES 193	497517	1923.P23.gz43_252982
M00043301D:B12	ES 193	450999	1924.C17.gz43_245558
M00043303B:E11	ES 193	450349	1924.D15.gz43_245527
M00043304B:A10	ES 193	450805	1924.E04.gz43_245352
M00043304C:E01	ES 193	496957	1924.E09.gz43_245432
M00043305A:H06	ES 193	204862	1924.E13.gz43_245496
M00043306B:A09	ES 193	493746	1924.E24.gz43_245672
M00043307B:F11	ES 193	498242	1924.F18.gz43_245577
M00043308A:D09	ES 193	496752	1924.G03.gz43_245338
M00043308A:F06	ES 193	451456	1924.G04.gz43_245354
M00043309A:H06	ES 193	499693	1924.G17.gz43_245562
M00043310A:F01	ES 193	498509	1924.H03.gz43_245339
M00043310C:B04	ES 193	495105	1924.H08.gz43_245419
M00043311B:H08	ES 193	499700	1924.H18.gz43_245579
M00043312B:A10	ES 193	494325	1924.H24.gz43_245675
M00043312D:A02	ES 193	494306	1924.I10.gz43_245452
M00043313D:B04	ES 193	492544	1924.J11.gz43_245469
M00043315C:D05	ES 193	495951	1924.K14.gz43_245518
M00043316C:F06	ES 193	498951	1924.L15.gz43_245535
M00043316D:F04	ES 193	479604	1924.L19.gz43_245599
M00043316D:F09	ES 193	553779	1924.L21.gz43_245631
M00043317B:B12	ES 193	494625	1924.M04.gz43_245360
M00043317D:C02	ES 193	451081	1924.M11.gz43_245472
M00043318A:G05	ES 193	454815	1924.M17.gz43_245568
M00043319A:D01	ES 193	562516	1924.N19.gz43_245601
M00043321B:E05	ES 193	490401	1924.P05.gz43_245379
M00043322C:F07	ES 193	446732	1924.P23.gz43_245667
M00043324D:D05	ES 193	451245	1933.A19.gz43_245972
M00043326A:H06	ES 193	500040	1933.B12.gz43_245861
M00043328A:E12	ES 193	496909	1933.C10.gz43_245830
M00043329B:H07	ES 193	492779	1933.C17.gz43_245942
M00043329C:D12	ES 193	453068	1933.C18.gz43_245958
M00043330D:G05	ES 193	412621	1933.D06.gz43_245767
M00043331C:G01	ES 193	491933	1933.D10.gz43_245831
M00043332A:D06	ES 193	454873	1933.D15.gz43_245911
M00043332A:E05	ES 193	490550	1933.D16.gz43_245927
M00043334A:F10	ES 193	491212	1933.E07.gz43_245784
M00043335A:D04	ES 193	450252	1933.E21.gz43_246008
M00043335D:E02	ES 193	450283	1933.F05.gz43_245753
M00043336A:D01	ES 193	496678	1933.F08.gz43_245801
M00043336C:A04	ES 193	450804	1933.F18.gz43_245961
M00043337A:C12	ES 193	495610	1933.G03.gz43_245722
M00043340A:B05	ES 193	494973	1933.H02.gz43_245707
M00043340B:B04	ES 193	453078	1933.H03.gz43_245723

Table 13

CloneID	ES No	ClusterID	SequenceName
M00043340D:C03	ES 193	447057	1933.H09.gz43_245819
M00043342B:H07	ES 193	450727	1933.I02.gz43_245708
M00043342C:G02	ES 193	492629	1933.I06.gz43_245772
M00043342D:D09	ES 193	128697	1933.I09.gz43_245820
M00043343B:B10	ES 193	451307	1933.I15.gz43_245916
M00043343D:H03	ES 193	492887	1933.J04.gz43_245741
M00043344C:C11	ES 193	450027	1933.J15.gz43_245917
M00043346D:E10	ES 193	449299	1933.K07.gz43_245790
M00043348A:D02	ES 193	450129	1933.K16.gz43_245934
M00043349A:C08	ES 193	448927	1933.L01.gz43_245695
M00043351C:A07	ES 193	494271	1933.M05.gz43_245760
M00043353D:E12	ES 193	496870	1933.N10.gz43_245841
M00043354A:C12	ES 193	529733	1933.N13.gz43_245889
M00043354A:E06	ES 193	561712	1933.N14.gz43_245905
M00043354B:C04	ES 193	561480	1933.N18.gz43_245969
M00043354B:F12	ES 193	561834	1933.N20.gz43_246001
M00043354D:C01	ES 193	448110	1933.O05.gz43_245762
M00043354D:G01	ES 193	515328	1933.O10.gz43_245842
M00043354D:G02	ES 193	552445	1933.O11.gz43_245858
M00043354D:H08	ES 193	553594	1933.O12.gz43_245874
M00043355A:D01	ES 193	561593	1933.O18.gz43_245970
M00043355B:B01	ES 193	552687	1933.O23.gz43_246050
M00043355B:D12	ES 193	517346	1933.O24.gz43_246066
M00043355C:G12	ES 193	487106	1933.P08.gz43_245811
M00043356B:E12	ES 193	452586	1934.A03.gz43_253031
M00043356C:F03	ES 193	448230	1934.A06.gz43_253079
M00043356C:H07	ES 193	447429	1934.A07.gz43_253095
M00043357A:G04	ES 193	450583	1934.A11.gz43_253159
M00043357B:B02	ES 193	487893	1934.A12.gz43_253175
M00043357B:D01	ES 193	450189	1934.A13.gz43_253191
M00043358A:D02	ES 193	450242	1934.A21.gz43_253319
M00043358B:D06	ES 193	450122	1934.A23.gz43_253351
M00043358C:F07	ES 193	449061	1934.B04.gz43_253048
M00043359B:A04	ES 193	449795	1934.B09.gz43_253128
M00043359B:D06	ES 193	450193	1934.B11.gz43_253160
M00043359C:C06	ES 193	449994	1934.B14.gz43_253208
M00043360C:E07	ES 193	452719	1934.C01.gz43_253001
M00043360C:F11	ES 194	491177	1934.C03.gz43_253033
M00043360D:D01	ES 194	489368	1934.C05.gz43_253065
M00043361B:F02	ES 194	491402	1934.C08.gz43_253113
M00043361D:A02	ES 194	450080	1934.C10.gz43_253145
M00043362C:E02	ES 194	490846	1934.C18.gz43_253273
M00043363A:G03	ES 194	492022	1934.D02.gz43_253018

Table 13

CloneID	ES No	ClusterID	SequenceName
M00043363B:A11	ES 194	450756	1934.D04.gz43_253050
M00043363D:F07	ES 194	491507	1934.D12.gz43_253178
M00043364B:H10	ES 194	447355	1934.D21.gz43_253322
M00043364D:H11	ES 194	450756	1934.E05.gz43_253067
M00043365A:C06	ES 194	449956	1934.E08.gz43_253115
M00043365B:A10	ES 194	486833	1934.E11.gz43_253163
M00043365B:C08	ES 194	488613	1934.E13.gz43_253195
M00043365C:A09	ES 194	449780	1934.E16.gz43_253243
M00043365C:F06	ES 194	491240	1934.E19.gz43_253291
M00043366A:B12	ES 194	488023	1934.E24.gz43_253371
M00043366D:B07	ES 194	488310	1934.F09.gz43_253132
M00043367C:D10	ES 194	450147	1934.F14.gz43_253212
M00043368A:F03	ES 194	491492	1934.F16.gz43_253244
M00043369D:B01	ES 194	449842	1934.G02.gz43_253021
M00043369D:G10	ES 194	450551	1934.G07.gz43_253101
M00043370A:C08	ES 194	449959	1934.G08.gz43_253117
M00043370B:D08	ES 194	450207	1934.G14.gz43_253213
M00043371A:D06	ES 194	490060	1934.G19.gz43_253293
M00043371B:C10	ES 194	450080	1934.G22.gz43_253341
M00043371C:B02	ES 194	449908	1934.G23.gz43_253357
M00043372B:A07	ES 194	43013	1934.H05.gz43_253070
M00043372B:B01	ES 194	455707	1934.H06.gz43_253086
M00043373A:G11	ES 194	452710	1934.H19.gz43_253294
M00043373B:G12	ES 194	450658	1934.H24.gz43_253374
M00043373D:G04	ES 194	456492	1934.I04.gz43_253055
M00043374A:E05	ES 194	560213	1934.I08.gz43_253119
M00043374A:G04	ES 194	510272	1934.I10.gz43_253151
M00043374D:D07	ES 194	631526	1934.I15.gz43_253231
M00043374D:H09	ES 194	515423	1934.I17.gz43_253263
M00043375A:E01	ES 194	451292	1934.I20.gz43_253311
M00043375A:E02	ES 194	451294	1934.I21.gz43_253327
M00043375B:A04	ES 194	456103	1934.I24.gz43_253375
M00043376B:C03	ES 194	451144	1934.J07.gz43_253104
M00043376B:F06	ES 194	450482	1934.J08.gz43_253120
M00043376D:A04	ES 194	493622	1934.J11.gz43_253168
M00043376D:A12	ES 194	233814	1934.J12.gz43_253184
M00043376D:D12	ES 194	451185	1934.J14.gz43_253216
M00043377C:A11	ES 194	449959	1934.J20.gz43_253312
M00043377D:E01	ES 194	451361	1934.J22.gz43_253344
M00043378B:B05	ES 194	494450	1934.J24.gz43_253376
M00043378D:D12	ES 194	496084	1934.K05.gz43_253073
M00043379C:B09	ES 194	451011	1934.K13.gz43_253201
M00043379D:A05	ES 194	494099	1934.K16.gz43_253249
M00043380D:E10	ES 194	450193	1934.L05.gz43_253074

Table 13

CloneID	ES No	ClusterID	SequenceName
M00043380D:E11	ES 194	451326	1934.L06.gz43_253090
M00043381B:E10	ES 194	551380	1934.L14.gz43_253218
M00043381C:D08	ES 194	561641	1934.L16.gz43_253250
M00043381C:E10	ES 194	556511	1934.L18.gz43_253282
M00043381D:F09	ES 194	467035	1934.L24.gz43_253378
M00043382C:D07	ES 194	496586	1934.M03.gz43_253043
M00043382C:G09	ES 194	499240	1934.M05.gz43_253075
M00043383B:F12	ES 194	456367	1934.M11.gz43_253171
M00043383D:C07	ES 194	495143	1934.M14.gz43_253219
M00043383D:G07	ES 194	451467	1934.M15.gz43_253235
M00043384B:A04	ES 194	487437	1934.M18.gz43_253283
M00043384C:A07	ES 194	487448	1934.M20.gz43_253315
M00043384C:C02	ES 194	489207	1934.M22.gz43_253347
M00043384C:G01	ES 194	492627	1934.M24.gz43_253379
M00043384D:D05	ES 194	489506	1934.N02.gz43_253028
M00043385A:E01	ES 194	496760	1934.N06.gz43_253092
M00043385A:G12	ES 194	448448	1934.N08.gz43_253124
M00043385C:D06	ES 194	496234	1934.N11.gz43_253172
M00043386A:A11	ES 194	450819	1934.N16.gz43_253252
M00043387A:E02	ES 194	490393	1934.O03.gz43_253045
M00043387A:E03	ES 194	490395	1934.O04.gz43_253061
M00043387B:A03	ES 194	486856	1934.O09.gz43_253141
M00043387C:A11	ES 194	487183	1934.O14.gz43_253221
M00043387C:G08	ES 194	455460	1934.O18.gz43_253285
M00043387D:A02	ES 194	449802	1934.O21.gz43_253333
M00043387D:B02	ES 194	488030	1934.O22.gz43_253349
M00043387D:D06	ES 194	450211	1934.O23.gz43_253365
M00043388A:D05	ES 194	453893	1934.P02.gz43_253030
M00043388B:C02	ES 194	489275	1934.P04.gz43_253062
M00043389D:B10	ES 194	488349	1934.P16.gz43_253254
M00043390B:C04	ES 194	449978	1934.P20.gz43_253318
M00043391D:D05	ES 194	217042	1935.A19.gz43_246512
M00043392C:F02	ES 194	491448	1935.B05.gz43_246289
M00043397B:H07	ES 194	335078	1935.D06.gz43_246307
M00043397C:G02	ES 194	450623	1935.D08.gz43_246339
M00043401A:E09	ES 194	490805	1935.E18.gz43_246500
M00043402C:F12	ES 194	456213	1935.F12.gz43_246405
M00043403B:A12	ES 194	450335	1935.F18.gz43_246501
M00043406D:C04	ES 194	448924	1935.H08.gz43_246343
M00043407C:H08	ES 194	451456	1935.H15.gz43_246455
M00043407D:G06	ES 194	498629	1935.H17.gz43_246487
M00043409C:C07	ES 194	402070	1935.I07.gz43_246328
M00043410C:C05	ES 194	451781	1935.I17.gz43_246488
M00043501A:D07	ES 194	553890	1935.K06.gz43_246314

Table 13

CloneID	ES No	ClusterID	SequenceName
M00043501D:C01	ES 194	562378	1935.K19.gz43_246522
M00043502A:H01	ES 194	491644	1935.L06.gz43_246315
M00043503C:F08	ES 194	402823	1935.M10.gz43_246380
M00043504A:E06	ES 194	477674	1935.M23.gz43_246588
M00043504B:C02	ES 194	635439	1935.N06.gz43_246317
M00043504C:E03	ES 194	555399	1935.N16.gz43_246477
M00043504D:G08	ES 194	446964	1935.N22.gz43_246573
M00043505B:G03	ES 194	562886	1935.O08.gz43_246350
M00043505B:G07	ES 194	558055	1935.O09.gz43_246366
M00043506D:F06	ES 194	522703	1935.P24.gz43_246607
M00043508A:H02	ES 194	456742	1936.B10.gz43_246753
M00043508B:G11	ES 194	562823	1936.B18.gz43_246881
M00043508D:C01	ES 194	414739	1936.C08.gz43_246722
M00054486B:E09	ES 194	562382	1936.D18.gz43_246883
M00054486B:H01	ES 194	549757	1936.D21.gz43_246931
M00054487C:A01	ES 194	559574	1936.E21.gz43_246932
M00054488A:F01	ES 194	556768	1936.F13.gz43_246805
M00054488C:D04	ES 194	564967	1936.G03.gz43_246646
M00054492A:D04	ES 194	449978	1936.I15.gz43_246840
M00054493C:E04	ES 194	489368	1936.J16.gz43_246857
M00054494A:H04	ES 194	549853	1936.K05.gz43_246682
M00054494D:A10	ES 194	560188	1936.K13.gz43_246810
M00054497B:C10	ES 194	560275	1936.M05.gz43_246684
M00054497C:G12	ES 194	450037	1936.M10.gz43_246764
M00054497D:A04	ES 194	554908	1936.M11.gz43_246780
M00054498C:B08	ES 194	558500	1936.N04.gz43_246669
M00054498D:F01	ES 194	449000	1936.N11.gz43_246781
M00054500A:F04	ES 194	559720	1936.O08.gz43_246734
M00054501A:E11	ES 194	552920	1936.O23.gz43_246974
M00054501A:G12	ES 194	488171	1936.O24.gz43_246990
M00054501C:E08	ES 194	481057	1936.P05.gz43_246687
M00054502C:E02	ES 194	550571	1936.P24.gz43_246991
M00054502C:H10	ES 194	449776	1945.A02.gz43_248938
M00054503D:E07	ES 194	562019	1945.B03.gz43_248955
M00054504B:A04	ES 194	524721	1945.B11.gz43_249083
M00054504D:E02	ES 194	551475	1945.B21.gz43_249243
M00054504D:G07	ES 194	289201	1945.B23.gz43_249275
M00054505A:G12	ES 194	572807	1945.C05.gz43_248988
M00054506A:D05	ES 194	554839	1945.C24.gz43_249292
M00054506B:A07	ES 194	388055	1945.D04.gz43_248973
M00054506B:H01	ES 194	550986	1945.D11.gz43_249085
M00054507B:A07	ES 194	505907	1945.E05.gz43_248990
M00054508B:E08	ES 194	557681	1945.F12.gz43_249103
M00054508C:B04	ES 194	550129	1945.F15.gz43_249151

Table 13

CloneID	ES No	ClusterID	SequenceName
M00054508C:C08	ES 194	555771	1945.F17.gz43_249183
M00054509A:C01	ES 194	547866	1945.F23.gz43_249279
M00054509B:F01	ES 194	559127	1945.G08.gz43_249040
M00054509C:G01	ES 194	499696	1945.G11.gz43_249088
M00054510C:G07	ES 194	452471	1945.H07.gz43_249025
M00054511A:D11	ES 194	570573	1945.H15.gz43_249153
M00054511B:C06	ES 194	389065	1945.H19.gz43_249217
M00054512D:H08	ES 194	487658	1945.I24.gz43_249298
M00054513A:B08	ES 194	550063	1945.J03.gz43_248963
M00054513A:F09	ES 194	455814	1945.J05.gz43_248995
M00054513B:E11	ES 194	551518	1945.J07.gz43_249027
M00054513C:A01	ES 194	555660	1945.J09.gz43_249059
M00054513D:F04	ES 194	550678	1945.J13.gz43_249123
M00054514C:B01	ES 194	461313	1945.J21.gz43_249251
M00054515B:E11	ES 194	554246	1945.K13.gz43_249124
M00054516C:A04	ES 194	559343	1945.L14.gz43_249141
M00054516D:F09	ES 194	554456	1945.L21.gz43_249253
M00054517A:C01	ES 194	488023	1945.L23.gz43_249285
M00054517B:B04	ES 194	549129	1945.M05.gz43_248998
M00054518C:F11	ES 194	549581	1945.N05.gz43_248999
M00054518D:D03	ES 194	552905	1945.N09.gz43_249063
M00054519A:C04	ES 194	554611	1945.N11.gz43_249095
M00054521D:H01	ES 194	572992	1945.O18.gz43_249208
M00054523C:A11	ES 194	458974	1945.P23.gz43_249289
M00054523D:D07	ES 194	558497	1946.A06.gz43_249386
M00054523D:E08	ES 194	550022	1946.A08.gz43_249418
M00054523D:G09	ES 194	454336	1946.A10.gz43_249450
M00054525D:H05	ES 194	559676	1946.B07.gz43_249403
M00054526A:E04	ES 194	550475	1946.B11.gz43_249467
M00054526B:C09	ES 194	556809	1946.B15.gz43_249531
M00054526C:F03	ES 194	524966	1946.B19.gz43_249595
M00054527B:A07	ES 194	552006	1946.C06.gz43_249388
M00054529A:H01	ES 194	585380	1946.D21.gz43_249629
M00054529C:D11	ES 194	551157	1946.E06.gz43_249390
M00054529D:E01	ES 194	490308	1946.E10.gz43_249454
M00054530D:C10	ES 194	312036	1946.E23.gz43_249662
M00054530D:H07	ES 194	553002	1946.E24.gz43_249678
M00054531D:F05	ES 194	584071	1946.F11.gz43_249471
M00054532A:A07	ES 194	549919	1946.F13.gz43_249503
M00054532B:C05	ES 194	550204	1946.F21.gz43_249631
M00054532D:A01	ES 194	559574	1946.G06.gz43_249392
M00054532D:E07	ES 194	526984	1946.G08.gz43_249424
M00054533A:F05	ES 194	571899	1946.G12.gz43_249488
M00054533B:F04	ES 194	550714	1946.G20.gz43_249616

Table 13

CloneID	ES No	ClusterID	SequenceName
M00054533C:B04	ES 194	556940	1946.H01.gz43_249313
M00054533C:E07	ES 194	466020	1946.H05.gz43_249377
M00054534A:B06	ES 194	498433	1946.H15.gz43_249537
M00054534D:D02	ES 194	556216	1946.I06.gz43_249394
M00054535A:G03	ES 194	553338	1946.I14.gz43_249522
M00054535B:H08	ES 194	560205	1946.I22.gz43_249650
M00054536B:A03	ES 194	550018	1946.J07.gz43_249411
M00054536B:D02	ES 194	550370	1946.J10.gz43_249459
M00054536B:F08	ES 194	550730	1946.J11.gz43_249475
M00054536C:B11	ES 194	555019	1946.J15.gz43_249539
M00054536C:D12	ES 195	82864	1946.J17.gz43_249571
M00054537B:H03	ES 195	451778	1946.K02.gz43_249332
M00054537C:B03	ES 195	51103	1946.K06.gz43_249396
M00054538A:E10	ES 195	455821	1946.K16.gz43_249556
M00054538B:B05	ES 195	550172	1946.K18.gz43_249588
M00054538D:F05	ES 195	557339	1946.L07.gz43_249413
M00054538D:G12	ES 195	550830	1946.L11.gz43_249477
M00054538D:H11	ES 195	560014	1946.L13.gz43_249509
M00054539B:D06	ES 195	560519	1946.L17.gz43_249573
M00054539B:G03	ES 195	549734	1946.L19.gz43_249605
M00054540A:H07	ES 195	464154	1946.M10.gz43_249462
M00054541B:A09	ES 195	549233	1946.M22.gz43_249654
M00054541C:C10	ES 195	493575	1946.N03.gz43_249351
M00054541C:F11	ES 195	481594	1946.N09.gz43_249447
M00054542B:B01	ES 195	409262	1946.N17.gz43_249575
M00054542C:B12	ES 195	558024	1946.N21.gz43_249639
M00054543B:E06	ES 195	552638	1946.O12.gz43_249496
M00054543C:F01	ES 195	552753	1946.O18.gz43_249592
M00054543D:G08	ES 195	549131	1946.P01.gz43_249321
M00054544B:E03	ES 195	550618	1946.P09.gz43_249449
M00054544C:F04	ES 195	560717	1946.P17.gz43_249577
M00054545C:B09	ES 195	555502	1947.A10.gz43_253539
M00054545D:E04	ES 195	561406	1947.A14.gz43_253603
M00054553D:E09	ES 195	515707	1947.G22.gz43_253737
M00054555A:H09	ES 195	550952	1947.I06.gz43_253483
M00054555D:C03	ES 195	550246	1947.J01.gz43_253404
M00054566D:G08	ES 195	496586	1947.P21.gz43_253730
M00054567C:B03	ES 195	556065	1948.A04.gz43_249738
M00054567C:D09	ES 195	550403	1948.A07.gz43_249786
M00054568A:G02	ES 195	549716	1948.A14.gz43_249898
M00054568A:H03	ES 195	549858	1948.A16.gz43_249930
M00054568B:A07	ES 195	554793	1948.A17.gz43_249946
M00054568C:D06	ES 195	450963	1948.A21.gz43_250010

Table 13

CloneID	ES No	ClusterID	SequenceName
M00054568C:G12	ES 195	557656	1948.A23.gz43_250042
M00054569D:E01	ES 195	468613	1948.C02.gz43_249708
M00054570A:F02	ES 195	549597	1948.C08.gz43_249804
M00054571A:B10	ES 195	451049	1948.C21.gz43_250012
M00054572C:B12	ES 195	562805	1948.E07.gz43_249790
M00054572C:E09	ES 195	561876	1948.E11.gz43_249854
M00054572C:G05	ES 195	550035	1948.E13.gz43_249886
M00054574C:B11	ES 195	562725	1948.G01.gz43_249696
M00054574D:F11	ES 195	559300	1948.G10.gz43_249840
M00054575A:B06	ES 195	560080	1948.G12.gz43_249872
M00054575B:A07	ES 195	562469	1948.G16.gz43_249936
M00054576D:C07	ES 195	378610	1948.I02.gz43_249714
M00054577B:A09	ES 195	558729	1948.I13.gz43_249890
M00054577B:F01	ES 195	509202	1948.I19.gz43_249986
M00054579A:G10	ES 195	550804	1948.K03.gz43_249732
M00054579B:C11	ES 195	454205	1948.K07.gz43_249796
M00054579B:D10	ES 195	553749	1948.K08.gz43_249812
M00054579C:A10	ES 195	552907	1948.K11.gz43_249860
M00054579D:D08	ES 195	313600	1948.K18.gz43_249972
M00054580A:B11	ES 195	528404	1948.K21.gz43_250020
M00054580A:C10	ES 195	492139	1948.K22.gz43_250036
M00054580A:D03	ES 195	550318	1948.K23.gz43_250052
M00054580A:D04	ES 195	570248	1948.K24.gz43_250068
M00054581B:A01	ES 195	559752	1948.M02.gz43_249718
M00054581B:D03	ES 195	550397	1948.M04.gz43_249750
M00054581B:G10	ES 195	550874	1948.M05.gz43_249766
M00054581D:C12	ES 195	555000	1948.M10.gz43_249846
M00054581D:D01	ES 195	556488	1948.M11.gz43_249862
M00054581D:E04	ES 195	556336	1948.M12.gz43_249878
M00054581D:G02	ES 195	550811	1948.M13.gz43_249894
M00054582A:A05	ES 195	568467	1948.M14.gz43_249910
M00054582A:A07	ES 195	549994	1948.M15.gz43_249926
M00054583A:B04	ES 195	550106	1948.N13.gz43_249895
M00054583A:F05	ES 195	550694	1948.N14.gz43_249911
M00054583D:E04	ES 195	394567	1948.O01.gz43_249704
M00054584A:A07	ES 195	549956	1948.O03.gz43_249736
M00054584A:B03	ES 195	533812	1948.O05.gz43_249768
M00054584B:A03	ES 195	554887	1948.O10.gz43_249848
M00054584B:G03	ES 195	572249	1948.O13.gz43_249896
M00054584D:C01	ES 195	466020	1948.O17.gz43_249960
M00054585A:E07	ES 195	160320	1948.O21.gz43_250024
M00054586A:F05	ES 195	550662	1948.P19.gz43_249993
M00054586C:H02	ES 195	560751	1957.A05.gz43_250138
M00054586D:A03	ES 195	559857	1957.A06.gz43_250154

Table 13

CloneID	ES No	ClusterID	SequenceName
M00054586D:G01	ES 195	559419	1957.A09.gz43_250202
M00054587A:A08	ES 195	558413	1957.A13.gz43_250266
M00054587A:F06	ES 195	471181	1957.A16.gz43_250314
M00054587A:F09	ES 195	452506	1957.A18.gz43_250346
M00054587B:F06	ES 195	562174	1957.A23.gz43_250426
M00054587C:G02	ES 195	535129	1957.B03.gz43_250107
M00054587D:D04	ES 195	550322	1957.B05.gz43_250139
M00054588A:G08	ES 195	550855	1957.B11.gz43_250235
M00054588B:B12	ES 195	553331	1957.B13.gz43_250267
M00054588C:F04	ES 195	550217	1957.B19.gz43_250363
M00054589A:D09	ES 195	555920	1957.C04.gz43_250124
M00054589A:E05	ES 195	477097	1957.C05.gz43_250140
M00054589B:A07	ES 195	446164	1957.C06.gz43_250156
M00054589B:F05	ES 195	551463	1957.C10.gz43_250220
M00054589B:G10	ES 195	43656	1957.C13.gz43_250268
M00054589C:G11	ES 195	427723	1957.C18.gz43_250348
M00054589D:C06	ES 195	556376	1957.C20.gz43_250380
M00054590A:A01	ES 195	447311	1957.C23.gz43_250428
M00054590A:C10	ES 195	553755	1957.D02.gz43_250093
M00054590A:E02	ES 195	550594	1957.D03.gz43_250109
M00054590B:B11	ES 195	550088	1957.D06.gz43_250157
M00054590C:A03	ES 195	498827	1957.D08.gz43_250189
M00054590D:B01	ES 195	550084	1957.D16.gz43_250317
M00054590D:C12	ES 195	551975	1957.D18.gz43_250349
M00054591C:A01	ES 195	550044	1957.E04.gz43_250126
M00054591C:H09	ES 195	554764	1957.E06.gz43_250158
M00054591D:G11	ES 195	550886	1957.E11.gz43_250238
M00054592A:D09	ES 195	550315	1957.E17.gz43_250334
M00054592C:A05	ES 195	549964	1957.E20.gz43_250382
M00054593A:D01	ES 195	547509	1957.F03.gz43_250111
M00054593B:B03	ES 195	473859	1957.F09.gz43_250207
M00054593B:E03	ES 195	557970	1957.F12.gz43_250255
M00054593D:B11	ES 195	550153	1957.F18.gz43_250351
M00054594A:D04	ES 195	561836	1957.G01.gz43_250080
M00054594C:E06	ES 195	498777	1957.G08.gz43_250192
M00054595B:A11	ES 195	161489	1957.G20.gz43_250384
M00054595B:C12	ES 195	560357	1957.G23.gz43_250432
M00054595B:H09	ES 195	485431	1957.H06.gz43_250161
M00054595C:G06	ES 195	549665	1957.H12.gz43_250257
M00054595D:A10	ES 195	485029	1957.H18.gz43_250353
M00054596A:G11	ES 195	549731	1957.H24.gz43_250449
M00054596B:C01	ES 195	447356	1957.I04.gz43_250130
M00054596C:A06	ES 195	451594	1957.I11.gz43_250242
M00054596C:F09	ES 195	549609	1957.I14.gz43_250290

Table 13

CloneID	ES No	ClusterID	SequenceName
M00054596C:F10	ES 195	455298	1957.I15.gz43_250306
M00054596C:G09	ES 195	561130	1957.I17.gz43_250338
M00054597A:A07	ES 195	467035	1957.I23.gz43_250434
M00054597A:C11	ES 195	558332	1957.J01.gz43_250083
M00054597A:D08	ES 195	558981	1957.J02.gz43_250099
M00054597A:G08	ES 195	549781	1957.J03.gz43_250115
M00054597B:F09	ES 195	493622	1957.J08.gz43_250195
M00054597D:E12	ES 195	461718	1957.J17.gz43_250339
M00054597D:F08	ES 195	449649	1957.J19.gz43_250371
M00054599B:A12	ES 195	446783	1957.K18.gz43_250356
M00054599B:C06	ES 195	549228	1957.K20.gz43_250388
M00054599B:F09	ES 195	549611	1957.K23.gz43_250436
M00054599C:E05	ES 195	561593	1957.L06.gz43_250165
M00054599D:B07	ES 195	559883	1957.L08.gz43_250197
M00054600A:G12	ES 195	559554	1957.L17.gz43_250341
M00054600A:H03	ES 195	549816	1957.L18.gz43_250357
M00054600C:B10	ES 195	459581	1957.L20.gz43_250389
M00054600C:D03	ES 195	554193	1957.L22.gz43_250421
M00054600D:H07	ES 195	554869	1957.M08.gz43_250198
M00054601A:E08	ES 195	555949	1957.M09.gz43_250214
M00054601B:D08	ES 195	446503	1957.M12.gz43_250262
M00054602A:B03	ES 195	550085	1957.M23.gz43_250438
M00054602A:E06	ES 195	416884	1957.N05.gz43_250151
M00054602C:B06	ES 195	547509	1957.N15.gz43_250311
M00054602C:C12	ES 195	487176	1957.N16.gz43_250327
M00054602D:A06	ES 195	562722	1957.N20.gz43_250391
M00054603A:G06	ES 195	552907	1957.O07.gz43_250184
M00054603A:G12	ES 195	552913	1957.O09.gz43_250216
M00054603B:B04	ES 195	526733	1957.O11.gz43_250248
M00054603B:C09	ES 195	447308	1957.O13.gz43_250280
M00054603B:G08	ES 195	356058	1957.O16.gz43_250328
M00054603C:G09	ES 195	408130	1957.O18.gz43_250360
M00054603D:B02	ES 195	552121	1957.O20.gz43_250392
M00054604C:B05	ES 195	562529	1957.P07.gz43_250185
M00054604C:F03	ES 195	549599	1957.P12.gz43_250265
M00054604D:A04	ES 195	563514	1957.P15.gz43_250313
M00054605A:A03	ES 195	558927	1957.P18.gz43_250361
M00054605B:F10	ES 195	460493	1957.P24.gz43_250457
M00054605B:G01	ES 195	549649	1958.A02.gz43_250474
M00054605C:A04	ES 195	548864	1958.A05.gz43_250522
M00054605C:D03	ES 195	188753	1958.A06.gz43_250538
M00054605C:H02	ES 195	549810	1958.A09.gz43_250586
M00054606A:A03	ES 195	449994	1958.A13.gz43_250650
M00054606A:D02	ES 195	562508	1958.A16.gz43_250698

Table 13

CloneID	ES No	ClusterID	SequenceName
M00054606C:B06	ES 195	549131	1958.A23.gz43_250810
M00054606C:E04	ES 195	549481	1958.B01.gz43_250459
M00054606D:B05	ES 195	557190	1958.B02.gz43_250475
M00054607A:B06	ES 195	560862	1958.B05.gz43_250523
M00054607A:G02	ES 195	552823	1958.B07.gz43_250555
M00054608B:D08	ES 195	490393	1958.B19.gz43_250747
M00054608C:H04	ES 195	549889	1958.B24.gz43_250827
M00054609A:D01	ES 195	423947	1958.C05.gz43_250524
M00054609A:F01	ES 195	561892	1958.C08.gz43_250572
M00054609A:H04	ES 195	549912	1958.C09.gz43_250588
M00054609B:E01	ES 195	556530	1958.C12.gz43_250636
M00054609B:H11	ES 195	507349	1958.C13.gz43_250652
M00054609C:G06	ES 195	549779	1958.C17.gz43_250716
M00054609D:E12	ES 195	490152	1958.C22.gz43_250796
M00054609D:H06	ES 195	549829	1958.C24.gz43_250828
M00054610A:E05	ES 195	558332	1958.D05.gz43_250525
M00054611B:F12	ES 195	549626	1958.E13.gz43_250654
M00054611B:G09	ES 195	478511	1958.E14.gz43_250670
M00054611C:C02	ES 195	561144	1958.E16.gz43_250702
M00054611C:E01	ES 195	555660	1958.E18.gz43_250734
M00054612A:D12	ES 195	549347	1958.F08.gz43_250575
M00054612B:B11	ES 195	549114	1958.F10.gz43_250607
M00054612B:E02	ES 195	488108	1958.F12.gz43_250639
M00054612D:B12	ES 195	552364	1958.F22.gz43_250799
M00054613A:D07	ES 195	550177	1958.G06.gz43_250544
M00054613B:H04	ES 195	550018	1958.G11.gz43_250624
M00054613D:H09	ES 195	553028	1958.G21.gz43_250784
M00054614A:G11	ES 196	557559	1958.G24.gz43_250832
M00054614B:E01	ES 196	405042	1958.H01.gz43_250465
M00054615B:E03	ES 196	497477	1958.H16.gz43_250705
M00054615C:D09	ES 196	557947	1958.H23.gz43_250817
M00054616A:H01	ES 196	553758	1958.I15.gz43_250690
M00054616A:H03	ES 196	481360	1958.I16.gz43_250706
M00054616D:C10	ES 196	552418	1958.J01.gz43_250467
M00054616D:G09	ES 196	549739	1958.J03.gz43_250499
M00054616D:H06	ES 196	513115	1958.J05.gz43_250531
M00054617A:C07	ES 196	553453	1958.J08.gz43_250579
M00054617B:A09	ES 196	548965	1958.J10.gz43_250611
M00054617B:C05	ES 196	549233	1958.J12.gz43_250643
M00054617B:D06	ES 196	549388	1958.J13.gz43_250659
M00054618B:B04	ES 196	549122	1958.K06.gz43_250548
M00054618C:H02	ES 196	555371	1958.K14.gz43_250676
M00054618D:D04	ES 196	552437	1958.K16.gz43_250708

Table 13

CloneID	ES No	ClusterID	SequenceName
M00054618D:E06	ES 196	490890	1958.K19.gz43_250756
M00054618D:E11	ES 196	451009	1958.K20.gz43_250772
M00054619A:C05	ES 196	447913	1958.K24.gz43_250836
M00054619C:F04	ES 196	554036	1958.L09.gz43_250597
M00054619D:C10	ES 196	562749	1958.L12.gz43_250645
M00054620A:C09	ES 196	553204	1958.L15.gz43_250693
M00054620B:B10	ES 196	552194	1958.L20.gz43_250773
M00054620C:C08	ES 196	448276	1958.L22.gz43_250805
M00054620C:C12	ES 196	560491	1958.L23.gz43_250821
M00054620D:D06	ES 196	561116	1958.M03.gz43_250502
M00054620D:D11	ES 196	473111	1958.M04.gz43_250518
M00054620D:F11	ES 196	556896	1958.M06.gz43_250550
M00054620D:G11	ES 196	395411	1958.M07.gz43_250566
M00054621B:A10	ES 196	548859	1958.M13.gz43_250662
M00054621C:G03	ES 196	451025	1958.M20.gz43_250774
M00054621D:A10	ES 196	518049	1958.M24.gz43_250838
M00054621D:C06	ES 196	558642	1958.N01.gz43_250471
M00054621D:D11	ES 196	549320	1958.N02.gz43_250487
M00054622A:D06	ES 196	27480	1958.N07.gz43_250567
M00054622A:H01	ES 196	561068	1958.N08.gz43_250583
M00054622B:F05	ES 196	491644	1958.N10.gz43_250615
M00054622B:H09	ES 196	556308	1958.N12.gz43_250647
M00054622D:C02	ES 196	562932	1958.N18.gz43_250743
M00054622D:D10	ES 196	551463	1958.N20.gz43_250775
M00054622D:F05	ES 196	485504	1958.N21.gz43_250791
M00054622D:G11	ES 196	556835	1958.N22.gz43_250807
M00054622D:H03	ES 196	453864	1958.N23.gz43_250823
M00054623B:B11	ES 196	556424	1958.O06.gz43_250552
M00054623C:E09	ES 196	558175	1958.O09.gz43_250600
M00054623D:C12	ES 196	551305	1958.O12.gz43_250648
M00054624A:B11	ES 196	550164	1958.O16.gz43_250712
M00054624B:G10	ES 196	559938	1958.O21.gz43_250792
M00054624D:B06	ES 196	554810	1958.O23.gz43_250824
M00054625A:D07	ES 196	558103	1958.P04.gz43_250521
M00054625A:E05	ES 196	557199	1958.P05.gz43_250537
M00054625B:B02	ES 196	551250	1958.P07.gz43_250569
M00054625D:F06	ES 196	562712	1958.P21.gz43_250793
M00054625D:H07	ES 196	461734	1958.P22.gz43_250809
M00054627A:B08	ES 196	556790	1959.A20.gz43_254083
M00054628C:G11	ES 196	557559	1959.C14.gz43_253989
M00054629C:G06	ES 196	555923	1959.D08.gz43_253894
M00054630A:D08	ES 196	562541	1959.D17.gz43_254038
M00054630B:A06	ES 196	551975	1959.D19.gz43_254070
M00054631D:C02	ES 196	552092	1959.F03.gz43_253816

Table 13

CloneID	ES No	ClusterID	SequenceName
M00054635B:G05	ES 196	268197	1959.H16.gz43_254026
M00054638D:F02	ES 196	555949	1959.K24.gz43_254157
M00054640B:C05	ES 196	549210	1959.M04.gz43_253839
M00054642D:F11	ES 196	549516	1959.N22.gz43_254128
M00054643B:G09	ES 196	552618	1959.O10.gz43_253937
M00054644B:F02	ES 196	557345	1959.P08.gz43_253906
M00054644D:F11	ES 196	549624	1959.P20.gz43_254098
M00054647D:H02	ES 196	502683	1960.B23.gz43_254516
M00054648C:H10	ES 196	450867	1960.C12.gz43_254341
M00054650A:B08	ES 196	410667	1960.D12.gz43_254342
M00054651D:D02	ES 196	452662	1960.E24.gz43_254535
M00054652B:A04	ES 196	387728	1960.F04.gz43_254216
M00054656C:E10	ES 196	561590	1960.I07.gz43_254267
M00054657D:E05	ES 196	551531	1960.J11.gz43_254332
M00054661A:B03	ES 196	193991	1960.L03.gz43_254206
M00054661D:A07	ES 196	551065	1960.L12.gz43_254350
M00054663D:D09	ES 196	466851	1960.M24.gz43_254543
M00054664D:A01	ES 196	264575	1960.N14.gz43_254384
M00054668A:D01	ES 196	450624	1969.A10.gz43_254691
M00054670D:F10	ES 196	556424	1969.B21.gz43_254868
M00054671A:H07	ES 196	579481	1969.C07.gz43_254645
M00054671D:A12	ES 196	573733	1969.C24.gz43_254917
M00054672C:F01	ES 196	140763	1969.D20.gz43_254854
M00054673B:G08	ES 196	551845	1969.E09.gz43_254679
M00054674B:B03	ES 196	551269	1969.F03.gz43_254584
M00054677D:H08	ES 196	556959	1969.I02.gz43_254571
M00054683D:F01	ES 196	551630	1969.M04.gz43_254607
M00054685D:D09	ES 196	415326	1969.N11.gz43_254720
M00054689C:B11	ES 196	557935	1970.A03.gz43_263422
M00054689D:E12	ES 196	551527	1970.A06.gz43_263470
M00054690B:B02	ES 196	559389	1970.A14.gz43_263598
M00054690B:D10	ES 196	552418	1970.A16.gz43_263630
M00054690D:G03	ES 196	549388	1970.B04.gz43_263439
M00054692B:C06	ES 196	550330	1970.B20.gz43_263695
M00054692B:D01	ES 196	420686	1970.B21.gz43_263711
M00054692C:B02	ES 196	42994	1970.B23.gz43_263743
M00054692D:F09	ES 196	479208	1970.B24.gz43_263759
M00054693A:C09	ES 196	551243	1970.C05.gz43_263456
M00054693A:E06	ES 196	558938	1970.C08.gz43_263504
M00054693B:B01	ES 196	559036	1970.C09.gz43_263520
M00054693C:A02	ES 196	549995	1970.C14.gz43_263600
M00054693D:A05	ES 196	551150	1970.C18.gz43_263664
M00054693D:A08	ES 196	448332	1970.C19.gz43_263680
M00054693D:C04	ES 196	450755	1970.C20.gz43_263696

Table 13

CloneID	ES No	ClusterID	SequenceName
M00054695A:A12	ES 196	552051	1970.D08.gz43_263505
M00054696B:H11	ES 196	553128	1970.E06.gz43_263474
M00054697A:E03	ES 196	552649	1970.E12.gz43_263570
M00054697A:G06	ES 196	562216	1970.E14.gz43_263602
M00054697C:E11	ES 196	552581	1970.E21.gz43_263714
M00054699A:G01	ES 196	584499	1970.F15.gz43_263619
M00054699B:A05	ES 196	551996	1970.F16.gz43_263635
M00054699B:F05	ES 196	552733	1970.F18.gz43_263667
M00054699C:A04	ES 196	551995	1970.F21.gz43_263715
M00054699D:A12	ES 196	552055	1970.G02.gz43_263412
M00054700A:B03	ES 196	552254	1970.G04.gz43_263444
M00054700A:F12	ES 196	552733	1970.G06.gz43_263476
M00054701D:H05	ES 196	555255	1970.G23.gz43_263748
M00054702A:C06	ES 196	556896	1970.H01.gz43_263397
M00054702A:F03	ES 196	483141	1970.H02.gz43_263413
M00054702A:H03	ES 196	509202	1970.H03.gz43_263429
M00054702C:G06	ES 196	551754	1970.H09.gz43_263525
M00054702D:E07	ES 196	389201	1970.H12.gz43_263573
M00054702D:F05	ES 196	452392	1970.H14.gz43_263605
M00054702D:H10	ES 196	549945	1970.H16.gz43_263637
M00054703C:F01	ES 196	521552	1970.H22.gz43_263733
M00054703D:E07	ES 196	549238	1970.I01.gz43_263398
M00054703D:F04	ES 196	561434	1970.I02.gz43_263414
M00054704B:B11	ES 196	549038	1970.I06.gz43_263478
M00054704D:F02	ES 196	552682	1970.I12.gz43_263574
M00054705B:C08	ES 196	552314	1970.I14.gz43_263606
M00054705B:D02	ES 196	527679	1970.I16.gz43_263638
M00054705B:E04	ES 196	498454	1970.I18.gz43_263670
M00054705C:B02	ES 196	475730	1970.I21.gz43_263718
M00054705C:D11	ES 196	554477	1970.I24.gz43_263766
M00054705D:G03	ES 196	184995	1970.J03.gz43_263431
M00054706A:G10	ES 196	491827	1970.J09.gz43_263527
M00054706B:F10	ES 196	562884	1970.J15.gz43_263623
M00054706C:A04	ES 196	551955	1970.J17.gz43_263655
M00054706C:B12	ES 196	550053	1970.J19.gz43_263687
M00054706D:B03	ES 196	553358	1970.J22.gz43_263735
M00054707B:B08	ES 196	453708	1970.K02.gz43_263416
M00054707C:D02	ES 196	549151	1970.K06.gz43_263480
M00054707C:G07	ES 196	552894	1970.K09.gz43_263528
M00054708A:F11	ES 196	552686	1970.K12.gz43_263576
M00054708B:F04	ES 196	391511	1970.K16.gz43_263640
M00054709A:A10	ES 196	560317	1970.K24.gz43_263768
M00054710B:B10	ES 196	552197	1970.L17.gz43_263657
M00054710C:A12	ES 196	558768	1970.L22.gz43_263737

Table 13

CloneID	ES No	ClusterID	SequenceName
M00054710D:A02	ES 196	551941	1970.M01.gz43_263402
M00054711A:B05	ES 196	553685	1970.M05.gz43_263466
M00054711C:A08	ES 196	552073	1970.M11.gz43_263562
M00054712C:A04	ES 196	558046	1970.N01.gz43_263403
M00054712C:C07	ES 196	549557	1970.N05.gz43_263467
M00054713B:B10	ES 196	551479	1970.N14.gz43_263611
M00054713C:D07	ES 196	553938	1970.N18.gz43_263675
M00054714A:C05	ES 196	430917	1970.O01.gz43_263404
M00054714B:F05	ES 196	32021	1970.O06.gz43_263484
M00054714C:E01	ES 196	552625	1970.O09.gz43_263532
M00054715A:C06	ES 196	452559	1970.O15.gz43_263628
M00054715A:G02	ES 196	550975	1970.O17.gz43_263660
M00054715C:D05	ES 196	451032	1970.O23.gz43_263756
M00054715C:D11	ES 196	419281	1970.O24.gz43_263772
M00054715D:E11	ES 196	552598	1970.P07.gz43_263501
M00054715D:F09	ES 196	583641	1970.P08.gz43_263517
M00054716B:D06	ES 196	490393	1970.P16.gz43_263645
M00054716D:D03	ES 196	552497	1970.P23.gz43_263757
M00054717A:A03	ES 196	552086	1971.A01.gz43_246992
M00054717A:C07	ES 196	549550	1971.A03.gz43_247024
M00054717A:G09	ES 196	450278	1971.A06.gz43_247072
M00054717C:G07	ES 196	554913	1971.A18.gz43_247264
M00054718A:D11	ES 196	555571	1971.A24.gz43_247360
M00054718B:D03	ES 196	555837	1971.B05.gz43_247057
M00054719A:A02	ES 196	552028	1971.B13.gz43_247185
M00054719A:H06	ES 196	553012	1971.B16.gz43_247233
M00054720C:A01	ES 196	553123	1971.D01.gz43_246995
M00054720C:G10	ES 196	557714	1971.D05.gz43_247059
M00054720C:H01	ES 196	561313	1971.D06.gz43_247075
M00054721C:D11	ES 196	446999	1971.E05.gz43_247060
M00054722C:D01	ES 196	450410	1971.F05.gz43_247061
M00054722D:C08	ES 196	553316	1971.F09.gz43_247125
M00054724A:G02	ES 196	421959	1971.G14.gz43_247206
M00054724B:F06	ES 196	551826	1971.G18.gz43_247270
M00054724D:C05	ES 196	561636	1971.H01.gz43_246999
M00054724D:G12	ES 196	553805	1971.H07.gz43_247095
M00054725A:A03	ES 196	448136	1971.H09.gz43_247127
M00054725A:A05	ES 196	551096	1971.H10.gz43_247143
M00054725A:F09	ES 196	555491	1971.H11.gz43_247159
M00054725A:H06	ES 196	86175	1971.H12.gz43_247175
M00054725B:G12	ES 196	555676	1971.H19.gz43_247287
M00054725D:F04	ES 196	553731	1971.I04.gz43_247048
M00054726A:B11	ES 196	552933	1971.I07.gz43_247096
M00054726A:D02	ES 196	555818	1971.I09.gz43_247128

Table 13

CloneID	ES No	ClusterID	SequenceName
M00054726A:E01	ES 197	551487	1971.I10.gz43_247144
M00054726B:F08	ES 197	553739	1971.I16.gz43_247240
M00054726B:F09	ES 197	557747	1971.I17.gz43_247256
M00054726C:D10	ES 197	449035	1971.I21.gz43_247320
M00054726C:E07	ES 197	524721	1971.I22.gz43_247336
M00054727A:B12	ES 197	553264	1971.J09.gz43_247129
M00054727D:C06	ES 197	496772	1971.K01.gz43_247002
M00054728B:C10	ES 197	557356	1971.K09.gz43_247130
M00054728C:B08	ES 197	559113	1971.K13.gz43_247194
M00054728D:B07	ES 197	554048	1971.K18.gz43_247274
M00054729B:A08	ES 197	484043	1971.L05.gz43_247067
M00054729B:B03	ES 197	557426	1971.L06.gz43_247083
M00054729B:E06	ES 197	451812	1971.L09.gz43_247131
M00054729C:C08	ES 197	561830	1971.L12.gz43_247179
M00054729C:G07	ES 197	562263	1971.L15.gz43_247227
M00054729D:D05	ES 197	550315	1971.L18.gz43_247275
M00054730B:F11	ES 197	559380	1971.M11.gz43_247164
M00054731A:D07	ES 197	452488	1971.N05.gz43_247069
M00054731B:C12	ES 197	553310	1971.N13.gz43_247197
M00054731B:D04	ES 197	448453	1971.N14.gz43_247213
M00054731B:G02	ES 197	553751	1971.N17.gz43_247261
M00054731C:H12	ES 197	553869	1971.N24.gz43_247373
M00054731D:H11	ES 197	215005	1971.O04.gz43_247054
M00054732A:B07	ES 197	561379	1971.O06.gz43_247086
M00054734B:C06	ES 197	556654	1971.P10.gz43_247151
M00054734B:G10	ES 197	549288	1971.P15.gz43_247231
M00054734C:A07	ES 197	553108	1971.P17.gz43_247263
M00054735A:G09	ES 197	552686	1971.P24.gz43_247375
M00054736B:H03	ES 197	522322	1972.B13.gz43_247569
M00054737B:H11	ES 197	556167	1972.C05.gz43_247442
M00054737C:B01	ES 197	454186	1972.C06.gz43_247458
M00054738B:E12	ES 197	560282	1972.C21.gz43_247698
M00054738D:F01	ES 197	558679	1972.D13.gz43_247571
M00054738D:G07	ES 197	495832	1972.D15.gz43_247603
M00054739A:F07	ES 197	555773	1972.D24.gz43_247747
M00054739C:B12	ES 197	466235	1972.E08.gz43_247492
M00054739C:E05	ES 197	450142	1972.E12.gz43_247556
M00054740C:H08	ES 197	493122	1972.F15.gz43_247605
M00054741C:D08	ES 197	493135	1972.G15.gz43_247606
M00054741D:C05	ES 197	551778	1972.G19.gz43_247670
M00054743A:C07	ES 197	424723	1972.I03.gz43_247416
M00054743A:E04	ES 197	473455	1972.I04.gz43_247432
M00054743C:E11	ES 197	452257	1972.I13.gz43_247576

Table 13

CloneID	ES No	ClusterID	SequenceName
M00054743D:F04	ES 197	555077	1972.I19.gz43_247672
M00054744A:G10	ES 197	553834	1972.J05.gz43_247449
M00054744C:D02	ES 197	587854	1972.J16.gz43_247625
M00054744D:G02	ES 197	557068	1972.K03.gz43_247418
M00054745C:B12	ES 197	562793	1972.K15.gz43_247610
M00054745C:H02	ES 197	557871	1972.K19.gz43_247674
M00054745D:G09	ES 197	551441	1972.L04.gz43_247435
M00054746A:H02	ES 197	559494	1972.L09.gz43_247515
M00054746D:E05	ES 197	503452	1972.L22.gz43_247723
M00054747D:B05	ES 197	474309	1972.M24.gz43_247756
M00054748B:G10	ES 197	523753	1972.N13.gz43_247581
M00054748B:H09	ES 197	59202	1972.N14.gz43_247597
M00054750A:E11	ES 197	446997	1972.O06.gz43_247470
M00054750A:G10	ES 197	562323	1972.O09.gz43_247518
M00054750B:F02	ES 197	557568	1972.O12.gz43_247566
M00054750C:D01	ES 197	553457	1972.O18.gz43_247662
M00054750D:F01	ES 197	559215	1972.P01.gz43_247391
M00054750D:H12	ES 197	499517	1972.P03.gz43_247423
M00054751A:A05	ES 197	86145	1972.P04.gz43_247439
M00054751B:F12	ES 197	553702	1972.P14.gz43_247599
M00054751D:G10	ES 197	553800	1972.P24.gz43_247759
M00054752A:C12	ES 197	562451	1981.A03.gz43_247792
M00054752B:H06	ES 197	495942	1981.A10.gz43_247904
M00054753A:A05	ES 197	554000	1981.A18.gz43_248032
M00054753C:H02	ES 197	553918	1981.B08.gz43_247873
M00054753D:A03	ES 197	477046	1981.B09.gz43_247889
M00054753D:C12	ES 197	256179	1981.B11.gz43_247921
M00054753D:H10	ES 197	553922	1981.B13.gz43_247953
M00054754B:F04	ES 197	558609	1981.B16.gz43_248001
M00054754C:H09	ES 197	550580	1981.B22.gz43_248097
M00054754D:F11	ES 197	551693	1981.C04.gz43_247810
M00054755A:E10	ES 197	493135	1981.C10.gz43_247906
M00054755C:D04	ES 197	561412	1981.C24.gz43_248130
M00054755D:E02	ES 197	562360	1981.D02.gz43_247779
M00054755D:E05	ES 197	513632	1981.D03.gz43_247795
M00054756A:C12	ES 197	551289	1981.D09.gz43_247891
M00054756C:C08	ES 197	551288	1981.D15.gz43_247987
M00054756D:F05	ES 197	451993	1981.D19.gz43_248051
M00054757A:H07	ES 197	555343	1981.D21.gz43_248083
M00054757B:H04	ES 197	561433	1981.E04.gz43_247812
M00054758A:F03	ES 197	554336	1981.E13.gz43_247956
M00054758B:C10	ES 197	122169	1981.E15.gz43_247988
M00054758B:D03	ES 197	554352	1981.E16.gz43_248004
M00054758B:H03	ES 197	554049	1981.E18.gz43_248036

Table 13

CloneID	ES No	ClusterID	SequenceName
M00054758D:D03	ES 197	551415	1981.E24.gz43_248132
M00054759A:B08	ES 197	553158	1981.F03.gz43_247797
M00054759C:D07	ES 197	553800	1981.F11.gz43_247925
M00054759C:G10	ES 197	560529	1981.F13.gz43_247957
M00054759D:E01	ES 197	556064	1981.F17.gz43_248021
M00054760A:A12	ES 197	551117	1981.F22.gz43_248101
M00054760A:D10	ES 197	561535	1981.F24.gz43_248133
M00054760B:A10	ES 197	549588	1981.G04.gz43_247814
M00054760D:B03	ES 197	263800	1981.G09.gz43_247894
M00054761C:E02	ES 197	558719	1981.G24.gz43_248134
M00054761D:C11	ES 197	493604	1981.H04.gz43_247815
M00054762A:D09	ES 197	556183	1981.H10.gz43_247911
M00054762B:F02	ES 197	558900	1981.H14.gz43_247975
M00054762B:F07	ES 197	551617	1981.H15.gz43_247991
M00054762C:A12	ES 197	558503	1981.H18.gz43_248039
M00054762D:C06	ES 197	551338	1981.H24.gz43_248135
M00054763A:A10	ES 197	472196	1981.I02.gz43_247784
M00054763C:D07	ES 197	554021	1981.I04.gz43_247816
M00054763C:F10	ES 197	558900	1981.I05.gz43_247832
M00054763C:H04	ES 197	450840	1981.I06.gz43_247848
M00054764A:E11	ES 197	576803	1981.I14.gz43_247976
M00054764C:G04	ES 197	555754	1981.I22.gz43_248104
M00054764D:F01	ES 197	556019	1981.J01.gz43_247769
M00054765B:C03	ES 197	561487	1981.J07.gz43_247865
M00054765B:C11	ES 197	554181	1981.J09.gz43_247897
M00054765C:F10	ES 197	553131	1981.J20.gz43_248073
M00054765D:D05	ES 197	554294	1981.K05.gz43_247834
M00054766A:H10	ES 197	508126	1981.K17.gz43_248026
M00054766C:B08	ES 197	498662	1981.L03.gz43_247803
M00054766C:E01	ES 197	552541	1981.L07.gz43_247867
M00054766D:H02	ES 197	260558	1981.L15.gz43_247995
M00054766D:H12	ES 197	554851	1981.L16.gz43_248011
M00054767A:F08	ES 197	556475	1981.L22.gz43_248107
M00054767C:C08	ES 197	552535	1981.M13.gz43_247964
M00054767C:D03	ES 197	455220	1981.M14.gz43_247980
M00054767C:H06	ES 197	549576	1981.M17.gz43_248028
M00054767D:G09	ES 197	552549	1981.M22.gz43_248108
M00054768B:B05	ES 197	559369	1981.N01.gz43_247773
M00054768B:D10	ES 197	400628	1981.N05.gz43_247837
M00054768D:A01	ES 197	448357	1981.N10.gz43_247917
M00054768D:B11	ES 197	451051	1981.N11.gz43_247933
M00054769A:G10	ES 197	512432	1981.N21.gz43_248093
M00054769B:D12	ES 197	550402	1981.O04.gz43_247822
M00054769B:F03	ES 197	554635	1981.O06.gz43_247854

Table 13

CloneID	ES No	ClusterID	SequenceName
M00054770A:C06	ES 197	558949	1981.O19.gz43_248062
M00054770B:A12	ES 197	552733	1981.O24.gz43_248142
M00054770B:B11	ES 197	556918	1981.P01.gz43_247775
M00054770B:D09	ES 197	448510	1981.P04.gz43_247823
M00054770C:A04	ES 197	528775	1981.P07.gz43_247871
M00054770C:C04	ES 197	554161	1981.P10.gz43_247919
M00054770C:D05	ES 197	555478	1981.P11.gz43_247935
M00054770C:F10	ES 197	554581	1981.P12.gz43_247951
M00054771A:E01	ES 197	470351	1981.P23.gz43_248127
M00054771B:F12	ES 197	492779	1982.A02.gz43_248160
M00054771C:A11	ES 197	551068	1982.A04.gz43_248192
M00054771D:G01	ES 197	551718	1982.A08.gz43_248256
M00054772B:B01	ES 197	586600	1982.A15.gz43_248368
M00054772B:D04	ES 197	472672	1982.A17.gz43_248400
M00054772B:F03	ES 197	493085	1982.A18.gz43_248416
M00054772D:G12	ES 197	553774	1982.B06.gz43_248225
M00054773A:E09	ES 197	551169	1982.B08.gz43_248257
M00054773A:H05	ES 197	402147	1982.B09.gz43_248273
M00054773C:D06	ES 197	42323	1982.B15.gz43_248369
M00054773C:F09	ES 197	557834	1982.B18.gz43_248417
M00054773C:F10	ES 197	448629	1982.B19.gz43_248433
M00054774B:A07	ES 197	555686	1982.C03.gz43_248178
M00054774B:G08	ES 197	554072	1982.C06.gz43_248226
M00054774C:A03	ES 197	552019	1982.C07.gz43_248242
M00054774C:D12	ES 197	552495	1982.C08.gz43_248258
M00054774D:D06	ES 197	559050	1982.C10.gz43_248290
M00054775A:D07	ES 197	555462	1982.C16.gz43_248386
M00054775A:G03	ES 197	595181	1982.C17.gz43_248402
M00054776A:D10	ES 197	557269	1982.D09.gz43_248275
M00054776A:F01	ES 197	560520	1982.D10.gz43_248291
M00054776A:F07	ES 197	447926	1982.D11.gz43_248307
M00054776A:G01	ES 197	412621	1982.D12.gz43_248323
M00054776C:G06	ES 197	554828	1982.E06.gz43_248228
M00054776D:G09	ES 197	553743	1982.E11.gz43_248308
M00054778A:D01	ES 197	555958	1982.F01.gz43_248149
M00054778A:F08	ES 197	551003	1982.F05.gz43_248213
M00054778B:A02	ES 197	551080	1982.F08.gz43_248261
M00054778C:F09	ES 197	548998	1982.F18.gz43_248421
M00054779B:A07	ES 197	465207	1982.G05.gz43_248214
M00054779B:B07	ES 197	559872	1982.G06.gz43_248230
M00054779B:B11	ES 197	556183	1982.G07.gz43_248246
M00054779D:F07	ES 197	554627	1982.G17.gz43_248406
M00054779D:F08	ES 197	551425	1982.G18.gz43_248422
M00054780A:B06	ES 197	550422	1982.G21.gz43_248470

Table 13

CloneID	ES No	ClusterID	SequenceName
M00054780B:B06	ES 197	555524	1982.H03.gz43_248183
M00054780B:E03	ES 197	533991	1982.H05.gz43_248215
M00054780B:G10	ES 197	491570	1982.H06.gz43_248231
M00054780C:G11	ES 197	558519	1982.H14.gz43_248359
M00054781A:H09	ES 197	505792	1982.H21.gz43_248471
M00054781D:F10	ES 197	556171	1982.I02.gz43_248168
M00054782B:B02	ES 197	551167	1982.I05.gz43_248216
M00054782B:D09	ES 197	551425	1982.I07.gz43_248248
M00054782D:D12	ES 197	575924	1982.I10.gz43_248296
M00054783C:C02	ES 197	557039	1982.I16.gz43_248392
M00054783C:C03	ES 197	552325	1982.I17.gz43_248408
M00054784C:D11	ES 197	552535	1982.J07.gz43_248249
M00054784D:B01	ES 197	554582	1982.J10.gz43_248297
M00054785B:B07	ES 197	552188	1982.J13.gz43_248345
M00054785C:C02	ES 197	562263	1982.J15.gz43_248377
M00054785C:G11	ES 197	462511	1982.J17.gz43_248409
M00054785D:A07	ES 197	552005	1982.J19.gz43_248441
M00054786A:G11	ES 198	561422	1982.J21.gz43_248473
M00054786C:G01	ES 198	553330	1982.K02.gz43_248170
M00054786D:F08	ES 198	553868	1982.K05.gz43_248218
M00054787D:A10	ES 198	580179	1982.K12.gz43_248330
M00054788C:G04	ES 198	552813	1982.K17.gz43_248410
M00054789A:A02	ES 198	490414	1982.K18.gz43_248426
M00054790D:D05	ES 198	548874	1982.L06.gz43_248235
M00054801C:G01	ES 198	549233	1982.L17.gz43_248411
M00054802A:G03	ES 198	446394	1982.M01.gz43_248156
M00054802A:H05	ES 198	490507	1982.M03.gz43_248188
M00054802C:A07	ES 198	374282	1982.M06.gz43_248236
M00054802D:A09	ES 198	555696	1982.M10.gz43_248300
M00054802D:C02	ES 198	497477	1982.M12.gz43_248332
M00054802D:C03	ES 198	456052	1982.M13.gz43_248348
M00054803A:D08	ES 198	175758	1982.M17.gz43_248412
M00054803A:E10	ES 198	551553	1982.M18.gz43_248428
M00054803B:B12	ES 198	554116	1982.M20.gz43_248460
M00054803C:G01	ES 198	551755	1982.M24.gz43_248524
M00054804A:G08	ES 198	496570	1982.N08.gz43_248269
M00054804A:H04	ES 198	539353	1982.N09.gz43_248285
M00054804B:E07	ES 198	553979	1982.N11.gz43_248317
M00054804C:F04	ES 198	553237	1982.N14.gz43_248365
M00054804D:A11	ES 198	559896	1982.N16.gz43_248397
M00054804D:D07	ES 198	555571	1982.N18.gz43_248429
M00054804D:H12	ES 198	417259	1982.N22.gz43_248493
M00054805A:E09	ES 198	553612	1982.O03.gz43_248190

Table 13

CloneID	ES No	ClusterID	SequenceName
M00054805A:H04	ES 198	552183	1982.O04.gz43_248206
M00054805B:E06	ES 198	556856	1982.O10.gz43_248302
M00054805B:E11	ES 198	497912	1982.O11.gz43_248318
M00054805B:G02	ES 198	556856	1982.O14.gz43_248366
M00054805B:G10	ES 198	394168	1982.O16.gz43_248398
M00054806A:G04	ES 198	553848	1982.P02.gz43_248175
M00054806C:C12	ES 198	517146	1982.P08.gz43_248271
M00054806D:C01	ES 198	553331	1982.P10.gz43_248303
M00054811A:C10	ES 198	551512	1983.C10.gz43_255077
M00054811B:H12	ES 198	494471	1983.C19.gz43_255221
M00054811D:F01	ES 198	551659	1983.D01.gz43_254934
M00054812D:H05	ES 198	549816	1983.E06.gz43_255015
M00054813B:D11	ES 198	456520	1983.E19.gz43_255223
M00054814A:F07	ES 198	557525	1983.F09.gz43_255064
M00054823B:E07	ES 198	450788	1983.K11.gz43_255101
M00054824A:E02	ES 198	555641	1983.L07.gz43_255038
M00054826B:G08	ES 198	447087	1983.N07.gz43_255040
M00054831A:E11	ES 198	554196	1984.A12.gz43_255491
M00054831B:E05	ES 198	451081	1984.A20.gz43_255619
M00054839D:F08	ES 198	562302	1984.G07.gz43_255417
M00054840D:B03	ES 198	557703	1984.G21.gz43_255641
M00054842B:B12	ES 198	554696	1984.I08.gz43_255435
M00054848B:E02	ES 198	533520	1984.N02.gz43_255344
M00054851B:E03	ES 198	560984	1984.P06.gz43_255410
M00054852C:G03	ES 198	559885	1993.A04.gz43_263822
M00054852D:D09	ES 198	556715	1993.A09.gz43_263902
M00054853A:A10	ES 198	556132	1993.A11.gz43_263934
M00054853B:E07	ES 198	522703	1993.A18.gz43_264046
M00054853B:E10	ES 198	599433	1993.A19.gz43_264062
M00054854A:H06	ES 198	554524	1993.B05.gz43_263839
M00054854B:C04	ES 198	548861	1993.B07.gz43_263871
M00054854C:H02	ES 198	450829	1993.B12.gz43_263951
M00054855B:E04	ES 198	554672	1993.C05.gz43_263840
M00054855B:F10	ES 198	556918	1993.C07.gz43_263872
M00054855C:B06	ES 198	496897	1993.C09.gz43_263904
M00054855C:H08	ES 198	557209	1993.C13.gz43_263968
M00054855D:G12	ES 198	557077	1993.C14.gz43_263984
M00054856A:F08	ES 198	554613	1993.C20.gz43_264080
M00054856D:E11	ES 198	560714	1993.D05.gz43_263841
M00054857A:B11	ES 198	554084	1993.D09.gz43_263905
M00054857A:G09	ES 198	554756	1993.D14.gz43_263985
M00054857A:G12	ES 198	554989	1993.D15.gz43_264001
M00054857B:D08	ES 198	593343	1993.D19.gz43_264065
M00054857C:G09	ES 198	555740	1993.E02.gz43_263794

Table 13

CloneID	ES No	ClusterID	SequenceName
M00054857D:E12	ES 198	554500	1993.E07.gz43_263874
M00054858A:B05	ES 198	554497	1993.E10.gz43_263922
M00054858A:D06	ES 198	482306	1993.E14.gz43_263986
M00054858A:D08	ES 198	550714	1993.E15.gz43_264002
M00054858B:A10	ES 198	451491	1993.E18.gz43_264050
M00054858D:C04	ES 198	551212	1993.F02.gz43_263795
M00054859A:D10	ES 198	555968	1993.F10.gz43_263923
M00054859A:E02	ES 198	555667	1993.F11.gz43_263939
M00054859D:D02	ES 198	557719	1993.F24.gz43_264147
M00054859D:E01	ES 198	594013	1993.G02.gz43_263796
M00054859D:E09	ES 198	554456	1993.G03.gz43_263812
M00054859D:G04	ES 198	557852	1993.G05.gz43_263844
M00054860B:F11	ES 198	549481	1993.G16.gz43_264020
M00054860C:C04	ES 198	554221	1993.G19.gz43_264068
M00054860C:E04	ES 198	497365	1993.G21.gz43_264100
M00054860C:F01	ES 198	490629	1993.G24.gz43_264148
M00054860D:D01	ES 198	554257	1993.H04.gz43_263829
M00054861B:H08	ES 198	560259	1993.H14.gz43_263989
M00054861C:E10	ES 198	551811	1993.H18.gz43_264053
M00054862C:D05	ES 198	522507	1993.I07.gz43_263878
M00054862D:D10	ES 198	476843	1993.I13.gz43_263974
M00054863A:A11	ES 198	562962	1993.I15.gz43_264006
M00054863D:C07	ES 198	463060	1993.I23.gz43_264134
M00054863D:H05	ES 198	554900	1993.J01.gz43_263783
M00054864B:B02	ES 198	553295	1993.J05.gz43_263847
M00054864B:D08	ES 198	501534	1993.J08.gz43_263895
M00054864C:A01	ES 198	519109	1993.J11.gz43_263943
M00054865A:A10	ES 198	462767	1993.J20.gz43_264087
M00054865B:H04	ES 198	43642	1993.K10.gz43_263928
M00054865D:F05	ES 198	394567	1993.K16.gz43_264024
M00054866B:C01	ES 198	560254	1993.L01.gz43_263785
M00054866B:G01	ES 198	408840	1993.L04.gz43_263833
M00054866C:G07	ES 198	595506	1993.L10.gz43_263929
M00054866D:C03	ES 198	402742	1993.L14.gz43_263993
M00054867A:C07	ES 198	549320	1993.L21.gz43_264105
M00054867A:G01	ES 198	551591	1993.L24.gz43_264153
M00054867B:D02	ES 198	493303	1993.M03.gz43_263818
M00054867D:H03	ES 198	463513	1993.M13.gz43_263978
M00054868B:A05	ES 198	557974	1993.M23.gz43_264138
M00054868C:G11	ES 198	559027	1993.N06.gz43_263867
M00054869A:A09	ES 198	552396	1993.N13.gz43_263979
M00054869A:D03	ES 198	457825	1993.N17.gz43_264043
M00054869C:A05	ES 198	182113	1993.O01.gz43_263788
M00054869C:H04	ES 198	549946	1993.O06.gz43_263868

Table 13

CloneID	ES No	ClusterID	SequenceName
M00054869D:F02	ES 198	594434	1993.O10.gz43_263932
M00054870A:D11	ES 198	549666	1993.O13.gz43_263980
M00054870B:A12	ES 198	553072	1993.O17.gz43_264044
M00054870B:G12	ES 198	555553	1993.O21.gz43_264108
M00054870C:C05	ES 198	522648	1993.P03.gz43_263821
M00054870C:E06	ES 198	556382	1993.P04.gz43_263837
M00054870D:G08	ES 198	555702	1993.P10.gz43_263933
M00054871A:C04	ES 198	390017	1993.P14.gz43_263997
M00054871A:E03	ES 198	553582	1993.P15.gz43_264013
M00054871A:E07	ES 198	524464	1993.P18.gz43_264061
M00054871A:H07	ES 198	481641	1993.P21.gz43_264109
M00054871B:E10	ES 198	553586	1993.P24.gz43_264157
M00054871B:F06	ES 198	556839	1994.A02.gz43_255715
M00054872A:H10	ES 198	559531	1994.A19.gz43_255987
M00054873C:E09	ES 198	553636	1994.B17.gz43_255956
M00054877A:F01	ES 198	562243	1994.E15.gz43_255927
M00054878B:G03	ES 198	447483	1994.F22.gz43_256040
M00054885C:G06	ES 198	549391	1994.K24.gz43_256077
M00054887C:E09	ES 198	558564	1994.M12.gz43_255887
M00054891D:D03	ES 198	556722	1995.A01.gz43_256083
M00054891D:H05	ES 198	557218	1995.A03.gz43_256115
M00054892C:G05	ES 198	555998	1995.A14.gz43_256291
M00054892D:D06	ES 198	454812	1995.A19.gz43_256371
M00054893A:F08	ES 198	550047	1995.B06.gz43_256164
M00054893C:A06	ES 198	562106	1995.B14.gz43_256292
M00054893C:A07	ES 198	554002	1995.B15.gz43_256308
M00054893C:B02	ES 198	556365	1995.B16.gz43_256324
M00054893C:E04	ES 198	551463	1995.B20.gz43_256388
M00054893C:G06	ES 198	474163	1995.B22.gz43_256420
M00054893D:D12	ES 198	556632	1995.B24.gz43_256452
M00054893D:F07	ES 198	550204	1995.C02.gz43_256101
M00054893D:G09	ES 198	562152	1995.C03.gz43_256117
M00054894A:F05	ES 198	469605	1995.C06.gz43_256165
M00054894C:B11	ES 198	556404	1995.C12.gz43_256261
M00054894D:F04	ES 198	446186	1995.C15.gz43_256309
M00054895B:A02	ES 198	558779	1995.C23.gz43_256437
M00054895B:A08	ES 198	596809	1995.C24.gz43_256453
M00054895B:D09	ES 198	447858	1995.D05.gz43_256150
M00054895C:B07	ES 198	82864	1995.D11.gz43_256246
M00054895D:B02	ES 198	549228	1995.D16.gz43_256326
M00054895D:C10	ES 198	552122	1995.D18.gz43_256358
M00054896B:E09	ES 198	562672	1995.E04.gz43_256135
M00054896C:D08	ES 198	556725	1995.E09.gz43_256215
M00054896C:F01	ES 198	451049	1995.E10.gz43_256231

Table 13

CloneID	ES No	ClusterID	SequenceName
M00054896D:C01	ES 198	556499	1995.E13.gz43_256279
M00054896D:C11	ES 198	557326	1995.E14.gz43_256295
M00054896D:E11	ES 198	557283	1995.E16.gz43_256327
M00054897C:F03	ES 198	562679	1995.F03.gz43_256120
M00054897D:E08	ES 198	556804	1995.F07.gz43_256184
M00054898A:G09	ES 198	453715	1995.F13.gz43_256280
M00054898B:A03	ES 198	556328	1995.F16.gz43_256328
M00054898B:D01	ES 198	549997	1995.F20.gz43_256392
M00054898B:D04	ES 198	458035	1995.F21.gz43_256408
M00054898D:H12	ES 198	543855	1995.G03.gz43_256121
M00054899A:D09	ES 198	460690	1995.G05.gz43_256153
M00054899C:D11	ES 198	553534	1995.G16.gz43_256329
M00054899D:C11	ES 198	558011	1995.G20.gz43_256393
M00054899D:F07	ES 198	555830	1995.G23.gz43_256441
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M00054900B:D12	ES 198	559554	1995.H08.gz43_256202
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M00054900C:C03	ES 198	516691	1995.H12.gz43_256266
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M00054903C:G04	ES 199	558935	1995.J14.gz43_256300
M00054903D:B05	ES 199	555184	1995.J15.gz43_256316
M00054903D:G01	ES 199	558177	1995.J19.gz43_256380
M00054903D:G10	ES 199	555967	1995.J21.gz43_256412
M00054904A:F07	ES 199	554604	1995.K02.gz43_256109
M00054904A:H10	ES 199	549376	1995.K03.gz43_256125

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M00054904D:B01	ES 199	559036	1995.K14.gz43_256301
M00054904D:F07	ES 199	411272	1995.K18:gz43_256365
M00054904D:G04	ES 199	558868	1995.K20.gz43_256397
M00054906D:D06	ES 199	492256	1995.L05.gz43_256158
M00054907A:D01	ES 199	554344	1995.L08.gz43_256206
M00054907B:E07	ES 199	489001	1995.L13.gz43_256286
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M00054907C:A12	ES 199	553969	1995.L16.gz43_256334
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M00054908A:F10	ES 199	522220	1995.M03.gz43_256127
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M00054908D:A07	ES 199	558326	1995.N02.gz43_256112
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M00054921C:G01	ES 199	554747	1995.N23.gz43_256448
M00054921C:G06	ES 199	495365	1995.N24.gz43_256464
M00054922A:C11	ES 199	550710	1995.O03.gz43_256129
M00054922B:A08	ES 199	553975	1995.O08.gz43_256209
M00054922B:A10	ES 199	150839	1995.O09.gz43_256225
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M00054930D:D04	ES 199	558024	1996.D13.gz43_256686
M00054931C:F10	ES 199	549171	1996.E06.gz43_256575
M00054933A:H09	ES 199	44608	1996.F18.gz43_256768
M00054933B:C02	ES 199	562106	1996.F20.gz43_256800
M00054936B:G02	ES 199	555739	1996.I18.gz43_256771
M00054936C:B08	ES 199	549805	1996.I19.gz43_256787

Table 13

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M00054939A:B11	ES 199	560088	1996.L08.gz43_256614
M00054939D:E03	ES 199	552566	1996.M08.gz43_256615
M00054940C:H12	ES 199	227777	1996.N13.gz43_256696
M00054940D:E06	ES 199	553535	1996.N16.gz43_256744
M00054941A:A08	ES 199	558397	1996.N18.gz43_256776
M00054941C:G04	ES 199	562550	1996.O06.gz43_256585
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M00054942C:B04	ES 199	67060	1996.P05.gz43_256570
M00054943A:H11	ES 199	481166	1996.P20.gz43_256810
M00054943D:F12	ES 199	562053	2005.A14.gz43_257085
M00054945B:G09	ES 199	554833	2005.C07.gz43_256975
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M00054951A:G03	ES 199	555996	2005.H14.gz43_257092
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M00054953B:D07	ES 199	555526	2005.J12.gz43_257062
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M00054960C:C03	ES 199	456795	2006.A03.gz43_257293
M00054961A:E10	ES 199	550149	2006.A11.gz43_257421
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M00054962A:H07	ES 199	129715	2006.B22.gz43_257598
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M00054962C:D02	ES 199	599012	2006.C06.gz43_257343
M00054963A:C12	ES 199	531145	2006.C17.gz43_257519
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M00054963A:G12	ES 199	553976	2006.C22.gz43_257599
M00054963A:H04	ES 199	471257	2006.C23.gz43_257615
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M00054963C:C08	ES 199	555394	2006.D06.gz43_257344
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M00054964A:B09	ES 199	561984	2006.D22.gz43_257600
M00054964A:C06	ES 199	562386	2006.D23.gz43_257616
M00054964A:F09	ES 199	556954	2006.E03.gz43_257297
M00054964C:B07	ES 199	553204	2006.E10.gz43_257409
M00054965C:C04	ES 199	557883	2006.F18.gz43_257538
M00054966A:C02	ES 199	465339	2006.G01.gz43_257267

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M00054966A:G02	ES 199	556126	2006.G10.gz43_257411
M00054966D:C05	ES 199	497938	2006.G22.gz43_257603
M00054966D:H12	ES 199	494306	2006.H03.gz43_257300
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M00054967D:F08	ES 199	208278	2006.I03.gz43_257301
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M00054969A:B08	ES 199	436888	2006.J05.gz43_257334
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M00054969A:F12	ES 199	554646	2006.J11.gz43_257430
M00054969B:F12	ES 199	556552	2006.J19.gz43_257558
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M00054969C:H05	ES 199	557080	2006.J23.gz43_257622
M00054969D:D04	ES 199	554379	2006.K06.gz43_257351
M00054969D:G11	ES 199	450932	2006.K09.gz43_257399
M00054970A:G03	ES 199	470386	2006.K18.gz43_257543
M00054970B:B02	ES 199	218113	2006.K20.gz43_257575
M00054970C:C08	ES 199	504400	2006.L03.gz43_257304
M00054971A:D04	ES 199	557559	2006.L20.gz43_257576
M00054971A:D07	ES 199	554275	2006.L22.gz43_257608
M00054971C:C11	ES 199	554204	2006.M11.gz43_257433
M00054971C:H06	ES 199	596152	2006.M18.gz43_257545
M00054971D:F04	ES 199	554643	2006.M23.gz43_257625
M00054972B:E06	ES 199	554524	2006.N12.gz43_257450
M00054972C:F09	ES 199	552669	2006.N18.gz43_257546
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M00054973B:A10	ES 199	555103	2006.O06.gz43_257355
M00054973D:B09	ES 199	555155	2006.O16.gz43_257515
M00054974C:A04	ES 199	557780	2006.P02.gz43_257292
M00054974D:C11	ES 199	556552	2006.P11.gz43_257436
M00054975A:C08	ES 199	559047	2006.P12.gz43_257452
M00054975A:E02	ES 199	552941	2006.P13.gz43_257468
M00054975B:B06	ES 199	554365	2006.P15.gz43_257500
M00054975C:D08	ES 199	549579	2006.P22.gz43_257612
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M00054976A:A03	ES 199	551967	2007.A05.gz43_257709
M00054976B:C10	ES 199	556512	2007.A08.gz43_257757
M00054976C:A03	ES 199	558670	2007.A11.gz43_257805
M00054976C:G10	ES 199	476517	2007.A19.gz43_257933
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M00054977C:A09	ES 199	458257	2007.B13.gz43_257838

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M00054977C:F09	ES 199	561112	2007.B18.gz43_257918
M00054977D:B06	ES 199	551694	2007.B20.gz43_257950
M00054978C:E07	ES 199	556768	2007.C04.gz43_257695
M00054978D:H09	ES 199	562750	2007.C09.gz43_257775
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M00054979B:G12	ES 199	557054	2007.C18.gz43_257919
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M00054980D:H07	ES 199	555197	2007.D13.gz43_257840
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M00054981D:C06	ES 199	556561	2007.E08.gz43_257761
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M00054989B:C11	ES 199	471827	2007.J03.gz43_257686

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M00054990C:A08	ES 199	556288	2007.J17.gz43_257910
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M00054991C:E01	ES 200	454463	2007.K08.gz43_257767
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M00054994A:E05	ES 200	550833	2007.M06.gz43_257737
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M00054994C:G06	ES 200	553797	2007.M16.gz43_257897
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M00055001C:G07	ES 200	549690	2008.A18.gz43_258303
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M00055005D:B08	ES 200	460445	2008.D17.gz43_258290
M00055005D:C11	ES 200	555289	2008.D18.gz43_258306
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M00055006B:E05	ES 200	347057	2008.E10.gz43_258179
M00055006B:G03	ES 200	557026	2008.E11.gz43_258195
M00055007C:D01	ES 200	34381	2008.F08.gz43_258148
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M00055008C:H10	ES 200	554932	2008.G05.gz43_258101
M00055008D:A02	ES 200	554015	2008.G06.gz43_258117
M00055008D:E02	ES 200	556041	2008.G12.gz43_258213
M00055008D:F05	ES 200	560563	2008.G13.gz43_258229
M00055008D:F12	ES 200	449314	2008.G14.gz43_258245
M00055008D:H11	ES 200	22308	2008.G18.gz43_258309
M00055009C:A07	ES 200	554040	2008.H02.gz43_258054
M00055009C:F06	ES 200	549195	2008.H08.gz43_258150
M00055009C:F07	ES 200	594994	2008.H09.gz43_258166

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055009D:D12	ES 200	558378	2008.H10.gz43_258182
M00055010A:B07	ES 200	552977	2008.H17.gz43_258294
M00055010A:H05	ES 200	551656	2008.H20.gz43_258342
M00055010B:A06	ES 200	460169	2008.H22.gz43_258374
M00055010B:C11	ES 200	497513	2008.H24.gz43_258406
M00055010C:C10	ES 200	597780	2008.I06.gz43_258119
M00055010D:A02	ES 200	555371	2008.I09.gz43_258167
M00055010D:D08	ES 200	555512	2008.I13.gz43_258231
M00055010D:E08	ES 200	555658	2008.I14.gz43_258247
M00055010D:F11	ES 200	600021	2008.I15.gz43_258263
M00055011A:B11	ES 200	362109	2008.I17.gz43_258295
M00055011A:C06	ES 200	559464	2008.I18.gz43_258311
M00055011A:F06	ES 200	556998	2008.I21.gz43_258359
M00055011A:G07	ES 200	557115	2008.I22.gz43_258375
M00055011A:G12	ES 200	495984	2008.I23.gz43_258391
M00055011B:D08	ES 200	549864	2008.J01.gz43_258040
M00055011B:F09	ES 200	557308	2008.J02.gz43_258056
M00055011C:E04	ES 200	548858	2008.J05.gz43_258104
M00055011D:G03	ES 200	557025	2008.J09.gz43_258168
M00055012B:A10	ES 200	556320	2008.J17.gz43_258296
M00055012B:H12	ES 200	476438	2008.J21.gz43_258360
M00055013B:B07	ES 200	497086	2008.K10.gz43_258185
M00055013B:H01	ES 200	516018	2008.K14.gz43_258249
M00055014B:C12	ES 200	556611	2008.L04.gz43_258090
M00055014B:E08	ES 200	605117	2008.L05.gz43_258106
M00055014C:F05	ES 200	554084	2008.L08.gz43_258154
M00055014C:F11	ES 200	143207	2008.L09.gz43_258170
M00055014D:A11	ES 200	451118	2008.L11.gz43_258202
M00055015A:C08	ES 200	556530	2008.L12.gz43_258218
M00055015A:E04	ES 200	143218	2008.L13.gz43_258234
M00055015B:A04	ES 200	556266	2008.L17.gz43_258298
M00055015B:E09	ES 200	560097	2008.L21.gz43_258362
M00055015D:C09	ES 200	560525	2008.M05.gz43_258107
M00055015D:D06	ES 200	562945	2008.M07.gz43_258139
M00055015D:G05	ES 200	557059	2008.M11.gz43_258203
M00055016A:E04	ES 200	604859	2008.M14.gz43_258251
M00055016B:E02	ES 200	494300	2008.M17.gz43_258299
M00055016C:F11	ES 200	557000	2008.M20.gz43_258347
M00055016C:G04	ES 200	557308	2008.M21.gz43_258363
M00055016D:C07	ES 200	555967	2008.N01.gz43_258044
M00055016D:C11	ES 200	549723	2008.N02.gz43_258060
M00055017A:A11	ES 200	411113	2008.N06.gz43_258124
M00055017C:C12	ES 200	556616	2008.N13.gz43_258236
M00055017C:D05	ES 200	450010	2008.N14.gz43_258252

Table 13

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M00055017D:D05	ES 200	453908	2008.N17.gz43_258300
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M00055017D:E08	ES 200	554245	2008.N20.gz43_258348
M00055018C:C06	ES 200	495942	2008.O07.gz43_258141
M00055018D:D01	ES 200	604179	2008.O11.gz43_258205
M00055018D:E05	ES 200	524897	2008.O12.gz43_258221
M00055018D:H03	ES 200	551268	2008.O16.gz43_258285
M00055019B:B11	ES 200	556488	2008.P01.gz43_258046
M00055019B:H10	ES 200	557240	2008.P03.gz43_258078
M00055019C:C01	ES 200	556115	2008.P04.gz43_258094
M00055019C:G06	ES 200	557121	2008.P08.gz43_258158
M00055019D:B02	ES 200	556487	2008.P11.gz43_258206
M00055019D:B11	ES 200	556490	2008.P12.gz43_258222
M00055020A:G11	ES 200	562142	2008.P20.gz43_258350
M00055020B:C12	ES 200	608873	2017.A02.gz43_258433
M00055020D:G06	ES 200	557910	2017.B02.gz43_258434
M00055021A:F08	ES 200	610986	2017.B05.gz43_258482
M00055021B:G09	ES 200	450059	2017.B14.gz43_258626
M00055021D:F06	ES 200	549114	2017.B22.gz43_258754
M00055022B:F07	ES 200	557759	2017.C09.gz43_258547
M00055022C:B12	ES 200	557353	2017.C14.gz43_258627
M00055023C:G11	ES 200	561935	2017.D08.gz43_258532
M00055023D:G02	ES 200	557049	2017.D10.gz43_258564
M00055024A:B04	ES 200	481930	2017.D11.gz43_258580
M00055024A:C07	ES 200	560898	2017.D14.gz43_258628
M00055024B:E02	ES 200	508671	2017.D18.gz43_258692
M00055024B:E03	ES 200	561868	2017.D19.gz43_258708
M00055024B:E06	ES 200	529356	2017.D21.gz43_258740
M00055024B:F02	ES 200	556933	2017.D22.gz43_258756
M00055024D:E09	ES 200	551884	2017.E05.gz43_258485
M00055024D:F07	ES 200	559447	2017.E06.gz43_258501
M00055024D:G09	ES 200	550815	2017.E07.gz43_258517
M00055025A:D11	ES 200	560250	2017.E10.gz43_258565
M00055025B:A03	ES 200	550986	2017.E11.gz43_258581
M00055026A:G08	ES 200	322123	2017.F06.gz43_258502
M00055026C:E07	ES 200	552891	2017.F16.gz43_258662
M00055026D:E12	ES 200	556856	2017.F19.gz43_258710
M00055027A:D03	ES 200	447438	2017.F21.gz43_258742
M00055027A:E04	ES 200	494314	2017.F22.gz43_258758
M00055027A:H02	ES 200	557975	2017.G01.gz43_258423
M00055027C:G06	ES 200	524100	2017.G09.gz43_258551
M00055027D:E08	ES 200	454483	2017.G16.gz43_258663
M00055028C:D05	ES 200	390017	2017.H04.gz43_258472
M00055028D:A08	ES 200	556258	2017.H06.gz43_258504

Table 13

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M00055028D:E10	ES 200	560294	2017.H10.gz43_258568
M00055029A:A02	ES 200	560621	2017.H11.gz43_258584
M00055029C:D05	ES 200	557603	2017.I02.gz43_258441
M00055030B:E03	ES 200	549599	2017.I11.gz43_258585
M00055030B:H07	ES 200	461850	2017.I14.gz43_258633
M00055031B:E02	ES 200	561301	2017.J06.gz43_258506
M00055031B:E05	ES 200	557733	2017.J08.gz43_258538
M00055031B:H08	ES 200	558004	2017.J11.gz43_258586
M00055031C:B11	ES 200	552848	2017.J14.gz43_258634
M00055032B:D08	ES 200	561279	2017.K06.gz43_258507
M00055032D:B06	ES 200	454014	2017.K16.gz43_258667
M00055033B:H01	ES 200	562590	2017.L12.gz43_258604
M00055033C:A08	ES 200	557283	2017.L13.gz43_258620
M00055033D:D03	ES 200	557010	2017.L19.gz43_258716
M00055033D:G01	ES 200	557883	2017.L21.gz43_258748
M00055034A:G01	ES 200	460078	2017.L23.gz43_258780
M00055034B:G04	ES 200	523495	2017.M03.gz43_258461
M00055034D:A10	ES 200	556458	2017.M13.gz43_258621
M00055035B:D11	ES 200	408586	2017.M22.gz43_258765
M00055035C:G10	ES 200	555651	2017.N07.gz43_258526
M00055035D:E07	ES 200	556852	2017.N09.gz43_258558
M00055035D:F09	ES 200	558755	2017.N12.gz43_258606
M00055036A:H10	ES 200	456183	2017.N18.gz43_258702
M00055036B:H02	ES 201	561836	2017.N23.gz43_258782
M00055036C:G10	ES 201	491127	2017.O02.gz43_258447
M00055037C:D01	ES 201	557578	2017.O18.gz43_258703
M00055038A:H08	ES 201	134734	2017.P07.gz43_258528
M00055039A:G06	ES 201	561438	2018.A03.gz43_264190
M00055039B:E02	ES 201	555660	2018.A07.gz43_264254
M00055039B:G11	ES 201	555993	2018.A08.gz43_264270
M00055039B:G11	ES 201	555993	2018.A08.gz43_264654
M00055039B:H10	ES 201	601365	2018.A09.gz43_264286
M00055039C:B05	ES 201	529733	2018.A11.gz43_264318
M00055039C:D11	ES 201	397338	2018.A12.gz43_264718
M00055039D:D07	ES 201	561259	2018.A15.gz43_264382
M00055039D:D07	ES 201	561259	2018.A15.gz43_264766
M00055040A:C02	ES 201	555399	2018.A17.gz43_264414
M00055040A:C02	ES 201	555399	2018.A17.gz43_264798
M00055040A:F01	ES 201	555883	2018.A18.gz43_264430
M00055040B:F02	ES 201	555751	2018.A22.gz43_264878
M00055040C:G08	ES 201	447815	2018.A23.gz43_264510
M00055040D:B05	ES 201	555160	2018.A24.gz43_264910
M00055040D:G05	ES 201	561761	2018.B02.gz43_264175

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CloneID	ES No	ClusterID	SequenceName
M00055041A:C02	ES 201	555340	2018.B05.gz43_264223
M00055041B:B06	ES 201	417274	2018.B08.gz43_264655
M00055041B:C10	ES 201	551711	2018.B09.gz43_264671
M00055041B:D11	ES 201	555524	2018.B10.gz43_264303
M00055041B:D11	ES 201	555524	2018.B10.gz43_264687
M00055041B:F04	ES 201	561994	2018.B13.gz43_264735
M00055041C:C10	ES 201	554149	2018.B17.gz43_264799
M00055041C:H12	ES 201	470617	2018.B22.gz43_264495
M00055041D:B07	ES 201	555250	2018.B23.gz43_264895
M00055042A:D09	ES 201	561901	2018.C07.gz43_264256
M00055042A:F07	ES 201	551328	2018.C08.gz43_264656
M00055042B:B09	ES 201	549008	2018.C10.gz43_264304
M00055042B:E02	ES 201	555708	2018.C12.gz43_264336
M00055042B:E05	ES 201	448098	2018.C13.gz43_264736
M00055042B:E08	ES 201	450765	2018.C14.gz43_264368
M00055042B:E08	ES 201	450765	2018.C14.gz43_264752
M00055042C:B05	ES 201	555172	2018.C16.gz43_264400
M00055042C:F04	ES 201	551805	2018.C19.gz43_264832
M00055042D:G03	ES 201	555940	2018.C21.gz43_264864
M00055042D:H02	ES 201	423588	2018.C22.gz43_264880
M00055043A:B06	ES 201	555173	2018.C24.gz43_264912
M00055043B:B01	ES 201	555213	2018.D07.gz43_264641
M00055043B:G01	ES 201	551714	2018.D08.gz43_264273
M00055043D:D10	ES 201	558254	2018.D13.gz43_264737
M00055043D:F07	ES 201	553356	2018.D14.gz43_264753
M00055044A:A08	ES 201	562949	2018.D17.gz43_264417
M00055044A:C02	ES 201	450755	2018.D18.gz43_264817
M00055044B:F12	ES 201	549444	2018.D21.gz43_264865
M00055045A:C06	ES 201	561911	2018.E08.gz43_264658
M00055045A:F03	ES 201	555771	2018.E10.gz43_264306
M00055045A:F12	ES 201	553850	2018.E11.gz43_264322
M00055045B:A04	ES 201	559699	2018.E12.gz43_264338
M00055045B:A04	ES 201	559699	2018.E12.gz43_264722
M00055045B:A12	ES 201	347486	2018.E13.gz43_264738
M00055045B:C08	ES 201	560720	2018.E14.gz43_264370
M00055045B:C08	ES 201	560720	2018.E14.gz43_264754
M00055045C:F09	ES 201	555892	2018.E18.gz43_264818
M00055045C:H05	ES 201	556158	2018.E19.gz43_264450
M00055045D:A01	ES 201	108755	2018.E21.gz43_264482
M00055045D:A07	ES 201	551578	2018.E22.gz43_264882
M00055045D:D01	ES 201	446664	2018.E24.gz43_264914
M00055045D:F10	ES 201	561838	2018.F02.gz43_264179
M00055046A:D06	ES 201	562585	2018.F05.gz43_264227
M00055046B:C07	ES 201	375380	2018.F09.gz43_264291

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CloneID	ES No	ClusterID	SequenceName
M00055046B:C12	ES 201	557546	2018.F10.gz43_264307
M00055046B:D02	ES 201	559052	2018.F11.gz43_264707
M00055046B:E08	ES 201	557420	2018.F13.gz43_264739
M00055046B:F06	ES 201	491799	2018.F14.gz43_264755
M00055046C:C05	ES 201	558389	2018.F18.gz43_264435
M00055046C:E07	ES 201	488970	2018.F21.gz43_264867
M00055046C:E11	ES 201	514418	2018.F23.gz43_264515
M00055046C:G10	ES 201	551641	2018.F24.gz43_264915
M00055047A:E07	ES 201	557735	2018.G11.gz43_264324
M00055047A:H04	ES 201	558007	2018.G13.gz43_264740
M00055047A:H05	ES 201	558120	2018.G14.gz43_264372
M00055047A:H05	ES 201	558120	2018.G14.gz43_264756
M00055047B:A10	ES 201	557326	2018.G15.gz43_264388
M00055047B:B03	ES 201	289316	2018.G16.gz43_264404
M00055047B:B10	ES 201	553603	2018.G17.gz43_264804
M00055047B:C03	ES 201	551793	2018.G18.gz43_264820
M00055047B:G06	ES 201	556171	2018.G22.gz43_264884
M00055047B:G10	ES 201	476268	2018.G23.gz43_264900
M00055047C:D11	ES 201	447455	2018.H06.gz43_264245
M00055047C:F07	ES 201	554936	2018.H07.gz43_264261
M00055047C:F08	ES 201	465207	2018.H08.gz43_264277
M00055047C:F08	ES 201	465207	2018.H08.gz43_264661
M00055047D:C12	ES 201	555798	2018.H11.gz43_264325
M00055048A:A04	ES 201	557279	2018.H16.gz43_264405
M00055048A:B12	ES 201	465447	2018.H17.gz43_264421
M00055048A:D12	ES 201	557606	2018.H19.gz43_264453
M00055048A:F04	ES 201	453893	2018.H20.gz43_264469
M00055048C:C06	ES 201	556490	2018.I04.gz43_264214
M00055048D:D08	ES 201	419153	2018.I08.gz43_264278
M00055048D:D08	ES 201	419153	2018.I08.gz43_264662
M00055048D:H04	ES 201	349744	2018.I14.gz43_264374
M00055049A:F10	ES 201	559762	2018.I19.gz43_264838
M00055049A:G03	ES 201	561046	2018.I20.gz43_264854
M00055049B:A01	ES 201	557249	2018.I22.gz43_264502
M00055049B:F05	ES 201	553983	2018.J01.gz43_264167
M00055049C:H12	ES 201	555010	2018.J07.gz43_264263
M00055049C:H12	ES 201	555010	2018.J07.gz43_264647
M00055049D:D09	ES 201	561216	2018.J09.gz43_264295
M00055049D:D10	ES 201	446739	2018.J10.gz43_264695
M00055050A:D11	ES 201	449437	2018.J15.gz43_264391
M00055050A:H08	ES 201	556169	2018.J16.gz43_264407
M00055050B:E11	ES 201	206098	2018.J19.gz43_264455
M00055050B:E11	ES 201	206098	2018.J19.gz43_264839
M00055050D:C01	ES 201	559775	2018.K06.gz43_264248

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055050D:E03	ES 201	486150	2018.K07.gz43_264264
M00055050D:F04	ES 201	557834	2018.K08.gz43_264664
M00055051A:B02	ES 201	454810	2018.K11.gz43_264328
M00055051A:C09	ES 201	551068	2018.K12.gz43_264344
M00055051A:E11	ES 201	432970	2018.K14.gz43_264760
M00055051A:G09	ES 201	555340	2018.K15.gz43_264392
M00055051A:G09	ES 201	555340	2018.K15.gz43_264776
M00055051A:H10	ES 201	551897	2018.K16.gz43_264408
M00055051B:B08	ES 201	552641	2018.K17.gz43_264424
M00055051B:B08	ES 201	552641	2018.K17.gz43_264808
M00055051B:D07	ES 201	557572	2018.K19.gz43_264840
M00055051B:G09	ES 201	451027	2018.K21.gz43_264872
M00055051C:B05	ES 201	553349	2018.K23.gz43_264904
M00055051C:F10	ES 201	554372	2018.L04.gz43_264217
M00055051D:D12	ES 201	540000	2018.L05.gz43_264233
M00055051D:F01	ES 201	560801	2018.L07.gz43_264265
M00055051D:G01	ES 201	557882	2018.L08.gz43_264665
M00055052A:F07	ES 201	559246	2018.L12.gz43_264345
M00055052A:H11	ES 201	558029	2018.L14.gz43_264761
M00055052B:E03	ES 201	551371	2018.L17.gz43_264425
M00055052B:E03	ES 201	551371	2018.L17.gz43_264809
M00055052C:B12	ES 201	454664	2018.L20.gz43_264857
M00055052D:B05	ES 201	557382	2018.L24.gz43_264921
M00055052D:G12	ES 201	493261	2018.M06.gz43_264250
M00055053B:A02	ES 201	553108	2018.M11.gz43_264330
M00055053B:A02	ES 201	553108	2018.M11.gz43_264714
M00055053B:C02	ES 201	557525	2018.M13.gz43_264362
M00055053B:C02	ES 201	557525	2018.M13.gz43_264746
M00055053B:C11	ES 201	558560	2018.M14.gz43_264762
M00055053C:A12	ES 201	557345	2018.M16.gz43_264794
M00055053C:B03	ES 201	562292	2018.M17.gz43_264426
M00055053C:B03	ES 201	562292	2018.M17.gz43_264810
M00055053C:F06	ES 201	551334	2018.M19.gz43_264842
M00055053D:G04	ES 201	557939	2018.N01.gz43_264171
M00055054A:A10	ES 201	447555	2018.N03.gz43_264203
M00055054B:E10	ES 201	8997	2018.N13.gz43_264363
M00055054B:E10	ES 201	8997	2018.N13.gz43_264747
M00055054B:F05	ES 201	562115	2018.N15.gz43_264395
M00055054B:G12	ES 201	555082	2018.N17.gz43_264427
M00055054C:G10	ES 201	551616	2018.N20.gz43_264859
M00055054D:A02	ES 201	557308	2018.N21.gz43_264491
M00055054D:E12	ES 201	555057	2018.N22.gz43_264507
M00055054D:H07	ES 201	467081	2018.N23.gz43_264523
M00055054D:H07	ES 201	467081	2018.N23.gz43_264907

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055055A:B03	ES 201	561963	2018.N24.gz43_264539
M00055055B:H11	ES 201	528775	2018.O05.gz43_264236
M00055055C:C09	ES 201	498629	2018.O09.gz43_264300
M00055055C:C09	ES 201	498629	2018.O09.gz43_264684
M00055055C:D02	ES 201	515115	2018.O10.gz43_264316
M00055055C:D02	ES 201	515115	2018.O10.gz43_264700
M00055055C:E08	ES 201	553975	2018.O12.gz43_264348
M00055055C:E08	ES 201	553975	2018.O12.gz43_264732
M00055055D:D11	ES 201	551630	2018.O15.gz43_264780
M00055055D:E11	ES 201	476342	2018.O16.gz43_264412
M00055056A:H09	ES 201	394373	2018.O17.gz43_264812
M00055056A:H12	ES 201	463341	2018.O18.gz43_264444
M00055056B:G01	ES 201	551561	2018.O23.gz43_264908
M00055056C:A05	ES 201	549858	2018.P01.gz43_264173
M00055056C:C05	ES 201	557504	2018.P04.gz43_264221
M00055056C:D07	ES 201	553012	2018.P05.gz43_264237
M00055056C:E10	ES 201	505451	2018.P07.gz43_264653
M00055056C:F04	ES 201	562808	2018.P08.gz43_264285
M00055056C:H07	ES 201	385531	2018.P10.gz43_264701
M00055056D:B06	ES 201	557401	2018.P12.gz43_264349
M00055056D:H12	ES 201	556391	2018.P16.gz43_264413
M00055057A:A04	ES 201	562272	2018.P17.gz43_264429
M00055057A:A04	ES 201	562272	2018.P17.gz43_264813
M00055057A:A05	ES 201	553002	2018.P18.gz43_264445
M00055057A:A05	ES 201	553002	2018.P18.gz43_264829
M00055057A:D10	ES 201	559294	2018.P20.gz43_264861
M00055057A:F10	ES 201	451172	2018.P22.gz43_264893
M00055057B:B01	ES 201	551544	2018.P24.gz43_264541
M00055073D:F06	ES 201	555512	2020.A04.gz43_264974
M00055074B:E05	ES 201	455820	2020.A14.gz43_265134
M00055074D:B04	ES 201	562229	2020.A22.gz43_265262
M00055075A:C09	ES 201	556635	2020.B05.gz43_264991
M00055075B:D12	ES 201	556742	2020.B12.gz43_265103
M00055075D:D05	ES 201	560069	2020.B20.gz43_265231
M00055076A:C06	ES 201	558720	2020.C03.gz43_264960
M00055076A:D11	ES 201	555368	2020.C05.gz43_264992
M00055076A:G12	ES 201	557024	2020.C07.gz43_265024
M00055076B:E08	ES 201	452822	2020.C11.gz43_265088
M00055076B:F04	ES 201	549810	2020.C12.gz43_265104
M00055076B:H06	ES 201	550701	2020.C16.gz43_265168
M00055076C:B10	ES 201	559965	2020.C18.gz43_265200
M00055076C:H07	ES 201	557954	2020.C20.gz43_265232
M00055076D:F11	ES 201	557783	2020.C23.gz43_265280
M00055076D:H11	ES 201	553131	2020.D02.gz43_264945

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CloneID	ES No	ClusterID	SequenceName
M00055077A:B07	ES 201	549129	2020.D04.gz43_264977
M00055077A:H10	ES 201	561707	2020.D10.gz43_265073
M00055077D:B01	ES 201	556471	2020.E02.gz43_264946
M00055078A:C05	ES 201	142614	2020.E08.gz43_265042
M00055078A:E10	ES 201	464905	2020.E11.gz43_265090
M00055078A:F01	ES 201	557760	2020.E12.gz43_265106
M00055078A:F04	ES 201	553303	2020.E13.gz43_265122
M00055078B:F05	ES 201	561489	2020.E15.gz43_265154
M00055078D:A07	ES 201	555996	2020.E21.gz43_265250
M00055078D:G04	ES 201	495408	2020.F06.gz43_265011
M00055079A:H05	ES 201	509505	2020.F11.gz43_265091
M00055079B:D02	ES 201	402683	2020.F12.gz43_265107
M00055079C:G06	ES 201	558616	2020.F15.gz43_265155
M00055079D:A03	ES 201	612961	2020.F17.gz43_265187
M00055080A:A07	ES 201	555111	2020.F22.gz43_265267
M00055080A:F05	ES 201	451185	2020.F24.gz43_265299
M00055080B:G10	ES 201	556040	2020.G09.gz43_265060
M00055080D:A01	ES 201	551976	2020.G16.gz43_265172
M00055080D:E07	ES 201	553318	2020.G19.gz43_265220
M00055080D:E10	ES 201	556357	2020.G20.gz43_265236
M00055080D:F01	ES 201	494625	2020.G21.gz43_265252
M00055081A:E08	ES 202	555616	2020.H01.gz43_264933
M00055081B:E10	ES 202	552361	2020.H06.gz43_265013
M00055081C:A12	ES 202	555061	2020.H11.gz43_265093
M00055081C:G01	ES 202	553372	2020.H18.gz43_265205
M00055081C:H04	ES 202	449613	2020.H19.gz43_265221
M00055082A:A12	ES 202	552019	2020.H24.gz43_265301
M00055082D:E08	ES 202	555710	2020.I14.gz43_265142
M00055082D:G01	ES 202	460244	2020.I16.gz43_265174
M00055082D:H02	ES 202	465446	2020.I17.gz43_265190
M00055083B:E05	ES 202	549607	2020.J01.gz43_264935
M00055083B:E07	ES 202	452434	2020.J02.gz43_264951
M00055083B:F10	ES 202	552618	2020.J03.gz43_264967
M00055083C:C05	ES 202	556497	2020.J04.gz43_264983
M00055083C:F05	ES 202	556882	2020.J05.gz43_264999
M00055083D:D08	ES 202	556668	2020.J11.gz43_265095
M00055084A:E10	ES 202	556802	2020.J16.gz43_265175
M00055084A:F10	ES 202	556925	2020.J17.gz43_265191
M00055084B:A04	ES 202	558231	2020.J18.gz43_265207
M00055084D:B01	ES 202	556446	2020.K06.gz43_265016
M00055084D:C09	ES 202	548943	2020.K07.gz43_265032
M00055085A:F12	ES 202	500833	2020.K12.gz43_265112
M00055085B:D02	ES 202	454910	2020.K16.gz43_265176

Table 13

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M00055085C:E05	ES 202	561753	2020.K19.gz43_265224
M00055085D:D10	ES 202	451134	2020.K21.gz43_265256
M00055085D:F03	ES 202	556881	2020.K23.gz43_265288
M00055085D:G09	ES 202	555725	2020.K24.gz43_265304
M00055086A:B10	ES 202	492893	2020.L01.gz43_264937
M00055086A:C09	ES 202	556542	2020.L02.gz43_264953
M00055086B:D10	ES 202	557476	2020.L06.gz43_265017
M00055086D:C07	ES 202	551342	2020.L13.gz43_265129
M00055086D:H07	ES 202	557214	2020.L16.gz43_265177
M00055087B:C03	ES 202	122169	2020.L22.gz43_265273
M00055087B:C05	ES 202	451885	2020.L23.gz43_265289
M00055087D:D08	ES 202	453756	2020.M08.gz43_265050
M00055088C:B02	ES 202	450352	2020.M20.gz43_265242
M00055088C:D01	ES 202	561975	2020.M22.gz43_265274
M00055088C:D02	ES 202	557747	2020.M23.gz43_265290
M00055088D:A01	ES 202	551283	2020.N02.gz43_264955
M00055088D:B08	ES 202	561422	2020.N04.gz43_264987
M00055089A:H06	ES 202	557454	2020.N09.gz43_265067
M00055089B:C01	ES 202	554084	2020.N12.gz43_265115
M00055089C:B06	ES 202	556465	2020.N16.gz43_265179
M00055089C:D06	ES 202	560507	2020.N19.gz43_265227
M00055090A:F02	ES 202	560080	2020.N22.gz43_265275
M00055090C:B03	ES 202	556408	2020.O04.gz43_264988
M00055090C:C12	ES 202	556559	2020.O06.gz43_265020
M00055090C:D01	ES 202	556675	2020.O07.gz43_265036
M00055090C:G06	ES 202	451370	2020.O09.gz43_265068
M00055090D:E03	ES 202	497086	2020.O14.gz43_265148
M00055090D:F03	ES 202	98869	2020.O17.gz43_265196
M00055091A:C09	ES 202	598101	2020.O23.gz43_265292
M00055091A:F05	ES 202	459581	2020.P04.gz43_264989
M00055091B:A07	ES 202	555126	2020.P07.gz43_265037
M00055091B:C11	ES 202	555418	2020.P08.gz43_265053
M00055091C:B04	ES 202	468262	2020.P12.gz43_265117
M00055091C:D11	ES 202	559071	2020.P15.gz43_265165
M00055091C:G11	ES 202	561593	2020.P18.gz43_265213
M00055091D:A03	ES 202	554828	2020.P21.gz43_265261
M00055092B:G09	ES 202	637966	2029.A15.gz43_265534
M00055093A:E09	ES 202	562542	2029.B05.gz43_265375
M00055093A:F07	ES 202	562768	2029.B06.gz43_265391
M00055093B:G08	ES 202	562881	2029.B14.gz43_265519
M00055094B:B11	ES 202	562307	2029.C11.gz43_265472
M00055094C:C10	ES 202	402488	2029.C21.gz43_265632
M00055094D:F09	ES 202	491127	2029.D06.gz43_265393
M00055095A:D08	ES 202	98484	2029.D11.gz43_265473

Table 13

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M00055096A:G08	ES 202	551967	2029.E09.gz43_265442
M00055096C:C03	ES 202	554496	2029.E16.gz43_265554
M00055096D:F02	ES 202	553380	2029.E22.gz43_265650
M00055097A:G06	ES 202	455820	2029.F06.gz43_265395
M00055097B:B12	ES 202	453533	2029.F09.gz43_265443
M00055097B:F08	ES 202	562719	2029.F10.gz43_265459
M00055098D:A09	ES 202	561215	2029.G03.gz43_265348
M00055099A:G05	ES 202	558118	2029.G11.gz43_265476
M00055100A:C05	ES 202	555330	2029.H07.gz43_265413
M00055100B:F11	ES 202	558186	2029.H15.gz43_265541
M00055100C:E03	ES 202	559125	2029.H22.gz43_265653
M00055100C:F11	ES 202	452349	2029.I01.gz43_265318
M00055100C:H06	ES 202	562989	2029.I02.gz43_265334
M00055100D:B02	ES 202	562243	2029.I03.gz43_265350
M00055102A:E11	ES 202	560628	2029.I20.gz43_265622
M00055102B:B03	ES 202	560111	2029.I21.gz43_265638
M00055103A:H11	ES 202	561144	2029.J16.gz43_265559
M00055103C:B07	ES 202	558511	2029.J20.gz43_265623
M00055103C:D05	ES 202	556613	2029.J21.gz43_265639
M00055103C:G03	ES 202	560898	2029.J22.gz43_265655
M00055104B:F09	ES 202	553548	2029.K14.gz43_265528
M00055104D:E02	ES 202	455878	2029.K20.gz43_265624
M00055105A:A05	ES 202	559955	2029.K23.gz43_265672
M00055105D:B06	ES 202	552704	2029.L07.gz43_265417
M00055106A:E04	ES 202	560575	2029.L15.gz43_265545
M00055106C:B06	ES 202	454499	2029.L22.gz43_265657
M00055109C:G10	ES 202	455529	2029.O01.gz43_265324
M00055110A:C03	ES 202	561426	2029.O08.gz43_265436
M00055110A:C05	ES 202	394189	2029.O09.gz43_265452
M00055111A:F10	ES 202	562748	2029.P01.gz43_265325
M00055111C:B07	ES 202	558186	2029.P05.gz43_265389
M00055111D:F10	ES 202	518735	2029.P16.gz43_265565
M00055113A:G08	ES 202	562822	2030.A11.gz43_265854
M00055113B:F02	ES 202	562714	2030.A12.gz43_265870
M00055113C:F09	ES 202	551734	2030.A14.gz43_265902
M00055114A:E02	ES 202	561741	2030.A18.gz43_265966
M00055115C:F04	ES 202	549948	2030.B23.gz43_266047
M00055115C:G09	ES 202	449035	2030.C02.gz43_265712
M00055116A:C07	ES 202	453274	2030.C12.gz43_265872
M00055116A:H06	ES 202	453692	2030.C19.gz43_265984
M00055117A:G08	ES 202	312036	2030.D10.gz43_265841
M00055117C:C03	ES 202	549591	2030.D16.gz43_265937
M00055117C:F02	ES 202	561265	2030.D17.gz43_265953
M00055118B:A09	ES 202	554737	2030.D24.gz43_266065

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M00055118C:B03	ES 202	452525	2030.E03.gz43_265730
M00055118D:B04	ES 202	560868	2030.E05.gz43_265762
M00055119B:B08	ES 202	560077	2030.E12.gz43_265874
M00055119D:F08	ES 202	526334	2030.E14.gz43_265906
M00055120B:F12	ES 202	556310	2030.E19.gz43_265986
M00055120C:F10	ES 202	560506	2030.E22.gz43_266034
M00055120D:H07	ES 202	63602	2030.F01.gz43_265699
M00055121D:H11	ES 202	507660	2030.F09.gz43_265827
M00055122C:B12	ES 202	448905	2030.F16.gz43_265939
M00055123A:D12	ES 202	560399	2030.F23.gz43_266051
M00055124A:F01	ES 202	479732	2030.G08.gz43_265812
M00055124B:A11	ES 202	558060	2030.G11.gz43_265860
M00055124C:C12	ES 202	553142	2030.G17.gz43_265956
M00055124D:A09	ES 202	451089	2030.G23.gz43_266052
M00055124D:B10	ES 202	553841	2030.H02.gz43_265717
M00055125A:A02	ES 202	538830	2030.H05.gz43_265765
M00055125B:F01	ES 202	558534	2030.H09.gz43_265829
M00055125C:H03	ES 202	557895	2030.H16.gz43_265941
M00055125D:E02	ES 202	558452	2030.H20.gz43_266005
M00055126C:G05	ES 202	561685	2030.I06.gz43_265782
M00055127B:A01	ES 202	559938	2030.I12.gz43_265878
M00055128A:C10	ES 202	554233	2030.J01.gz43_265703
M00055128B:B08	ES 202	561679	2030.J06.gz43_265783
M00055128B:B12	ES 202	528369	2030.J07.gz43_265799
M00055128B:E12	ES 202	461653	2030.J10.gz43_265847
M00055128B:G01	ES 202	407964	2030.J13.gz43_265895
M00055128C:E03	ES 202	554989	2030.J16.gz43_265943
M00055128D:C11	ES 202	561279	2030.J22.gz43_266039
M00055128D:D04	ES 202	557615	2030.K01.gz43_265704
M00055129A:B03	ES 202	486683	2030.K05.gz43_265768
M00055129B:H07	ES 202	558024	2030.K18.gz43_265976
M00055129C:H08	ES 202	452759	2030.K24.gz43_266072
M00055129D:C02	ES 202	452775	2030.L03.gz43_265737
M00055129D:F11	ES 202	488030	2030.L06.gz43_265785
M00055130A:D10	ES 202	557610	2030.L11.gz43_265865
M00055130B:D07	ES 202	380636	2030.L17.gz43_265961
M00055130D:F08	ES 202	66678	2030.M06.gz43_265786
M00055131A:A04	ES 202	518007	2030.M10.gz43_265850
M00055131A:D07	ES 202	449454	2030.M13.gz43_265898
M00055131C:H12	ES 202	562822	2030.N04.gz43_265755
M00055132B:B12	ES 202	288134	2030.N12.gz43_265883
M00055132D:E07	ES 202	610269	2030.N21.gz43_266027
M00055132D:E10	ES 202	557719	2030.N22.gz43_266043
M00055132D:F05	ES 202	548991	2030.N23.gz43_266059

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M00055133B:B06	ES 202	400628	2030.O05.gz43_265772
M00055133B:E04	ES 202	557741	2030.O07.gz43_265804
M00055133B:E08	ES 202	557747	2030.O08.gz43_265820
M00055133B:F07	ES 202	451618	2030.O10.gz43_265852
M00055133C:C06	ES 202	562760	2030.O13.gz43_265900
M00055133C:G07	ES 202	451392	2030.O15.gz43_265932
M00055133C:H11	ES 202	558015	2030.O17.gz43_265964
M00055133D:A02	ES 202	477295	2030.O18.gz43_265980
M00055133D:F02	ES 202	451391	2030.O22.gz43_266044
M00055134A:C03	ES 202	553871	2030.O24.gz43_266076
M00055134C:A01	ES 202	557284	2030.P11.gz43_265869
M00055134C:B01	ES 202	551068	2030.P12.gz43_265885
M00055134C:E09	ES 202	557710	2030.P13.gz43_265901
M00055134D:B03	ES 202	407077	2030.P17.gz43_265965
M00055135A:D08	ES 202	557549	2030.P23.gz43_266061
M00055135A:E07	ES 202	562683	2031.A01.gz43_266078
M00055135A:H10	ES 202	562725	2031.A02.gz43_266094
M00055136C:F11	ES 202	562449	2031.A24.gz43_266446
M00055136D:D09	ES 202	558768	2031.B05.gz43_266143
M00055137A:E05	ES 202	550047	2031.B10.gz43_266223
M00055137B:B11	ES 202	556630	2031.B14.gz43_266287
M00055137B:F12	ES 202	558477	2031.B16.gz43_266319
M00055138A:E08	ES 202	558463	2031.C04.gz43_266128
M00055138A:F01	ES 202	558544	2031.C05.gz43_266144
M00055138A:G08	ES 202	558619	2031.C06.gz43_266160
M00055138B:H12	ES 202	446873	2031.C11.gz43_266240
M00055138C:A07	ES 202	556328	2031.C12.gz43_266256
M00055139B:E10	ES 202	553969	2031.D09.gz43_266209
M00055139B:G03	ES 202	558230	2031.D11.gz43_266241
M00055140A:G07	ES 202	557893	2031.D22.gz43_266417
M00055143B:C11	ES 202	555754	2031.G02.gz43_266100
M00055144A:A11	ES 202	561245	2031.G05.gz43_266148
M00055144A:E09	ES 202	450630	2031.G06.gz43_266164
M00055144B:A12	ES 202	506372	2031.G11.gz43_266244
M00055145B:F03	ES 202	490032	2031.H18.gz43_266357
M00055146A:B12	ES 202	211273	2031.I04.gz43_266134
M00055146B:E09	ES 202	562000	2031.I10.gz43_266230
M00055148A:E06	ES 202	289328	2031.J13.gz43_266279
M00055149B:F09	ES 203	557783	2031.K05.gz43_266152
M00055149C:A11	ES 203	553500	2031.K08.gz43_266200
M00055150D:C06	ES 203	160289	2031.L10.gz43_266233
M00055151A:C10	ES 203	557522	2031.L14.gz43_266297
M00055151A:F10	ES 203	610893	2031.L18.gz43_266361

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CloneID	ES No	ClusterID	SequenceName
M00055152A:B05	ES 203	490846	2031.M08.gz43_266202
M00055152A:E09	ES 203	549739	2031.M12.gz43_266266
M00055152B:A03	ES 203	557250	2031.M16.gz43_266330
M00055152D:C03	ES 203	468257	2031.N04.gz43_266139
M00055152D:H09	ES 203	497493	2031.N07.gz43_266187
M00055154D:F06	ES 203	549930	2031.O05.gz43_266156
M00055154D:G12	ES 203	524721	2031.O06.gz43_266172
M00055155D:B02	ES 203	557708	2031.O24.gz43_266460
M00055156A:D02	ES 203	561624	2031.P06.gz43_266173
M00055156B:C11	ES 203	558645	2031.P08.gz43_266205
M00055156C:A08	ES 203	558007	2031.P09.gz43_266221
M00055156C:D06	ES 203	561558	2031.P12.gz43_266269
M00055156D:A02	ES 203	561178	2031.P15.gz43_266317
M00055157A:B04	ES 203	556288	2031.P17.gz43_266349
M00055157C:C11	ES 203	559389	2032.A05.gz43_266526
M00055158A:D09	ES 203	555210	2032.A10.gz43_266606
M00055158D:C01	ES 203	394772	2032.A19.gz43_266750
M00055158D:D10	ES 203	560296	2032.A20.gz43_266766
M00055159B:B08	ES 203	561308	2032.B04.gz43_266511
M00055159B:G09	ES 203	561911	2032.B12.gz43_266639
M00055159C:B02	ES 203	215005	2032.B16.gz43_266703
M00055159D:F09	ES 203	554885	2032.B24.gz43_266831
M00055160C:D02	ES 203	553537	2032.C10.gz43_266608
M00055161A:C02	ES 203	561507	2032.C21.gz43_266784
M00055161A:E05	ES 203	558395	2032.C23.gz43_266816
M00055161B:A07	ES 203	452901	2032.D06.gz43_266545
M00055161D:H03	ES 203	447386	2032.D23.gz43_266817
M00055162A:B03	ES 203	562881	2032.E01.gz43_266466
M00055162A:C12	ES 203	451458	2032.E03.gz43_266498
M00055162A:G12	ES 203	561994	2032.E07.gz43_266562
M00055162B:B04	ES 203	561413	2032.E10.gz43_266610
M00055162C:E12	ES 203	553877	2032.E19.gz43_266754
M00055162C:G03	ES 203	323165	2032.E20.gz43_266770
M00055162D:B01	ES 203	555883	2032.E22.gz43_266802
M00055162D:G04	ES 203	561918	2032.E24.gz43_266834
M00055163B:F07	ES 203	561876	2032.F10.gz43_266611
M00055164C:C10	ES 203	558965	2032.G11.gz43_266628
M00055164D:C05	ES 203	555200	2032.G18.gz43_266740
M00055165A:F05	ES 203	559389	2032.G24.gz43_266836
M00055165B:G09	ES 203	559562	2032.H05.gz43_266533
M00055165C:H08	ES 203	558917	2032.H07.gz43_266565
M00055165D:C03	ES 203	553797	2032.H10.gz43_266613
M00055166B:D07	ES 203	452874	2032.H19.gz43_266757
M00055166C:G01	ES 203	488108	2032.H23.gz43_266821

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055166D:F02	ES 203	559464	2032.I04.gz43_266518
M00055166D:F09	ES 203	555418	2032.I05.gz43_266534
M00055167A:A02	ES 203	493261	2032.I07.gz43_266566
M00055167B:A08	ES 203	557961	2032.I12.gz43_266646
M00055167B:H07	ES 203	415538	2032.I15.gz43_266694
M00055167D:B05	ES 203	558858	2032.I19.gz43_266758
M00055168B:F11	ES 203	557316	2032.J06.gz43_266551
M00055169B:F04	ES 203	559355	2032.J19.gz43_266759
M00055169B:H08	ES 203	550674	2032.J21.gz43_266791
M00055169D:A11	ES 203	558720	2032.K02.gz43_266488
M00055170A:A09	ES 203	557209	2032.K06.gz43_266552
M00055170A:A11	ES 203	558755	2032.K07.gz43_266568
M00055170B:B06	ES 203	558022	2032.K12.gz43_266648
M00055170D:B09	ES 203	494198	2032.L01.gz43_266473
M00055171C:C01	ES 203	450566	2032.L23.gz43_266825
M00055172A:A01	ES 203	550085	2032.M02.gz43_266490
M00055172A:C09	ES 203	559015	2032.M05.gz43_266538
M00055172A:F03	ES 203	554604	2032.M06.gz43_266554
M00055172B:B04	ES 203	558900	2032.M09.gz43_266602
M00055172B:H07	ES 203	409262	2032.M12.gz43_266650
M00055172D:D04	ES 203	559057	2032.M15.gz43_266698
M00055172D:D07	ES 203	556542	2032.M16.gz43_266714
M00055172D:F12	ES 203	551693	2032.M19.gz43_266762
M00055174A:H12	ES 203	555202	2032.M24.gz43_266842
M00055174B:B04	ES 203	550175	2032.N01.gz43_266475
M00055176A:A02	ES 203	553047	2032.N11.gz43_266635
M00055176A:B03	ES 203	553713	2032.N13.gz43_266667
M00055176D:H01	ES 203	559752	2032.N24.gz43_266843
M00055177A:F05	ES 203	551475	2032.O01.gz43_266476
M00055177D:F07	ES 203	562989	2032.O17.gz43_266732
M00055178A:C07	ES 203	558981	2032.O20.gz43_266780
M00055178A:D03	ES 203	559088	2032.O22.gz43_266812
M00055179A:G08	ES 203	561975	2041.A02.gz43_266862
M00055179A:H11	ES 203	479851	2041.A03.gz43_266878
M00055179B:C07	ES 203	450289	2041.A04.gz43_266894
M00055179B:D05	ES 203	559050	2041.A05.gz43_266910
M00055179B:G07	ES 203	559000	2041.A08.gz43_266958
M00055179C:F11	ES 203	559383	2041.A10.gz43_266990
M00055179C:H02	ES 203	559710	2041.A11.gz43_267006
M00055179D:C10	ES 203	555739	2041.A14.gz43_267054
M00055181A:E01	ES 203	549829	2041.A20.gz43_267150
M00055181A:G02	ES 203	557644	2041.A22.gz43_267182
M00055181A:H01	ES 203	559194	2041.A24.gz43_267214
M00055181B:A10	ES 203	478511	2041.B01.gz43_266847

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055181B:E06	ES 203	549472	2041.B03.gz43_266879
M00055181C:B07	ES 203	476199	2041.B07.gz43_266943
M00055181C:B12	ES 203	553002	2041.B08.gz43_266959
M00055181C:C09	ES 203	561513	2041.B09.gz43_266975
M00055181C:D06	ES 203	562569	2041.B11.gz43_267007
M00055181C:H01	ES 203	561351	2041.B17.gz43_267103
M00055181D:D05	ES 203	473742	2041.B21.gz43_267167
M00055182A:D07	ES 203	554520	2041.C05.gz43_266912
M00055182B:C07	ES 203	226324	2041.C08.gz43_266960
M00055182B:F05	ES 203	556632	2041.C09.gz43_266976
M00055182C:E09	ES 203	556881	2041.C17.gz43_267104
M00055182D:E06	ES 203	559333	2041.C21.gz43_267168
M00055182D:H08	ES 203	557961	2041.C23.gz43_267200
M00055183A:C06	ES 203	456517	2041.D01.gz43_266849
M00055183A:E10	ES 203	557714	2041.D02.gz43_266865
M00055183C:A02	ES 203	562840	2041.D08.gz43_266961
M00055183C:D07	ES 203	561963	2041.D12.gz43_267025
M00055184A:G02	ES 203	557935	2041.D19.gz43_267137
M00055184B:H01	ES 203	560308	2041.E02.gz43_266866
M00055184C:C07	ES 203	558212	2041.E04.gz43_266898
M00055184C:D02	ES 203	409612	2041.E05.gz43_266914
M00055184C:D11	ES 203	551879	2041.E07.gz43_266946
M00055184C:F01	ES 203	561513	2041.E08.gz43_266962
M00055185A:B01	ES 203	451761	2041.E12.gz43_267026
M00055185A:G11	ES 203	558582	2041.E14.gz43_267058
M00055185B:B01	ES 203	559883	2041.E16.gz43_267090
M00055185C:B01	ES 203	411113	2041.E22.gz43_267186
M00055185D:A02	ES 203	561687	2041.F03.gz43_266883
M00055185D:D11	ES 203	555394	2041.F06.gz43_266931
M00055185D:F07	ES 203	477046	2041.F08.gz43_266963
M00055185D:H01	ES 203	502343	2041.F10.gz43_266995
M00055186A:D04	ES 203	552629	2041.F11.gz43_267011
M00055186A:E08	ES 203	557867	2041.F12.gz43_267027
M00055186C:A01	ES 203	459103	2041.F15.gz43_267075
M00055186C:A02	ES 203	481136	2041.F16.gz43_267091
M00055187A:F02	ES 203	516484	2041.G07.gz43_266948
M00055187A:F06	ES 203	492627	2041.G08.gz43_266964
M00055187A:G02	ES 203	552629	2041.G09.gz43_266980
M00055187B:C01	ES 203	364462	2041.G11.gz43_267012
M00055187C:C02	ES 203	551855	2041.G15.gz43_267076
M00055187C:E07	ES 203	549588	2041.G17.gz43_267108
M00055187D:A08	ES 203	557298	2041.G19.gz43_267140
M00055187D:F01	ES 203	560294	2041.G23.gz43_267204
M00055187D:G11	ES 203	557895	2041.H01.gz43_266853

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055188A:G11	ES 203	559610	2041.H06.gz43_266933
M00055188A:H10	ES 203	187704	2041.H07.gz43_266949
M00055188B:E06	ES 203	559262	2041.H08.gz43_266965
M00055188B:G06	ES 203	555649	2041.H09.gz43_266981
M00055188C:A08	ES 203	448046	2041.H12.gz43_267029
M00055188C:F08	ES 203	549665	2041.H14.gz43_267061
M00055188D:D05	ES 203	559146	2041.H19.gz43_267141
M00055188D:F10	ES 203	561685	2041.H20.gz43_267157
M00055188D:H03	ES 203	559825	2041.H21.gz43_267173
M00055189A:C11	ES 203	558463	2041.H24.gz43_267221
M00055189B:B02	ES 203	452094	2041.I04.gz43_266902
M00055189B:B12	ES 203	560080	2041.I06.gz43_266934
M00055189C:C01	ES 203	413915	2041.I10.gz43_266998
M00055190A:A05	ES 203	523332	2041.I15.gz43_267078
M00055190A:F11	ES 203	455814	2041.I19.gz43_267142
M00055190C:G08	ES 203	560859	2041.I24.gz43_267222
M00055191B:A10	ES 203	488613	2041.J05.gz43_266919
M00055191B:E04	ES 203	560674	2041.J07.gz43_266951
M00055191C:C06	ES 203	447412	2041.J10.gz43_266999
M00055191D:C05	ES 203	560213	2041.J13.gz43_267047
M00055192A:A09	ES 203	559883	2041.J15.gz43_267079
M00055192C:A03	ES 203	499903	2041.J22.gz43_267191
M00055192C:D04	ES 203	491992	2041.K01.gz43_266856
M00055192C:E04	ES 203	550874	2041.K02.gz43_266872
M00055192C:H06	ES 203	558326	2041.K05.gz43_266920
M00055193A:A08	ES 203	560003	2041.K11.gz43_267016
M00055193A:C06	ES 203	451544	2041.K14.gz43_267064
M00055193B:A08	ES 203	624044	2041.K18.gz43_267128
M00055193C:C11	ES 203	539142	2041.L02.gz43_266873
M00055193C:E10	ES 203	504880	2041.L03.gz43_266889
M00055193D:G07	ES 203	552977	2041.L08.gz43_266969
M00055194A:A01	ES 203	495591	2041.L10.gz43_267001
M00055194A:E07	ES 203	558413	2041.L13.gz43_267049
M00055194B:C01	ES 203	559234	2041.L15.gz43_267081
M00055194B:G04	ES 203	513168	2041.L16.gz43_267097
M00055194D:C05	ES 203	549911	2041.M02.gz43_266874
M00055195A:B08	ES 203	549304	2041.M09.gz43_266986
M00055195A:C10	ES 203	550704	2041.M11.gz43_267018
M00055195A:E07	ES 203	143218	2041.M12.gz43_267034
M00055195B:B09	ES 203	450623	2041.M14.gz43_267066
M00055195B:C04	ES 203	614369	2041.M15.gz43_267082
M00055195C:F09	ES 203	561659	2041.N01.gz43_266859
M00055195C:H05	ES 203	561830	2041.N02.gz43_266875
M00055195D:B10	ES 203	555742	2041.N06.gz43_266939

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055195D:E11	ES 203	550652	2041.N09.gz43_266987
M00055196A:C04	ES 203	495074	2041.N12.gz43_267035
M00055196A:E01	ES 203	551977	2041.N13.gz43_267051
M00055196A:H07	ES 203	553237	2041.N15.gz43_267083
M00055196B:A09	ES 203	552879	2041.N17.gz43_267115
M00055196B:C06	ES 203	562336	2041.N18.gz43_267131
M00055196C:B07	ES 203	456697	2041.N24.gz43_267227
M00055196D:A10	ES 203	556538	2041.O08.gz43_266972
M00055196D:F07	ES 203	481231	2041.O10.gz43_267004
M00055196D:H02	ES 203	562569	2041.O11.gz43_267020
M00055197B:A10	ES 203	559885	2041.O16.gz43_267100
M00055197B:B06	ES 204	558642	2041.O18.gz43_267132
M00055197C:D10	ES 204	625988	2041.O21.gz43_267180
M00055198A:E05	ES 204	460727	2041.P06.gz43_266941
M00055198B:H08	ES 204	490154	2041.P09.gz43_266989
M00055198C:C12	ES 204	551374	2041.P11.gz43_267021
M00055198C:F02	ES 204	557852	2041.P13.gz43_267053
M00055198C:G07	ES 204	561753	2041.P14.gz43_267069
M00055198D:A12	ES 204	551415	2041.P16.gz43_267101
M00055198D:B08	ES 204	556343	2041.P17.gz43_267117
M00055198D:G01	ES 204	550782	2041.P20.gz43_267165
M00055198D:G03	ES 204	491260	2041.P21.gz43_267181
M00055219B:B04	ES 204	554627	2043.A06.gz43_259273
M00055219C:C10	ES 204	556790	2043.A14.gz43_259401
M00055219C:H06	ES 204	558652	2043.A17.gz43_259449
M00055220B:H06	ES 204	490414	2043.B06.gz43_259274
M00055220D:G07	ES 204	557965	2043.B12.gz43_259370
M00055221A:D10	ES 204	549634	2043.B17.gz43_259450
M00055221D:A06	ES 204	558055	2043.C07.gz43_259291
M00055221D:H08	ES 204	467710	2043.C11.gz43_259355
M00055222A:A06	ES 204	460493	2043.C12.gz43_259371
M00055222A:C08	ES 204	464067	2043.C13.gz43_259387
M00055222B:A01	ES 204	552086	2043.C18.gz43_259467
M00055222B:A06	ES 204	451966	2043.C19.gz43_259483
M00055222D:B11	ES 204	558185	2043.D03.gz43_259228
M00055223B:C04	ES 204	552521	2043.D13.gz43_259388
M00055223D:F10	ES 204	621635	2043.D23.gz43_259548
M00055223D:H03	ES 204	559764	2043.D24.gz43_259564
M00055224B:E12	ES 204	561289	2043.E04.gz43_259245
M00055225B:H01	ES 204	560717	2043.E24.gz43_259565
M00055225C:E08	ES 204	550632	2043.F03.gz43_259230
M00055225D:G11	ES 204	491240	2043.F09.gz43_259326
M00055226B:F10	ES 204	556123	2043.F20.gz43_259502

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055226C:A11	ES 204	489275	2043.F23.gz43_259550
M00055226C:H05	ES 204	558679	2043.G08.gz43_259311
M00055227C:D02	ES 204	550815	2043.H09.gz43_259328
M00055227D:E07	ES 204	550571	2043.H16.gz43_259440
M00055227D:G10	ES 204	559101	2043.H17.gz43_259456
M00055228B:E07	ES 204	554181	2043.H21.gz43_259520
M00055229B:E12	ES 204	452598	2043.I12.gz43_259377
M00055229B:H11	ES 204	559729	2043.I15.gz43_259425
M00055229C:D01	ES 204	559053	2043.I17.gz43_259457
M00055229D:D07	ES 204	543540	2043.I22.gz43_259537
M00055230A:H01	ES 204	551677	2043.J03.gz43_259234
M00055231D:G01	ES 204	560986	2043.J22.gz43_259538
M00055232A:A09	ES 204	460680	2043.J23.gz43_259554
M00055232C:D04	ES 204	557411	2043.K14.gz43_259411
M00055233C:F09	ES 204	559447	2043.L05.gz43_259268
M00055233D:G11	ES 204	559884	2043.L15.gz43_259428
M00055234A:G12	ES 204	552430	2043.L18.gz43_259476
M00055235B:C01	ES 204	374281	2043.M12.gz43_259381
M00055236A:B01	ES 204	466887	2043.M19.gz43_259493
M00055236B:C07	ES 204	450193	2043.M23.gz43_259557
M00055236C:E05	ES 204	451720	2043.N03.gz43_259238
M00055236D:E04	ES 204	558422	2043.N06.gz43_259286
M00055236D:E10	ES 204	557140	2043.N07.gz43_259302
M00055238D:D10	ES 204	557656	2043.O23.gz43_259559
M00055239B:C05	ES 204	558230	2043.P05.gz43_259272
M00055239C:F08	ES 204	481362	2043.P10.gz43_259352
M00055239D:C01	ES 204	552019	2043.P13.gz43_259400
M00055239D:G04	ES 204	557676	2043.P16.gz43_259448
M00055240A:B07	ES 204	562317	2043.P19.gz43_259496
M00055240B:E12	ES 204	552249	2043.P24.gz43_259576
M00055240C:A03	ES 204	558093	2044.A03.gz43_259613
M00055240C:D06	ES 204	43349	2044.A04.gz43_259629
M00055240D:D12	ES 204	497119	2044.A10.gz43_259725
M00055241A:C06	ES 204	450025	2044.A15.gz43_259805
M00055241D:F10	ES 204	616134	2044.B03.gz43_259614
M00055242D:E02	ES 204	541784	2044.B22.gz43_259918
M00055243D:C06	ES 204	486787	2044.C16.gz43_259823
M00055244A:C06	ES 204	238121	2044.C20.gz43_259887
M00055244B:F02	ES 204	558500	2044.D01.gz43_259584
M00055244B:G10	ES 204	38280	2044.D04.gz43_259632
M00055244D:C07	ES 204	560317	2044.D09.gz43_259712
M00055244D:D09	ES 204	549493	2044.D10.gz43_259728
M00055244D:G08	ES 204	549889	2044.D13.gz43_259776
M00055245B:H01	ES 204	629002	2044.D20.gz43_259888

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055245C:D04	ES 204	560507	2044.D22.gz43_259920
M00055245D:A04	ES 204	558355	2044.E03.gz43_259617
M00055245D:D01	ES 204	551305	2044.E06.gz43_259665
M00055246A:C01	ES 204	560317	2044.E09.gz43_259713
M00055246A:E10	ES 204	560669	2044.E10.gz43_259729
M00055246B:C04	ES 204	560204	2044.E14.gz43_259793
M00055246B:D10	ES 204	484086	2044.E15.gz43_259809
M00055246C:A10	ES 204	557389	2044.E16.gz43_259825
M00055246C:F08	ES 204	561579	2044.E17.gz43_259841
M00055247B:A11	ES 204	607430	2044.F04.gz43_259634
M00055247C:B01	ES 204	557389	2044.F05.gz43_259650
M00055248A:F10	ES 204	558461	2044.F14.gz43_259794
M00055248B:B03	ES 204	560099	2044.F15.gz43_259810
M00055248C:B11	ES 204	555340	2044.F22.gz43_259922
M00055248D:B12	ES 204	556829	2044.G02.gz43_259603
M00055249B:G08	ES 204	550830	2044.G18.gz43_259859
M00055249C:B12	ES 204	560059	2044.G22.gz43_259923
M00055250B:A05	ES 204	504415	2044.H06.gz43_259668
M00055250B:G09	ES 204	552357	2044.H09.gz43_259716
M00055250C:F03	ES 204	616196	2044.H10.gz43_259732
M00055251A:B09	ES 204	488143	2044.H18.gz43_259860
M00055251C:D01	ES 204	549052	2044.I06.gz43_259669
M00055251C:H07	ES 204	523732	2044.I11.gz43_259749
M00055251D:B09	ES 204	464205	2044.I14.gz43_259797
M00055251D:H11	ES 204	500737	2044.I18.gz43_259861
M00055252A:H09	ES 204	558670	2044.I24.gz43_259957
M00055252B:D07	ES 204	558785	2044.J03.gz43_259622
M00055252C:B04	ES 204	557256	2044.J05.gz43_259654
M00055252C:E02	ES 204	159419	2044.J08.gz43_259702
M00055252D:C10	ES 204	447380	2044.J14.gz43_259798
M00055253A:C07	ES 204	560205	2044.J17.gz43_259846
M00055253D:C03	ES 204	560261	2044.K01.gz43_259591
M00055254A:E02	ES 204	557928	2044.K05.gz43_259655
M00055254C:A06	ES 204	493359	2044.K11.gz43_259751
M00055254D:B10	ES 204	558861	2044.K15.gz43_259815
M00055255A:F11	ES 204	494130	2044.K24.gz43_259959
M00055255B:A10	ES 204	450405	2044.L01.gz43_259592
M00055255B:F05	ES 204	558512	2044.L04.gz43_259640
M00055256A:D12	ES 204	562256	2044.L16.gz43_259832
M00055256B:C07	ES 204	562256	2044.L21.gz43_259912
M00055256B:G05	ES 204	557928	2044.L24.gz43_259960
M00055257A:D01	ES 204	549456	2044.M16.gz43_259833
M00055257B:B10	ES 204	558134	2044.M17.gz43_259849
M00055257D:A11	ES 204	488574	2044.N04.gz43_259642

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055257D:E02	ES 204	554246	2044.N07.gz43_259690
M00055258A:C07	ES 204	423884	2044.N10.gz43_259738
M00055259A:G06	ES 204	138927	2044.O06.gz43_259675
M00055259B:G11	ES 204	558559	2044.O14.gz43_259803
M00055259C:G10	ES 204	476373	2044.O17.gz43_259851
M00055260B:A05	ES 204	558098	2044.P04.gz43_259644
M00055260B:H06	ES 204	460049	2044.P08.gz43_259708
M00055260C:A11	ES 204	560144	2044.P09.gz43_259724
M00055260C:A12	ES 204	557734	2044.P10.gz43_259740
M00055260D:D04	ES 204	562926	2044.P20.gz43_259900
M00055261A:D11	ES 204	558357	2053.A03.gz43_260006
M00055261B:G12	ES 204	550863	2053.A12.gz43_260150
M00055261D:D09	ES 204	128962	2053.A20.gz43_260278
M00055262A:C05	ES 204	558281	2053.B02.gz43_259991
M00055262B:A11	ES 204	558120	2053.B05.gz43_260039
M00055262B:C01	ES 204	554373	2053.B06.gz43_260055
M00055262C:B08	ES 204	558052	2053.B11.gz43_260135
M00055262C:F05	ES 204	446557	2053.B14.gz43_260183
M00055263C:D02	ES 204	478087	2053.C10.gz43_260120
M00055263C:F10	ES 204	450242	2053.C13.gz43_260168
M00055263C:G09	ES 204	505858	2053.C15.gz43_260200
M00055263D:C03	ES 204	554000	2053.C19.gz43_260264
M00055264A:F03	ES 204	511276	2053.D05.gz43_260041
M00055264B:E06	ES 204	556019	2053.D08.gz43_260089
M00055264B:H12	ES 204	450507	2053.D10.gz43_260121
M00055264D:A03	ES 204	551272	2053.D14.gz43_260185
M00055264D:E09	ES 204	557713	2053.D18.gz43_260249
M00055265A:G01	ES 204	34381	2053.E02.gz43_259994
M00055265A:G07	ES 204	555564	2053.E03.gz43_260010
M00055265C:A04	ES 204	512721	2053.E10.gz43_260122
M00055265C:D09	ES 204	560520	2053.E13.gz43_260170
M00055265C:E01	ES 204	560678	2053.E14.gz43_260186
M00055265C:F01	ES 204	557561	2053.E15.gz43_260202
M00055266A:H08	ES 204	559910	2053.F03.gz43_260011
M00055266B:C12	ES 204	550074	2053.F05.gz43_260043
M00055266D:C09	ES 204	557561	2053.F14.gz43_260187
M00055267A:D01	ES 204	487961	2053.F21.gz43_260299
M00055267A:G11	ES 204	511847	2053.F22.gz43_260315
M00055267B:B06	ES 204	561666	2053.F24.gz43_260347
M00055267D:G08	ES 204	562269	2053.G18.gz43_260252
M00055268B:D12	ES 204	556447	2053.H02.gz43_259997
M00055268D:G09	ES 204	448450	2053.H15.gz43_260205
M00055270D:B05	ES 204	475578	2053.I15.gz43_260206
M00055271A:C05	ES 204	562992	2053.I19.gz43_260270

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055271B:C01	ES 204	553665	2053.I24.gz43_260350
M00055271B:D02	ES 204	446964	2053.J01.gz43_259983
M00055272D:E04	ES 204	559321	2053.K01.gz43_259984
M00055274B:A10	ES 204	562314	2053.K21.gz43_260304
M00055274C:C06	ES 204	558867	2053.L05.gz43_260049
M00055274C:F02	ES 204	452506	2053.L10.gz43_260129
M00055274C:F10	ES 204	557115	2053.L11.gz43_260145
M00055274D:A11	ES 204	560957	2053.L12.gz43_260161
M00055274D:B10	ES 204	549052	2053.L15.gz43_260209
M00055274D:C10	ES 204	558263	2053.L18.gz43_260257
M00055275B:H06	ES 204	558360	2053.M03.gz43_260018
M00055275D:E12	ES 204	560621	2053.M12.gz43_260162
M00055275D:G09	ES 204	362109	2053.M13.gz43_260178
M00055275D:H08	ES 204	562871	2053.M15.gz43_260210
M00055276B:C09	ES 204	560278	2053.M20.gz43_260290
M00055277D:A02	ES 204	555564	2053.N05.gz43_260051
M00055279A:E03	ES 204	551798	2053.O05.gz43_260052
M00055279B:D02	ES 204	480960	2053.O09.gz43_260116
M00055280A:C09	ES 204	560538	2053.O18.gz43_260260
M00055280C:G09	ES 204	560977	2053.P05.gz43_260053
M00055281A:E04	ES 204	558437	2053.P20.gz43_260293
M00055281A:F08	ES 204	558513	2053.P21.gz43_260309
M00055281B:D04	ES 204	481958	2053.P22.gz43_260325
M00055282A:A01	ES 204	559113	2054.A07.gz43_267326
M00055286A:H08	ES 204	559728	2054.C19.gz43_267520
M00055288B:D01	ES 204	559127	2054.E01.gz43_267234
M00055288B:D08	ES 204	399121	2054.E02.gz43_267250
M00055288C:A09	ES 205	549575	2054.E07.gz43_267330
M00055288D:A03	ES 205	558730	2054.E14.gz43_267442
M00055294B:C03	ES 205	484617	2054.H17.gz43_267493
M00055294B:D04	ES 205	559043	2054.H18.gz43_267509
M00055294B:G01	ES 205	559531	2054.H20.gz43_267541
M00055296A:C05	ES 205	561779	2054.I14.gz43_267446
M00055296C:E08	ES 205	558446	2054.I21.gz43_267558
M00055297A:C01	ES 205	558940	2054.I24.gz43_267606
M00055297D:C02	ES 205	500337	2054.J13.gz43_267431
M00055300A:B06	ES 205	551930	2054.K20.gz43_267544
M00055300C:F11	ES 205	559460	2054.L01.gz43_267241
M00055302B:B10	ES 205	624133	2054.M03.gz43_267274
M00055302B:F07	ES 205	561096	2054.M05.gz43_267306
M00055305C:D08	ES 205	560420	2054.O18.gz43_267516
M00055305D:F07	ES 205	448519	2054.O23.gz43_267596
M00055307B:G08	ES 205	451834	2054.P22.gz43_267581

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055308D:C09	ES 205	551811	2055.A23.gz43_267966
M00055308D:E10	ES 205	559965	2055.B01.gz43_267615
M00055310B:E02	ES 205	138470	2055.B20.gz43_267919
M00055312A:D11	ES 205	559112	2055.C08.gz43_267728
M00055312A:E10	ES 205	440707	2055.C09.gz43_267744
M00055312B:F01	ES 205	559452	2055.C15.gz43_267840
M00055312D:A09	ES 205	558813	2055.C23.gz43_267968
M00055313D:E10	ES 205	560369	2055.D17.gz43_267873
M00055314B:F03	ES 205	430146	2055.D22.gz43_267953
M00055314B:G07	ES 205	551912	2055.D23.gz43_267969
M00055315C:A09	ES 205	617813	2055.E13.gz43_267810
M00055316B:B10	ES 205	477757	2055.E22.gz43_267954
M00055317C:D04	ES 205	555359	2055.F12.gz43_267795
M00055319B:H06	ES 205	559794	2055.G19.gz43_267908
M00055319C:C03	ES 205	553709	2055.G22.gz43_267956
M00055319C:C07	ES 205	552857	2055.G23.gz43_267972
M00055320A:F04	ES 205	553986	2055.H09.gz43_267749
M00055320D:E09	ES 205	558105	2055.H20.gz43_267925
M00055321A:A04	ES 205	555200	2055.I01.gz43_267622
M00055321A:D11	ES 205	558161	2055.I03.gz43_267654
M00055321B:B10	ES 205	558890	2055.I05.gz43_267686
M00055321D:C12	ES 205	559027	2055.I13.gz43_267814
M00055322A:C08	ES 205	558254	2055.I23.gz43_267974
M00055322C:G11	ES 205	559574	2055.J04.gz43_267671
M00055322D:A01	ES 205	552673	2055.J05.gz43_267687
M00055322D:C12	ES 205	446900	2055.J07.gz43_267719
M00055323D:A12	ES 205	562236	2055.K01.gz43_267624
M00055324C:H10	ES 205	448677	2055.K13.gz43_267816
M00055324D:B02	ES 205	555277	2055.K15.gz43_267848
M00055325A:E12	ES 205	473343	2055.K21.gz43_267944
M00055325A:H02	ES 205	554585	2055.K22.gz43_267960
M00055330C:F05	ES 205	451118	2055.M20.gz43_267930
M00055330D:C05	ES 205	558980	2055.M22.gz43_267962
M00055330D:H12	ES 205	559776	2055.N01.gz43_267627
M00055333C:F12	ES 205	451429	2055.N22.gz43_267963
M00055333C:H07	ES 205	555349	2055.N23.gz43_267979
M00055334C:E11	ES 205	560538	2055.O16.gz43_267868
M00055334D:G07	ES 205	554176	2055.O21.gz43_267948
M00055335A:B06	ES 205	497493	2055.O24.gz43_267996
M00055335D:A03	ES 205	472188	2055.P12.gz43_267805
M00055336D:B03	ES 205	558562	2056.A04.gz43_268046
M00055337D:B10	ES 205	558867	2056.A15.gz43_268222
M00055338A:A02	ES 205	453004	2056.A16.gz43_268238
M00055338A:A03	ES 205	559971	2056.A17.gz43_268254

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055338A:H10	ES 205	561116	2056.A21.gz43_268318
M00055338B:F06	ES 205	560714	2056.A23.gz43_268350
M00055338C:F03	ES 205	551912	2056.B04.gz43_268047
M00055338C:G04	ES 205	552430	2056.B05.gz43_268063
M00055338C:H06	ES 205	561024	2056.B07.gz43_268095
M00055338D:E11	ES 205	512657	2056.B09.gz43_268127
M00055339A:B06	ES 205	560091	2056.B10.gz43_268143
M00055339B:D10	ES 205	562883	2056.B13.gz43_268191
M00055340B:C03	ES 205	449405	2056.C06.gz43_268080
M00055340B:E06	ES 205	560652	2056.C07.gz43_268096
M00055340C:D01	ES 205	560369	2056.C09.gz43_268128
M00055340D:D01	ES 205	560370	2056.C11.gz43_268160
M00055340D:F08	ES 205	560717	2056.C13.gz43_268192
M00055341B:A01	ES 205	558653	2056.C16.gz43_268240
M00055341B:C07	ES 205	560254	2056.C19.gz43_268288
M00055341C:C01	ES 205	560252	2056.C24.gz43_268368
M00055341C:F04	ES 205	627386	2056.D03.gz43_268033
M00055341C:G12	ES 205	552669	2056.D04.gz43_268049
M00055341D:H07	ES 205	552357	2056.D08.gz43_268113
M00055342A:E08	ES 205	562576	2056.D14.gz43_268209
M00055342B:C08	ES 205	403419	2056.D19.gz43_268289
M00055342C:E03	ES 205	496460	2056.D23.gz43_268353
M00055342C:H06	ES 205	561124	2056.E03.gz43_268034
M00055342D:B02	ES 205	163336	2056.E04.gz43_268050
M00055342D:F07	ES 205	627139	2056.E08.gz43_268114
M00055342D:H05	ES 205	561124	2056.E11.gz43_268162
M00055343A:C09	ES 205	560199	2056.E13.gz43_268194
M00055343A:D08	ES 205	560377	2056.E14.gz43_268210
M00055343A:G03	ES 205	560868	2056.E16.gz43_268242
M00055343C:B11	ES 205	400047	2056.E19.gz43_268290
M00055343C:G09	ES 205	560939	2056.E21.gz43_268322
M00055343C:G10	ES 205	560939	2056.E22.gz43_268338
M00055343D:C12	ES 205	560259	2056.F01.gz43_268003
M00055343D:G03	ES 205	560932	2056.F05.gz43_268067
M00055343D:G06	ES 205	554101	2056.F06.gz43_268083
M00055343D:H04	ES 205	559296	2056.F07.gz43_268099
M00055344A:G11	ES 205	448285	2056.F12.gz43_268179
M00055344B:A12	ES 205	618311	2056.F13.gz43_268195
M00055344C:C08	ES 205	491240	2056.F18.gz43_268275
M00055344C:E04	ES 205	557264	2056.F19.gz43_268291
M00055344C:F09	ES 205	558890	2056.F20.gz43_268307
M00055344C:H09	ES 205	559806	2056.F24.gz43_268371
M00055344D:A09	ES 205	550063	2056.G01.gz43_268004
M00055345A:D05	ES 205	559049	2056.G05.gz43_268068

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055345B:B03	ES 205	558769	2056.G06.gz43_268084
M00055345B:F03	ES 205	559375	2056.G09.gz43_268132
M00055345D:A04	ES 205	551305	2056.G16.gz43_268244
M00055345D:D01	ES 205	559087	2056.G18.gz43_268276
M00055345D:D12	ES 205	559093	2056.G19.gz43_268292
M00055345D:E02	ES 205	559246	2056.G20.gz43_268308
M00055345D:E05	ES 205	558334	2056.G21.gz43_268324
M00055346A:B01	ES 205	560088	2056.G24.gz43_268372
M00055346A:E12	ES 205	418482	2056.H03.gz43_268037
M00055346B:G03	ES 205	509505	2056.H08.gz43_268117
M00055347A:C03	ES 205	559004	2056.H16.gz43_268245
M00055347C:F01	ES 205	559359	2056.I04.gz43_268054
M00055348B:A02	ES 205	559963	2056.I17.gz43_268262
M00055348B:B05	ES 205	103123	2056.I18.gz43_268278
M00055348B:F05	ES 205	552258	2056.I22.gz43_268342
M00055348B:H05	ES 205	550973	2056.I23.gz43_268358
M00055348D:A01	ES 205	559857	2056.J04.gz43_268055
M00055349A:F07	ES 205	549041	2056.J11.gz43_268167
M00055349C:G07	ES 205	458618	2056.J19.gz43_268295
M00055349C:H12	ES 205	562849	2056.J20.gz43_268311
M00055349D:F02	ES 205	556011	2056.J24.gz43_268375
M00055350A:F01	ES 205	556216	2056.K06.gz43_268088
M00055350B:B12	ES 205	449927	2056.K09.gz43_268136
M00055350B:D09	ES 205	560695	2056.K11.gz43_268168
M00055350C:G11	ES 205	553875	2056.K15.gz43_268232
M00055351A:A08	ES 205	553505	2056.K21.gz43_268328
M00055351A:C09	ES 205	560311	2056.K22.gz43_268344
M00055351B:D11	ES 205	560498	2056.L01.gz43_268009
M00055351B:H12	ES 205	512014	2056.L02.gz43_268025
M00055352B:E01	ES 205	555095	2056.L24.gz43_268377
M00055352B:E06	ES 205	560544	2056.M01.gz43_268010
M00055352B:H05	ES 205	557372	2056.M04.gz43_268058
M00055352C:A07	ES 205	553591	2056.M06.gz43_268090
M00055353B:B09	ES 205	455379	2056.M13.gz43_268202
M00055353C:A05	ES 205	426698	2056.M18.gz43_268282
M00055353D:C05	ES 205	558959	2056.M24.gz43_268378
M00055354A:A01	ES 205	558182	2056.N04.gz43_268059
M00055354A:G11	ES 205	471712	2056.N11.gz43_268171
M00055354A:H08	ES 205	561068	2056.N12.gz43_268187
M00055354C:C12	ES 205	238146	2056.N16.gz43_268251
M00055354C:E01	ES 205	184995	2056.N17.gz43_268267
M00055354C:F04	ES 205	560805	2056.N18.gz43_268283
M00055355A:A10	ES 205	487623	2056.N23.gz43_268363
M00055355A:H04	ES 205	562719	2056.O02.gz43_268028

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055355C:A11	ES 205	559910	2056.O07.gz43_268108
M00055356A:B06	ES 205	471272	2056.O13.gz43_268204
M00055356A:D04	ES 205	626061	2056.O14.gz43_268220
M00055356A:D09	ES 205	556365	2056.O15.gz43_268236
M00055356B:B04	ES 205	549781	2056.O17.gz43_268268
M00055356C:H02	ES 205	561108	2056.P01.gz43_268013
M00055356D:C11	ES 205	560174	2056.P07.gz43_268109
M00055356D:G09	ES 205	549464	2056.P08.gz43_268125
M00055357A:A09	ES 205	449751	2056.P10.gz43_268157
M00055357B:A08	ES 205	554591	2056.P15.gz43_268237
M00055357B:B01	ES 205	448989	2056.P16.gz43_268253
M00055357B:B07	ES 205	551412	2056.P17.gz43_268269
M00055357C:H07	ES 205	492821	2056.P22.gz43_268349
M00055358A:F09	ES 205	627297	2065.A06.gz43_268462
M00055358B:C01	ES 205	561485	2065.A09.gz43_268510
M00055358D:G04	ES 205	465610	2065.A17.gz43_268638
M00055359B:F03	ES 205	559495	2065.A21.gz43_268702
M00055359B:G09	ES 205	559676	2065.A23.gz43_268734
M00055359B:H07	ES 205	491635	2065.A24.gz43_268750
M00055359C:H09	ES 205	501534	2065.B08.gz43_268495
M00055359D:C12	ES 205	451124	2065.B11.gz43_268543
M00055359D:H02	ES 205	559828	2065.B15.gz43_268607
M00055360C:C05	ES 205	495799	2065.C02.gz43_268400
M00055360C:F08	ES 205	471718	2065.C05.gz43_268448
M00055360C:G11	ES 205	456469	2065.C06.gz43_268464
M00055360D:H10	ES 205	449593	2065.C12.gz43_268560
M00055361A:C01	ES 205	559022	2065.C15.gz43_268608
M00055361B:F12	ES 205	553615	2065.C20.gz43_268688
M00055361B:G08	ES 205	559675	2065.C21.gz43_268704
M00055361C:E05	ES 205	562459	2065.C22.gz43_268720
M00055361D:C05	ES 205	558927	2065.D02.gz43_268401
M00055361D:H12	ES 205	559696	2065.D05.gz43_268449
M00055362C:B06	ES 205	558412	2065.D11.gz43_268545
M00055362C:G08	ES 205	559675	2065.D14.gz43_268593
M00055362C:H07	ES 205	484091	2065.D15.gz43_268609
M00055363A:C03	ES 205	556947	2065.D22.gz43_268721
M00055363A:D02	ES 205	32021	2065.D24.gz43_268753
M00055363A:F07	ES 205	550562	2065.E02.gz43_268402
M00055363C:E02	ES 205	91178	2065.E08.gz43_268498
M00055364B:B01	ES 205	558504	2065.E15.gz43_268610
M00055364B:D01	ES 205	463304	2065.E17.gz43_268642
M00055364B:E10	ES 205	559963	2065.E18.gz43_268658
M00055364C:B08	ES 205	534054	2065.E20.gz43_268690
M00055364D:E09	ES 205	636651	2065.F03.gz43_268419

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055365B:G10	ES 206	559919	2065.F09.gz43_268515
M00055365C:D12	ES 206	558334	2065.F11.gz43_268547
M00055365C:F11	ES 206	561825	2065.F13.gz43_268579
M00055366A:B04	ES 206	556850	2065.F15.gz43_268611
M00055366A:H08	ES 206	551551	2065.F17.gz43_268643
M00055366B:C04	ES 206	511746	2065.F20.gz43_268691
M00055366C:B11	ES 206	505971	2065.F23.gz43_268739
M00055366D:G10	ES 206	527410	2065.G07.gz43_268484
M00055367A:B11	ES 206	556430	2065.G12.gz43_268564
M00055367D:A05	ES 206	523606	2065.H02.gz43_268405
M00055368C:G06	ES 206	482515	2065.H21.gz43_268709
M00055368D:E03	ES 206	558813	2065.H23.gz43_268741
M00055369A:H08	ES 206	556959	2065.I07.gz43_268486
M00055369C:D04	ES 206	557783	2065.I09.gz43_268518
M00055370A:B03	ES 206	335714	2065.I17.gz43_268646
M00055370B:F07	ES 206	549163	2065.J02.gz43_268407
M00055370C:B08	ES 206	562280	2065.J05.gz43_268455
M00055370C:D02	ES 206	552031	2065.J06.gz43_268471
M00055370D:F06	ES 206	549984	2065.J12.gz43_268567
M00055370D:H07	ES 206	560959	2065.J13.gz43_268583
M00055370D:H12	ES 206	554885	2065.J14.gz43_268599
M00055371A:B05	ES 206	508515	2065.J15.gz43_268615
M00055371A:H10	ES 206	562027	2065.J18.gz43_268663
M00055371B:D01	ES 206	561610	2065.J19.gz43_268679
M00055371B:F01	ES 206	553705	2065.J21.gz43_268711
M00055371D:B08	ES 206	484748	2065.K05.gz43_268456
M00055372A:H02	ES 206	552265	2065.K11.gz43_268552
M00055372B:B02	ES 206	556357	2065.K13.gz43_268584
M00055372B:E01	ES 206	632260	2065.K14.gz43_268600
M00055372B:F11	ES 206	561868	2065.K18.gz43_268664
M00055372C:E03	ES 206	553904	2065.K22.gz43_268728
M00055372D:C11	ES 206	556416	2065.L04.gz43_268441
M00055372D:G11	ES 206	516008	2065.L09.gz43_268521
M00055373B:A09	ES 206	490308	2065.L14.gz43_268601
M00055373C:F05	ES 206	466887	2065.M01.gz43_268394
M00055373C:H03	ES 206	446890	2065.M02.gz43_268410
M00055373C:H10	ES 206	543323	2065.M03.gz43_268426
M00055373D:B08	ES 206	498509	2065.M04.gz43_268442
M00055374A:B11	ES 206	555796	2065.M11.gz43_268554
M00055374A:E01	ES 206	636876	2065.M13.gz43_268586
M00055374B:D05	ES 206	562565	2065.M19.gz43_268682
M00055374B:F06	ES 206	559764	2065.M21.gz43_268714
M00055374C:F01	ES 206	376726	2065.N04.gz43_268443

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055374D:C09	ES 206	504167	2065.N10.gz43_268539
M00055374D:F10	ES 206	558507	2065.N11.gz43_268555
M00055375B:H02	ES 206	482090	2065.N21.gz43_268715
M00055375B:H07	ES 206	555878	2065.N22.gz43_268731
M00055375C:C08	ES 206	448741	2065.N24.gz43_268763
M00055375C:F02	ES 206	143210	2065.O01.gz43_268396
M00055376A:A08	ES 206	561229	2065.O05.gz43_268460
M00055376B:A03	ES 206	474580	2065.O09.gz43_268524
M00055376B:A11	ES 206	561279	2065.O10.gz43_268540
M00055376B:B01	ES 206	453846	2065.O11.gz43_268556
M00055377A:B11	ES 206	207099	2065.O23.gz43_268748
M00055377B:E10	ES 206	562844	2065.P02.gz43_268413
M00055377C:G01	ES 206	461325	2065.P08.gz43_268509
M00055377C:H08	ES 206	450637	2065.P09.gz43_268525
M00055377D:F12	ES 206	562801	2065.P13.gz43_268589
M00055378A:B12	ES 206	235456	2065.P19.gz43_268685
M00055378D:B07	ES 206	559938	2066.A12.gz43_270570
M00055378D:D04	ES 206	562524	2066.A13.gz43_270586
M00055379A:D07	ES 206	468565	2066.A17.gz43_270650
M00055380A:C06	ES 206	448949	2066.B17.gz43_270651
M00055380D:H02	ES 206	562085	2066.C12.gz43_270572
M00055381A:F02	ES 206	549082	2066.C14.gz43_270604
M00055381B:C10	ES 206	562386	2066.C22.gz43_270732
M00055381C:G03	ES 206	562876	2066.D09.gz43_270525
M00055381D:D08	ES 206	560868	2066.D15.gz43_270621
M00055382B:E02	ES 206	493487	2066.D23.gz43_270749
M00055382C:D08	ES 206	558437	2066.E06.gz43_270478
M00055382C:H06	ES 206	446399	2066.E12.gz43_270574
M00055382D:C05	ES 206	562382	2066.E14.gz43_270606
M00055382D:D04	ES 206	459764	2066.E15.gz43_270622
M00055383A:F03	ES 206	562757	2066.E22.gz43_270734
M00055383B:H09	ES 206	551995	2066.F08.gz43_270511
M00055383C:A08	ES 206	562216	2066.F09.gz43_270527
M00055383D:F02	ES 206	498390	2066.F17.gz43_270655
M00055383D:G08	ES 206	454031	2066.F22.gz43_270735
M00055383D:H11	ES 206	559854	2066.F24.gz43_270767
M00055384A:F05	ES 206	562725	2066.G06.gz43_270480
M00055384B:D10	ES 206	562498	2066.G12.gz43_270576
M00055384C:G07	ES 206	562870	2066.G18.gz43_270672
M00055384D:H06	ES 206	550766	2066.G20.gz43_270704
M00055385C:C04	ES 206	549045	2066.H06.gz43_270481
M00055385C:F06	ES 206	561325	2066.H08.gz43_270513
M00055385C:G09	ES 206	450349	2066.H10.gz43_270545
M00055385D:D03	ES 206	418622	2066.H14.gz43_270609

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055386A:G05	ES 206	562849	2066.H21.gz43_270721
M00055386D:G02	ES 206	558297	2066.I11.gz43_270562
M00055386D:H04	ES 206	557247	2066.I12.gz43_270578
M00055387B:H12	ES 206	550829	2066.I22.gz43_270738
M00055388A:A09	ES 206	553244	2066.J08.gz43_270515
M00055388A:B06	ES 206	560948	2066.J09.gz43_270531
M00055388B:B02	ES 206	465836	2066.J13.gz43_270595
M00055388B:E01	ES 206	636532	2066.J17.gz43_270659
M00055388B:H04	ES 206	557249	2066.J20.gz43_270707
M00055388C:D01	ES 206	635965	2066.J22.gz43_270739
M00055388D:A01	ES 206	555681	2066.J24.gz43_270771
M00055388D:F11	ES 206	556793	2066.K10.gz43_270548
M00055389A:D08	ES 206	238196	2066.K14.gz43_270612
M00055389C:F12	ES 206	282015	2066.K24.gz43_270772
M00055390A:A05	ES 206	515115	2066.L06.gz43_270485
M00055390C:E06	ES 206	50604	2066.L18.gz43_270677
M00055391B:D05	ES 206	499690	2066.M10.gz43_270550
M00055391B:D07	ES 206	453508	2066.M11.gz43_270566
M00055391B:H07	ES 206	418921	2066.M14.gz43_270614
M00055391B:H08	ES 206	555639	2066.M15.gz43_270630
M00055392A:H06	ES 206	446242	2066.N03.gz43_270439
M00055392C:G07	ES 206	551640	2066.N11.gz43_270567
M00055392D:A06	ES 206	562701	2066.N13.gz43_270599
M00055393B:F04	ES 206	44015	2066.N23.gz43_270759
M00055393C:B02	ES 206	549889	2066.N24.gz43_270775
M00055394B:C06	ES 206	561457	2066.O13.gz43_270600
M00055394B:D08	ES 206	556011	2066.O15.gz43_270632
M00055394D:F03	ES 206	554908	2066.P07.gz43_270505
M00055395A:C02	ES 206	446531	2066.P09.gz43_270537
M00055395A:E09	ES 206	452808	2066.P13.gz43_270601
M00055395B:C04	ES 206	561487	2066.P17.gz43_270665
M00055396B:C06	ES 206	560003	2067.A11.gz43_270938
M00055396B:G02	ES 206	561922	2067.A14.gz43_270986
M00055397A:B10	ES 206	562236	2067.A23.gz43_271130
M00055397A:C06	ES 206	154980	2067.A24.gz43_271146
M00055397A:H07	ES 206	556380	2067.B06.gz43_270859
M00055397B:F12	ES 206	562736	2067.B08.gz43_270891
M00055397D:A01	ES 206	562147	2067.B12.gz43_270955
M00055398A:C11	ES 206	561438	2067.B20.gz43_271083
M00055398B:A05	ES 206	469852	2067.B21.gz43_271099
M00055398B:C05	ES 206	456687	2067.B23.gz43_271131
M00055398C:A11	ES 206	555882	2067.B24.gz43_271147
M00055398C:D01	ES 206	448511	2067.C02.gz43_270796
M00055398C:F07	ES 206	511792	2067.C06.gz43_270860

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055399C:A08	ES 206	513715	2067.C21.gz43_271100
M00055400B:H12	ES 206	562029	2067.D19.gz43_271069
M00055400D:G01	ES 206	556382	2067.E04.gz43_270830
M00055401A:C08	ES 206	449258	2067.E06.gz43_270862
M00055401D:E03	ES 206	551731	2067.E21.gz43_271102
M00055402A:A05	ES 206	561206	2067.F02.gz43_270799
M00055402A:H03	ES 206	98869	2067.F06.gz43_270863
M00055402C:C12	ES 206	551928	2067.F22.gz43_271119
M00055402D:A11	ES 206	486834	2067.G02.gz43_270800
M00055402D:H04	ES 206	562059	2067.G06.gz43_270864
M00055403A:C07	ES 206	555856	2067.G11.gz43_270944
M00055403B:A05	ES 206	490060	2067.G16.gz43_271024
M00055403B:A10	ES 206	558180	2067.G18.gz43_271056
M00055403B:D04	ES 206	555726	2067.G21.gz43_271104
M00055403B:D07	ES 206	553173	2067.G22.gz43_271120
M00055403B:G09	ES 206	551675	2067.G23.gz43_271136
M00055403B:G12	ES 206	561236	2067.G24.gz43_271152
M00055404A:B10	ES 206	561325	2067.H10.gz43_270929
M00055404A:D08	ES 206	553766	2067.H12.gz43_270961
M00055404C:C11	ES 206	530715	2067.H23.gz43_271137
M00055405A:A02	ES 206	561236	2067.I05.gz43_270850
M00055405A:C01	ES 206	452761	2067.I06.gz43_270866
M00055405A:G11	ES 206	419489	2067.I07.gz43_270882
M00055405B:H05	ES 206	554742	2067.I10.gz43_270930
M00055405B:H06	ES 206	473617	2067.I11.gz43_270946
M00055405C:C04	ES 206	63669	2067.I13.gz43_270978
M00055405C:H07	ES 206	559102	2067.I14.gz43_270994
M00055405D:G05	ES 206	551617	2067.I20.gz43_271090
M00055406B:E07	ES 206	562584	2067.J05.gz43_270851
M00055406B:F10	ES 206	562369	2067.J07.gz43_270883
M00055406D:A03	ES 206	491260	2067.J13.gz43_270979
M00055406D:C10	ES 206	487893	2067.J16.gz43_271027
M00055406D:G12	ES 206	557853	2067.J18.gz43_271059
M00055407A:F08	ES 206	465828	2067.J24.gz43_271155
M00055407B:G07	ES 206	550730	2067.K02.gz43_270804
M00055407C:E04	ES 206	465284	2067.K06.gz43_270868
M00055407C:G04	ES 206	556105	2067.K08.gz43_270900
M00055407C:G11	ES 206	560252	2067.K09.gz43_270916
M00055408A:A05	ES 206	561212	2067.K15.gz43_271012
M00055408A:F12	ES 206	66014	2067.K23.gz43_271140
M00055408A:G09	ES 206	446650	2067.L01.gz43_270789
M00055408B:G04	ES 206	447800	2067.L08.gz43_270901
M00055408C:C04	ES 206	451938	2067.L11.gz43_270949
M00055408C:E04	ES 206	559776	2067.L13.gz43_270981

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055408D:E05	ES 206	548939	2067.L17.gz43_271045
M00055408D:E11	ES 206	558720	2067.L18.gz43_271061
M00055409A:E06	ES 206	100821	2067.L23.gz43_271141
M00055409A:E10	ES 206	516043	2067.L24.gz43_271157
M00055410C:G08	ES 206	550135	2067.N05.gz43_270855
M00055410C:H11	ES 206	562001	2067.N08.gz43_270903
M00055410D:B02	ES 206	288626	2067.N09.gz43_270919
M00055410D:G01	ES 206	633189	2067.N11.gz43_270951
M00055411A:H04	ES 206	558583	2067.N16.gz43_271031
M00055411B:D12	ES 206	356058	2067.N22.gz43_271127
M00055411C:E02	ES 206	450060	2067.O03.gz43_270824
M00055412A:C05	ES 206	440833	2067.O14.gz43_271000
M00055412A:F09	ES 206	556734	2067.O15.gz43_271016
M00055412B:A07	ES 206	495958	2067.O16.gz43_271032
M00055412D:A12	ES 206	560838	2067.P03.gz43_270825
M00055413A:A02	ES 206	540000	2067.P07.gz43_270889
M00055413C:B09	ES 206	446171	2067.P19.gz43_271081
M00042583D:F03	ES 207	452204	2078.A10.gz43_269168
M00042583D:F11	ES 207	506901	2078.A11.gz43_269184
M00042586B:A04	ES 207	451722	2078.A22.gz43_269360
M00042586B:A09	ES 207	451933	2078.A23.gz43_269376
M00042586B:A10	ES 207	448453	2078.A24.gz43_269392
M00042586C:E01	ES 207	451923	2078.B03.gz43_269057
M00042586D:C07	ES 207	451868	2078.B06.gz43_269105
M00042587B:G07	ES 207	452260	2078.B09.gz43_269153
M00042588A:G10	ES 207	508088	2078.B16.gz43_269265
M00042588C:E07	ES 207	505858	2078.B19.gz43_269313
M00042589A:G06	ES 207	452236	2078.B21.gz43_269345
M00042589B:D04	ES 207	504007	2078.B22.gz43_269361
M00042589B:E03	ES 207	452066	2078.B23.gz43_269377
M00042589D:D08	ES 207	415825	2078.C08.gz43_269138
M00042589D:F02	ES 207	452182	2078.C09.gz43_269154
M00042590B:G02	ES 207	507349	2078.C11.gz43_269186
M00042590C:C09	ES 207	418340	2078.C12.gz43_269202
M00042621B:G01	ES 207	452257	2078.C16.gz43_269266
M00042621D:A03	ES 207	501401	2078.C19.gz43_269314
M00042622C:H12	ES 207	452315	2078.D03.gz43_269059
M00042623B:B09	ES 207	451802	2078.D06.gz43_269107
M00042623D:C02	ES 207	447210	2078.D09.gz43_269155
M00042624D:B05	ES 207	452462	2078.D14.gz43_269235
M00042625B:H10	ES 207	517247	2078.D20.gz43_269331
M00042625D:C07	ES 207	511746	2078.E06.gz43_269108
M00042625D:E08	ES 207	513888	2078.E07.gz43_269124

Table 13

CloneID	ES No	ClusterID	SequenceName
M00042626B:A12	ES 207	452432	2078.E10.gz43_269172
M00042626D:D12	ES 207	452031	2078.E16.gz43_269268
M00042627B:A10	ES 207	452376	2078.E18.gz43_269300
M00042628B:G11	ES 207	451401	2078.F04.gz43_269077
M00042628C:G10	ES 207	516522	2078.F06.gz43_269109
M00042628D:F12	ES 207	447904	2078.F08.gz43_269141
M00042629A:E11	ES 207	452052	2078.F11.gz43_269189
M00042630B:C04	ES 207	451885	2078.F20.gz43_269333
M00042630C:C12	ES 207	503499	2078.F22.gz43_269365
M00042951D:C05	ES 207	451841	2078.G05.gz43_269094
M00042952A:H12	ES 207	452324	2078.G10.gz43_269174
M00042952B:A08	ES 207	500853	2078.G11.gz43_269190
M00042952B:C08	ES 207	451887	2078.G12.gz43_269206
M00042952C:H09	ES 207	452323	2078.G16.gz43_269270
M00042953B:D02	ES 207	504560	2078.H01.gz43_269031
M00042954A:F04	ES 207	452142	2078.H12.gz43_269207
M00042954D:D04	ES 207	451993	2078.H18.gz43_269303
M00042955D:C02	ES 207	502815	2078.I02.gz43_269048
M00042955D:H03	ES 207	448594	2078.I04.gz43_269080
M00042956A:H02	ES 207	448090	2078.I05.gz43_269096
M00042957A:D06	ES 207	451994	2078.I12.gz43_269208
M00042957D:C09	ES 207	451929	2078.I18.gz43_269304
M00042958B:H04	ES 207	452981	2078.J02.gz43_269049
M00042958C:D04	ES 207	512721	2078.J03.gz43_269065
M00042958C:G10	ES 207	516018	2078.J04.gz43_269081
M00042959A:B07	ES 207	423578	2078.J06.gz43_269113
M00042959A:E08	ES 207	514142	2078.J08.gz43_269145
M00042959B:E11	ES 207	514160	2078.J11.gz43_269193
M00042959C:C06	ES 207	452615	2078.J12.gz43_269209
M00042959D:A05	ES 207	510169	2078.J14.gz43_269241
M00042960A:B10	ES 207	448332	2078.J17.gz43_269289
M00042960D:C11	ES 207	512051	2078.K03.gz43_269066
M00042962A:G04	ES 207	452899	2078.K12.gz43_269210
M00042962B:A03	ES 207	446438	2078.K13.gz43_269226
M00042962C:D05	ES 207	513155	2078.K16.gz43_269274
M00042962D:B09	ES 207	511351	2078.K18.gz43_269306
M00042963B:A02	ES 207	452459	2078.K23.gz43_269386
M00042963B:E12	ES 207	514594	2078.L02.gz43_269051
M00042963D:F11	ES 207	452801	2078.L07.gz43_269131
M00042964C:D06	ES 207	513156	2078.L16.gz43_269275
M00042964C:D10	ES 207	513168	2078.L17.gz43_269291
M00042964D:C02	ES 207	512059	2078.L21.gz43_269355
M00042965A:B03	ES 207	452506	2078.L23.gz43_269387
M00042965A:G02	ES 207	516415	2078.M01.gz43_269036

Table 13

CloneID	ES No	ClusterID	SequenceName
M00042965B:G08	ES 207	452898	2078.M04.gz43_269084
M00042965C:A05	ES 207	452454	2078.M06.gz43_269116
M00042965C:E06	ES 207	452775	2078.M07.gz43_269132
M00042967A:E06	ES 207	513585	2078.M18.gz43_269308
M00042969B:E01	ES 207	505679	2078.N04.gz43_269085
M00042969B:G10	ES 207	452279	2078.N05.gz43_269101
M00042970D:D02	ES 207	452695	2078.N16.gz43_269277
M00042971A:B09	ES 207	510717	2078.N17.gz43_269293
M00042971A:D12	ES 207	452662	2078.N19.gz43_269325
M00042972C:F07	ES 207	451618	2078.O04.gz43_269086
M00042972C:F09	ES 207	373239	2078.O05.gz43_269102
M00042973B:B10	ES 207	452500	2078.O09.gz43_269166
M00042974D:B07	ES 207	456545	2078.O17.gz43_269294
M00042975C:A08	ES 207	450805	2078.O21.gz43_269358
M00042975D:G07	ES 207	453124	2078.P01.gz43_269039
M00042976B:F05	ES 207	506920	2078.P03.gz43_269071
M00042978B:F03	ES 207	452833	2078.P17.gz43_269295
M00042978D:E02	ES 207	27534	2078.P20.gz43_269343
M00042982C:G02	ES 207	448687	2079.A18.gz43_271818
M00042983A:E09	ES 207	504880	2079.A22.gz43_271882
M00042983D:A03	ES 207	456756	2079.B06.gz43_271627
M00042985B:C05	ES 207	448200	2079.B14.gz43_271755
M00042985B:F05	ES 207	506372	2079.B15.gz43_271771
M00042985C:B03	ES 207	451811	2079.B16.gz43_271787
M00042985C:D02	ES 207	504501	2079.B17.gz43_271803
M00042985C:D04	ES 207	451491	2079.B18.gz43_271819
M00042986B:E06	ES 207	447445	2079.B22.gz43_271883
M00042986C:B07	ES 207	501534	2079.B24.gz43_271915
M00042987C:E04	ES 207	505226	2079.C06.gz43_271628
M00042988D:G10	ES 207	452220	2079.C13.gz43_271740
M00042989C:A06	ES 207	510254	2079.C15.gz43_271772
M00042989C:B07	ES 207	511348	2079.C16.gz43_271788
M00042989D:A07	ES 207	509505	2079.C20.gz43_271852
M00042990A:E05	ES 207	448813	2079.C21.gz43_271868
M00042990B:A08	ES 207	500795	2079.C23.gz43_271900
M00042991B:G01	ES 207	452874	2079.D05.gz43_271613
M00042991C:C02	ES 207	238196	2079.D06.gz43_271629
M00042991D:C09	ES 207	452603	2079.D09.gz43_271677
M00042991D:F06	ES 207	452830	2079.D12.gz43_271725
M00042992B:B03	ES 207	451812	2079.D15.gz43_271773
M00042992B:B11	ES 207	502343	2079.D16.gz43_271789
M00042992D:H02	ES 207	75212	2079.D19.gz43_271837
M00042993A:D12	ES 207	513178	2079.D21.gz43_271869
M00042993B:C12	ES 207	446520	2079.D23.gz43_271901

Table 13

CloneID	ES No	ClusterID	SequenceName
M00042994C:C09	ES 207	503628	2079.E05.gz43_271614
M00042995C:E04	ES 207	455716	2079.E11.gz43_271710
M00042996D:D12	ES 207	453804	2079.E21.gz43_271870
M00042997B:B07	ES 207	451806	2079.E23.gz43_271902
M00042999A:D01	ES 207	403634	2079.F07.gz43_271647
M00043000C:H06	ES 207	509027	2079.F14.gz43_271759
M00055413C:G09	ES 207	556126	2067.P21.gz43_271113
M00055414C:C02	ES 207	456520	2068.A13.gz43_271354
M00055414D:G10	ES 207	482425	2068.A21.gz43_271482
M00055415D:C12	ES 207	561500	2068.B15.gz43_271387
M00055415D:E10	ES 207	204557	2068.B17.gz43_271419
M00055416A:C04	ES 207	561497	2068.B21.gz43_271483
M00055416B:F11	ES 207	561770	2068.C07.gz43_271260
M00055416D:B03	ES 207	562477	2068.C12.gz43_271340
M00055416D:D11	ES 207	558679	2068.C14.gz43_271372
M00055416D:H11	ES 207	555880	2068.C18.gz43_271436
M00055417A:G11	ES 207	131130	2068.C21.gz43_271484
M00055417C:A05	ES 207	550166	2068.D04.gz43_271213
M00055417C:G03	ES 207	561112	2068.D05.gz43_271229
M00055417D:D08	ES 207	557760	2068.D08.gz43_271277
M00055417D:H08	ES 207	470667	2068.D10.gz43_271309
M00055418A:C12	ES 207	561454	2068.D12.gz43_271341
M00055418A:E07	ES 207	561682	2068.D15.gz43_271389
M00055418A:F03	ES 207	560252	2068.D16.gz43_271405
M00055418A:H04	ES 207	554774	2068.D17.gz43_271421
M00055418C:D08	ES 207	418562	2068.E05.gz43_271230
M00055418D:A03	ES 207	552561	2068.E10.gz43_271310
M00055418D:B05	ES 207	630348	2068.E11.gz43_271326
M00055419D:D04	ES 207	561646	2068.F04.gz43_271215
M00055419D:H07	ES 207	550018	2068.F09.gz43_271295
M00055420A:E12	ES 207	561707	2068.F14.gz43_271375
M00055420A:F01	ES 207	558958	2068.F15.gz43_271391
M00055420C:E08	ES 207	524736	2068.F22.gz43_271503
M00055421A:A09	ES 207	556793	2068.G10.gz43_271312
M00055421B:E05	ES 207	58680	2068.G22.gz43_271504
M00055421C:F06	ES 207	561837	2068.H09.gz43_271297
M00055421C:G07	ES 207	491728	2068.H11.gz43_271329
M00055421D:G11	ES 207	559884	2068.H16.gz43_271409
M00055422B:B01	ES 207	554489	2068.H22.gz43_271505
M00055422C:E10	ES 207	554028	2068.I09.gz43_271298
M00055422D:E12	ES 207	631966	2068.I12.gz43_271346
M00055423A:A10	ES 207	561180	2068.I14.gz43_271378
M00055423A:D02	ES 207	560118	2068.I15.gz43_271394
M00055423A:G08	ES 207	449356	2068.I16.gz43_271410

Table 13

CloneID	ES No	ClusterID	SequenceName
M00055423B:A06	ES 207	553987	2068.I17.gz43_271426
M00055423C:C11	ES 207	559514	2068.J04.gz43_271219
M00055423C:D05	ES 207	559385	2068.J05.gz43_271235
M00055424A:A08	ES 207	556511	2068.J12.gz43_271347
M00055424A:C10	ES 207	492982	2068.J13.gz43_271363
M00055424A:F04	ES 207	512392	2068.J15.gz43_271395
M00055424A:F06	ES 207	48977	2068.J16.gz43_271411
M00055424B:D04	ES 207	559380	2068.K01.gz43_271172
M00055425A:H03	ES 207	554953	2068.K14.gz43_271380
M00055425B:D12	ES 207	561645	2068.K17.gz43_271428
M00055425B:F06	ES 207	493410	2068.K20.gz43_271476
M00055471C:A06	ES 207	412282	2068.L13.gz43_271365
M00055471C:B01	ES 207	492876	2068.L14.gz43_271381
M00055471C:D04	ES 207	447098	2068.L16.gz43_271413
M00055472A:B12	ES 207	561411	2068.M05.gz43_271238
M00055472A:F02	ES 207	468672	2068.M08.gz43_271286
M00055472A:H01	ES 207	551166	2068.M09.gz43_271302
M00055472C:G11	ES 207	549511	2068.M18.gz43_271446
M00055472D:H09	ES 207	562017	2068.N03.gz43_271207
M00055473B:D01	ES 207	556490	2068.N08.gz43_271287
M00055473B:E10	ES 207	561718	2068.N10.gz43_271319
M00055473C:A05	ES 207	559076	2068.N12.gz43_271351
M00055473C:E06	ES 207	554181	2068.N15.gz43_271399
M00055473C:H05	ES 207	522220	2068.N16.gz43_271415
M00055473D:E01	ES 207	561753	2068.N20.gz43_271479
M00055474A:B05	ES 207	562302	2068.N22.gz43_271511
M00055474A:G06	ES 207	449795	2068.O03.gz43_271208
M00055474B:G02	ES 207	486512	2068.O09.gz43_271304
M00055474C:H12	ES 207	555933	2068.O14.gz43_271384
M00055474D:E07	ES 207	268197	2068.O18.gz43_271448
M00055475D:A05	ES 207	417426	2068.P12.gz43_271353
M00055475D:A10	ES 207	562137	2068.P14.gz43_271385
M00055475D:B07	ES 207	453715	2068.P16.gz43_271417
M00055475D:G08	ES 207	560700	2068.P18.gz43_271449
M00042611A:A01	ES 208	449068	2089.A01.gz43_269708
M00042612A:B06	ES 208	405102	2089.A06.gz43_269788
M00042613A:H01	ES 208	453783	2089.A15.gz43_269932
M00042613C:F06	ES 208	453783	2089.A18.gz43_269980
M00042614A:C04	ES 208	520074	2089.A22.gz43_270044
M00042614A:H02	ES 208	524157	2089.A23.gz43_270060
M00042614C:B09	ES 208	447446	2089.A24.gz43_270076
M00042614D:A12	ES 208	453220	2089.B03.gz43_269741
M00042616A:D03	ES 208	527590	2089.B10.gz43_269853

Table 13

CloneID	ES No	ClusterID	SequenceName
M00042617C:B07	ES 208	453385	2089.B20.gz43_270013
M00042618B:G04	ES 208	453893	2089.C03.gz43_269742
M00043001A:C10	ES 208	451850	2079.F16.gz43_271791
M00043001B:C01	ES 208	503122	2079.F17.gz43_271807
M00043001B:E02	ES 208	452969	2079.F18.gz43_271823
M00043001B:H01	ES 208	452325	2079.F19.gz43_271839
M00043001C:C03	ES 208	451891	2079.F20.gz43_271855
M00043002A:G09	ES 208	507450	2079.F23.gz43_271903
M00043002B:E06	ES 208	454849	2079.F24.gz43_271919
M00043003A:H07	ES 208	452976	2079.G11.gz43_271712
M00043003C:A02	ES 208	452392	2079.G15.gz43_271776
M00043003C:G10	ES 208	452866	2079.G18.gz43_271824
M00043003D:D10	ES 208	455132	2079.G20.gz43_271856
M00043004A:C08	ES 208	503625	2079.G22.gz43_271888
M00043004A:C10	ES 208	448381	2079.G23.gz43_271904
M00043005A:B06	ES 208	452504	2079.H06.gz43_271633
M00043007B:D12	ES 208	366607	2079.H24.gz43_271921
M00043007D:F07	ES 208	452186	2079.I05.gz43_271618
M00043008D:E12	ES 208	504812	2079.I15.gz43_271778
M00043008D:H09	ES 208	508126	2079.I17.gz43_271810
M00043009B:C09	ES 208	502984	2079.I19.gz43_271842
M00043009B:F11	ES 208	452160	2079.I20.gz43_271858
M00043010B:B02	ES 208	451794	2079.J09.gz43_271683
M00043011B:D03	ES 208	504431	2079.J15.gz43_271779
M00043011C:H09	ES 208	508125	2079.J19.gz43_271843
M00043011D:C12	ES 208	502614	2079.J22.gz43_271891
M00043012A:E02	ES 208	452110	2079.K03.gz43_271588
M00043012A:F06	ES 208	453572	2079.K04.gz43_271604
M00043012D:A06	ES 208	449510	2079.K10.gz43_271700
M00043013B:A06	ES 208	500896	2079.K13.gz43_271748
M00043013C:A01	ES 208	455117	2079.K16.gz43_271796
M00043013D:F03	ES 208	455621	2079.K18.gz43_271828
M00043014B:G12	ES 208	454226	2079.K22.gz43_271892
M00043014C:F07	ES 208	505933	2079.K23.gz43_271908
M00043014C:G06	ES 208	507066	2079.K24.gz43_271924
M00043017D:B06	ES 208	455855	2079.L13.gz43_271749
M00043020A:A03	ES 208	452440	2079.L15.gz43_271781
M00043020A:G12	ES 208	452922	2079.L16.gz43_271797
M00043021A:A09	ES 208	452445	2079.L18.gz43_271829
M00043021A:B06	ES 208	452528	2079.L19.gz43_271845
M00043021A:C04	ES 208	454286	2079.L20.gz43_271861
M00043021A:H06	ES 208	453078	2079.L21.gz43_271877
M00043021B:H03	ES 208	452973	2079.L22.gz43_271893
M00043021D:F10	ES 208	514824	2079.M01.gz43_271558

Table 13

CloneID	ES No	ClusterID	SequenceName
M00043022D:A07	ES 208	500622	2079.M06.gz43_271638
M00043023D:D06	ES 208	513381	2079.M13.gz43_271750
M00043024B:H11	ES 208	453079	2079.M20.gz43_271862
M00043025A:C01	ES 208	456755	2079.M22.gz43_271894
M00043025A:D09	ES 208	452648	2079.M23.gz43_271910
M00043026D:D06	ES 208	452031	2079.N11.gz43_271719
M00043027B:C04	ES 208	452618	2079.N14.gz43_271767
M00043027D:G12	ES 208	452873	2079.N18.gz43_271831
M00043028B:F08	ES 208	454487	2079.N21.gz43_271879
M00043028C:H09	ES 208	453038	2079.N23.gz43_271911
M00043029A:E11	ES 208	452759	2079.O05.gz43_271624
M00043029B:C09	ES 208	512432	2079.O07.gz43_271656
M00043029B:F09	ES 208	269927	2079.O09.gz43_271688
M00043029B:G10	ES 208	516799	2079.O10.gz43_271704
M00043029C:D01	ES 208	448550	2079.O11.gz43_271720
M00043030C:B11	ES 208	452501	2079.O21.gz43_271880
M00043030C:F03	ES 208	515127	2079.O22.gz43_271896
M00043030D:G03	ES 208	449242	2079.P01.gz43_271561
M00043031A:B01	ES 208	452523	2079.P02.gz43_271577
M00043032B:H01	ES 208	452957	2079.P11.gz43_271721
M00043033C:C05	ES 208	452611	2079.P21.gz43_271881
M00043033C:D05	ES 208	452611	2079.P23.gz43_271913
M00043075A:B12	ES 208	519109	2089.C14.gz43_269918
M00043076A:A09	ES 208	518566	2089.C22.gz43_270046
M00043077B:H01	ES 208	448985	2089.D07.gz43_269807
M00043077D:E12	ES 208	417549	2089.D09.gz43_269839
M00043077D:F04	ES 208	522648	2089.D10.gz43_269855
M00043078C:C04	ES 208	519641	2089.D14.gz43_269919
M00043078C:H05	ES 208	523732	2089.D16.gz43_269951
M00043079C:D08	ES 208	453554	2089.D19.gz43_269999
M00043079D:G10	ES 208	523182	2089.E01.gz43_269712
M00043080A:C03	ES 208	451583	2089.E02.gz43_269728
M00043080B:B05	ES 208	453297	2089.E03.gz43_269744
M00043080B:C11	ES 208	519988	2089.E04.gz43_269760
M00043081D:A10	ES 208	446614	2089.E09.gz43_269840
M00043082D:B05	ES 208	454562	2089.E17.gz43_269968
M00043085C:A03	ES 208	453160	2089.E24.gz43_270080
M00043086A:C02	ES 208	453470	2089.F03.gz43_269745
M00043086D:B09	ES 208	453248	2089.F08.gz43_269825
M00043087B:D10	ES 208	449430	2089.F13.gz43_269905
M00043088B:D07	ES 208	395536	2089.F16.gz43_269953
M00043089A:D06	ES 208	520616	2089.F21.gz43_270033
M00043090B:H06	ES 208	524470	2089.F24.gz43_270081
M00043090D:H07	ES 208	524478	2089.G03.gz43_269746

Table 13

CloneID	ES No	ClusterID	SequenceName
M00043091C:H05	ES 208	530656	2089.G07.gz43_269810
M00043091C:H08	ES 208	454910	2089.G08.gz43_269826
M00043091D:C01	ES 208	454374	2089.G09.gz43_269842
M00043091D:F03	ES 208	402242	2089.G11.gz43_269874
M00043092D:D06	ES 208	454531	2089.G18.gz43_269986
M00043093A:A06	ES 208	454177	2089.G20.gz43_270018
M00043093D:F12	ES 208	454701	2089.H02.gz43_269731
M00043094A:F01	ES 208	529219	2089.H03.gz43_269747
M00043094C:A12	ES 208	525023	2089.H06.gz43_269795
M00043096A:B02	ES 208	449202	2089.H12.gz43_269891
M00043096A:E01	ES 208	528134	2089.H13.gz43_269907
M00043096C:D02	ES 208	454509	2089.H16.gz43_269955
M00043096C:H04	ES 208	451972	2089.H17.gz43_269971
M00043097A:D11	ES 208	527873	2089.H21.gz43_270035
M00043097A:F06	ES 208	387530	2089.H22.gz43_270051
M00043097D:B12	ES 208	454226	2089.I02.gz43_269732
M00043100C:D08	ES 208	453533	2089.I15.gz43_269940
M00043100D:C12	ES 208	520057	2089.I17.gz43_269972
M00043101A:F12	ES 208	522548	2089.I20.gz43_270020
M00043101C:F12	ES 208	453846	2089.I22.gz43_270052
M00043102A:B10	ES 208	453364	2089.J01.gz43_269717
M00043102A:G12	ES 208	523590	2089.J04.gz43_269765
M00043102B:F05	ES 208	453761	2089.J05.gz43_269781
M00043102D:C05	ES 208	446728	2089.J09.gz43_269845
M00043102D:F11	ES 208	453766	2089.J11.gz43_269877
M00043103A:G05	ES 208	449335	2089.J12.gz43_269893
M00043104B:C09	ES 208	453494	2089.J20.gz43_270021
M00043105A:F02	ES 208	453809	2089.K01.gz43_269718
M00043106B:F07	ES 208	450287	2089.K11.gz43_269878
M00043106C:D05	ES 208	453572	2089.K12.gz43_269894
M00043107A:E07	ES 208	453726	2089.K17.gz43_269974
M00043107D:H04	ES 208	450566	2089.K21.gz43_270038
M00043108B:A01	ES 208	453132	2089.K23.gz43_270070
M00043108B:D12	ES 208	453549	2089.L01.gz43_269719
M00043109C:F04	ES 208	454720	2089.L06.gz43_269799
M00043131B:A11	ES 208	454134	2089.L07.gz43_269815
M00043131B:G10	ES 208	454825	2089.L11.gz43_269879
M00043131C:A11	ES 208	451391	2089.L13.gz43_269911
M00043131D:B02	ES 208	525719	2089.L15.gz43_269943
M00043132C:D02	ES 208	454483	2089.L22.gz43_270055
M00043134C:D06	ES 208	454518	2089.M09.gz43_269848
M00043135C:E07	ES 208	454550	2089.M12.gz43_269896
M00043135D:A11	ES 208	454126	2089.M13.gz43_269912
M00043135D:C07	ES 208	526575	2089.M14.gz43_269928

Table 13

CloneID	ES No	ClusterID	SequenceName
M00043136A:D03	ES 208	527361	2089.M17.gz43_269976
M00043137C:D02	ES 208	452936	2089.N04.gz43_269769
M00043137D:D10	ES 208	454438	2089.N06.gz43_269801
M00043138A:H03	ES 208	523753	2089.N09.gz43_269849
M00043138B:B08	ES 208	407275	2089.N10.gz43_269865
M00043138B:F02	ES 208	93125	2089.N12.gz43_269897
M00043138B:G11	ES 208	437064	2089.N13.gz43_269913
M00043138C:D09	ES 208	449394	2089.N15.gz43_269945
M00043139C:A05	ES 208	524622	2089.N23.gz43_270073
M00043139D:A06	ES 208	524624	2089.O02.gz43_269738
M00043140C:D03	ES 208	527446	2089.O04.gz43_269770
M00043140C:H11	ES 208	530919	2089.O07.gz43_269818
M00043141C:C12	ES 208	415326	2089.O10.gz43_269866
M00043141D:A12	ES 208	454129	2089.O13.gz43_269914
M00043144D:H01	ES 208	454050	2089.P03.gz43_269755
M00043146C:D10	ES 208	520595	2089.P09.gz43_269851
M00043146C:F10	ES 208	453756	2089.P10.gz43_269867
M00043146D:H03	ES 208	455941	2089.P13.gz43_269915
M00043147D:H03	ES 208	524363	2089.P15.gz43_269947
M00043148C:E01	ES 208	453692	2089.P17.gz43_269979
M00043149B:A01	ES 208	453202	2089.P20.gz43_270027
M00043149D:F02	ES 208	522220	2090.A03.gz43_273939
M00043150A:B12	ES 208	518949	2090.A04.gz43_273955
M00043151B:D02	ES 208	454460	2090.A12.gz43_274083
M00043152A:F10	ES 208	454731	2090.A17.gz43_274163
M00043152A:G08	ES 208	456723	2090.A18.gz43_274179
M00043152B:H04	ES 208	530939	2090.A23.gz43_274259
M00043153B:B09	ES 208	519378	2090.B01.gz43_273908
M00043156C:E05	ES 208	528404	2090.C03.gz43_273941
M00043158A:F03	ES 208	522869	2090.C12.gz43_274085
M00043159A:C01	ES 208	526449	2090.C18.gz43_274181
M00043160B:E05	ES 208	521840	2090.D02.gz43_273926
M00043162D:E06	ES 208	453730	2090.D17.gz43_274166
M00043168C:F03	ES 208	446768	2090.F05.gz43_273976
M00043169A:F05	ES 208	453804	2090.F09.gz43_274040
M00043169A:H08	ES 208	524100	2090.F11.gz43_274072
M00043169C:D10	ES 208	453569	2090.F15.gz43_274136
M00043171B:G05	ES 208	523602	2090.G12.gz43_274089
M00043171D:G08	ES 208	450784	2090.G17.gz43_274169
M00043172A:D08	ES 208	401160	2090.G18.gz43_274185
M00043172C:B05	ES 208	234270	2090.G23.gz43_274265
M00043172C:G06	ES 208	453946	2090.H01.gz43_273914
M00043172D:H03	ES 208	128749	2090.H06.gz43_273994
M00043173B:F03	ES 208	453354	2090.H11.gz43_274074

Table 13

CloneID	ES No	ClusterID	SequenceName
M00043173C:B05	ES 208	453256	2090.H13.gz43_274106
M00043173C:D12	ES 208	520599	2090.H15.gz43_274138
M00043174A:G04	ES 208	454810	2090.H17.gz43_274170
M00043174B:B06	ES 208	413693	2090.H18.gz43_274186
M00043174C:C06	ES 208	526733	2090.H20.gz43_274218
M00043176C:A01	ES 208	525315	2090.I11.gz43_274075
M00043176C:E12	ES 208	454664	2090.I13.gz43_274107
M00042592A:H02	ES 209	539142	2092.A07.gz43_274486
M00042594C:D02	ES 209	455405	2092.A22.gz43_274726
M00042595A:B07	ES 209	447278	2092.B01.gz43_274391
M00042599D:E07	ES 209	455460	2092.B15.gz43_274615
M00042600D:B08	ES 209	455117	2092.B20.gz43_274695
M00042600D:E11	ES 209	452392	2092.B21.gz43_274711
M00042637C:E12	ES 209	536171	2092.B22.gz43_274727
M00042637D:B12	ES 209	455814	2092.B23.gz43_274743
M00042638D:G10	ES 209	455784	2092.C02.gz43_274408
M00042639D:H04	ES 209	455880	2092.C09.gz43_274520
M00042640C:C10	ES 209	455201	2092.C11.gz43_274552
M00042640D:D01	ES 209	455375	2092.C12.gz43_274568
M00043178C:C01	ES 209	454324	2090.I22.gz43_274251
M00043178C:G06	ES 209	529742	2090.I24.gz43_274283
M00043180C:B02	ES 209	452325	2090.J08.gz43_274028
M00043181C:C10	ES 209	526539	2090.J14.gz43_274124
M00043181C:F06	ES 209	529037	2090.J15.gz43_274140
M00043182B:C02	ES 209	454311	2090.J18.gz43_274188
M00043183A:C04	ES 209	454363	2090.K02.gz43_273933
M00043183C:B08	ES 209	525781	2090.K06.gz43_273997
M00043184D:A02	ES 209	447536	2090.K17.gz43_274173
M00043184D:G06	ES 209	432159	2090.K20.gz43_274221
M00043185B:D02	ES 209	527679	2090.L01.gz43_273918
M00043186C:A11	ES 209	524721	2090.L07.gz43_274014
M00043186D:A06	ES 209	524706	2090.L09.gz43_274046
M00043186D:B09	ES 209	425455	2090.L10.gz43_274062
M00043187B:G03	ES 209	530094	2090.L12.gz43_274094
M00043187C:E06	ES 209	528369	2090.L13.gz43_274110
M00043187D:H04	ES 209	530971	2090.L16.gz43_274158
M00043188D:B07	ES 209	525456	2090.L17.gz43_274174
M00043189C:F08	ES 209	528981	2090.M02.gz43_273935
M00043189D:B11	ES 209	452231	2090.M05.gz43_273983
M00043190A:B10	ES 209	454202	2090.M07.gz43_274015
M00043191C:G05	ES 209	404081	2090.M17.gz43_274175
M00043192B:H06	ES 209	453983	2090.M20.gz43_274223
M00043193C:G11	ES 209	523674	2090.N04.gz43_273968

Table 13

CloneID	ES No	ClusterID	SequenceName
M00043193C:H09	ES 209	452775	2090.N06.gz43_274000
M00043194A:G06	ES 209	453890	2090.N11.gz43_274080
M00043194C:A05	ES 209	453177	2090.N14.gz43_274128
M00043194D:E10	ES 209	289316	2090.N16.gz43_274160
M00043195D:A05	ES 209	518172	2090.N20.gz43_274224
M00043197D:H12	ES 209	454007	2090.O09.gz43_274049
M00043198A:F01	ES 209	453818	2090.O11.gz43_274081
M00043199A:F03	ES 209	452182	2090.O14.gz43_274129
M00043201D:D03	ES 209	454463	2090.P01.gz43_273922
M00043203B:E07	ES 209	528616	2090.P10.gz43_274066
M00043210C:E08	ES 209	454629	2090.P22.gz43_274258
M00043417A:H12	ES 209	539804	2092.C18.gz43_274664
M00043417B:F12	ES 209	455601	2092.C20.gz43_274696
M00043417C:F12	ES 209	447380	2092.C21.gz43_274712
M00043418A:A06	ES 209	422223	2092.C23.gz43_274744
M00043420C:C02	ES 209	455289	2092.D09.gz43_274521
M00043421C:G07	ES 209	449067	2092.D12.gz43_274569
M00043422B:C03	ES 209	455162	2092.D13.gz43_274585
M00043425C:H11	ES 209	539452	2092.E07.gz43_274490
M00043427C:E11	ES 209	544355	2092.E10.gz43_274538
M00043428C:A08	ES 209	531461	2092.E15.gz43_274618
M00043428D:C10	ES 209	455220	2092.E17.gz43_274650
M00043428D:E02	ES 209	536038	2092.E18.gz43_274666
M00043430D:C01	ES 209	455254	2092.E20.gz43_274698
M00043433A:F02	ES 209	537451	2092.F08.gz43_274507
M00043434A:H02	ES 209	452128	2092.F10.gz43_274539
M00043434B:D06	ES 209	535129	2092.F11.gz43_274555
M00043434B:E04	ES 209	452801	2092.F12.gz43_274571
M00043438B:E10	ES 209	404461	2092.G04.gz43_274444
M00043438C:D12	ES 209	535436	2092.G05.gz43_274460
M00043439C:D05	ES 209	535123	2092.G08.gz43_274508
M00043441D:A09	ES 209	455132	2092.G17.gz43_274652
M00043442A:D02	ES 209	534519	2092.G18.gz43_274668
M00043446B:H01	ES 209	456020	2092.H09.gz43_274525
M00043446C:E04	ES 209	455808	2092.H11.gz43_274557
M00043446C:E08	ES 209	400258	2092.H12.gz43_274573
M00043446C:E10	ES 209	456530	2092.H13.gz43_274589
M00043446C:G09	ES 209	547652	2092.H14.gz43_274605
M00043447A:F02	ES 209	455572	2092.H15.gz43_274621
M00043447C:A06	ES 209	454994	2092.H18.gz43_274669
M00043448B:E08	ES 209	455501	2092.H22.gz43_274733
M00043448C:D05	ES 209	456742	2092.H23.gz43_274749
M00043448C:G07	ES 209	538582	2092.H24.gz43_274765
M00043448D:H09	ES 209	451023	2092.I04.gz43_274446

Table 13

CloneID	ES No	ClusterID	SequenceName
M00043449C:H09	ES 209	448946	2092.I09.gz43_274526
M00043449D:A06	ES 209	447534	2092.I10.gz43_274542
M00043449D:E09	ES 209	215366	2092.I11.gz43_274558
M00043450B:C11	ES 209	456249	2092.I14.gz43_274606
M00043450B:H05	ES 209	456783	2092.I15.gz43_274622
M00043450C:F11	ES 209	454563	2092.I17.gz43_274654
M00043451A:B02	ES 209	456103	2092.I20.gz43_274702
M00043451B:D08	ES 209	448250	2092.I21.gz43_274718
M00043451C:H03	ES 209	447238	2092.I24.gz43_274766
M00043452D:D05	ES 209	452830	2092.J08.gz43_274511
M00043453B:C06	ES 209	456254	2092.J11.gz43_274559
M00043453B:F02	ES 209	546121	2092.J12.gz43_274575
M00043453C:A06	ES 209	446866	2092.J13.gz43_274591
M00043453D:D02	ES 209	543855	2092.J19.gz43_274687
M00043455B:G11	ES 209	546838	2092.K04.gz43_274448
M00043455C:G07	ES 209	450914	2092.K07.gz43_274496
M00043457C:B12	ES 209	454621	2092.K12.gz43_274576
M00043459A:B08	ES 209	541901	2092.K17.gz43_274656
M00043460D:C03	ES 209	534054	2092.L08.gz43_274513
M00043460D:H01	ES 209	539353	2092.L09.gz43_274529
M00043462A:H06	ES 209	455834	2092.L14.gz43_274609
M00043462C:E12	ES 209	536225	2092.L17.gz43_274657
M00043462D:C09	ES 209	415326	2092.L19.gz43_274689
M00043465B:G08	ES 209	162851	2092.M08.gz43_274514
M00043468C:D08	ES 209	455379	2092.M17.gz43_274658
M00043470C:A01	ES 209	456001	2092.N05.gz43_274467
M00043472A:E06	ES 209	536415	2092.N11.gz43_274563
M00043473C:B11	ES 209	37186	2092.N15.gz43_274627
M00043473D:D11	ES 209	452618	2092.N18.gz43_274675
M00043474C:H05	ES 209	455864	2092.N20.gz43_274707
M00043475C:G08	ES 209	446866	2092.N23.gz43_274755
M00043478B:D01	ES 209	450724	2092.O06.gz43_274484
M00043481A:B01	ES 209	532904	2092.O14.gz43_274612
M00043481A:G02	ES 209	402534	2092.O16.gz43_274644
M00043483B:G01	ES 209	455808	2092.O22.gz43_274740
M00043483B:G11	ES 209	455814	2092.O23.gz43_274756
M00043484C:E12	ES 209	455492	2092.P05.gz43_274469
M00043484D:H08	ES 209	455855	2092.P07.gz43_274501
M00043485A:A04	ES 209	452910	2092.P08.gz43_274517
M00043485A:C04	ES 209	450658	2092.P09.gz43_274533
M00043485B:C09	ES 209	455256	2092.P10.gz43_274549
M00043486B:D02	ES 209	543429	2092.P13.gz43_274597
M00043486C:D02	ES 209	543431	2092.P15.gz43_274629
M00043486C:F07	ES 209	456567	2092.P17.gz43_274661

Table 13

CloneID	ES No	ClusterID	SequenceName
M00043489C:H06	ES 209	446873	2092.P20.gz43_274709
M00043490A:F03	ES 209	456577	2092.P24.gz43_274773
M00063157B:B09	ES 209	464791	2102.A16.gz43_275283
M00063165C:F10	ES 209	449206	2116.A13.gz43_306321
M00063457A:B12	ES 209	558147	2102.B18.gz43_275316
M00063493D:G07	ES 209	644927	2102.F08.gz43_275160
M00063496B:F07	ES 209	558900	2102.F14.gz43_275256
M00063507B:B08	ES 209	621081	2102.G10.gz43_275193
M00063514B:E04	ES 209	498509	2102.H02.gz43_275066
M00063546B:F01	ES 209	730600	2116.D21.gz43_306452
M00063552B:B06	ES 209	89082	2116.E15.gz43_306357
M00063580A:A07	ES 209	649744	2116.I06.gz43_306217
M00063592B:E09	ES 209	378453	2116.J09.gz43_306266
M00063601D:C05	ES 209	379154	2102.I24.gz43_275419
M00063803B:F11	ES 209	402353	2103.B13.gz43_275620
M00063861C:F09	ES 209	544229	2103.E13.gz43_275623
M00063864A:H10	ES 209	380514	2103.E17.gz43_275687
M00063865A:F01	ES 209	427540	2103.E21.gz43_275751
M00063866B:H02	ES 209	643609	2103.F01.gz43_275432
M00063900B:B04	ES 209	730845	2103.H23.gz43_275786
M00063923B:A04	ES 209	402941	2103.J21.gz43_275756
M00063927A:B08	ES 209	554395	2103.K10.gz43_275581
M00063943B:G12	ES 209	377696	2103.M06.gz43_275519
M00063943B:G12	ES 209	377696	RTA22200255F.f.15.1.P
M00063970A:D09	ES 209	642263	2116.M13.gz43_306333
M00063980B:A08	ES 209	378447	2116.N09.gz43_306270
M00063988A:C02	ES 209	404453	2116.O22.gz43_306479
M00063994B:D10	ES 209	535955	2116.P08.gz43_306256
M00064064D:D11	ES 209	554032	2104.A21.gz43_297640
M00064077B:H02	ES 209	639578	2104.C08.gz43_297434
M00064081A:D04	ES 209	52644	2104.C19.gz43_297610
M00064082C:D11	ES 209	505275	2104.D01.gz43_297323
M00064085B:A12	ES 209	649035	2104.D11.gz43_297483
M00064101B:E12	ES 209	376559	2104.E08.gz43_297436
M00064104B:A01	ES 209	558382	2104.E17.gz43_297580
M00064107C:E03	ES 209	463217	2104.E23.gz43_297676
M00064112A:G03	ES 209	646187	2104.F12.gz43_297501
M00064131B:A09	ES 209	647586	2104.H11.gz43_297487
M00064147B:G08	ES 209	454622	2104.I20.gz43_297632
M00064194B:A02	ES 209	11379	2104.N01.gz43_297333
M00064195C:B02	ES 209	446397	2104.N03.gz43_297365
M00064196D:C10	ES 209	469367	2104.N05.gz43_297397
M00064201A:C08	ES 209	727888	2104.N13.gz43_297525
M00064220B:E01	ES 209	418763	2104.P04.gz43_297383

Table 13

CloneID	ES No	ClusterID	SequenceName
M00064307C:E12	ES 209	404453	2117.D05.gz43_306580
M00064371B:E01	ES 209	728687	2117.J15.gz43_306746
M00064383B:B04	ES 209	551960	2117.K19.gz43_306811
M00064387A:H05	ES 209	447461	2117.L05.gz43_306588
M00064391C:D09	ES 209	471364	2117.L18.gz43_306796
M00064394A:C02	ES 209	416886	2117.M03.gz43_306557
M00064446D:C08	ES 209	446397	2118.A09.gz43_307025
M00064534D:H04	ES 209	730238	2118.H24.gz43_307272
M00064592D:F05	ES 209	177443	2118.M09.gz43_307037
M00064601C:H06	ES 209	644919	2118.N03.gz43_306942

We Claim:

1. An isolated polynucleotide comprising a nucleotide sequence which hybridizes under stringent conditions to a sequence selected from the group consisting of SEQ ID NOS: 1-6010.

2. An isolated polynucleotide comprising at least 15 contiguous nucleotides of a nucleotide sequence having at least 90% sequence identity to a sequence selected from the group consisting of: SEQ ID NOS:1-6010, a degenerate variant of SEQ ID NOS:1-6010, an antisense of SEQ ID NOS:1-6010, and a complement of SEQ ID NOS:1-6010.

3. An isolated polynucleotide comprising at least 15 contiguous nucleotides of a nucleotide sequence selected from the group consisting of: SEQ ID NOS:1-6010, a degenerate variant of SEQ ID NOS:1-6010, an antisense of SEQ ID NOS:1-6010, and a complement of SEQ ID NOS:1-6010.

4. The isolated polynucleotide of claim 3, wherein the polynucleotide comprises at least 100 contiguous nucleotides of the nucleotide sequence.

5. The isolated polynucleotide of claim 3, wherein the polynucleotide comprises at least 200 contiguous nucleotides of the selected nucleotide sequence.

6. An isolated polynucleotide comprising a nucleotide sequence of at least 90% sequence identity to a sequence selected from the group consisting of: SEQ ID NOS:1-6010, a degenerate variant of SEQ ID NOS:1-6010, an antisense of SEQ ID NOS:1-6010, and a complement of SEQ ID NOS:1-6010.

7. The isolated polynucleotide of claim 6, wherein the polynucleotide comprises a nucleotide sequence of at least 95% sequence identity to the selected nucleotide sequence.

8. The isolated polynucleotide of claim 6, wherein the polynucleotide comprises a nucleotide sequence that is identical to the selected nucleotide sequence.

9. A polynucleotide comprising a nucleotide sequence of an insert contained in a clone deposited as ATCC Accession No. PTA-2027, PTA-2028, PTA-2029, PTA-2030, PTA-2031, PTA-2032, PTA-2033, PTA-2034, PTA-2035, PTA-2036, PTA-2037, PTA-2038, PTA-2039, PTA-2040, PTA-2041, PTA-2042, PTA-2043, PTA-2044, PTA-2045, PTA-2046, PTA-2047, PTA-2050, PTA-2051, PTA-2052, PTA-2053, PTA-2054, PTA-2055, PTA-2056, PTA-2057, PTA-2058, PTA-

2059, PTA-2060, PTA-2061, PTA-2062, PTA-2048, PTA-2049, PTA-2063, PTA-2064, PTA-2065, PTA-2066, PTA-2067, or PTA-2068.

10. An isolated cDNA obtained by the process of amplification using a polynucleotide comprising at least 15 contiguous nucleotides of a nucleotide sequence of a sequence selected from the group consisting of SEQ ID NOS:1-6010.

11. The isolated cDNA of claim 10, wherein the polynucleotide comprises at least 25 contiguous nucleotides of the selected nucleotide sequence.

12. The isolated cDNA of claim 10, wherein the polynucleotide comprises at least 100 contiguous nucleotides of the selected nucleotide sequence.

13. The isolated cDNA of claims 10, 11, or 12, wherein amplification is by polymerase chain reaction (PCR) amplification.

14. An isolated recombinant host cell containing the polynucleotide according to claims 1, 2, 3, 6, 9, or 10.

15. An isolated vector comprising the polynucleotide according to claims claims 1, 2, 3, 6, 9, or 10.

16. A method for producing a polypeptide, the method comprising the steps of:

culturing a recombinant host cell containing the polynucleotide according to claims claims 1, 2, 3, 6, 9, or 10., said culturing being under conditions suitable for the expression of an encoded polypeptide;

recovering the polypeptide from the host cell culture.

17. An isolated polypeptide encoded by the polynucleotide according to claims claims 1, 2, 3, 6, 9, or 10.

18. An antibody that specifically binds the polypeptide of claim 17.

19. A method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, the method comprising the step of:

detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where the gene product is encoded by a gene comprising an identifying sequence of at least one of SEQ ID NOS:1-6010;

wherein detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived.

20. A library of polynucleotides, wherein at least one of the polynucleotides comprises the sequence information of the polynucleotide according to claims 1, 2, 3, 6, 9, or 10.

21. The library of claim 20, wherein the library is provided on a nucleic acid array.

22. The library of claim 20, wherein the library is provided in a computer-readable format.

23. A method of inhibiting tumor growth by modulating expression of a gene product, the gene product being encoded by a gene identified by a sequence selected from the group consisting of SEQ ID NOS:1-6010.