HUMAN GENES AND GENE EXPRESSION PRODUCTS ISOLATED FROM HUMAN PROSTATE

159159

Cross-Reference to Related Application

Ths application claims the benefit of earlier-filed U.S. provisional application serial no. 60/254,648 filed December 11, 2000, and of ealier-filed U.S. provisional application serial no. 60/275,688 filed March 13, 2001, which applications are incorporated herein by reference in their entirety.

Field of the Invention

The present invention relates to polynucleotides of human origin, particularly in human prostate, and the encoded gene products.

Background of the Invention

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.

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

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:1-1477. The polypeptides of the invention correspond to a polypeptide comprising the amino acid sequence information of at least one of SEQ ID NOS:1478-1568.

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

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:1-1477; 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:1-1477 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: 1-1477.

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:1-1477) 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:1-1477. 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:1-1477, 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, or TeraBLAST available from TimeLogic Corp. (Crystal Bay, Nevada).

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:1-1477. 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:1-1477.

Probes specific to the polynucleotides of the invention can be generated using the polynucleotide sequences disclosed in SEQ ID NOS:1-1477. 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:1-1477, and can be less than 10, 5, 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:1-1477. 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, RepeatMasker, etc.) 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, for example, to 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:1-1477 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:1-1477, 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 prostate cells, more preferably, human prostate cancer cells

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:1-1477. 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:1-1477) 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:1-1477; (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:1-1477, preferably the entire sequence of at least any one of SEQ ID NOS:1-1477, 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:1-1477 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:1-1477.

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:1-1477), 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:1-1477 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:1-1477 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 as identified through, for example, BLAST-based searching,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, or TeraBLAST available from TimeLogic Corp. (Crystal Bay, Nevada). 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 or TeraBLAST, 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), TeraBLAST (available from TimeLogic Corp., Crystal Bay, Nevada), 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:1-1477 or a variant thereof. Also included in the invention are the polypeptides comprising the amino acid sequences of SEQ ID NOS:1478-1568.

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 or TeraBLAST 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 or TeraBLAST 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:1-1477, a polypeptide comrpsing a sequence of at least one of SEQ ID NOS:1478-1568, 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:1-1477. By plurality is meant at least 2, usually at least 3 and can include up to all of SEQ ID NOS:1-1477. 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:1-1477, 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, or the TeraBLAST (TimeLogic, Crystal Bay, Nevada) program optionally running on a specialized computer platform available from TimeLogic, 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), TeraBLAST (TimeLogic, Crystal Bay, Nevada). 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:1-1477 , 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:1-1477 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:1-1477.

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. The present invention further provides antibodies, which may be isolated antibodies, that are specific for a polypeptide encoded by a polynucleotide described herein (*e.g.*, a polypeptide encoded by a sequence corresponding to SEQ ID NOS:1-1477, a polypeptide comprising an amino acid sequence of SEQ ID NOS:1478-1568). Antibodies can be provided in a composition comprising the antibody and a buffer and/or a pharmaceutically acceptable excipient. Antibodies specific for a polypeptide associated with prostate cancer are useful in a variety of diagnostic and therapeutic methods, as discussed in detail herein.

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.

The invention also contemplates other molecules that can specifically bind a polynucleotide or polypeptide of the invention. Examples of such molecules include, but are not necessarily limited to, single-chain binding proteins (*e.g.*, mono- and multi-valent single chain antigen binding proteins (*see, e.g.*, U.S. Patent Nos. 4,704,692; 4,946,778; 4,946,778; 6,027,725; 6,121,424)), oligonucleotide-based synthetic antibodies (*e.g.*, oligobodies (*see, e.g.*, Radrizzani *et al., Medicina* (B Aires) (1999) 59:753-8; Radrizzani *et al., Medicina* (B Aires) (2000) 60(Suppl 2):55-60)), aptamers (*see, e.g.*, Gening *et al., Biotechniques* (2001) 3:828, 830, 832, 834; Cox and Ellington, *Bioorg. Med. Chem.* (2001) 9:2525-31), and the like.

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:1-1477. 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:1-1477, and can involve detection of expression of genes corresponding to all of SEQ ID NOS:1-1477 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, such as a polypeptide of a gene corresponding to SEQ ID NOS:1-1477 and/or a polypeptide comprising a sequence of SEQ ID NO:1478-1568. 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.

For prostate cancer, the Gleason Grading/Scoring system is most commonly used. A prostate biopsy tissue sample is examined under a microscope and a grade is assigned to the tissue based on: 1) the appearance of the cells, and 2) the arrangement of the cells. Each parameter is assessed on a scale of one (cells are almost normal) to five (abnormal), and the individual Gleason Grades are presented separated by a "+" sign. Alternatively, the two grades are combined to give a Gleason Score of 2-10. Thus, for a tissue sample that received a grade of 3 for each parameter, the Gleason Grade would be 3+3 and the Gleason Score would be 6. A lower Gleason Score indicates a well-differentiated tumor, while a higher Gleason Score indicates a poorly differentiated cancer that is more likely to spread. The majority of biopsies in general are Gleason Scores 5, 6 and 7.

Gleason Score 2, 3, 4	Gleason Score 5, 6, 7	Gleason Score 8, 9, 10
Low-grade tumor	Medium-grade tumor	High-grade tumor
Slow Growth	Unpredictable Growth	Aggressive Growth
Least dangerous. Cells look most like normal prostate cells and are described as being "well-differentiated". Tends to be slow growing.	Intermediate cancers may behave like low-grade or high-grade cancers. The cells' behavior may depend on the volume of the cancer and the PSA level. This is the most common grade of prostate cancer.	High-grade cancers are usually very aggressive and quick to spread to the tissue surrounding the prostate. These cancer cells look least like normal prostate cells and are usually described as "poorly-differentiated".

The polynucleotides of the Sequence Listing, and their corresponding genes and gene products, 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. Prostate cancer is quite common in humans, with one out of every six men at a lifetime risk for prostate cancer, and can be relatively harmless or extremely aggressive. Some prostate tumors are slow growing, causing few clinical symptoms, while aggressive tumors spread rapidly to the lymph nodes, other organs and especially bone. 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.

The prostate is divided into three areas - the peripheral zone, the transition zone, and the central zone - with a layer of tissue surrounding all three. Most prostate tumors form in the peripheral zone; the larger, glandular portion of the organ. Prostate cancer can also form in the tissue of the central zone. Surrounding the prostate is the prostate capsule, a tissue that separates the prostate from the rest of the body. When prostate cancer remains inside the prostate capsule, it is considered localized and treatable with surgery. Once the cancer punctures the capsule and spreads outside, treatment options are more limited. Prevention and early detection are key factors in controlling and curing prostate cancer.

While the Gleason Grade or Score of a prostate cancer can provide information useful in determining the appropriate treatment of a prostate cancer, the majority of prostate cancers are Gleason Scores 5, 6, and 7, which exhibit unpredictable behavior. These cancers may behave like less dangerous low-grade cancers or like extremely dangerous high-grade cancers. As a result, a patient living with a medium-grade prostate cancer is at constant risk of developing high-grade cancer.

The expression of appropriate polynucleotides can be used in the diagnosis, prognosis and management of prostate cancer. Detection of prostate cancer can be determined using expression levels of any of these sequences alone or in combination with the levels of expression of any other nucleotide sequences. Determination of the aggressive nature and/or the metastatic potential of a prostate cancer can be determined by comparing levels of one or more gene products of the genes corresponding to the polynucleotides described herein, and comparing total levels of another sequence known to vary in cancerous tissue, *e.g.*, expression of p53, DCC, ras, 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 prostate cancer can be detected by examining the level of expression of a gene corresponding to a polynucleotides described herein 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 prostate tissue, to discriminate between prostate cancers with different cells of origin, to discriminate between prostate 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.

In addition, 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.

Identification of Therapeutic Targets and Anti-Cancer Therapeutic Agents

The present invention also encompasses methods for identification of agents having the ability to modulate activity of a differentially expressed gene product, as well as methods for identifying a differentially expressed gene product as a therapeutic target for treatment of cancer, especially prostate cancer.

Candidate agents

Identification of compounds that modulate activity of a differentially expressed gene product can be accomplished using any of a variety of drug screening techniques. Such agents are candidates for development of cancer therapies. Of particular interest are screening assays for agents that have tolerable toxicity for normal, non-cancerous human cells. The screening assays of the invention are generally based upon the ability of the agent to modulate an activity of a differentially expressed gene product and/or to inhibit or suppress phenomenon associated with cancer (*e.g.*, cell proliferation, colony formation, cell cycle arrest, metastasis, and the like).

The term "agent" as used herein describes any molecule, *e.g.* protein or pharmaceutical, with the capability of modulating a biological activity of a gene product of a differentially expressed gene. Generally a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, *i.e.* at zero concentration or below the level of detection.

Candidate agents encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 50 and less than about 2,500 daltons. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including, but not limited to: peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs or combinations thereof.

Candidate agents are obtained from a wide variety of sources including libraries of synthetic or natural compounds. For example, numerous means are available for random and directed synthesis of a wide variety of organic compounds and biomolecules, including expression of randomized oligonucleotides and oligopeptides. Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant and animal extracts (including extracts from human tissue to identify endogenous factors affecting differentially expressed gene products) are available or readily produced. Additionally, natural or synthetically produced libraries and compounds are readily modified through conventional chemical, physical and biochemical means, and may be used to produce combinatorial libraries. Known pharmacological agents may be subjected to directed or random chemical modifications, such as acylation, alkylation, esterification, amidification, *etc.* to produce structural analogs.

Exemplary candidate agents of particular interest include, but are not limited to, antisense polynucleotides, and antibodies, soluble receptors, and the like. Antibodies and soluble receptors are of particular interest as candidate agents where the target differentially expressed gene product is secreted or accessible at the cell-surface (*e.g.*, receptors and other molecule stably-associated with the outer cell membrane).

Screening of candidate agents

Screening assays can be based upon any of a variety of techniques readily available and known to one of ordinary skill in the art. In general, the screening assays involve contacting a cancerous cell (preferably a cancerous prostate cell) with a candidate agent, and assessing the effect upon biological activity of a differentially expressed gene product. The effect upon a biological activity can be detected by, for example, detection of expression of a gene product of a differentially expressed gene (*e.g.*, a decrease in mRNA or polypeptide levels, would in turn cause a decrease in biological activity of the gene product). Alternatively or in addition, the effect of the candidate agent can be assessed by examining the effect of the candidate agent in a functional assay. For example, where the differentially expressed gene product is an enzyme, then the effect upon biological activity can be assessed by detecting a level of enzymatic activity associated with the differentially expressed

gene product. The functional assay will be selected according to the differentially expressed gene product. In general, where the differentially expressed gene is increased in expression in a cancerous cell, agents of interest are those that decrease activity of the differentially expressed gene product.

Assays described infra can be readily adapted in the screening assay embodiments of the invention. Exemplary assays useful in screening candidate agents include, but are not limited to, hybridization-based assays (*e.g.*, use of nucleic acid probes or primers to assess expression levels), antibody-based assays (*e.g.*, to assess levels of polypeptide gene products), binding assays (*e.g.*, to detect interaction of a candidate agent with a differentially expressed polypeptide, which assays may be competitive assays where a natural or synthetic ligand for the polypeptide is available), and the like. Additional exemplary assays include, but are not necessarily limited to, cell proliferation assays, antisense knockout assays, assays to detect inhibition of cell cycle, assays of induction of cell death/apoptosis, and the like. Generally such assays are conducted *in vitro*, but many assays can be adapted for *in vivo* analyses, *e.g.*, in an animal model of the cancer.

Identification of therapeutic targets

In another embodiment, the invention contemplates identification of differentially expressed genes and gene products as therapeutic targets. In some respects, this is the converse of the assays described above for identification of agents having activity in modulating (*e.g.*, decreasing or increasing) activity of a differentially expressed gene product.

In this embodiment, therapeutic targets are identified by examining the effect(s) of an agent that can be demonstrated or has been demonstrated to modulate a cancerous phenotype (*e.g.*, inhibit or suppress or prevent development of a cancerous phenotype). Such agents are generally referred to herein as an "anti-cancer agent", which agents encompass chemotherapeutic agents. For example, the agent can be an antisense oligonucleotide that is specific for a selected gene transcript. For example, the antisense oligonucleotide may have a sequence corresponding to a sequence of a differentially expressed gene described herein, *e.g.*, a sequence of one of SEQ ID NOS:1-2164.

Assays for identification of therapeutic targets can be conducted in a variety of ways using methods that are well known to one of ordinary skill in the art. For example, a test cancerous cell that expresses or overexpresses a differentially expressed gene is contacted with an anti-cancer agent, the effect upon a cancerous phenotype and a biological activity of the candidate gene product assessed. The biological activity of the candidate gene product can be assayed be examining, for example, modulation of expression of a gene encoding the candidate gene product (*e.g.*, as detected by, for example, an increase or decrease in transcript levels or polypeptide levels), or modulation of an enzymatic or other activity of the gene product. The cancerous phenotype can be, for example,

cellular proliferation, loss of contact inhibition of growth (*e.g.*, colony formation), tumor growth (*in vitro* or *in vivo*), and the like. Alternatively or in addition, the effect of modulation of a biological activity of the candidate target gene upon cell death/apoptosis or cell cycle regulation can be assessed.

Inhibition or suppression of a cancerous phenotype, or an increase in cell/death apoptosis as a result of modulation of biological activity of a candidate gene product indicates that the candidate gene product is a suitable target for cancer therapy. Assays described infra can be readily adapted in for assays for identification of therapeutic targets. Generally such assays are conducted *in vitro*, but many assays can be adapted for *in vivo* analyses, *e.g.*, in an appropriate, art-accepted animal model of the cancer.

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.

Vaccines and Uses

The differentially expressed nucleic acids and polypeptides produced by the nucleic acids of the invention can also be used to modulate primary immune response to prevent or treat cancer. Every immune response is a complex and intricately regulated sequence of events involving several cell types. It is triggered when an antigen enters the body and encounters a specialized class of cells called

antigen-presenting cells (APCs). These APCs capture a minute amount of the antigen and display it in a form that can be recognized by antigen-specific helper T lymphocytes. The helper (Th) cells become activated and, in turn, promote the activation of other classes of lymphocytes, such as B cells or cytotoxic T cells. The activated lymphocytes then proliferate and carry out their specific effector functions, which in many cases successfully activate or eliminate the antigen. Thus, activating the immune response to a particular antigen associated with a cancer cell can protect the patient from developing cancer or result in lymphocytes eliminating cancer cells expressing the antigen.

Gene products, including polypeptides, mRNA (particularly mRNAs having distinct secondary and/or tertiary structures), cDNA, or complete gene, can be prepared and used in vaccines for the treatment or prevention of hyperproliferative disorders and cancers. The nucleic acids and polypeptides can be utilized to enhance the immune response, prevent tumor progression, prevent hyperproliferative cell growth, and the like. Methods for selecting nucleic acids and polypeptides that are capable of enhancing the immune response are known in the art. Preferably, the gene products for use in a vaccine are gene products which are present on the surface of a cell and are recognizable by lymphocytes and antibodies.

The gene products may be formulated with pharmaceutically acceptable carriers into pharmaceutical compositions by methods known in the art. The composition is useful as a vaccine to prevent or treat cancer. The composition may further comprise at least one co-immunostimulatory molecule, including but not limited to one or more major histocompatibility complex (MHC) molecules, such as a class I or class II molecule, preferably a class I molecule. The composition may further comprise other stimulator molecules including B7.1, B7.2, ICAM-1, ICAM-2, LFA-1, LFA-3, CD72 and the like, immunostimulatory polynucleotides (which comprise an 5'-CG-3' wherein the cytosine is unmethylated), and cytokines which include but are not limited to IL-1 through IL-15, TNF-α, IFN-γ, RANTES, G-CSF, M-CSF, IFN-α, CTAP III, ENA-78, GRO, I-309, PF-4, IP-10, LD-78, MGSA, MIP-1α, MIP-1β, or combination thereof, and the like for immunopotentiation. In one embodiment, the immunopotentiators of particular interest are those which facilitate a Th1 immune response.

The gene products may also be prepared with a carrier that will protect the gene products against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, polylactic acid, and the like. Methods for preparation of such formulations are known in the art.

In the methods of preventing or treating cancer, the gene products may be administered via one of several routes including but not limited to transdermal, transmucosal, intravenous, intramuscular, subcutaneous, intradermal, intraperitoneal, intrathecal, intrapleural, intrauterine, rectal, vaginal, topical, intratumor, and the like. For transmucosal or transdermal administration, penetrants

appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, administration bile salts and fusidic acid derivatives. In addition, detergents may be used to facilitate permeation. Transmucosal administration may be by nasal sprays or suppositories. For oral administration, the gene products are formulated into conventional oral administration form such as capsules, tablets and toxics.

The gene product is administered to a patient in an amount effective to prevent or treat cancer. In general, it is desirable to provide the patient with a dosage of gene product of at least about 1 pg per Kg body weight, preferably at least about 1 ng per Kg body weight, more preferably at least about 1 μg or greater per Kg body weight of the recipient. A range of from about 1 ng per Kg body weight to about 100 mg per Kg body weight is preferred although a lower or higher dose may be administered. The dose is effective to prime, stimulate and/or cause the clonal expansion of antigen-specific T lymphocytes, preferably cytotoxic T lymphocytes, which in turn are capable of preventing or treating cancer in the recipient. The dose is administered at least once and may be provided as a bolus or a continuous administration. Multiple administrations of the dose over a period of several weeks to months may be preferable. Subsequent doses may be administered as indicated.

In another method of treatment, autologous cytotoxic lymphocytes or tumor infiltrating lymphocytes may be obtained from a patient with cancer. The lymphocytes are grown in culture, and antigen-specific lymphocytes are expanded by culturing in the presence of the specific gene products alone or in combination with at least one co-immunostimulatory molecule with cytokines. The antigen-specific lymphocytes are then infused back into the patient in an amount effective to reduce or eliminate the tumors in the patient. Cancer vaccines and their uses are further described in USPN 5,961,978; USPN 5,993,829; USPN 6,132,980; and WO 00/38706.

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.

GRRpz was derived from normal prostate epithelium. The WOca cell line is a Gleason Grade 4 cell line.

The source materials for generating the normalized prostate libraries of libraries 25 and 26 were cryopreserved prostate tumor tissue from a patient with Gleason grade 3+3 adenocarcinoma and matched normal prostate biopsies from a pool of at-risk subjects under medical surveillance. The source materials for generating the normalized prostate libraries of libraries 30 and 31 were cryopreserved prostate tumor tissue from a patient with Gleason grade 4+4 adenocarcinoma and matched normal prostate biopsies from a pool of at-risk subjects under medical surveillance.

The source materials for generating the normalized breast libraries of libraries 27, 28 and 29 were cryopreserved breast tissue from a primary breast tumor (infiltrating ductal carcinoma)(library 28), from a lymph node metastasis (library 29), or matched normal breast biopsies from a pool of at-risk subjects under medical surveillance. In each case, prostate or breast epithelia were harvested directly from frozen sections of tissue by laser capture microdissection (LCM, Arcturus Enginering Inc., Mountain View, CA), carried out according to methods well known in the art (*see*, Simone et al. Am J Pathol. 156(2):445-52 (2000)), to provide substantially homogenous cell samples.

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

Library (lib#)	Description	Number of Clones in Library
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
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 polynucleotides were compared against the public databases to identify any homologous sequences. The sequences of the isolated polynucleotides were first masked to eliminate low complexity sequences using the RepeatMasker masking program, publicly available through a web site supported by the University of Washington (*See also* Smit, A.F.A. and Green, P., unpublished results). 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 homology search of the GenBank database using the TeraBLAST program (TimeLogic, Crystal Bay, Nevada). TeraBLAST is a version of the publicly available BLAST search algorithm developed by the National Center for Biotechnology, modified to operate at an accelerated speed with increased sensitivity on a specialized computer hardware platform. The program was run with the default parameters recommended by TimeLogic to provide the best sensitivity and speed for searching DNA and protein sequences. 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 TeraBLASTX 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 TeraBLAST 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 TeraBLASTN 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 sequences listed as SEQ ID NOS:1-1267 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 6) the name of the library from which the sequence was isolated ("LIBRARY"). 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. Clones which comprise the sequences described herein were deposited as set out in the tables indicated below (see Example entitled "Deposit Information").

Example 2: Contig Assembly

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 was 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 of the above-described polynucleotides were used in the contig assembly. The contig was assembled using the software program Sequencher, version 4.05, according to the manufacturer's instructions. The sequence information obtained in the contig assembly was then used to obtain a consensus sequence derived from the contig using the Sequencher program. The resulting consensus sequence was used to search both the public databases as well as databases internal to the applicants to match the consensus polynucleotide with homology data and/or differential gene expressed data.

The final result provided the sequences listed as SEQ ID NOS: 1268-1385 in the accompanying Sequence Listing and summarized in Table 3 (inserted prior to claims). Table 3 provides a summary of the consensus sequences assembled as described. Specifically, Table 3 provides: 1) the SEQ ID NO ("SEQ ID") assigned to each sequence for use in the present specification; 2) the consensus sequence name ("CONSENSUS SEQ NAME") used as an internal identifier of the sequence; and 3) the sequence name ("POLYNTD SEQ NAME") of a polynucleotide of SEQ ID NOS: 1-1267 used in assembly of the consensus sequence.

Example 3: Additional Gene Characterization

Sequences of the polynucleotides of SEQ ID NOS: 1-1267 were used as a query sequence in a TeraBLASTN search of the DoubleTwist Human Genome Sequence Database (DoubleTwist, Inc., Oakland, CA), which contains all the human genomic sequences that have been assembled into a contiguous model of the human genome. Predicted cDNA and protein sequences were obtained where a polynucleotide of the invention was homologous to a predicted full-length gene sequence. Alternatively, a sequence of a contig or consensus sequence described herein could be used directly as a query sequence in a TeraBLASTN search of the DoubleTwist Human Genome Sequence Database.

The final results of the search provided the predicted cDNA sequences listed as SEQ ID NOS: 1386-1477 in the accompanying Sequence Listing and summarized in Table 4 (inserted prior to claims), and the predicted protein sequences listed as SEQ ID NOS:1478-1568 in the accompanying Sequence Listing and summarized in Table 5 (inserted prior to claims). Specifically, Table 4 provides: 1) the SEQ ID NO ("SEQ ID") assigned to each cDNA sequence for use in the present specification; 2) the cDNA sequence name ("cDNA SEQ NAME") used as an internal identifier of the sequence; 3) the sequence name ("POLYNTD SEQ NAME") of the polynucleotide of SEQ ID NOS: 1-1267 that maps to the cDNA; 4)The gene id number (GENE) of the DoubleTwist predicted gene ; 5) the chromosome ("CHROM") containing the gene corresponding to the cDNA sequence; Table 5

provides: 1) the SEQ ID NO ("SEQ ID") assigned to each protein sequence for use in the present specification; 2) the protein sequence name ("PROTEIN SEQ NAME") used as an internal identifier of the sequence; 3) the sequence name ("POLYNTD SEQ NAME") of the polynucleotide of SEQ ID NOS: 1-1267 that maps to the protein sequence; 4)The gene id number (GENE) of the DoubleTwist predicted gene ; 5) the chromosome ("CHROM") containing the gene corresponding to the cDNA sequence.

A correlation between the polynucleotide used as a query sequence as described above and the corresponding predicted cDNA and protein sequences is contained in Table 6. Specifically Table 6 provides: 1) the SEQ ID NO of the cDNA ("cDNA SEQ ID"); 2) the cDNA sequence name ("cDNA SEQ NAME") used as an internal identifier of the sequence; 3) the SEQ ID NO of the protein ("PROTEIN SEQ ID") encoded by the cDNA sequence 4) the sequence name of the protein ("PROTEIN SEQ NAME") encoded by the cDNA sequence; 5) the SEQ ID NO of the polynucleotide ("POLYNTD SEQ ID") of SEQ ID NOS: 1-1267 that maps to the cDNA and protein; and 6) the sequence name ("POLYNTD SEQ NAME") of the polynucleotide of SEQ ID NOS: 1-1267 that maps to the cDNA and protein.

Through contig and consensus sequence 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).

Example 4:Results of Public Database Search to Identify Function of Gene Products

SEQ ID NOS:1-1477 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 the GenBank (nucleotide sequences) database. Query and individual sequences were aligned using the TeraBLAST program available from TimeLogic, Crystal Bay, Nevada. The sequences were masked to various extents to prevent searching of repetitive sequences or poly-A sequences, using the RepeatMasker masking program for masking low complexity as described above.

Table 7 (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 7 provides: 1) the SEQ ID NO ("SEQ ID") of the query sequence; 2) the sequence name ("SEQ NAME") used as an internal identifier of the query sequence; 3) the accession number ("ACCESSION") of the GenBank database entry of the

homologous sequence; 4) a description of the GenBank sequences ("GENBANK DESCRIPTION"); and 5) the score of the similarity of the polynucleotide sequence and the GenBank sequence ("GENBANK SCORE"). The alignments provided in Table 7 are the best available alignment to a DNA sequence at a time just prior to filing of the present specification. Also incorporated by reference is all publicly available information regarding the sequence listed in Table 6 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 can be used as probes and primers to identify and isolate the full length sequence of the corresponding polynucleotide.

Example 5:Members of Protein Families

SEQ ID NOS:1-1477 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 8 (inserted prior to claims) provides: 1) the SEQ ID NO ("SEQ ID") of the query polynucleotide sequence; 2) the sequence name ("SEQ NAME") used as an internal identifier of the query sequence; 3) the accession number ("PFAM ID") of the the protein family profile hit; 4) a brief description of the profile hit ("PFAM DESCRIPTION"); 5) the score ("SCORE") of the profile hit; 6) the starting nucleotide of the profile hit ("START"); and 7) the ending nucleotide of the profile hit ("END").

In addition, SEQ ID NOS:1478-1568 were also used to conduct a profile search as described above. Several of the polypeptides of the invention were found to have 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 9 (inserted prior to claims) provides: 1) the SEQ ID NO ("SEQ ID") of the query protein sequence; 2) the sequence name ("PROTEIN SEQ NAME") used as an internal identifier of the query sequence; 3) the accession number ("PFAM ID") of the the protein family profile hit; 4) a brief description of the profile hit ("PFAM DESCRIPTION"); 5) the score ("SCORE") of the profile hit; 6) the starting residue of the profile hit ("START"); and 7) the ending residue of the profile hit ("END").

Some SEQ ID NOS 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 Tables 8 and 9 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.

Ank Repeats (ANK; Pfam Accession No. PF0023). SEQ ID NOS:482, 818, 914, 1216, 1484, 1537, and 1564 represent 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).

Epidermal Growth Factor (EGF; Pfam Accession No. PF00008). SEQ ID NO:967 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. These 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.

Zinc Finger, C2H2 Type (Zincfing_C2H2; Pfam Accession No. PF00096). SEQ ID NO:521 corresponds 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.

PDZ Domain (PDZ; Pfam Accession No. PF00595.) SEQ ID NOS:527, 1523, and 1551 correspond to genes comprising a PDZ domain (also known as DHR or GLGF domain). PDZ domains comprise 80-100 residue repeats, several of which interact with the C-terminal tetrapeptide motifs X-Ser/Thr-X-Val-COO- of ion channels and/or receptors, and are found in mammalian proteins as well as in bacteria, yeast, and plants (Pontig *et al. Protein Sci* (1997) *6*(2):464-8). Proteins comprising one or more PDZ domains are found in diverse membrane-associated proteins, including members of the MAGUK family of guanylate kinase homologues, several protein phosphatases and kinases, neuronal nitric oxide synthase, and several dystrophin-associated proteins, collectively known as syntrophins (Ponting *et al. Bioessays* (1997) *19*(6):469-79). Many PDZ domain-containing proteins are localised to highly specialised submembranous sites, suggesting their participation in cellular junction formation, receptor or channel clustering, and intracellular signalling events. For example, PDZ domains of several MAGUKs interact with the C-terminal polypeptides of a subset of NMDA receptor subunits and/or with Shaker-type K+ channels. Other PDZ domains have been shown to bind similar ligands of other transmembrane receptors. In cell junction-associated proteins,the PDZ mediates the clustering of membrane ion channels by binding to their C-terminus. The X-ray crystallographic structure of some proteins comrpising PDZ domains have been solved (see, *e.g.*, Doyle *et al. Cell* (1996) *85*(7):1067-76).

Zinc knuckle, CCHC type (Zf-CCHC; Pfam Accession No. PF00098). SEQ ID NOS:543 and 1069 correspond to a gene encoding a member of the family of CCHC zinc fingers. Because the prototype CCHC type zinc finger structure is from an HIV protein, this domain is also referred to as a retrovrial-type zinc finger domain. The family also contains proteins involved in eukaryotic gene regulation, such as C. elegans GLH-1. The structure is an 18-residue zinc finger; no examples of indels in the alignment. The motif that defines a CCHC type zinc finger domain is: C-X2-C-X4-H-X4-C (Summers J Cell Biochem 1991 Jan;45(1):41-8). The domain is found in, for example, HIV-1 nucleocapsid protein, Moloney murine leukemia virus nucleocapsid protine NCp10 (De Rocquigny *et al. Nucleic Acids Res.* (1993) *21*:823-9), and myelin transcription factor 1 (Myt1) (Kim *et al. J. Neurosci. Res.* (1997) *50*:272-90).

RNA Recognition Motif (rrm; Pfam Accession No. PF00076). SEQ ID NOS:514 and 910 correspond to sequence encoding an RNA recognition motif, also known as an RRM, RBD, or RNP domain. This domain, which is about 90 amino acids long, is contained in eukaryotic proteins that bind single-stranded RNA (Bandziulis et al. *Genes Dev.* (1989) *3*:431-437; Dreyfuss et al. *Trends Biochem. Sci.* (1988) *13*:86-91). Two regions within the RNA-binding domain are highly conserved: the first is a hydrophobic segment of six residues (which is called the RNP-2 motif), the second is an

octapeptide motif (which is called RNP-1 or RNP-CS). The consensus pattern is: [RK]-G-{EDRKHPCG}-[AGSCI]-[FY]-[LIVA]-x-[FYLM].

Metallothioneins (metalthio; Pfam Accession No. PF00131). SEQ ID NO:335 corresponds to a polynucleotide encoding a member of the metallothionein (MT) protein family (Hamer *Annu. Rev. Biochem.* (1986) *55*:913-951; and Kagi *et al. Biochemistry* (1988) *27*:8509-8515), small proteins which bind heavy metals such as zinc, copper, cadmium, nickel, *etc.*, through clusters of thiolate bonds. MT's occur throughout the animal kingdom and are also found in higher plants, fungi and some prokaryotes. On the basis of structural relationships MT's have been subdivided into three classes. Class I includes mammalian MT's as well as MT's from crustacean and molluscs, but with clearly related primary structure. Class II groups together MT's from various species such as sea urchins, fungi, insects and cyanobacteria which display none or only very distant correspondence to class I MT's. Class III MT's are atypical polypeptides containing gamma-glutamylcysteinyl units. The consensus pattern for this protein family is: C-x-C-[GSTAP]-x(2)-C-x-C-x(2)-C-x-C-x(2)-C-x-K.

Trypsin (trypsin; Pfam Accession No. PF00089). SEQ ID NOS:422 and 1558 correspond to a novel serine protease of the trypsin family. The catalytic activity of the serine proteases from the trypsin family is provided by a charge relay system involving an aspartic acid residue hydrogen-bonded to a histidine, which itself is hydrogen-bonded to a serine. The sequences in the vicinity of the active site serine and histidine residues are well conserved in this family of proteases (Brenner S., *Nature* (1988) *334*:528). The consensus patterns for this trypsin protein family are: 1) [LIVM]-[ST]-A-[STAG]-H-C, where H is the active site residue; and 2) [DNSTAGC]-[GSTAPIMVQH]-x(2)-G-[DE]-S-G-[GS]-[SAPHV]- [LIVMFYWH]-[LIVMFYSTANQH], where S is the active site residue. All sequences known to belong to this family are detected by the above consensus sequences, except for 18 different proteases which have lost the first conserved glycine. If a protein includes both the serine and the histidine active site signatures, the probability of it being a trypsin family serine protease is 100%.

HSP70 protein (HSP70; Pfam Accession No. PF00012) SEQ ID NOS:952 and 1482 correspond to members of the family of ATP-binding heat shock proteins having an average molecular weight of 70kD (Pelham, *Cell* (1986) 46:959-961; Pelham, *Nature* (1988) 332:776-77; Craig, *BioEssays* (1989) 11:48-52). In most species, there are many proteins that belong to the hsp70 family, some of which are expressed under unstressed conditions. Hsp70 proteins can be found in different cellular compartments, including nuclear, cytosolic, mitochondrial, endoplasmic reticulum, etc. A variety of functions have been postulated for hsp70 proteins. Some play an important role in the transport of proteins across membranes (Deshaies *et al., Trends Biochem. Sci.* (1988) 13:384-388), while others are involved in protein folding and in the assembly/disassembly of protein complexes (Craig and Gross, *Trends Biochem. Sci.* (1991) 16:135-140).

There are three signature patterns for the hsp70 family of proteins. The first is centered on a conserved pentapeptide found in the N-terminal section of these proteins and the two others on conserved regions located in the central part of the sequence. The consensus patterns are: 1) [IV]-D-L-G-T-[ST]-x-[SC]; 2) [LIVMF]-[LIVMFY]-[DN]-[LIVMFS]-G-[GSH]-[GS]-[AST]-x(3)- [ST]-[LIVM]-[LIVMFC]; and 3) [LIVMY]-x-[LIVMF]-x-G-G-x-[ST]-x-[LIVM]-P-x-[LIVM]-x-[DEQKRSTA].

WD Domain (WD40), G-Beta Repeats (WD_domain; Pfam Accession No. PF00400). SEQ ID NOS: 1510 and 1536 represent members 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].

Protein Kinase (protkinase; Pfam Accession No. PF00069). SEQ ID NO: 1540 represents a protein kinase. Protein kinases catalyze phosphorylation of proteins in a variety of pathways, and are implicated in cancer. Eukaryotic protein kinases (Hanks S.K., *et al.*, *FASEB J.* (1995) *9*:576; Hunter T., *Meth. Enzymol.* (1991) *200*:3; Hanks S.K., *et al.*, *Meth. Enzymol.* (1991) *200*:38; Hanks S.K., *Curr. Opin. Struct. Biol.* (1991) *1*:369; Hanks S.K., *et al.*, *Science* (1988) *241*:42) are enzymes that belong to a very extensive family of proteins which 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, which is 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, which is located in the central part of the catalytic domain, contains a conserved aspartic acid residue which is important for the catalytic activity of the enzyme (Knighton D.R., *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 S.K., *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.

If a protein analyzed includes the two of the above protein kinase signatures, the probability of it being a protein kinase is close to 100%. Eukaryotic-type protein kinases have also been found in prokaryotes such as Myxococcus xanthus (Munoz-Dorado J., *et al.*, *Cell* (1991) *67*:995) and Yersinia pseudotuberculosis. The patterns shown above has been updated since their publication in (Bairoch A., *et al.*, *Nature* (1988) *331*:22).

C2 domain (C2; Pfam Accession No. PF00168). SEQ ID NO: 1550 corresponds to a C2 domain, which is involved in calcium-dependent phospholipid binding (Davletov *J. Biol. Chem.* (1993) *268*:26386-26390) or, in proteins that do not bind calcium, the domain may facilitate binding to inositol-1,3,4,5-tetraphosphate (Fukuda et al. *J. Biol. Chem.* (1994) *269*:29206-29211; Sutton et al. *Cell* (1995) *80*:929-938). The consensus sequence is: [ACG]-x(2)-L-x(2,3)-D-x(1,2)-[NGSTLIF]-[GTMR]-x-[STAP]-D- [PA]-[FY].

Myosin head (motor domain) (myosin_head; Pfam Accession No. PF00063). SEQ ID NOS:189, 1548, and 1557 correspond to a myosin head domain, a glycine-rich region that typically forms a flexible loop between a beta-strand and an alpha-helix. This loop interacts with one of the phosphate groups of ATP or GTP in binding of a protein to the nucleotide. The myosin head sequence motif is generally referred to as the "A" consensus sequence (Walker *et al.*, *EMBO J.* (1982) 1:945-951) or the "P-loop" (Saraste *et al.*, *Trends Biochem. Sci.* (1990) 15:430-434). The consensus sequence is: [AG]-x(4)-G-K-[ST].

Sugar (and other) transporter (sugar_tr; Pfam Accession No. PF00083). SEQ ID NOS:334, 1244, and 1512 represent members of the sugar (and other) transporter family. In mammalian cells the uptake of glucose is mediated by a family of closely related transport proteins which are called the glucose transporters (Silverman, *Annu. Rev. Biochem.* (1991) 60:757-794; Gould and Bell, *Trends Biochem. Sci.* (1990) 15:18-23; Baldwin, *Biochim. Biophys. Acta* (1993) 1154:17-49). At least seven of these transporters are currently known to exist and in Humans are encoded by the GLUT1 to GLUT7 genes. These integral membrane proteins are predicted to comprise twelve membrane spanning domains and show sequence similarities with a number of other sugar or metabolite transport proteins (Maiden *et al.*, *Nature* (1987) 325:641-643; Henderson, *Curr. Opin. Struct. Biol.* (1991) 1:590-601).

Two patterns have been developed to detect this family of proteins. The first pattern is based on the G-R-[KR] motif; but because this motif is too short to be specific to this family of proteins, a second pattern has been derived from a larger region centered on the second copy of this motif. The second pattern is based on a number of conserved residues which are located at the end of the fourth transmembrane segment and in the short loop region between the fourth and fifth segments. The two consensus sequences are: 1) [LIVMSTAG]-[LIVMFSAG]-x(2)-[LIVMSA]-[DE]-x-[LIVMFYWA]-

G- R-[RK]-x(4,6)-[GSTA]; and 2) [LIVMF]-x-G-[LIVMFA]-x(2)-G-x(8)-[LIFY]-x(2)-[EQ]-x(6)-[RK].

HSP 90 protein (Pfam Accession No. PF00183). SEQ ID NO:1538 represents a polypeptide having a consensus sequence of a Hsp90 protein family member. Hsp90 proteins are proteins of an average molecular weight of approximately 90 kDa that respond to heat shock or other environmental stress by the induction of the synthesis of proteins collectively known as heat-shock proteins (hsp) (Lindquist et al. Annu. Rev. Genet. 22:631-677 (1988). Proteins known to belong to this family include vertebrate hsp 90-alpha (hsp 86) and hsp 90-beta (hsp 84); Drosophila hsp 82 (hsp 83); and the endoplasmic reticulum protein 'endoplasmin' (also known as Erp99 in mouse, GRP94 in hamster, and hsp 108 in chicken). Hsp90 proteins have been found associated with steroid hormone receptors, with tyrosine kinase oncogene products of several retroviruses, with eIF2alpha kinase, and with actin and tubulin. Without being held to theory, Hsp90 proteins are probable chaperonins that possess ATPase activity (Nadeau et al. J. Biol. Chem. 268:1479-1487 (1993); Jakob et al. Trends Biochem Sci 19:205-211 (1994). Hsp90 family proteins have the following signature pattern, which represents a highly conserved region found in the N-terminal part of these proteins: Y-x-[NQH]-K-[DE]-[IVA]-F-[LM]-R-[ED]

KOW motif (Ribosomal protein L24 signature; Pfam Accession No. PF00467). SEQ ID NO:1553 represents a polypeptide having a KOW motif such as that found in the ribosomal protein L24, one of the proteins from the large ribosomal subunit. L24 belongs to a family of ribosomal proteins. In their mature form, these proteins have 103 to 150 amino-acid residues. As a signature pattern, The consensus sequence is based on a conserved stretch of 20 residues in the N-terminal section: [GDEN]-D-x-[IV]-x-[IV]-[LIVMA]-x-G-x(2)-[KRA]-[GNQ]- x(2,3)-[GA]-x-[IV].

TPR Domain (Pfam Accession No. PF00515). SEQ ID NO:1532 represents a polypeptide having at least one or more tetratricopeptide repeat (TPR) domains. The TPR is a degenerate 34 amino acid sequence identified in a wide variety of proteins, present in tandem arrays of 3-16 motifs, which form scaffolds to mediate protein-protein interactions and often the assembly of multiprotein complexes. TPR-containing proteins include the anaphase promoting complex (APC) subunits cdc16, cdc23 and cdc27, the NADPH oxidase subunit p67 phox, hsp90-binding immunophilins, transcription factors, the PKR protein kinase inhibitor, and peroxisomal and mitochondrial import proteins (see, e.g., Das et al. EMBO J;17(5):1192-9 (1998); and Lamb Trends Biochem Sci 20:257-259 (1995).

tRNA synthetase class II core domain (G, H, P, S and T) (Pfam Accession No. PF00587). SEQ ID NO:1481 represents a polypeptide having a tRNA synthetase class II core domain. Aminoacyl-tRNA synthetases (EC 6.1.1.-) (Schimmel Annu. Rev. Biochem. 56:125-158(1987)) are a group of enzymes which activate amino acids and transfer them to specific tRNA molecules as the first step in protein biosynthesis. In prokaryotic organisms there are at least twenty different types of aminoacyl-tRNA synthetases, one for each different amino acid. In eukaryotes there are generally two

aminoacyl-tRNA synthetases for each different amino acid: one cytosolic form and a mitochondrial form. While all these enzymes have a common function, they are widely diverse in terms of subunit size and of quaternary structure.

The synthetases specific for alanine, asparagine, aspartic acid, glycine, histidine, lysine, phenylalanine, proline, serine, and threonine are referred to as class-II synthetases and probably have a common folding pattern in their catalytic domain for the binding of ATP and amino acid which is different to the Rossmann fold observed for the class I synthetases. Class-II tRNA synthetases do not share a high degree of similarity, however at least three conserved regions are present (Delarue et al. BioEssays 15:675-687(1993); Cusack et al. Nucleic Acids Res. 19:3489-3498(1991); Leveque et al. Nucleic Acids Res. 18:305-312(1990)]. The consensus sequences are derived from these regions: [FYH]-R-x-[DE]-x(4,12)-[RH]-x(3)-F-x(3)-[DE] (found in the majority of class-II tRNA synthetases with the exception of those specific for alanine, glycine as well as bacterial histidine); and [GSTALVF]-{DENQHRKP}-[GSTA]-[LIVMF]-[DE]-R-[LIVMF]-x- [LIVMSTAG]-[LIVMFY] (found in the majority of class-II tRNA synthetases with the exception of those specific for serine and proline).

IQ calmodulin-binding motif (Pfam Accession No. PF00612). SEQ ID NOS:189 and 1548 represent polypeptides having an IQ calmodulin-binding motif. The IQ motif is an extremely basic unit of about 23 amino acids, whose conserved core usually fits the consensus A-x(3)-I-Q-x(2)-F-R-x(4)-K-K. The IQ motif, which can be present in one or more copies, serves as a binding site for different EF-hand proteins including the essential and regulatory myosin light chains, calmodulin (CaM), and CaM-like proteins (see, e.g., Cheney et al. Curr. Opin. Cell Biol. 4:27-35(1992); and Rhoads et al. FASEB J. 11:331-340(1997)). Many IQ motis are protein kinase C (PKC) phosphorylation sites (Baudier et al. J. Biol. Chem. 266:229-237(1991); and Chen et al. Biochemistry 32:1032-1039(1993)). Resolution of the 3D structure of scallop myosin has shown that the IQ motif forms a basic amphipathic helix (Xie et al. Nature 368:306-312(1994)). Exemplary proteins containing an IQ motif include neuromodulin (GAP-43), neurogranin (NG/p17), sperm surface protein Sp17, and Ras GTPase-activating-like protein IQGAP1. IQGAP1 contains 4 IQ motifs.

Phophotyrosine interaction domain (PTB/PID) (Pfam Accession No. PF00640). SEQ ID NO:1523 represents a polypeptide having a phosphotyrosine interaction domain (PID or PI domain). PID is the second phosphotyrosine-binding domain found in the transforming protein Shc (Kavanaugh et al. Science 266:1862-1865(1994); Blaikie et al. J. Biol. Chem. 269:32031-32034(1994); and Bork et al. Cell 80:693-694(1995)). Shc couples activated growth factor receptors to a signaling pathway that regulates the proliferation of mammalian cells and it might participate in the transforming activity of oncogenic tyrosine kinases. The PID of Shc specifically binds to the Asn-Pro-Xaa-Tyr(P) motif found in many tyrosine-phosphorylated proteins including growth factor receptors. PID has also been found in, for example, human Shc-related protein Sck, mammalian protein X11 which is

expressed prominently in the nervous system, rat FE65, a transcription-factor activator expressed preferentially in liver, mammalian regulator of G-protein signalling 12 (RGS12), and N-terminal insulinase-type domain. PID has an average length of about 160 amino acids. It is probably a globular domain with an antiparallel beta sheet. The function of this domain might be phosphotyrosine-binding. It is at least expected to be involved in regulatory protein/protein-binding (Bork et al. Cell 80:693-694(1995)).

Syntaxin (Pfam Accession No. PF00804). SEQ ID NOS:1039 and 1496 represent polypeptides having sequence similarity to syntaxin protein family. Members of the syntaxin family of proteins include, for example, epimorphin (or syntaxin 2), a mammalian mesenchymal protein which plays an essential role in epithelial morphogenesis; syntaxin 1A, syntaxin 1B, and syntaxin 4, which are synaptic proteins involved in docking of synaptic vesicles at presynaptic active zones; syntaxin 3; syntaxin 5, which mediates endoplasmic reticulum to golgi transport; and syntaxin 6, which is involved in intracellular vesicle trafficking (Bennett et al. Cell 74:863-873(1993); Spring et al. Trends Biochem. Sci. 18:124-125(1993); Pelham et al. Cell 73:425-426(1993)). The syntaxin family of proteins each range in size from 30 Kd to 40 Kd; have a C-terminal extremity which is highly hydrophobic and is involved in anchoring the protein to the membrane; a central, well conserved region, which may be present in a coiled-coil conformation. The pattern specific for this family is based on the most conserved region of the coiled coil domain: [RQ]-x(3)-[LIVMA]-x(2)-[LIVM]-[ESH]-x(2)-[LIVMT]-x-[DEVM]- [LIVM]-x(2)-[LIVM]-[FS]-x(2)-[LIVM]-x(3)-[LIVT]-x(2)-Q- [GADEQ]-x(2)-[LIVM]-[DNQT]-x-[LIVMF]-[DESV]-x(2)-[LIVM].

Ribosomal L10 (Pfam Accession No. PF00826). SEQ ID NOS:759, 1207, and 1566 represents a polypeptide having sequence similarity to the ribosomal L10 protein family (see, e.g., Chan et al. Biochem. Biophys. Res. Commun. 225:952-956(1996)). The members of this family generally have 174 to 232 amino-acid residues and contain the following signature pattern (based on a conserved region located in the central section of the proten): A-D-R-x(3)-G-M-R-x-[SAP]-[FYW]-G-[KRVT]-[PA]-x-[GS]-x(2)- A-[KRLV]-[LIV]

GTP1/OBG Family (Pfam Accession No. PF01018). SEQ ID NO:126, 721, and 1518 represent polypeptides that have similarities to the members of the GTP1/OBG family, a widespread family of GTP-binding proteins (Sazuka et al. Biochem. Biophys. Res. Commun. 189:363-370(1992); Hudson et al. Gene 125:191-193(1993)). This family includes, for example, protein DRG (found in mouse, human, and xenopus), fission yeast protein gtp1, and Bacillus subtilis protein obg (which binds GTP). Family members are generally about 40 to 48 Kd and contain the five small sequence elements characteristic of GTP-binding proteins (Bourne et al. Nature 349:117-127(1991)). The signature pattern corresponds to the ATP/GTP B motif (also called G-3 in GTP-binding proteins): D-[LIVM]-P-G-[LIVM](2)-[DEY]-[GN]-A-x(2)-G-x-G

KRAB box (Pfam Accession No. PF01352). SEQ ID NOS:1556 and 349 represent polypeptides having a Krueppel-associated box (KRAB). A KRAB box is a domain of around 75 amino acids that is found in the N-terminal part of about one third of eukaryotic Krueppel-type C2H2 zinc finger proteins (ZFPs). It is enriched in charged amino acids and can be divided into subregions A and B, which are predicted to fold into two amphipathic alpha-helices. The KRAB A and B boxes can be separated by variable spacer segments and many KRAB proteins contain only the A box.

The KRAB domain functions as a transcriptional repressor when tethered to the template DNA by a DNA-binding domain. A sequence of 45 amino acids in the KRAB A subdomain has been shown to be necessary and sufficient for transcriptional repression. The B box does not repress by itself but does potentiate the repression exerted by the KRAB A subdomain. Gene silencing requires the binding of the KRAB domain to the RING-B box-coiled coil (RBCC) domain of the KAP-1/TIF1-beta corepressor. As KAP-1 binds to the heterochromatin proteins HP1, it has been proposed that the KRAB-ZFP-bound target gene could be silenced following recruitment to heterochromatin.

KRAB-ZFPs constitute one of the single largest class of transcription factors within the human genome, and appear to play important roles during cell differentiation and development. The KRAB domain is generally encoded by two exons. The regions coded by the two exons are known as KRAB-A and KRAB-B.

Small ribonucleoprotein (Sm protein; Pfam Accession No. PF01423). SEQ ID NO:1495 represents a polypeptide having sequence similarity to small ribonucleoprotein (Sm protein). The U1, U2, U4/U6, and U5 small nuclear ribonucleoprotein particles (snRNPs) involved in pre-mRNA splicing contain seven Sm proteins (B/B', D1, D2, D3, E, F and G) in common, which assemble around the Sm site present in four of the major spliceosomal small nuclear RNAs (Hermann et al. EMBO J. 14: 2076-2088(1995)). The Sm proteins are essential for pre-mRNA splicing and are implicated in the formation of stable, biologically active snRNP structures.

Cation efflux family (Pfam Accession No. PF01545). SEQ ID NO:563, 766, and 1545 represent polypeptides having sequence similarity to members of the cation efflux family. Members of this family are integral membrane proteins which increase tolerance to divalent metal ions such as cadmium, zinc, and cobalt. These proteins are efflux pumps that remove these ions from cells (Xiong et al. J. Bacteriol. 180: 4024-4029(1998); Kunito et al. Biosci. Biotechnol. Biochem. 60: 699-704(1996)).

FG-GAP repeat (Pfam Accession No. PF01839). SEQ ID NO:1486 represents a polypeptide having an FG-GAP repeat. This family contains the extracellular repeat that is found in up to seven copies in alpha integrins. This repeat has been predicted to fold into a beta propeller structure (Springer et al. Proc Natl Acad Sci U S A 1997;94:65-72). The repeat is called the FG-GAP repeat after two conserved motifs in the repeat (Spring, ibid). The FG-GAP repeats are found in the N terminus of integrin alpha chains, a region that has been shown to be important for ligand binding

(Loftus et al. J Biol Chem 1994;269:25235-25238). A putative Ca2+ binding motif is found in some of the repeats.

Dilute (DIL) domain (Pfam Accession No. PF01843). SEQ ID NO:1548 represents a polypeptide having a DIL domain. Dilute encodes a type of myosin heavy chain, with a tail, or C-terminal, region that has elements of both type II (alpha-helical coiled-coil) and type I (non-coiled-coil) myosin heavy chains. The DIL non alpha-helical domain is found in dilute myosin heavy chain proteins and other myosins. In mouse the dilute protein plays a role in the elaboration, maintenance, or function of cellular processes of melanocytes and neurons (Mercer et al. Nature 349(6311): 709-713(1991)). The DIL-containing MYO2 protein of Saccharomyces cerevisiae is implicated in vectorial vesicle transport and is homologous to the dilute protein over practically its entire length (Johnston et al. J. Cell Biol. 113(3): 539-551(1991).

Ubiquinol-cytochrome C reductase complex 14kD subunit (Pfam Accession No. PF022771). SEQ ID NOS:419 and 1519 represent a polypeptide having sequence similarity to Ubiquinol-cytochrome C reductase complex 14kD subunit. The cytochrome bd type terminal oxidases catalyse quinol dependent, Na+ independent oxygen uptake. Members of this family are integral membrane proteins and contain a protoheame IX center B558. Cytochrome bd plays a role in microaerobic nitrogen fixation in the enteric bacterium Klebsiella pneumoniae, where it is expressed under all conditions that permit diazotrophy . The 14kD (or VI) subunit of the complex is not directly involved in electron transfer, but has a role in assembly of the complex (Braun et al Plant Physiol. 107(4): 1217-1223(1995)).

Cytidylytransferase (Pfam Accession No. PF02348). SEQ ID NOS:109, 394, 569, 1128, and 1535 represent polypeptides having sequence similarity to the cytidylytransferase family of proteins, which are involved in lipopolysaccharide biosynthesis. This family consists of two main cytidylyltransferase activities: 1) 3-deoxy-manno-octulosonate cytidylyltransferase (Strohmaier et al. J Bacteriol 1995;177:4488-4500.) EC:2.7.7.38 catalysing the reaction:- CTP + 3-deoxy-D-manno-octulosonate <=> diphosphate + CMP-3-deoxy-D-manno-octulosonate; and 2) acylneuraminate cytidylyltransferase EC:2.7.7.43 (Munster et al. Proc Natl Acad Sci U S A 1998;95:9140-9145; Tullius et al. J Biol Chem 1996;271:15373-15380) catalysing the reaction:- CTP + N-acylneuraminate <=> diphosphate + CMP-N-acylneuraminate N-acetylneuraminic acid cytidylyltransferase (EC 2.7.7.43) (CMP-NeuAc synthetase) catalyzes the reaction of CTP and NeuAc to form CMP-NeuAc, which is the nucleotide sugar donor used by sialyltransferases. The outer membrane lipooligosaccharides of some microorganisms contain terminal sialic acid attached to N-acetyllactosamine; thus this modification may be important in pathogenesis.

Laminin G domain (Pfam Accession No. PF00054). SEQ ID NO:1521 represents a polypeptide having a laminin G domain, a homology domain first described in the long arm globular domain of laminin (Vuolteenaho et al. J. Biol. Chem. 265: 15611-15616(1990)). Similar sequences

also occurs in a large number of extracellular proteins. Laminin binds to heparin (Yurchenco et al. J. Biol. Chem. 268(11): 8356-8365(1993); Sung et al. Eur. J. Biochem. 250(1): 138-143(1997)). The structure of the laminin-G domain has been predicted to resemble that of pentraxin (Beckmann et al. J. Mol. Biol. 275: 725-730(1998)). Exemplary proteins having laminin-G domains include laminin, merosin, agrin, neurexins, vitamin K dependent protein S, and sex steroid binding protein SBP/SHBG.

4Fe-4S iron sulfur cluster binding proteins, NifH/frxC family (Pfam Accession No. PF00142). SEQ ID NO:1100 represents a polypeptide having sequence similarity to the 4Fe-4S iron sulfur cluster binding proteins, NifH/frxC family. Nitrogen fixing bacteria possess a nitrogenase enzyme complex (EC 1.18.6.1) that comprises 2 components, which catalyse the reduction of molecular nitrogen to ammonia: component I (nitrogenase MoFe protein or dinitrogenase) contains 2 molecules each of 2 non-identical subunits; component II (nitrogenase Fe protein or dinitrogenase reductase) is a homodimer, the monomer being coded for by the nifH gene. Component II has 2 ATP-binding domains and one 4Fe-4S cluster per homodimer: it supplies energy by ATP hydrolysis, and transfers electrons from reduced ferredoxin or flavodoxin to component I for the reduction of molecular nitrogen to ammonia. There are a number of conserved regions in the sequence of these proteins: in the N-terminal section there is an ATP-binding site motif 'A' (P-loop) and in the central section there are two conserved cysteines which have been shown, in nifH, to be the ligands of the 4Fe-4S cluster.

Cyclophilin-type peptidyl-prolyl cis-trans isomerase (Pfam Accession No. PF00160). SEQ ID NOS:134, 259, 363, 1101, and 1267 represent polypeptides having sqeuence simlarity to the cyclophilin-type peptidyl-prolyl cis-trans isomerase protein family. Cyclophilin (Stamnes et al. Trends Cell Biol. 2: 272-276(1992)) is the major high-affinity binding protein in vertebrates for the immunosuppressive drug cyclosporin A (CSA), but is also found in other organisms. It exhibits a peptidyl-prolyl cis-trans isomerase activity (EC 5.2.1.8) (PPIase or rotamase). PPIase is an enzyme that accelerates protein folding by catalyzing the cis-trans isomerization of proline imidic peptide bonds in oligopeptides (Fischer et al. Biochemistry 29: 2205-2212(1990)). It is probable that CSA mediates some of its effects via an inhibitory action on PPIase. Cyclophilin A is a cytosolic and highly abundant protein. The protein belongs to a family of isozymes, including cyclophilins B and C, and natural killer cell cyclophilin-related protein (Trandinh et al. FASEB J. 6: 3410-3420(1992); Galat Eur. J. Biochem. 216: 689-707(1993); Hacker et al. Mol. Microbiol. 10: 445-456(1993)). Major isoforms have been found throughout the cell, including the ER, and some are even secreted. The sequences of the different forms of cyclophilin-type PPIases are well conserved.

Ubiquitin-conjugating enyme (Pfam Accession No. PF00179). SEQ ID NO:7 represents a polypeptide having sequence similarity to ubiquitin-conjugating enyme. Ubiquitin-conjugating enzymes (EC 6.3.2.19) (UBC or E2 enzymes) (Jentsch et al. Biochim. Biophys. Acta 1089: 127-

139(1991); Jentsch et al. Trends Biochem. Sci. 15: 195-198(1990); Hershko et al. Trends Biochem. Sci. 16: 265-268(1991)). catalyze the covalent attachment of ubiquitin to target proteins. An activated ubiquitin moiety is transferred from an ubiquitin-activating enzyme (E1) to E2 which later ligates ubiquitin directly to substrate proteins with or without the assistance of 'N-end' recognizing proteins (E3). A cysteine residue is required for ubiquitin-thiolester formation. There is a single conserved cysteine in UBC's and the region around that residue is conserved in the sequence of known UBC isozymes. There are, however, exceptions, the breast cancer gene product TSG101 is one of several UBC homologues that lacks this active site cysteine (Ponting et al. J. Mol. Med. 75: 467-469(1997); Koonin et al. Nat. Genet. 16: 330-331(1997)). In most species there are many forms of UBC which are implicated in diverse cellular functions.

NADH-ubiquinone/plastoquinone oxidoreductase chain 6 (Pfam Accession No. PF00499). SEQ ID NOS: 507 and 1002 represent polypeptides having sequence similarity with NADH-ubiquinone/plastoquinone oxidoreductase chain 6 protein family. In bacteria, the proton-translocating NADH-quinone oxidoreductase (NDH-1) is composed of 14 different subunits. The chain belonging to this family is a subunit that constitutes the membrane sector of the complex. It reduces ubiquinone to ubiquinol utilising NADH. In plants, chloroplastic NADH-plastoquinone oxidoreductase reduces plastoquinone to plastoquinol. Mitochondrial NADH-ubiquinone oxidoreductase from a variety of sources reduces ubiquinone to ubiquinol.

AP endonucleases family 1 (Pfam Accession No. PF00895). SEQ ID NO:10 and 1107 represent polypeptides having sequence similarity to members of the AP endonucleases family 1. DNA damaging agents such as the antitumor drugs bleomycin and neocarzinostatin or those that generate oxygen radicals produce a variety of lesions in DNA. Amongst these is base-loss which forms apurinic/apyrimidinic (AP) sites or strand breaks with atypical 3'termini. DNA repair at the AP sites is initiated by specific endonuclease cleavage of the phosphodiester backbone. Such endonucleases are also generally capable of removing blocking groups from the 3'terminus of DNA strand breaks.

AP endonucleases can be classified into two families on the basis of sequence similarity. This family contains members of AP endonuclease family 1. Except for Rrp1 and arp, these enzymes are proteins of about 300 amino-acid residues. Rrp1 and arp both contain additional and unrelated sequences in their N-terminal section (about 400 residues for Rrp1 and 270 for arp). The proteins contain glutamate which has been shown (Mol et al. Nature 374: 381-386(1995), in the Escherichia coli enzyme to bind a divalent metal ion such as magnesium or manganese.

Late Expression Factor 2 (lef-2; Pfam Accession No. PF03041). SEQ ID NO: 405 represents a polynucleotide encoding a member of the late expression factor 2 family of polypeptides. The lef-2 gene from baculovirus is required for expression of late genes and has been shown to be specifically required for expression from the vp39 and polh promoters (Passarelli and Miller, *J. Virol.* (1993)

Apr;67(4):2149-58). Lef-2 has been found in both Lymantria dispar multicapsid nuclear polyhedrosis virus (LdMNPV) and Orgyia pseudotsugata multicapsid polyhedrosis virus (OpMNPV).

Papillomavirus E5 (Papilloma_E5; Pfam Accession No. PF03025). SEQ ID NO: 1051 corresponds to a polynucleotide encoding a member of the papillomavirus E5 family of polypeptides. The E5 protein from papillomaviruses is about 80 amino acids long and contains three regions that have been predicted to be transmembrane alpha helices.

Male sterility protein (Sterile; Pfam Accession No. PF03015). SEQ ID NO: 391 encodes a member of the male sterility protein family. This family represents the C-terminal region of the male sterility protein in a number of organisms. One member of this family, the *Arabidopsis thaliana* male sterility 2 (MS2) protein, is involved in male gametogenesis. The MS2 protein shows sequence similarity to reductases in elongation/condensation complexes, such as jojoba protein (also a member of this group), an acyl CoA reductase that converts wax fatty acids to fatty alcohols. The MS2 protein may be a fatty acyl reductase involved in the formation of pollen wall substances (Aarts *et al., Plant. J.* (1997) Sep;12(3):615-23).

Cytochrome C oxidase subunit II, transmembrane domain (COX2_TM; Pfam Accession No. PF02790). SEQ ID NO: 1183 corresponds to a gene comprising a cytochrome C oxidase subunit II transmembrane domain (COX2_TM). Cytochrome C oxidase is an oligomeric enzymatic complex which is a component of the respiratory chain and is involved in the transfer of electrons from cytochrome C to oxygen (Capaldi *et al., Biochim. Biophys.* Acta (1983) 726:135-148; Garcia-Horsman *et al., J. Bacteriol.* (1994) 176:5587-5600). In eukaryotes this enzyme complex is located in the mitochondrial inner membrane; in aerobic prokaryotes it is found in the plasma membrane. The enzyme complex consists of 3-4 subunits (prokaryotes) to up to 13 polypeptides (mammals).

Subunit 2 of cytochrome C oxidase (COX2_TM) transfers the electrons from cytochrome C to the catalytic subunit 1. It contains two adjacent transmembrane regions in its N-terminus and the major part of the protein is exposed to the periplasmic or to the mitochondrial intermembrane space, respectively. COX2_TM provides the substrate-binding site and contains a copper center called Cu(A), probably the primary acceptor in cytochrome C oxidase. Several bacterial COX2_TM have a C-terminal extension that contains a covalently bound heme c. The consensus pattern is: V-x-H-x(33,40)-C-x(3)-C-x(3)-H-x(2)-M, where the two C's and two H's are copper ligands.

Uncharacterized ACR, YggU family COG1872 (DUF167; Pfam Accession No. PF02594). SEQ ID NOS: 46, 813, 935, and 1225 correspond to a polynucleotide encoding a member of the uncharacterized ACR, YggU family COG1872 of proteins of E. coli. This protein in E. coli is a hypothetical 10.5 kDa protein in the GSHB-ANSB intergenic region.

Phosducin (Phosducin; Pfam Accession No. PF02114). SEQ ID NOS: 267 and 771 correspond to sequence encoding a Phosducin motif. The outer and inner segments of vertebrate rod photoreceptor cells contain phosducin, a soluble phosphoprotein that complexes with the beta/gamma-

subunits of the GTP-binding protein, transducin (Lee *et al., J. Biol. Chem.* (1990) 265:15867-15873). Light-induced changes in cyclic nucleotide levels modulate the phosphorylation of phosducin by protein kinase A (Lee *et al., J. Biol. Chem.* (1990) 265:15867-15873). The protein is thought to participate in the regulation of visual phototransduction or in the integration of photo-receptor metabolism. Similar proteins have been isolated from the pineal gland (Abe *et al., Gene* (1990) 91:209-215): the 33kDa proteins have the same sequences and the same phosphorylation site, suggesting that the functional role of the protein is the same in both retina and pineal gland.

The Phosducin motif is an 8-element fingerprint that provides a signature for phosducins. The fingerprint was derived from an initial alignment of 7 sequences where the motifs were drawn from conserved regions spanning virtually the full alignment length. The sequences of the 8 elements are as follows: (1) EEDFEGQASHTGPKGVINDW; (2) DSVAHSKKEILRQMSSPQSR; (3) SRKMSVQEYELIHKDKEDE; (4) CLRKYRRQCMQDMHQKLSF; (5) GPRYGFVYELESGEQFLETIEKE; (6) YEDGIKGCDALNSSLICLAAEY; (7) DRFSSDVLPTLLVYKGGELLSNF; and (8) EQLAEEFFTGDVESFLNEYG.

Example 6: Detection of Differential Expression Using Arrays and source of patient tissue samples

mRNA isolated from samples of cancerous and normal breast, colon, and prostate tissue obtained from patients were analyzed to identify genes differentially expressed in cancerous and normal cells. Normal and cancerous tissues were collected from patients 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 10 (inserted prior to 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 ("Lymph Met"); the incidence of lymph node metastases (provided as a number of lymph nodes positive for metastasis over the number of lymph nodes examined) ("Lymph Met Incid"); the regional lymphnode grade ("Reg Lymph 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 11 below provides information about each patient from which the prostate tissue samples were isolated, including: 1) the "Patient ID", which is a number assigned to the patient for identification purposes; 2) the "Tissue Type"; and 3) the "Gleason Grade" of the tumor. Histopathology of all primary tumors indicated the tumor was adenocarcinoma.

Table 11. Prostate patient data.

Patient ID	Tissue Type	Gleason Grade	Patient ID	Tissue Type	Gleason Grade
93	Prostate Cancer	3+4	391	Prostate Cancer	3+3
94	Prostate Cancer	3+3	420	Prostate Cancer	3+3
95	Prostate Cancer	3+3	425	Prostate Cancer	3+3
96	Prostate Cancer	3+3	428	Prostate Cancer	4+3
97	Prostate Cancer	3+2	431	Prostate Cancer	3+4
100	Prostate Cancer	3+3	492	Prostate Cancer	3+3
101	Prostate Cancer	3+3	493	Prostate Cancer	3+4
104	Prostate Cancer	3+3	496	Prostate Cancer	3+3
105	Prostate Cancer	3+4	510	Prostate Cancer	3+3
106	Prostate Cancer	3+3	511	Prostate Cancer	4+3
138	Prostate Cancer	3+3	514	Prostate Cancer	3+3
151	Prostate Cancer	3+3	549	Prostate Cancer	3+3
153	Prostate Cancer	3+3	552	Prostate Cancer	3+3
155	Prostate Cancer	4+3	858	Prostate Cancer	3+4
171	Prostate Cancer	3+4	859	Prostate Cancer	3+4
173	Prostate Cancer	3+4	864	Prostate Cancer	3+4
231	Prostate Cancer	3+4	883	Prostate Cancer	4+4
232	Prostate Cancer	3+3	895	Prostate Cancer	3+3
251	Prostate Cancer	3+4	901	Prostate Cancer	3+3
282	Prostate Cancer	4+3	909	Prostate Cancer	3+3
286	Prostate Cancer	3+3	921	Prostate Cancer	3+3
294	Prostate Cancer	3+4	923	Prostate Cancer	4+3
351	Prostate Cancer	5+4	934	Prostate Cancer	3+3
361	Prostate Cancer	3+3	1134	Prostate Cancer	3+4
362	Prostate Cancer	3+3	1135	Prostate Cancer	3+3
365	Prostate Cancer	3+2	1136	Prostate Cancer	3+4
368	Prostate Cancer	3+3	1137	Prostate Cancer	3+3
379	Prostate Cancer	3+4	1138	Prostate Cancer	4+3
388	Prostate Cancer	5+3			

Table 12 provides information about each patient from which the breast tissue samples were isolated, including: 1) the "Pat Num", a number assigned to the patient for identification purposes; 2) the "Histology", which indicates whether the tumor was characterized as an intraductal carcinoma (IDC) or ductal carcinoma in situ (DCIS); 3) the incidence of lymph node metastases (LMF),

represented as the number of lymph nodes positive to metastases out of the total number examined in the patient; 4) the "Tumor Size"; 5) "TNM Stage", which provides the tumor grade (T#), where the number indicates the grade and "p" indicates that the tumor grade is a pathological classification; regional lymph node metastasis (N#), where "0" indicates no lymph node metastases were found, "1" indicates lymph node metastases were found, and "X" means information not available and; the identification or detection of metastases to sites distant to the tumor and their location (M#), with "X" indicating that no distant mesatses were reported; and the stage of the tumor ("Stage Grouping"). "nr" indicates "no reported".

Table 12 Breast cancer patient data

Pat Num	Histology	LMF	Tumor Size	TNM Stage	Stage Grouping
280	IDC, DCIS+D2	nr	2 cm	T2NXMX	probable Stage II
284	IDC, DCIS	0/16	2 cm	T2pN0MX	Stage II
285	IDC, DCIS	nr	4.5 cm	T2NXMX	probable Stage II
291	IDC, DCIS	0/24	4.5 cm	T2pN0MX	Stage II
302	IDC, DCIS	nr	2.2 cm	T2NXMX	probable Stage II
375	IDC, DCIS	nr	1.5 cm	T1NXMX	probable Stage I
408	IDC	0/23	3.0 cm	T2pN0MX	Stage II
416	IDC	0/6	3.3 cm	T2pN0MX	Stage II
421	IDC, DCIS	nr	3.5 cm	T2NXMX	probable Stage II
459	IDC	2/5	4.9 cm	T2pN1MX	Stage II
465	IDC	0/10	6.5 cm	T3pN0MX	Stage II
470	IDC, DCIS	0/6	2.5 cm	T2pN0MX	Stage II
472	IDC, DCIS	6/45	5.0+ cm	T3pN1MX	Stage III
474	IDC	0/18	6.0 cm	T3pN0MX	Stage II
476	IDC	0/16	3.4 cm	T2pN0MX	Stage II
605	IDC, DCIS	1/25	5.0 cm	T2pN1MX	Stage II
649	IDC, DCIS	1/29	4.5 cm	T2pN1MX	Stage II

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. 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.

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 13 (inserted prior to claims) provides the results for gene products expressed by at least 2-fold or greater in cancerous prostate, colon, or breast tissue samples relative to normal tissue samples in at least 20% of the patients tested. Table 12 includes: 1) the SEQ ID NO ("SEQ ID") assigned to each sequence for use in the present specification; 2) the Cluster Identification No. ("CLUSTER"); 3) the percentage of patients tested in which expression levels (*e.g.*, as message level) of the gene was at least 2-fold greater in cancerous breast tissue than in matched normal tissue ("BREAST PATIENTS >=2x"); 4) the percentage of patients tested in which expression levels (*e.g.*, as message level) of the gene was less than or equal to ½ of the expression level in matched normal breast cells ("BREAST PATIENTS <=halfx"); 5) the percentage of patients tested in which expression levels (*e.g.*, as message level) of the gene was at least 2-fold greater in cancerous colon tissue than in matched normal tissue ("COLON PATIENTS >=2x"); 6) the percentage of patients tested in which expression levels (*e.g.*, as message level) of the gene was less than or equal to ½ of the expression level in matched normal colon cells ("COLON PATIENTS <=halfx"); 7) the percentage of patients tested in which expression levels (*e.g.*, as message level) of the gene was at least 2-fold greater in cancerous prostate tissue than in matched normal tissue ("PROSTATE PATIENTS >=2x");

and 8) the percentage of patients tested in which expression levels (*e.g.*, as message level) of the gene was less than or equal to ½ of the expression level in matched normal prostate cells ("PROSTATE PATIENTS <=halfx").

These data provide evidence that the genes represented by the polynucleotides having the indicated sequences are differentially expressed in breast cancer as compared to normal non-cancerous breast tissue, are differentially expressed in colon cancer as compared to normal non-cancerous colon tissue, and are differentially expressed in prostate cancer as compared to normal non-cancerous prostate tissue.

Example 7: 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 The expression of the differentially expressed genes represented by the polynucleotides in the cancerous cells can be analyzed using antisense knockout technology to confirm the role and function of the gene product in tumorigenesis, *e.g.*, in promoting a metastatic phenotype.

A number of different oligonucleotides complementary to the mRNA generated by the differentially expressed genes identified herein can be designed as potential 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 that are 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 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.

Using the sets of oligomers and the HYBsimulator program, three to ten antisense oligonucleotides and their reverse controls are designed and synthesized for each candidate mRNA transcript, which transcript is obtained from the gene corresponding to the target polynucleotide sequence of interest. 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.

The ability of each designed antisense oligonucleotide to inhibit gene expression is tested through transfection into LNCaP, PC3, 22Rv1, MDA-PCA-2b, or DU145 prostate carcinoma cells. For each transfection mixture, a carrier molecule (such as a lipid, lipid derivative, lipid-like molecule, cholesterol, cholesterol derivative, or cholesterol-like molecule) 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, the carrier molecule, typically in the amount of about 1.5-2 nmol carrier/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 carrier 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 is added to a total volume of 12.5 μl. To each tube is added 7.5 μl of a buffer/enzyme mixture, 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 is 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 is added, and amplification is carried out according to standard protocols. The results are 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 8: Effect of Expression on Proliferation

The effect of gene expression on the inhibition of cell proliferation can be assessed in metastatic breast cancer cell lines (MDA-MB-231 ("231")); SW620 colon colorectal carcinoma cells; SKOV3 cells (a human ovarian carcinoma cell line); or LNCaP, PC3, 22Rv1, MDA-PCA-2b, or DU145 prostate cancer cells.

Cells are plated to approximately 60-80% confluency in 96-well dishes. Antisense or reverse control oligonucleotide is diluted to 2 µM in OptiMEM™. The oligonucleotide-OptiMEM™ can then be added to a delivery vehicle, which delivery vehicle can be selected so as to be optimized for the particular cell type to be used in the assay. The oligo/delivery vehicle mixture is then further diluted into medium with serum on the cells. The final concentration of oligonucleotide for all experiments can be about 300 nM.

Antisense oligonucleotides are prepared as described above (see Example 3). Cells are transfected overnight at 37°C and the transfection mixture is replaced with fresh medium the next morning. Transfection is carried out as described above in Example 8.

Those antisense oligonucleotides that result in inhibition of proliferation of SW620 cells indicate that the corresponding gene plays a role in production or maintenance of the cancerous phenotype in cancerous colon cells. Those antisense oligonucleotides that inhibit proliferation in SKOV3 cells represent genes that play a role in production or maintenance of the cancerous phenotype in cancerous breast cells. Those antisense oligonucleotides that result in inhibition of proliferation of MDA-MB-231 cells indicate that the corresponding gene plays a role in production or maintenance of the cancerous phenotype in cancerous ovarian cells. Those antisense oligonucleotides that inhibit proliferation in LNCaP, PC3, 22Rv1, MDA-PCA-2b, or DU145 cells represent genes that play a role in production or maintenance of the cancerous phenotype in cancerous prostate cells.

Example 9: Effect of Gene Expression on Cell Migration

The effect of gene expression on the inhibition of cell migration can be assessed in LNCaP, PC3, 22Rv1, MDA-PCA-2b, or DU145 prostate cancer cells using static endothelial cell binding assays, non-static endothelial cell binding assays, and transmigration assays.

For the static endothelial cell binding assay, antisense oligonucleotides are prepared as described above (see Example 8). Two days prior to use, prostate cancer cells (CaP) are plated and

transfected with antisense oligonucleotide as described above (see Examples 3 and 4). On the day before use, the medium is replaced with fresh medium, and on the day of use, the medium is replaced with fresh medium containing 2 μM CellTracker green CMFDA (Molecular Probes, Inc.) and cells are incubated for 30 min. Following incubation, CaP medium is replaced with fresh medium (no CMFDA) and cells are incubated for an additional 30-60 min. CaP cells are detached using CMF PBS/2.5 mM EDTA or trypsin, spun and resuspended in DMEM/1% BSA/ 10 mM HEPES pH 7.0. Finally, CaP cells are counted and resuspended at a concentration of $1x10^6$ cells/ml.

Endothelial cells (EC) are plated onto 96-well plates at 40-50% confluence 3 days prior to use. On the day of use, EC are washed 1X with PBS and 50λ DMDM/1%BSA/10mM HEPES pH 7 is added to each well. To each well is then added 50K (50λ) CaP cells in DMEM/1% BSA/ 10mM HEPES pH 7. The plates are incubated for an additional 30 min and washed 5X with PBS containing Ca^{++} and Mg^{++}. After the final wash, 100 μL PBS is added to each well and fluorescence is read on a fluorescent plate reader (Ab492/Em 516 nm).

For the non-static endothelial cell binding assay, CaP are prepared as described above. EC are plated onto 24-well plates at 30-40% confluence 3 days prior to use. On the day of use, a subset of EC are treated with cytokine for 6 hours then washed 2X with PBS. To each well is then added 150-200K CaP cells in DMEM/1% BSA/ 10mM HEPES pH 7. Plates are placed on a rotating shaker (70 RPM) for 30 min and then washed 3X with PBS containing Ca^{++} and Mg^{++}. After the final wash, 500 μL PBS is added to each well and fluorescence is read on a fluorescent plate reader (Ab492/Em 516 nm).

For the transmigration assay, CaP are prepared as described above with the following changes. On the day of use, CaP medium is replaced with fresh medium containing 5 μM CellTracker green CMFDA (Molecular Probes, Inc.) and cells are incubated for 30 min. Following incubation, CaP medium is replaced with fresh medium (no CMFDA) and cells are incubated for an additional 30-60 min. CaP cells are detached using CMF PBS/2.5 mM EDTA or trypsin, spun and resuspended in EGM-2-MV medium. Finally, CaP cells are counted and resuspended at a concentration of $1x10^6$ cells/ml.

EC are plated onto FluorBlok transwells (BD Biosciences) at 30-40% confluence 5-7 days before use. Medium is replaced with fresh medium 3 days before use and on the day of use. To each transwell is then added 50K labeled CaP. 30 min prior to the first fluorescence reading, 10 μg of FITC-dextran (10K MW) is added to the EC plated filter. Fluorescence is then read at multiple time points on a fluorescent plate reader (Ab492/Em 516 nm).

Those antisense oligonucleotides that result in inhibition of binding of LNCaP, PC3, 22Rv1, MDA-PCA-2b, or DU145 prostate cancer cells to endothelial cells indicate that the corresponding gene plays a role in the production or maintenance of the cancerous phenotype in cancerous prostate cells. Those antisense oligonucleotides that result in inhibition of endothelial cell transmigration by

LNCaP, PC3, 22Rv1, MDA-PCA-2b, or DU145 prostate cancer cells indicate that the corresponding gene plays a role in the production or maintenance of the cancerous phenotype in cancerous prostate cells.

Example 10: Effect of Gene Expression on Colony Formation

The effect of gene expression upon colony formation of SW620 cells, SKOV3 cells, MDA-MB-231 cells, LNCaP cells, PC3 cells, 22Rv1 cells, MDA-PCA-2b cells, and DU145 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 8) is added without delivery vehicles. Fresh media and oligos are added every 3-4 days. Colonies 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 result in inhibition of colony formation of SW620 cells indicate that the corresponding gene plays a role in production or maintenance of the cancerous phenotype in cancerous colon cells. Those antisense oligonucleotides that inhibit colony formation in SKOV3 cells represent genes that play a role in production or maintenance of the cancerous phenotype in cancerous breast cells. Those antisense oligonucleotides that result in inhibition of colony formation of MDA-MB-231 cells indicate that the corresponding gene plays a role in production or maintenance of the cancerous phenotype in cancerous ovarian cells. Those antisense oligonucleotides that inhibit colony formation in LNCaP, PC3, 22Rv1, MDA-PCA-2b, or DU145 cells represent genes that play a role in production or maintenance of the cancerous phenotype in cancerous prostate cells.

Example 11: 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, LNCaP, PC3, 22Rv1, MDA-PCA-2b, or DU145 cells, or other cells derived from a cancer of interest, can be 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 is 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 12: 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. In order to generate antibodies, a clone corresponding to a selected gene product is selected, and a sequence that represents a partial or complete coding sequence is obtained. The resulting clone is expressed, the polypeptide produced isolated, and antibodies generated. The antibodies are then combined with cells and the effect upon tumorigenesis assessed.

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 13: 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 14A. 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 14 below provides the ATCC Accession Nos. of the clones deposited as a library named ES217. The deposit was made on January 18, 2001. Table 15 (inserted before the claims) provides the ATCC Accession Nos. of the clones deposited as libraries named ES210-ES216 on July 25, 2000.

Table 14B: Clones Deposited as Library No. ES217 with ATCC on or before January 18, 2001.

CloneID	CMCC#	ATCC#	CloneID	CMCC#	ATCC#
M00073094B:A01	5418	PTA-2918	M00073425A:H12	5418	PTA-2918
M00073096B:A12	5418	PTA-2918	M00073427B:E04	5418	PTA-2918
M00073412C:E07	5418	PTA-2918	M00073408A:D06	5418	PTA-2918
M00073408C:F06	5418	PTA-2918	M00073428D:H03	5418	PTA-2918
M00073435C:E06	5418	PTA-2918	M00073435B:E11	5418	PTA-2918
M00073403B:F06	5418	PTA-2918	M00074323D:F09	5418	PTA-2918
M00073412D:B07	5418	PTA-2918	M00074333D:A11	5418	PTA-2918
M00073421C:B07	5418	PTA-2918	M00074335A:H08	5418	PTA-2918
M00073429B:H10	5418	PTA-2918	M00074337A:G08	5418	PTA-2918
M00073412D:E02	5418	PTA-2918	M00074340B:D06	5418	PTA-2918
M00073097C:A03	5418	PTA-2918	M00074343C:A03	5418	PTA-2918
M00073403C:C10	5418	PTA-2918	M00074346A:H09	5418	PTA-2918
M00073425D:F08	5418	PTA-2918	M00074347B:F11	5418	PTA-2918
M00073403C:E11	5418	PTA-2918	M00074349A:E08	5418	PTA-2918
M00073431A:G02	5418	PTA-2918	M00074355D:H06	5418	PTA-2918
M00073412A:C03	5418	PTA-2918	M00074361C:B01	5418	PTA-2918
M00073424D:C03	5418	PTA-2918	M00074365A:E09	5418	PTA-2918
M00073430C:A01	5418	PTA-2918	M00074366A:D07	5418	PTA-2918
M00073407A:E12	5418	PTA-2918	M00074366A:H07	5418	PTA-2918
M00073412A:H09	5418	PTA-2918	M00074370D:G09	5418	PTA-2918
M00073418B:B09	5418	PTA-2918	M00074375D:E05	5418	PTA-2918
M00073403C:H09	5418	PTA-2918	M00074382D:F04	5418	PTA-2918
M00073416B:F01	5418	PTA-2918	M00074384D:G07	5418	PTA-2918
M00073425A:G10	5418	PTA-2918	M00074388B:E07	5418	PTA-2918

CloneID	CMCC#	ATCC#	CloneID	CMCC#	ATCC#
M00073427B:C08	5418	PTA-2918	M00074392C:D02	5418	PTA-2918
M00073430C:B02	5418	PTA-2918	M00074405B:A04	5418	PTA-2918
M00073418B:H09	5418	PTA-2918	M00074417D:F07	5418	PTA-2918
M00073423C:E01	5418	PTA-2918	M00074392D:D01	5418	PTA-2918
M00074391B:D02	5418	PTA-2918	M00074406B:F10	5418	PTA-2918
M00074390C:E04	5418	PTA-2918	M00074430D:G09	5418	PTA-2918
M00074411B:G07	5418	PTA-2918	M00074395A:B11	5418	PTA-2918
M00074415B:A01	5418	PTA-2918	M00074404B:H01	5418	PTA-2918

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.

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.

Table 2

SEQ ID	CLUSTER	SEQNAME	ORIENT	CLONE ID	LIBRARY
1	38838	2504.A17.GZ43_365806	F	M00072942B:E02	IF97-26811-NormBPHProstate
2	558959	2504.B06.GZ43_365819	F	M00072942D:F07	IF97-26811-NormBPHProstate
3	19061	2504.B11.GZ43_365824	F	M00072943B:E04	IF97-26811-NormBPHProstate
4	139979	2504.B21.GZ43_365834	F	M00072944A:C07	IF97-26811-NormBPHProstate
5	24540	2504.B23.GZ43_365836	F	M00072944A:E06	IF97-26811-NormBPHProstate
6	40164	2504.C08.GZ43_365845	F	M00072944C:C02	IF97-26811-NormBPHProstate
7	53675	2504.C11.GZ43_365848	F	M00072944D:C08	IF97-26811-NormBPHProstate
8	119614	2504.D09.GZ43_365870	F	M00072947B:G04	IF97-26811-NormBPHProstate
9	918867	2504.D16.GZ43_365877	F	M00072947D:G05	IF97-26811-NormBPHProstate
10	823	2504.E23.GZ43_365908	F	M00072950A:A06	IF97-26811-NormBPHProstate
11	604822	2504.F20.GZ43_365929	F	M00072961A:G04	IF97-26811-NormBPHProstate
12	343686	2504.G01.GZ43_365934	F	M00072961B:G10	IF97-26811-NormBPHProstate
13	21554	2504.G04.GZ43_365937	F	M00072961C:B06	IF97-26811-NormBPHProstate
14	204211	2504.G07.GZ43_365940	F	M00072962A:B05	IF97-26811-NormBPHProstate
15	21567	2504.H02.GZ43_365959	F	M00072963B:G11	IF97-26811-NormBPHProstate
16	956537	2504.I11.GZ43_365992	F	M00072967A:G07	IF97-26811-NormBPHProstate
17	44238	2504.I13.GZ43_365994	F	M00072967B:G06	IF97-26811-NormBPHProstate
18	56663	2504.I19.GZ43_366000	F	M00072968A:F08	IF97-26811-NormBPHProstate
19	49884	2504.I23.GZ43_366004	F	M00072968D:A06	IF97-26811-NormBPHProstate
20	402904	2504.J02.GZ43_366007	F	M00072968D:E05	IF97-26811-NormBPHProstate
21	845171	2504.J11.GZ43_366016	F	M00072970C:B07	IF97-26811-NormBPHProstate
22	471272	2504.K01.GZ43_366030	F	M00072971A:E04	IF97-26811-NormBPHProstate
23	660842	2504.K02.GZ43_366031	F	M00072971A:F11	IF97-26811-NormBPHProstate
24	764473	2504.K07.GZ43_366036	F	M00072971C:B07	IF97-26811-NormBPHProstate
25	406416	2504.K14.GZ43_366043	F	M00072972A:C03	IF97-26811-NormBPHProstate
26	842403	2504.L16.GZ43_366069	F	M00072974A:A11	IF97-26811-NormBPHProstate
27	401809	2504.M12.GZ43_366089	F	M00072974D:B04	IF97-26811-NormBPHProstate
28	28050	2504.M18.GZ43_366095	F	M00072975A:D11	IF97-26811-NormBPHProstate
29	37758	2504.M19.GZ43_366096	F	M00072975A:E02	IF97-26811-NormBPHProstate
30	85792	2504.O09.GZ43_366134	F	M00072977A:F06	IF97-26811-NormBPHProstate
31	400258	2504.O12.GZ43_366137	F	M00072977B:C05	IF97-26811-NormBPHProstate
32	9934	2505.B02.GZ43_366199	F	M00072980B:C05	IF97-26811-NormBPHProstate
33	448503	2505.B05.GZ43_366202	F	M00072980B:G01	IF97-26811-NormBPHProstate
34	731371	2505.B17.GZ43_366214	F	M00073001A:F07	IF97-26811-NormBPHProstate
35	171148	2505.B18.GZ43_366215	F	M00073001B:E07	IF97-26811-NormBPHProstate
36	49090	2505.C06.GZ43_366227	F	M00073002B:B12	IF97-26811-NormBPHProstate
37	57638	2505.C17.GZ43_366238	F	M00073002D:B08	IF97-26811-NormBPHProstate
38	523261	2505.C21.GZ43_366242	F	M00073003A:E06	IF97-26811-NormBPHProstate
39	85192	2505.D01.GZ43_366246	F	M00073003B:E10	IF97-26811-NormBPHProstate
40	696086	2505.D03.GZ43_366248	F	M00073003B:H01	IF97-26811-NormBPHProstate
41	41455	2505.D04.GZ43_366249	F	M00073003C:C05	IF97-26811-NormBPHProstate
42	336576	2505.E09.GZ43_366278	F	M00073006A:H08	IF97-26811-NormBPHProstate
43	36407	2505.E15.GZ43_366284	F	M00073006C:D07	IF97-26811-NormBPHProstate
44	397652	2505.F09.GZ43_366302	F	M00073007D:E05	IF97-26811-NormBPHProstate
45	85792	2505.G06.GZ43_366323	F	M00073009B:C08	IF97-26811-NormBPHProstate
46	376516	2505.G16.GZ43_366333	F	M00073009D:A02	IF97-26811-NormBPHProstate
47	588996	2505.H14.GZ43_366355	F	M00073012A:C11	IF97-26811-NormBPHProstate
48	8401	2505.I04.GZ43_366369	F	M00073013A:D10	IF97-26811-NormBPHProstate
49	11561	2505.I06.GZ43_366371	F	M00073013A:F10	IF97-26811-NormBPHProstate
50	726937	2505.I14.GZ43_366379	F	M00073013C:B10	IF97-26811-NormBPHProstate

Table 2

SEQ ID	CLUSTER	SEQNAME	ORIENT	CLONE ID	LIBRARY
51	672233	2505.I16.GZ43_366381	F	M00073013C:G05	IF97-26811-NormBPHProstate
52	31453	2505.J15.GZ43_366404	F	M00073014D:F01	IF97-26811-NormBPHProstate
53	40330	2505.J20.GZ43_366409	F	M00073015A:E12	IF97-26811-NormBPHProstate
54	38454	2505.J22.GZ43_366411	F	M00073015A:H06	IF97-26811-NormBPHProstate
55	666927	2505.J23.GZ43_366412	F	M00073015B:A05	IF97-26811-NormBPHProstate
56	163500	2505.K09.GZ43_366422	F	M00073015C:E10	IF97-26811-NormBPHProstate
57	42034	2505.L07.GZ43_366444	F	M00073017A:D06	IF97-26811-NormBPHProstate
58	455662	2505.L09.GZ43_366446	F	M00073017A:F03	IF97-26811-NormBPHProstate
59	985835	2505.M09.GZ43_366470	F	M00073019A:H12	IF97-26811-NormBPHProstate
60	502358	2505.M10.GZ43_366471	F	M00073019B:B12	IF97-26811-NormBPHProstate
61	189993	2505.N19.GZ43_366504	F	M00073020C:F07	IF97-26811-NormBPHProstate
62	605923	2505.N21.GZ43_366506	F	M00073020D:C06	IF97-26811-NormBPHProstate
63	935908	2505.O09.GZ43_366518	F	M00073021C:E04	IF97-26811-NormBPHProstate
64	568204	2505.O12.GZ43_366521	F	M00073021D:C03	IF97-26811-NormBPHProstate
65	640970	2505.O19.GZ43_366528	F	M00073023A:D10	IF97-26811-NormBPHProstate
66	558581	2505.P09.GZ43_366542	F	M00073025A:E11	IF97-26811-NormBPHProstate
67	823	2505.P23.GZ43_366556	F	M00073026B:F01	IF97-26811-NormBPHProstate
68	195498	2510.A11.GZ43_369036	F	M00073026D:G04	IF97-26811-NormBPHProstate
69	7885	2510.A19.GZ43_369044	F	M00073027B:H12	IF97-26811-NormBPHProstate
70	63363	2510.C06.GZ43_369079	F	M00073030A:G05	IF97-26811-NormBPHProstate
71	558602	2510.C07.GZ43_369080	F	M00073030B:C02	IF97-26811-NormBPHProstate
72	38454	2510.C10.GZ43_369083	F	M00073030C:A02	IF97-26811-NormBPHProstate
73	21546	2510.E13.GZ43_369134	F	M00073036C:H10	IF97-26811-NormBPHProstate
74	846506	2510.E16.GZ43_369137	F	M00073037A:C06	IF97-26811-NormBPHProstate
75	62816	2510.F11.GZ43_369156	F	M00073037D:H02	IF97-26811-NormBPHProstate
76	134226	2510.F23.GZ43_369168	F	M00073038C:C07	IF97-26811-NormBPHProstate
77	63363	2510.G05.GZ43_369174	F	M00073038D:D12	IF97-26811-NormBPHProstate
78	85192	2510.G06.GZ43_369175	F	M00073038D:F10	IF97-26811-NormBPHProstate
79	9048	2510.G09.GZ43_369178	F	M00073039A:D09	IF97-26811-NormBPHProstate
80	480019	2510.G14.GZ43_369183	F	M00073039C:B10	IF97-26811-NormBPHProstate
81	58429	2510.G21.GZ43_369190	F	M00073040A:B02	IF97-26811-NormBPHProstate
82	115787	2510.H03.GZ43_369196	F	M00073040D:F05	IF97-26811-NormBPHProstate
83	42891	2510.I08.GZ43_369225	F	M00073043B:C10	IF97-26811-NormBPHProstate
84	469837	2510.I10.GZ43_369227	F	M00073043B:E08	IF97-26811-NormBPHProstate
85	54634	2510.I16.GZ43_369233	F	M00073043C:F04	IF97-26811-NormBPHProstate
86	648899	2510.I23.GZ43_369240	F	M00073043D:H09	IF97-26811-NormBPHProstate
87	778001	2510.J06.GZ43_369247	F	M00073044B:F08	IF97-26811-NormBPHProstate
88	452714	2510.J10.GZ43_369251	F	M00073044C:C12	IF97-26811-NormBPHProstate
89	142502	2510.J11.GZ43_369252	F	M00073044C:D08	IF97-26811-NormBPHProstate
90	668962	2510.J12.GZ43_369253	F	M00073044C:G12	IF97-26811-NormBPHProstate
91	210229	2510.J14.GZ43_369255	F	M00073044D:F08	IF97-26811-NormBPHProstate
92	483211	2510.J18.GZ43_369259	F	M00073045B:A03	IF97-26811-NormBPHProstate
93	7307	2510.J22.GZ43_369263	F	M00073045B:D06	IF97-26811-NormBPHProstate
94	99399	2510.K05.GZ43_369270	F	M00073045C:E06	IF97-26811-NormBPHProstate
95	421869	2510.K06.GZ43_369271	F	M00073045C:E07	IF97-26811-NormBPHProstate
96	21827	2510.K11.GZ43_369276	F	M00073045D:B04	IF97-26811-NormBPHProstate
97	88462	2510.K15.GZ43_369280	F	M00073046A:A05	IF97-26811-NormBPHProstate
98	16176	2510.K16.GZ43_369281	F	M00073046A:A06	IF97-26811-NormBPHProstate
99	138646	2510.K21.GZ43_369286	F	M00073046B:A12	IF97-26811-NormBPHProstate
100	513744	2510.L10.GZ43_369299	F	M00073046D:F04	IF97-26811-NormBPHProstate

Table 2

SEQ ID	CLUSTER	SEQNAME	ORIENT	CLONE ID	LIBRARY
101	15951	2510.L17.GZ43_369306	F	M00073047B:E10	IF97-26811-NormBPHProstate
102	40270	2510.L21.GZ43_369310	F	M00073047C:G01	IF97-26811-NormBPHProstate
103	73796	2510.M14.GZ43_369327	F	M00073048A:H05	IF97-26811-NormBPHProstate
104	18508	2510.M20.GZ43_369333	F	M00073048C:A11	IF97-26811-NormBPHProstate
105	18629	2510.M21.GZ43_369334	F	M00073048C:B01	IF97-26811-NormBPHProstate
106	405925	2510.N01.GZ43_369338	F	M00073048C:E11	IF97-26811-NormBPHProstate
107	455862	2510.N12.GZ43_369349	F	M00073049A:H04	IF97-26811-NormBPHProstate
108	582134	2510.N13.GZ43_369350	F	M00073049B:B03	IF97-26811-NormBPHProstate
109	727966	2510.N14.GZ43_369351	F	M00073049B:B06	IF97-26811-NormBPHProstate
110	644299	2510.N24.GZ43_369361	F	M00073049C:C09	IF97-26811-NormBPHProstate
111	208449	2510.O07.GZ43_369368	F	M00073049C:H07	IF97-26811-NormBPHProstate
112	44480	2510.O14.GZ43_369375	F	M00073050A:D09	IF97-26811-NormBPHProstate
113	148227	2510.O21.GZ43_369382	F	M00073051A:D07	IF97-26811-NormBPHProstate
114	197343	2510.O22.GZ43_369383	F	M00073051A:F12	IF97-26811-NormBPHProstate
115	20571	2510.O23.GZ43_369384	F	M00073051A:F07	IF97-26811-NormBPHProstate
116	724818	2510.P08.GZ43_369393	F	M00073052B:H12	IF97-26811-NormBPHProstate
117	9051	2365.A13.GZ43_345239	F	M00073054A:A06	IF97-26811-NormBPHProstate
118	77849	2365.A14.GZ43_345240	F	M00073054A:C10	IF97-26811-NormBPHProstate
119	5823	2365.A23.GZ43_345249	F	M00073054B:E07	IF97-26811-NormBPHProstate
120	41430	2365.B02.GZ43_345252	F	M00073054C:E02	IF97-26811-NormBPHProstate
121	24115	2365.B20.GZ43_345270	F	M00073055D:E11	IF97-26811-NormBPHProstate
122	573764	2365.C10.GZ43_345284	F	M00073056C:A09	IF97-26811-NormBPHProstate
123	44480	2365.C13.GZ43_345287	F	M00073056C:C12	IF97-26811-NormBPHProstate
124	15604	2365.C20.GZ43_345294	F	M00073057A:F09	IF97-26811-NormBPHProstate
125	54203	2365.D03.GZ43_345301	F	M00073057D:A12	IF97-26811-NormBPHProstate
126	756337	2365.D10.GZ43_345308	F	M00073060B:C06	IF97-26811-NormBPHProstate
127	16852	2365.E03.GZ43_345325	F	M00073061B:F10	IF97-26811-NormBPHProstate
128	59018	2365.E08.GZ43_345330	F	M00073061C:G08	IF97-26811-NormBPHProstate
129	61166	2365.E11.GZ43_345333	F	M00073062B:D09	IF97-26811-NormBPHProstate
130	119614	2365.E12.GZ43_345334	F	M00073062C:D09	IF97-26811-NormBPHProstate
131	806992	2365.F07.GZ43_345353	F	M00073064C:A11	IF97-26811-NormBPHProstate
132	659483	2365.F12.GZ43_345358	F	M00073064C:H09	IF97-26811-NormBPHProstate
133	34077	2365.F13.GZ43_345359	F	M00073064D:B11	IF97-26811-NormBPHProstate
134	404081	2365.F24.GZ43_345370	F	M00073065D:D11	IF97-26811-NormBPHProstate
135	752623	2365.G09.GZ43_345379	F	M00073066B:G03	IF97-26811-NormBPHProstate
136	531505	2365.G11.GZ43_345381	F	M00073066C:D02	IF97-26811-NormBPHProstate
137	588059	2365.G17.GZ43_345387	F	M00073067A:E09	IF97-26811-NormBPHProstate
138	271456	2365.G19.GZ43_345389	F	M00073067B:D04	IF97-26811-NormBPHProstate
139	5791	2365.G22.GZ43_345392	F	M00073067D:B02	IF97-26811-NormBPHProstate
140	725987	2365.I04.GZ43_345422	F	M00073069D:G03	IF97-26811-NormBPHProstate
141	58218	2365.I06.GZ43_345424	F	M00073070A:B12	IF97-26811-NormBPHProstate
142	453526	2365.I11.GZ43_345429	F	M00073070B:B06	IF97-26811-NormBPHProstate
143	141010	2365.J14.GZ43_345456	F	M00073071D:D02	IF97-26811-NormBPHProstate
144	558342	2365.J19.GZ43_345461	F	M00073072A:A10	IF97-26811-NormBPHProstate
145	682065	2365.L07.GZ43_345497	F	M00073074B:G04	IF97-26811-NormBPHProstate
146	466312	2365.L08.GZ43_345498	F	M00073074D:A04	IF97-26811-NormBPHProstate
147	204211	2365.L23.GZ43_345513	F	M00073078B:F08	IF97-26811-NormBPHProstate
148	158853	2365.M03.GZ43_345517	F	M00073080B:A07	IF97-26811-NormBPHProstate
149	633646	2365.M09.GZ43_345523	F	M00073081A:F08	IF97-26811-NormBPHProstate
150	375488	2365.M13.GZ43_345527	F	M00073081D:C07	IF97-26811-NormBPHProstate

Table 2

SEQ ID	CLUSTER	SEQNAME	ORIENT	CLONE ID	LIBRARY
151	228149	2365.M20.GZ43_345534	F	M00073084C:E02	IF97-26811-NormBPHProstate
152	599028	2365.N12.GZ43_345550	F	M00073085D:B01	IF97-26811-NormBPHProstate
153	691653	2365.N23.GZ43_345561	F	M00073086D:B05	IF97-26811-NormBPHProstate
154	8231	2365.O07.GZ43_345569	F	M00073088C:B04	IF97-26811-NormBPHProstate
155	397652	2365.O13.GZ43_345575	F	M00073088D:F07	IF97-26811-NormBPHProstate
156	20863	2365.O20.GZ43_345582	F	M00073091B:C04	IF97-26811-NormBPHProstate
157	11121	2365.O24.GZ43_345586	F	M00073091D:B06	IF97-26811-NormBPHProstate
158	33725	2365.P04.GZ43_345590	F	M00073092A:D03	IF97-26811-NormBPHProstate
159	37420	2365.P10.GZ43_345596	F	M00073092D:B03	IF97-26811-NormBPHProstate
160	236390	2366.A01.GZ43_345611	F	M00073094B:A01	IF97-26811-NormBPHProstate
161	831518	2366.F02.GZ43_345632	F	M00073412A:C03	IF97-26811-NormBPHProstate
162	89912	2366.E03.GZ43_345647	F	M00073408C:F06	IF97-26811-NormBPHProstate
163	853371	2366.J03.GZ43_345652	F	M00073424D:C03	IF97-26811-NormBPHProstate
164	401741	2366.C04.GZ43_345661	F	M00073403B:F06	IF97-26811-NormBPHProstate
165	50062	2366.D04.GZ43_345662	F	M00073407A:E12	IF97-26811-NormBPHProstate
166	377367	2366.F04.GZ43_345664	F	M00073412A:H09	IF97-26811-NormBPHProstate
167	9741	2366.I04.GZ43_345667	F	M00073421C:B07	IF97-26811-NormBPHProstate
168	13951	2366.H05.GZ43_345682	F	M00073416B:F01	IF97-26811-NormBPHProstate
169	497520	2366.J05.GZ43_345684	F	M00073425A:G10	IF97-26811-NormBPHProstate
170	136530	2366.J06.GZ43_345700	F	M00073425A:H12	IF97-26811-NormBPHProstate
171	403134	2366.C07.GZ43_345709	F	M00073403C:C10	IF97-26811-NormBPHProstate
172	379939	2366.L07.GZ43_345718	F	M00073428D:H03	IF97-26811-NormBPHProstate
173	128835	2366.C08.GZ43_345725	F	M00073403C:E11	IF97-26811-NormBPHProstate
174	34475	2366.P08.GZ43_345738	F	M00073435B:E11	IF97-26811-NormBPHProstate
175	427808	2366.M09.GZ43_345751	F	M00073431A:G02	IF97-26811-NormBPHProstate
176	450472	2366.F10.GZ43_345760	F	M00073412C:E07	IF97-26811-NormBPHProstate
177	31060	2366.P11.GZ43_345786	F	M00073435C:E06	IF97-26811-NormBPHProstate
178	734776	2366.F12.GZ43_345792	F	M00073412D:B07	IF97-26811-NormBPHProstate
179	47789	2366.L12.GZ43_345798	F	M00073429B:H10	IF97-26811-NormBPHProstate
180	559440	2366.C13.GZ43_345805	F	M00073403C:H09	IF97-26811-NormBPHProstate
181	169728	2366.F13.GZ43_345808	F	M00073412D:E02	IF97-26811-NormBPHProstate
182	137023	2366.K13.GZ43_345813	F	M00073427B:C08	IF97-26811-NormBPHProstate
183	732434	2366.I14.GZ43_345827	F	M00073423C:E01	IF97-26811-NormBPHProstate
184	529	2366.K14.GZ43_345829	F	M00073427B:E04	IF97-26811-NormBPHProstate
185	32624	2366.J15.GZ43_345844	F	M00073425D:F08	IF97-26811-NormBPHProstate
186	378965	2366.A17.GZ43_345867	F	M00073096B:A12	IF97-26811-NormBPHProstate
187	16009	2366.L19.GZ43_345910	F	M00073430C:A01	IF97-26811-NormBPHProstate
188	134637	2366.H20.GZ43_345922	F	M00073418B:B09	IF97-26811-NormBPHProstate
189	1959	2366.L21.GZ43_345942	F	M00073430C:B02	IF97-26811-NormBPHProstate
190	805118	2366.A22.GZ43_345947	F	M00073097C:A03	IF97-26811-NormBPHProstate
191	411952	2366.H22.GZ43_345954	F	M00073418B:H09	IF97-26811-NormBPHProstate
192	887	2366.D23.GZ43_345966	F	M00073408A:D06	IF97-26811-NormBPHProstate
193	172916	2367.A21.GZ43_346015	F	M00073438A:A08	IF97-26811-NormBPHProstate
194	929222	2367.A22.GZ43_346016	F	M00073438A:B02	IF97-26811-NormBPHProstate
195	968417	2367.B10.GZ43_346028	F	M00073438D:G05	IF97-26811-NormBPHProstate
196	588996	2367.C06.GZ43_346048	F	M00073442A:F07	IF97-26811-NormBPHProstate
197	560612	2367.C08.GZ43_346050	F	M00073442B:D12	IF97-26811-NormBPHProstate
198	15307	2367.C12.GZ43_346054	F	M00073442D:E11	IF97-26811-NormBPHProstate
199	88462	2367.D11.GZ43_346077	F	M00073446C:A03	IF97-26811-NormBPHProstate
200	923732	2367.D18.GZ43_346084	F	M00073447B:A03	IF97-26811-NormBPHProstate

Table 2

SEQ ID	CLUSTER	SEQNAME	ORIENT	CLONE ID	LIBRARY
201	423085	2367.D21.GZ43_346087	F	M00073447D:F01	IF97-26811-NormBPHProstate
202	483211	2367.E03.GZ43_346093	F	M00073448B:F11	IF97-26811-NormBPHProstate
203	465814	2367.E04.GZ43_346094	F	M00073448B:F07	IF97-26811-NormBPHProstate
204	244504	2367.E23.GZ43_346113	F	M00073453C:C09	IF97-26811-NormBPHProstate
205	395761	2367.F06.GZ43_346120	F	M00073455C:G09	IF97-26811-NormBPHProstate
206	514044	2367.F13.GZ43_346127	F	M00073457A:G09	IF97-26811-NormBPHProstate
207	227227	2367.G11.GZ43_346149	F	M00073462C:H12	IF97-26811-NormBPHProstate
208	691653	2367.G13.GZ43_346151	F	M00073462D:D12	IF97-26811-NormBPHProstate
209	416124	2367.G17.GZ43_346155	F	M00073464B:E01	IF97-26811-NormBPHProstate
210	452486	2367.G20.GZ43_346158	F	M00073464D:G12	IF97-26811-NormBPHProstate
211	486366	2367.G22.GZ43_346160	F	M00073465A:H08	IF97-26811-NormBPHProstate
212	417672	2367.I09.GZ43_346195	F	M00073469B:A09	IF97-26811-NormBPHProstate
213	4481	2367.I15.GZ43_346201	F	M00073469D:A06	IF97-26811-NormBPHProstate
214	11528	2367.I22.GZ43_346208	F	M00073470D:A01	IF97-26811-NormBPHProstate
215	552537	2367.K06.GZ43_346240	F	M00073474A:G11	IF97-26811-NormBPHProstate
216	1049007	2367.K13.GZ43_346247	F	M00073474C:F08	IF97-26811-NormBPHProstate
217	14533	2367.K24.GZ43_346258	F	M00073475D:E05	IF97-26811-NormBPHProstate
218	192060	2367.L11.GZ43_346269	F	M00073478C:A07	IF97-26811-NormBPHProstate
219	571816	2367.M06.GZ43_346288	F	M00073483B:C07	IF97-26811-NormBPHProstate
220	660248	2367.M14.GZ43_346296	F	M00073484B:A05	IF97-26811-NormBPHProstate
221	192060	2367.M16.GZ43_346298	F	M00073484C:B04	IF97-26811-NormBPHProstate
222	606908	2367.M19.GZ43_346301	F	M00073486A:A12	IF97-26811-NormBPHProstate
223	466749	2367.N05.GZ43_346311	F	M00073487A:C07	IF97-26811-NormBPHProstate
224	396325	2367.N16.GZ43_346322	F	M00073489B:A07	IF97-26811-NormBPHProstate
225	400167	2367.O08.GZ43_346338	F	M00073493A:E12	IF97-26811-NormBPHProstate
226	446968	2367.O16.GZ43_346346	F	M00073493D:F05	IF97-26811-NormBPHProstate
227	160534	2367.O21.GZ43_346351	F	M00073495B:G11	IF97-26811-NormBPHProstate
228	621397	2367.P12.GZ43_346366	F	M00073497C:D03	IF97-26811-NormBPHProstate
229	391679	2368.A13.GZ43_346391	F	M00073504D:F03	IF97-26811-NormBPHProstate
230	605923	2368.A23.GZ43_346401	F	M00073505D:F01	IF97-26811-NormBPHProstate
231	416124	2368.B18.GZ43_346420	F	M00073509B:B11	IF97-26811-NormBPHProstate
232	464200	2368.B20.GZ43_346422	F	M00073509B:E03	IF97-26811-NormBPHProstate
233	640970	2368.C15.GZ43_346441	F	M00073513A:G07	IF97-26811-NormBPHProstate
234	858675	2368.C19.GZ43_346445	F	M00073513D:A11	IF97-26811-NormBPHProstate
235	467877	2368.D08.GZ43_346458	F	M00073515A:F09	IF97-26811-NormBPHProstate
236	752831	2368.D20.GZ43_346470	F	M00073517A:A06	IF97-26811-NormBPHProstate
237	423085	2368.E06.GZ43_346480	F	M00073517D:F11	IF97-26811-NormBPHProstate
238	474125	2368.F12.GZ43_346510	F	M00073520D:A04	IF97-26811-NormBPHProstate
239	70469	2368.F22.GZ43_346520	F	M00073524A:A03	IF97-26811-NormBPHProstate
240	39999	2368.G01.GZ43_346523	F	M00073524A:G05	IF97-26811-NormBPHProstate
241	847088	2368.H07.GZ43_346553	F	M00073529A:F03	IF97-26811-NormBPHProstate
242	510539	2368.H12.GZ43_346558	F	M00073530B:A02	IF97-26811-NormBPHProstate
243	402167	2368.H15.GZ43_346561	F	M00073531B:H02	IF97-26811-NormBPHProstate
244	389538	2368.H17.GZ43_346563	F	M00073531C:F12	IF97-26811-NormBPHProstate
245	858540	2368.I04.GZ43_346574	F	M00073537B:A12	IF97-26811-NormBPHProstate
246	113786	2368.I23.GZ43_346593	F	M00073539C:H05	IF97-26811-NormBPHProstate
247	468400	2368.J18.GZ43_346612	F	M00073541B:C10	IF97-26811-NormBPHProstate
248	605923	2368.K19.GZ43_346637	F	M00073547B:F04	IF97-26811-NormBPHProstate
249	1796	2368.K21.GZ43_346639	F	M00073547C:D02	IF97-26811-NormBPHProstate
250	15951	2368.L06.GZ43_346648	F	M00073549B:B03	IF97-26811-NormBPHProstate

Table 2

SEQ ID	CLUSTER	SEQNAME	ORIENT	CLONE ID	LIBRARY
251	43907	2368.L24.GZ43_346666	F	M00073551B:E10	IF97-26811-NormBPHProstate
252	48738	2368.M19.GZ43_346685	F	M00073552A:F06	IF97-26811-NormBPHProstate
253	597681	2368.N03.GZ43_346693	F	M00073554A:C01	IF97-26811-NormBPHProstate
254	821039	2368.N05.GZ43_346695	F	M00073554A:G04	IF97-26811-NormBPHProstate
255	954391	2368.N06.GZ43_346696	F	M00073554B:A08	IF97-26811-NormBPHProstate
256	404368	2368.N08.GZ43_346698	F	M00073554B:D11	IF97-26811-NormBPHProstate
257	460493	2368.N15.GZ43_346705	F	M00073555A:B09	IF97-26811-NormBPHProstate
258	778001	2368.N23.GZ43_346713	F	M00073555D:B04	IF97-26811-NormBPHProstate
259	404081	2368.O03.GZ43_346717	F	M00073557A:A05	IF97-26811-NormBPHProstate
260	368947	2368.O11.GZ43_346725	F	M00073558A:A02	IF97-26811-NormBPHProstate
261	421869	2368.P13.GZ43_346751	F	M00073561C:A04	IF97-26811-NormBPHProstate
262	621573	2535.A08.GZ43_370095	F	M00073565D:E05	IF97-26811-NormBPHProstate
263	640911	2535.A10.GZ43_370097	F	M00073566A:G01	IF97-26811-NormBPHProstate
264	450754	2535.B09.GZ43_370120	F	M00073568A:G06	IF97-26811-NormBPHProstate
265	455862	2535.B12.GZ43_370123	F	M00073568C:G07	IF97-26811-NormBPHProstate
266	22339	2535.B20.GZ43_370131	F	M00073569A:H02	IF97-26811-NormBPHProstate
267	372750	2535.C23.GZ43_370158	F	M00073571A:F12	IF97-26811-NormBPHProstate
268	677530	2535.E22.GZ43_370205	F	M00073575B:H12	IF97-26811-NormBPHProstate
269	605923	2535.F05.GZ43_370212	F	M00073576B:E03	IF97-26811-NormBPHProstate
270	35578	2535.F07.GZ43_370214	F	M00073576C:C11	IF97-26811-NormBPHProstate
271	568661	2535.F11.GZ43_370218	F	M00073577B:D12	IF97-26811-NormBPHProstate
272	64401	2535.G02.GZ43_370233	F	M00073579B:A04	IF97-26811-NormBPHProstate
273	76555	2535.G13.GZ43_370244	F	M00073580A:D08	IF97-26811-NormBPHProstate
274	36568	2535.J20.GZ43_370323	F	M00073587D:E12	IF97-26811-NormBPHProstate
275	533888	2535.K01.GZ43_370328	F	M00073588B:H07	IF97-26811-NormBPHProstate
276	13301	2535.L03.GZ43_370354	F	M00073590C:F07	IF97-26811-NormBPHProstate
277	52735	2535.L18.GZ43_370369	F	M00073592B:D09	IF97-26811-NormBPHProstate
278	33508	2535.M11.GZ43_370386	F	M00073594B:B11	IF97-26811-NormBPHProstate
279	436659	2535.N06.GZ43_370405	F	M00073595D:A11	IF97-26811-NormBPHProstate
280	451707	2535.O07.GZ43_370430	F	M00073598D:E11	IF97-26811-NormBPHProstate
281	481445	2535.O13.GZ43_370436	F	M00073599C:E08	IF97-26811-NormBPHProstate
282	135469	2535.P02.GZ43_370449	F	M00073601A:B06	IF97-26811-NormBPHProstate
283	36102	2535.P06.GZ43_370453	F	M00073601A:F07	IF97-26811-NormBPHProstate
284	6712	2535.P14.GZ43_370461	F	M00073601D:D08	IF97-26811-NormBPHProstate
285	87043	2536.A06.GZ43_370477	F	M00073603A:F04	IF97-26811-NormBPHProstate
286	375483	2536.A07.GZ43_370478	F	M00073603B:C03	IF97-26811-NormBPHProstate
287	415500	2536.A08.GZ43_370479	F	M00073603C:A11	IF97-26811-NormBPHProstate
288	7368	2536.A09.GZ43_370480	F	M00073603C:C02	IF97-26811-NormBPHProstate
289	553460	2536.A14.GZ43_370485	F	M00073603D:E07	IF97-26811-NormBPHProstate
290	210361	2536.A19.GZ43_370490	F	M00073604B:B07	IF97-26811-NormBPHProstate
291	260521	2536.A20.GZ43_370491	F	M00073604B:H06	IF97-26811-NormBPHProstate
292	70406	2536.A22.GZ43_370493	F	M00073604C:H09	IF97-26811-NormBPHProstate
293	21817	2536.B06.GZ43_370501	F	M00073605B:F10	IF97-26811-NormBPHProstate
294	62816	2536.B07.GZ43_370502	F	M00073605B:F11	IF97-26811-NormBPHProstate
295	10376	2536.B15.GZ43_370510	F	M00073606D:F12	IF97-26811-NormBPHProstate
296	35707	2536.C12.GZ43_370531	F	M00073610A:F06	IF97-26811-NormBPHProstate
297	738158	2536.D17.GZ43_370560	F	M00073614B:A12	IF97-26811-NormBPHProstate
298	974091	2536.D20.GZ43_370563	F	M00073614B:G09	IF97-26811-NormBPHProstate
299	374280	2536.D22.GZ43_370565	F	M00073614C:F06	IF97-26811-NormBPHProstate
300	375209	2536.E08.GZ43_370575	F	M00073615D:E03	IF97-26811-NormBPHProstate

Table 2

SEQ ID	CLUSTER	SEQNAME	ORIENT	CLONE ID	LIBRARY
301	176266	2536.E11.GZ43_370578	F	M00073616A:F06	IF97-26811-NormBPHProstate
302	31475	2536.E21.GZ43_370588	F	M00073617A:H04	IF97-26811-NormBPHProstate
303	235423	2536.G05.GZ43_370620	F	M00073620A:G05	IF97-26811-NormBPHProstate
304	88462	2536.G20.GZ43_370635	F	M00073621D:A04	IF97-26811-NormBPHProstate
305	186007	2536.G21.GZ43_370636	F	M00073621D:D02	IF97-26811-NormBPHProstate
306	12346	2536.G22.GZ43_370637	F	M00073621D:H05	IF97-26811-NormBPHProstate
307	98685	2536.H08.GZ43_370647	F	M00073623D:H10	IF97-26811-NormBPHProstate
308	861172	2536.H20.GZ43_370659	F	M00073625C:D09	IF97-26811-NormBPHProstate
309	164426	2536.I05.GZ43_370668	F	M00073626D:A01	IF97-26811-NormBPHProstate
310	428727	2536.I15.GZ43_370678	F	M00073628A:E03	IF97-26811-NormBPHProstate
311	573	2536.J05.GZ43_370692	F	M00073630A:C03	IF97-26811-NormBPHProstate
312	883034	2536.J09.GZ43_370696	F	M00073630B:E09	IF97-26811-NormBPHProstate
313	856743	2536.J11.GZ43_370698	F	M00073630C:D02	IF97-26811-NormBPHProstate
314	60888	2536.K12.GZ43_370723	F	M00073632A:B12	IF97-26811-NormBPHProstate
315	207397	2536.K21.GZ43_370732	F	M00073632C:A03	IF97-26811-NormBPHProstate
316	177456	2536.L18.GZ43_370753	F	M00073633D:A04	IF97-26811-NormBPHProstate
317	47454	2536.L22.GZ43_370757	F	M00073633D:G04	IF97-26811-NormBPHProstate
318	33967	2536.M10.GZ43_370769	F	M00073634C:H08	IF97-26811-NormBPHProstate
319	402043	2536.N05.GZ43_370788	F	M00073635D:C10	IF97-26811-NormBPHProstate
320	831101	2536.N20.GZ43_370803	F	M00073636C:F03	IF97-26811-NormBPHProstate
321	736938	2536.O12.GZ43_370819	F	M00073637C:B01	IF97-26811-NormBPHProstate
322	40144	2536.O14.GZ43_370821	F	M00073637C:E04	IF97-26811-NormBPHProstate
323	13473	2536.O22.GZ43_370829	F	M00073638A:A12	IF97-26811-NormBPHProstate
324	23951	2536.P14.GZ43_370845	F	M00073638D:D10	IF97-26811-NormBPHProstate
325	72334	2536.P17.GZ43_370848	F	M00073639A:G08	IF97-26811-NormBPHProstate
326	140322	2536.P22.GZ43_370853	F	M00073639B:F02	IF97-26811-NormBPHProstate
327	42714	2536.M04.GZ43_370763	F	M00073634B:C12	IF97-26811-NormBPHProstate
328	25714	2537.A21.GZ43_370876	F	M00073640B:G08	IF97-26811-NormBPHProstate
329	177456	2537.A23.GZ43_370878	F	M00073640C:A03	IF97-26811-NormBPHProstate
330	7546	2537.B07.GZ43_370886	F	M00073640D:A11	IF97-26811-NormBPHProstate
331	21102	2537.B14.GZ43_370893	F	M00073640D:G07	IF97-26811-NormBPHProstate
332	375856	2537.C10.GZ43_370913	F	M00073641B:G07	IF97-26811-NormBPHProstate
333	15080	2537.C18.GZ43_370921	F	M00073641C:E04	IF97-26811-NormBPHProstate
334	44198	2537.D11.GZ43_370938	F	M00073643B:E11	IF97-26811-NormBPHProstate
335	598913	2537.D20.GZ43_370947	F	M00073644A:G12	IF97-26811-NormBPHProstate
336	374952	2537.F01.GZ43_370976	F	M00073646A:C01	IF97-26811-NormBPHProstate
337	374839	2537.F18.GZ43_370993	F	M00073647B:H07	IF97-26811-NormBPHProstate
338	21817	2537.G05.GZ43_371004	F	M00073649A:A03	IF97-26811-NormBPHProstate
339	3211	2537.G09.GZ43_371008	F	M00073649A:G08	IF97-26811-NormBPHProstate
340	397144	2537.H24.GZ43_371047	F	M00073651C:F06	IF97-26811-NormBPHProstate
341	379025	2537.I03.GZ43_371050	F	M00073651C:H07	IF97-26811-NormBPHProstate
342	7368	2537.I08.GZ43_371055	F	M00073652D:B11	IF97-26811-NormBPHProstate
343	350	2537.J07.GZ43_371078	F	M00073655B:A04	IF97-26811-NormBPHProstate
344	55140	2537.J23.GZ43_371094	F	M00073657B:D05	IF97-26811-NormBPHProstate
345	4031	2537.K17.GZ43_371112	F	M00073659C:D03	IF97-26811-NormBPHProstate
346	48711	2537.L23.GZ43_371142	F	M00073663A:E02	IF97-26811-NormBPHProstate
347	744278	2537.M11.GZ43_371154	F	M00073663D:G06	IF97-26811-NormBPHProstate
348	436755	2537.M14.GZ43_371157	F	M00073664A:E03	IF97-26811-NormBPHProstate
349	148227	2537.N12.GZ43_371179	F	M00073666B:B01	IF97-26811-NormBPHProstate
350	402325	2537.N23.GZ43_371190	F	M00073668A:H03	IF97-26811-NormBPHProstate

Table 2

SEQ ID	CLUSTER	SEQNAME	ORIENT	CLONE ID	LIBRARY
351	14002	2537.N24.GZ43_371191	F	M00073668B:A08	IF97-26811-NormBPHProstate
352	714906	2537.O05.GZ43_371196	F	M00073668D:D10	IF97-26811-NormBPHProstate
353	557739	2537.O10.GZ43_371201	F	M00073669A:F04	IF97-26811-NormBPHProstate
354	296	2537.O13.GZ43_371204	F	M00073669B:E12	IF97-26811-NormBPHProstate
355	373515	2537.O21.GZ43_371212	F	M00073669D:G10	IF97-26811-NormBPHProstate
356	455443	2537.P14.GZ43_371229	F	M00073671B:D09	IF97-26811-NormBPHProstate
357	12272	2538.F24.GZ43_371383	F	M00073687A:D11	IF97-26811-NormBPHProstate
358	380624	2538.M23.GZ43_371550	F	M00073699C:E02	IF97-26811-NormBPHProstate
359	4442	2538.N23.GZ43_371574	F	M00073701D:G10	IF97-26811-NormBPHProstate
360	556517	2538.A08.GZ43_371247	F	M00073672D:B07	IF97-26811-NormBPHProstate
361	530582	2538.A10.GZ43_371249	F	M00073672D:E09	IF97-26811-NormBPHProstate
362	8126	2538.A12.GZ43_371251	F	M00073673A:D11	IF97-26811-NormBPHProstate
363	733673	2538.B03.GZ43_371266	F	M00073673D:H03	IF97-26811-NormBPHProstate
364	446	2538.B15.GZ43_371278	F	M00073674D:F10	IF97-26811-NormBPHProstate
365	449576	2538.B20.GZ43_371283	F	M00073676A:G08	IF97-26811-NormBPHProstate
366	555630	2538.C07.GZ43_371294	F	M00073676D:H04	IF97-26811-NormBPHProstate
367	19627	2538.C14.GZ43_371301	F	M00073677B:F01	IF97-26811-NormBPHProstate
368	401402	2538.D03.GZ43_371314	F	M00073678B:E08	IF97-26811-NormBPHProstate
369	296	2538.D04.GZ43_371315	F	M00073678B:H02	IF97-26811-NormBPHProstate
370	3843	2538.D11.GZ43_371322	F	M00073679A:D06	IF97-26811-NormBPHProstate
371	1239	2538.E01.GZ43_371336	F	M00073680D:F11	IF97-26811-NormBPHProstate
372	676448	2538.E05.GZ43_371340	F	M00073681A:F12	IF97-26811-NormBPHProstate
373	423064	2538.E22.GZ43_371357	F	M00073684B:F10	IF97-26811-NormBPHProstate
374	449749	2538.F03.GZ43_371362	F	M00073685A:F07	IF97-26811-NormBPHProstate
375	72417	2538.H02.GZ43_371409	F	M00073688C:A12	IF97-26811-NormBPHProstate
376	4650	2538.H08.GZ43_371415	F	M00073688D:C11	IF97-26811-NormBPHProstate
377	673484	2538.H19.GZ43_371426	F	M00073689C:C09	IF97-26811-NormBPHProstate
378	134226	2538.I06.GZ43_371437	F	M00073690B:G04	IF97-26811-NormBPHProstate
379	9516	2538.I17.GZ43_371448	F	M00073691A:G02	IF97-26811-NormBPHProstate
380	400463	2538.J10.GZ43_371465	F	M00073692D:H02	IF97-26811-NormBPHProstate
381	48289	2538.K17.GZ43_371496	F	M00073695C:D11	IF97-26811-NormBPHProstate
382	35380	2538.L09.GZ43_371512	F	M00073696C:D11	IF97-26811-NormBPHProstate
383	375810	2538.L11.GZ43_371514	F	M00073696D:A08	IF97-26811-NormBPHProstate
384	640911	2538.L20.GZ43_371523	F	M00073697C:F11	IF97-26811-NormBPHProstate
385	374382	2538.M16.GZ43_371543	F	M00073699B:D02	IF97-26811-NormBPHProstate
386	448604	2538.M17.GZ43_371544	F	M00073699B:D09	IF97-26811-NormBPHProstate
387	447798	2538.N06.GZ43_371557	F	M00073700A:C09	IF97-26811-NormBPHProstate
388	452289	2538.N11.GZ43_371562	F	M00073700B:D12	IF97-26811-NormBPHProstate
389	518084	2538.P16.GZ43_371615	F	M00073707B:G08	IF97-26811-NormBPHProstate
390	706359	2554.A04.GZ43_375851	F	M00073708D:E10	IF97-26811-NormBPHProstate
391	901160	2554.A06.GZ43_375853	F	M00073708D:F03	IF97-26811-NormBPHProstate
392	510479	2554.A12.GZ43_375859	F	M00073709B:F01	IF97-26811-NormBPHProstate
393	149529	2554.A15.GZ43_375862	F	M00073709C:A01	IF97-26811-NormBPHProstate
394	727966	2554.A16.GZ43_375863	F	M00073709C:A02	IF97-26811-NormBPHProstate
395	398682	2554.A23.GZ43_375870	F	M00073710B:A09	IF97-26811-NormBPHProstate
396	57638	2554.B12.GZ43_375883	F	M00073710D:G06	IF97-26811-NormBPHProstate
397	8956	2554.B17.GZ43_375888	F	M00073711C:E12	IF97-26811-NormBPHProstate
398	599028	2554.D02.GZ43_375921	F	M00073713D:E07	IF97-26811-NormBPHProstate
399	497138	2554.D09.GZ43_375928	F	M00073715A:F05	IF97-26811-NormBPHProstate
400	735042	2554.D12.GZ43_375931	F	M00073715B:B06	IF97-26811-NormBPHProstate

Table 2

SEQ ID	CLUSTER	SEQNAME	ORIENT	CLONE ID	LIBRARY
401	42867	2554.E10.GZ43_375953	F	M00073717C:A12	IF97-26811-NormBPHProstate
402	29906	2554.E17.GZ43_375960	F	M00073718A:F11	IF97-26811-NormBPHProstate
403	560612	2554.F20.GZ43_375987	F	M00073720D:H11	IF97-26811-NormBPHProstate
404	980	2554.G22.GZ43_376013	F	M00073724D:F04	IF97-26811-NormBPHProstate
405	642041	2554.I10.GZ43_376049	F	M00073732C:B09	IF97-26811-NormBPHProstate
406	163500	2554.I15.GZ43_376054	F	M00073733A:A05	IF97-26811-NormBPHProstate
407	1522	2554.I18.GZ43_376057	F	M00073733A:E03	IF97-26811-NormBPHProstate
408	573764	2554.J15.GZ43_376078	F	M00073735C:E04	IF97-26811-NormBPHProstate
409	40330	2554.K08.GZ43_376095	F	M00073737A:C12	IF97-26811-NormBPHProstate
410	525011	2554.L09.GZ43_376120	F	M00073739D:B04	IF97-26811-NormBPHProstate
411	847088	2554.L18.GZ43_376129	F	M00073740B:F08	IF97-26811-NormBPHProstate
412	36174	2554.M14.GZ43_376145	F	M00073741C:D05	IF97-26811-NormBPHProstate
413	455254	2554.N09.GZ43_376168	F	M00073743C:F03	IF97-26811-NormBPHProstate
414	89912	2554.O17.GZ43_376200	F	M00073746A:H03	IF97-26811-NormBPHProstate
415	451707	2554.P16.GZ43_376223	F	M00073748A:F09	IF97-26811-NormBPHProstate
416	43900	2554.P17.GZ43_376224	F	M00073748B:A12	IF97-26811-NormBPHProstate
417	752831	2554.P23.GZ43_376230	F	M00073748B:F07	IF97-26811-NormBPHProstate
418	558581	2565.B13.GZ43_398139	F	M00073750A:E08	IF97-26811-NormBPHProstate
419	7307	2565.B15.GZ43_398171	F	M00073750A:H08	IF97-26811-NormBPHProstate
420	403109	2565.B18.GZ43_398219	F	M00073750B:D05	IF97-26811-NormBPHProstate
421	60809	2565.C02.GZ43_397964	F	M00073750C:G06	IF97-26811-NormBPHProstate
422	375711	2565.C17.GZ43_398204	F	M00073751D:A06	IF97-26811-NormBPHProstate
423	1371	2565.D06.GZ43_398029	F	M00073753B:B05	IF97-26811-NormBPHProstate
424	402399	2565.D22.GZ43_398285	F	M00073754B:D05	IF97-26811-NormBPHProstate
425	18508	2565.E03.GZ43_397982	F	M00073754B:H02	IF97-26811-NormBPHProstate
426	617	2565.E05.GZ43_398014	F	M00073754C:C01	IF97-26811-NormBPHProstate
427	147634	2565.F18.GZ43_398223	F	M00073758C:G03	IF97-26811-NormBPHProstate
428	10334	2565.G20.GZ43_398256	F	M00073760B:B11	IF97-26811-NormBPHProstate
429	1530	2565.H01.GZ43_397953	F	M00073760D:F04	IF97-26811-NormBPHProstate
430	373261	2565.H12.GZ43_398129	F	M00073762A:B09	IF97-26811-NormBPHProstate
431	18746	2565.H21.GZ43_398273	F	M00073762D:C02	IF97-26811-NormBPHProstate
432	524083	2565.H24.GZ43_398321	F	M00073763A:D06	IF97-26811-NormBPHProstate
433	724819	2565.I22.GZ43_398290	F	M00073764B:B09	IF97-26811-NormBPHProstate
434	401809	2565.J08.GZ43_398067	F	M00073764D:A07	IF97-26811-NormBPHProstate
435	424776	2565.J09.GZ43_398083	F	M00073764D:B12	IF97-26811-NormBPHProstate
436	648899	2565.J13.GZ43_398147	F	M00073765A:E02	IF97-26811-NormBPHProstate
437	752623	2565.J19.GZ43_398243	F	M00073765C:B01	IF97-26811-NormBPHProstate
438	193333	2565.K04.GZ43_398004	F	M00073766A:B07	IF97-26811-NormBPHProstate
439	493811	2565.K07.GZ43_398052	F	M00073766B:B07	IF97-26811-NormBPHProstate
440	46581	2565.K09.GZ43_398084	F	M00073766B:C04	IF97-26811-NormBPHProstate
441	19736	2565.L21.GZ43_398277	F	M00073769D:G10	IF97-26811-NormBPHProstate
442	449073	2565.M14.GZ43_398166	F	M00073772B:E07	IF97-26811-NormBPHProstate
443	42891	2565.M24.GZ43_398326	F	M00073773A:F05	IF97-26811-NormBPHProstate
444	456043	2565.N02.GZ43_397975	F	M00073773A:G04	IF97-26811-NormBPHProstate
445	70411	2565.N03.GZ43_397991	F	M00073773B:A09	IF97-26811-NormBPHProstate
446	174228	2565.N20.GZ43_398263	F	M00073774C:G12	IF97-26811-NormBPHProstate
447	448795	2565.O07.GZ43_398056	F	M00073776C:F11	IF97-26811-NormBPHProstate
448	452714	2565.O12.GZ43_398136	F	M00073777A:A01	IF97-26811-NormBPHProstate
449	70908	2565.O16.GZ43_398200	F	M00073777A:H03	IF97-26811-NormBPHProstate
450	562386	2565.P08.GZ43_398073	F	M00073779B:B11	IF97-26811-NormBPHProstate

Table 2

SEQ ID	CLUSTER	SEQNAME	ORIENT	CLONE ID	LIBRARY
451	21817	2565.P24.GZ43_398329	F	M00073784A:A12	IF97-26811-NormBPHProstate
452	696086	2540.A24.GZ43_372031	F	M00073785C:A05	IF97-26811-NormBPHProstate
453	36174	2540.B02.GZ43_372033	F	M00073785D:D01	IF97-26811-NormBPHProstate
454	481445	2540.C04.GZ43_372059	F	M00073787D:H12	IF97-26811-NormBPHProstate
455	552537	2540.C10.GZ43_372065	F	M00073788C:A10	IF97-26811-NormBPHProstate
456	507628	2540.D02.GZ43_372081	F	M00073790C:E07	IF97-26811-NormBPHProstate
457	113786	2540.E09.GZ43_372112	F	M00073793C:E09	IF97-26811-NormBPHProstate
458	454796	2540.F03.GZ43_372130	F	M00073795A:F03	IF97-26811-NormBPHProstate
459	134637	2540.F05.GZ43_372132	F	M00073795B:B05	IF97-26811-NormBPHProstate
460	450227	2540.F06.GZ43_372133	F	M00073795B:B09	IF97-26811-NormBPHProstate
461	23300	2540.F13.GZ43_372140	F	M00073796A:C03	IF97-26811-NormBPHProstate
462	57350	2540.G11.GZ43_372162	F	M00073798A:H03	IF97-26811-NormBPHProstate
463	633752	2540.H07.GZ43_372182	F	M00073800D:F08	IF97-26811-NormBPHProstate
464	516985	2540.H13.GZ43_372188	F	M00073801B:A10	IF97-26811-NormBPHProstate
465	376272	2540.I10.GZ43_372209	F	M00073802D:B11	IF97-26811-NormBPHProstate
466	39862	2540.K12.GZ43_372259	F	M00073806D:C09	IF97-26811-NormBPHProstate
467	525801	2540.M05.GZ43_372300	F	M00073809C:E09	IF97-26811-NormBPHProstate
468	830453	2540.M22.GZ43_372317	F	M00073810C:F05	IF97-26811-NormBPHProstate
469	454796	2540.P02.GZ43_372369	F	M00073813D:B06	IF97-26811-NormBPHProstate
470	572170	2540.P13.GZ43_372380	F	M00073814C:B04	IF97-26811-NormBPHProstate
471	44044	2540.B15.GZ43_372046	F	M00073786D:B03	IF97-26811-NormBPHProstate
472	553297	2540.C19.GZ43_372074	F	M00073789C:B06	IF97-26811-NormBPHProstate
473	402167	2540.C21.GZ43_372076	F	M00073790A:A12	IF97-26811-NormBPHProstate
474	38334	2540.D19.GZ43_372098	F	M00073792B:A03	IF97-26811-NormBPHProstate
475	477271	2540.E17.GZ43_372120	F	M00073794B:G09	IF97-26811-NormBPHProstate
476	519354	2540.F01.GZ43_372128	F	M00073794D:G07	IF97-26811-NormBPHProstate
477	528957	2540.F15.GZ43_372142	F	M00073796A:D08	IF97-26811-NormBPHProstate
478	89912	2540.F17.GZ43_372144	F	M00073796B:A03	IF97-26811-NormBPHProstate
479	495563	2540.G16.GZ43_372167	F	M00073799A:A09	IF97-26811-NormBPHProstate
480	626993	2540.G19.GZ43_372170	F	M00073799A:G02	IF97-26811-NormBPHProstate
481	429609	2540.H01.GZ43_372176	F	M00073799D:G04	IF97-26811-NormBPHProstate
482	932437	2540.I17.GZ43_372216	F	M00073803B:B03	IF97-26811-NormBPHProstate
483	427559	2540.I20.GZ43_372219	F	M00073803B:C06	IF97-26811-NormBPHProstate
484	14214	2540.M15.GZ43_372310	F	M00073810B:G10	IF97-26811-NormBPHProstate
485	379689	2540.M18.GZ43_372313	F	M00073810C:A06	IF97-26811-NormBPHProstate
486	552374	2540.O16.GZ43_372359	F	M00073813A:E06	IF97-26811-NormBPHProstate
487	743053	2540.O19.GZ43_372362	F	M00073813B:A01	IF97-26811-NormBPHProstate
488	474125	2541.A06.GZ43_372397	F	M00073815D:E02	IF97-26811-NormBPHProstate
489	498886	2541.B15.GZ43_372430	F	M00073818A:A06	IF97-26811-NormBPHProstate
490	993554	2541.D03.GZ43_372466	F	M00073819D:C11	IF97-26811-NormBPHProstate
491	7170	2541.D14.GZ43_372477	F	M00073821A:B10	IF97-26811-NormBPHProstate
492	36866	2541.D21.GZ43_372484	F	M00073821B:H03	IF97-26811-NormBPHProstate
493	451707	2541.E16.GZ43_372503	F	M00073822C:E02	IF97-26811-NormBPHProstate
494	948383	2541.F05.GZ43_372516	F	M00073824A:C04	IF97-26811-NormBPHProstate
495	454796	2541.F18.GZ43_372529	F	M00073826B:C01	IF97-26811-NormBPHProstate
496	821039	2541.I08.GZ43_372591	F	M00073831B:H09	IF97-26811-NormBPHProstate
497	568204	2541.I17.GZ43_372600	F	M00073832A:A06	IF97-26811-NormBPHProstate
498	652099	2541.I23.GZ43_372606	F	M00073832A:G01	IF97-26811-NormBPHProstate
499	723822	2541.I24.GZ43_372607	F	M00073832B:B05	IF97-26811-NormBPHProstate
500	207018	2541.J17.GZ43_372624	F	M00073834A:H10	IF97-26811-NormBPHProstate

Table 2

SEQ ID	CLUSTER	SEQNAME	ORIENT	CLONE ID	LIBRARY
501	2745	2541.J23.GZ43_372630	F	M00073834D:E07	IF97-26811-NormBPHProstate
502	1049007	2541.K02.GZ43_372633	F	M00073834D:H06	IF97-26811-NormBPHProstate
503	558463	2541.K15.GZ43_372646	F	M00073836D:E05	IF97-26811-NormBPHProstate
504	20052	2541.K18.GZ43_372649	F	M00073837B:D12	IF97-26811-NormBPHProstate
505	208449	2541.L02.GZ43_372657	F	M00073838A:H07	IF97-26811-NormBPHProstate
506	853371	2541.L06.GZ43_372661	F	M00073838B:F09	IF97-26811-NormBPHProstate
507	398682	2541.L08.GZ43_372663	F	M00073838B:H06	IF97-26811-NormBPHProstate
508	40241	2541.L12.GZ43_372667	F	M00073838D:E01	IF97-26811-NormBPHProstate
509	423085	2541.L21.GZ43_372676	F	M00073839A:D05	IF97-26811-NormBPHProstate
510	640911	2541.M24.GZ43_372703	F	M00073840D:C08	IF97-26811-NormBPHProstate
511	520370	2541.N01.GZ43_372704	F	M00073841A:A03	IF97-26811-NormBPHProstate
512	643828	2541.P14.GZ43_372765	F	M00073845D:F05	IF97-26811-NormBPHProstate
513	384776	2506.C08.GZ43_366613	F	M00073850A:H09	IF97-26811-NormBPHProstate
514	765	2506.C15.GZ43_366620	F	M00073850D:G04	IF97-26811-NormBPHProstate
515	3188	2506.C18.GZ43_366623	F	M00073851A:C05	IF97-26811-NormBPHProstate
516	20818	2506.C20.GZ43_366625	F	M00073851A:E04	IF97-26811-NormBPHProstate
517	401067	2506.E01.GZ43_366654	F	M00073853C:A01	IF97-26811-NormBPHProstate
518	382	2506.E12.GZ43_366665	F	M00073854B:B04	IF97-26811-NormBPHProstate
519	237334	2506.E18.GZ43_366671	F	M00073854C:F08	IF97-26811-NormBPHProstate
520	379913	2506.G01.GZ43_366702	F	M00073857A:B12	IF97-26811-NormBPHProstate
521	663109	2506.G24.GZ43_366725	F	M00073859A:C09	IF97-26811-NormBPHProstate
522	702885	2506.H20.GZ43_366745	F	M00073860B:F12	IF97-26811-NormBPHProstate
523	374164	2506.I12.GZ43_366761	F	M00073861D:A09	IF97-26811-NormBPHProstate
524	402325	2506.I14.GZ43_366763	F	M00073861D:D08	IF97-26811-NormBPHProstate
525	2660	2506.I24.GZ43_366773	F	M00073862B:D11	IF97-26811-NormBPHProstate
526	373578	2506.J12.GZ43_366785	F	M00073862D:F06	IF97-26811-NormBPHProstate
527	403773	2506.J20.GZ43_366793	F	M00073863B:G09	IF97-26811-NormBPHProstate
528	4290	2506.J22.GZ43_366795	F	M00073863C:D04	IF97-26811-NormBPHProstate
529	117060	2506.K20.GZ43_366817	F	M00073865B:G04	IF97-26811-NormBPHProstate
530	42794	2506.L08.GZ43_366829	F	M00073866A:G07	IF97-26811-NormBPHProstate
531	40541	2506.M05.GZ43_366850	F	M00073867B:E01	IF97-26811-NormBPHProstate
532	401013	2506.M13.GZ43_366858	F	M00073867D:F10	IF97-26811-NormBPHProstate
533	374406	2506.O11.GZ43_366904	F	M00073871B:C12	IF97-26811-NormBPHProstate
534	40094	2506.P07.GZ43_366924	F	M00073872C:B09	IF97-26811-NormBPHProstate
535	374280	2506.P11.GZ43_366928	F	M00073872D:B01	IF97-26811-NormBPHProstate
536	376054	2506.P13.GZ43_366930	F	M00073872D:E10	IF97-26811-NormBPHProstate
537	172474	2506.P19.GZ43_366936	F	M00073873C:A06	IF97-26811-NormBPHProstate
538	8159	2542.A15.GZ43_372790	F	M00073875A:B03	IF97-26811-NormBPHProstate
539	51272	2542.B01.GZ43_372800	F	M00073875C:G02	IF97-26811-NormBPHProstate
540	709796	2542.C20.GZ43_372843	F	M00073878C:A03	IF97-26811-NormBPHProstate
541	380482	2542.D09.GZ43_372856	F	M00073879D:B08	IF97-26811-NormBPHProstate
542	573764	2542.D18.GZ43_372865	F	M00073880B:B02	IF97-26811-NormBPHProstate
543	5105	2542.D19.GZ43_372866	F	M00073880B:B09	IF97-26811-NormBPHProstate
544	551379	2542.F05.GZ43_372900	F	M00073883B:D03	IF97-26811-NormBPHProstate
545	615999	2542.F08.GZ43_372903	F	M00073883B:H03	IF97-26811-NormBPHProstate
546	464200	2542.H02.GZ43_372945	F	M00073886C:C12	IF97-26811-NormBPHProstate
547	743053	2542.I14.GZ43_372981	F	M00073889B:G08	IF97-26811-NormBPHProstate
548	483211	2542.J12.GZ43_373003	F	M00073891A:A06	IF97-26811-NormBPHProstate
549	519354	2542.K05.GZ43_373020	F	M00073892A:E02	IF97-26811-NormBPHProstate
550	595883	2542.K08.GZ43_373023	F	M00073892B:F12	IF97-26811-NormBPHProstate

Table 2

SEQ ID	CLUSTER	SEQNAME	ORIENT	CLONE ID	LIBRARY
551	374817	2542.L03.GZ43_373042	F	M00073893D:A04	IF97-26811-NormBPHProstate
552	604822	2542.M05.GZ43_373068	F	M00073895C:F02	IF97-26811-NormBPHProstate
553	454509	2542.M09.GZ43_373072	F	M00073896A:F07	IF97-26811-NormBPHProstate
554	184489	2542.O05.GZ43_373116	F	M00073899C:E12	IF97-26811-NormBPHProstate
555	565709	2542.P02.GZ43_373137	F	M00073905B:A03	IF97-26811-NormBPHProstate
556	13301	2542.P08.GZ43_373143	F	M00073905D:C11	IF97-26811-NormBPHProstate
557	723485	2542.P19.GZ43_373154	F	M00073907B:B06	IF97-26811-NormBPHProstate
558	418723	2542.F24.GZ43_372919	F	M00073884D:B06	IF97-26811-NormBPHProstate
559	847088	2542.H23.GZ43_372966	F	M00073888C:C10	IF97-26811-NormBPHProstate
560	534076	2542.J21.GZ43_373012	F	M00073891C:A12	IF97-26811-NormBPHProstate
561	240	2542.K21.GZ43_373036	F	M00073893B:C08	IF97-26811-NormBPHProstate
562	58218	2542.M24.GZ43_373087	F	M00073897B:B11	IF97-26811-NormBPHProstate
563	641662	2542.N21.GZ43_373108	F	M00073899A:C02	IF97-26811-NormBPHProstate
564	398642	2542.N22.GZ43_373109	F	M00073899A:D06	IF97-26811-NormBPHProstate
565	452289	2555.B08.GZ43_373191	F	M00073911B:G10	IF97-26811-NormBPHProstate
566	621397	2555.B20.GZ43_373203	F	M00073912B:C04	IF97-26811-NormBPHProstate
567	641662	2555.D22.GZ43_373253	F	M00073916A:B07	IF97-26811-NormBPHProstate
568	13903	2555.E20.GZ43_373275	F	M00073917B:B07	IF97-26811-NormBPHProstate
569	727966	2555.F16.GZ43_373295	F	M00073918C:B03	IF97-26811-NormBPHProstate
570	702885	2555.H18.GZ43_373345	F	M00073921B:H12	IF97-26811-NormBPHProstate
571	525801	2555.I05.GZ43_373356	F	M00073922C:E02	IF97-26811-NormBPHProstate
572	11561	2555.I21.GZ43_373372	F	M00073923C:A04	IF97-26811-NormBPHProstate
573	602052	2555.J07.GZ43_373382	F	M00073924B:H03	IF97-26811-NormBPHProstate
574	453398	2555.K17.GZ43_373416	F	M00073927D:E09	IF97-26811-NormBPHProstate
575	528957	2555.M18.GZ43_373465	F	M00073931D:E02	IF97-26811-NormBPHProstate
576	652099	2555.N05.GZ43_373476	F	M00073932D:G05	IF97-26811-NormBPHProstate
577	16641	2555.P05.GZ43_373524	F	M00073936D:E05	IF97-26811-NormBPHProstate
578	517481	2555.P22.GZ43_373541	F	M00073938B:D11	IF97-26811-NormBPHProstate
579	411128	2555.A11.GZ43_373170	F	M00073908C:D09	IF97-26811-NormBPHProstate
580	558342	2555.E11.GZ43_373266	F	M00073916C:H11	IF97-26811-NormBPHProstate
581	692282	2555.F09.GZ43_373288	F	M00073918A:F07	IF97-26811-NormBPHProstate
582	520370	2555.F10.GZ43_373289	F	M00073918A:G12	IF97-26811-NormBPHProstate
583	271	2555.G11.GZ43_373314	F	M00073919C:B04	IF97-26811-NormBPHProstate
584	525801	2555.H12.GZ43_373339	F	M00073920D:F08	IF97-26811-NormBPHProstate
585	467877	2555.I12.GZ43_373363	F	M00073922D:G04	IF97-26811-NormBPHProstate
586	502358	2555.J10.GZ43_373385	F	M00073924C:G05	IF97-26811-NormBPHProstate
587	15935	2555.K10.GZ43_373409	F	M00073927C:B07	IF97-26811-NormBPHProstate
588	451821	2555.N09.GZ43_373480	F	M00073933B:B12	IF97-26811-NormBPHProstate
589	604822	2556.A02.GZ43_373545	F	M00073938B:F09	IF97-26811-NormBPHProstate
590	50391	2556.B22.GZ43_373589	F	M00073941B:A06	IF97-26811-NormBPHProstate
591	139789	2556.C11.GZ43_373602	F	M00073941D:H09	IF97-26811-NormBPHProstate
592	649670	2556.C19.GZ43_373610	F	M00073942B:C01	IF97-26811-NormBPHProstate
593	20563	2556.D02.GZ43_373617	F	M00073942C:E04	IF97-26811-NormBPHProstate
594	113786	2556.D06.GZ43_373621	F	M00073942D:D09	IF97-26811-NormBPHProstate
595	420371	2556.D09.GZ43_373624	F	M00073942D:G05	IF97-26811-NormBPHProstate
596	1607	2556.E07.GZ43_373646	F	M00073944A:E10	IF97-26811-NormBPHProstate
597	60888	2556.E11.GZ43_373650	F	M00073944A:H05	IF97-26811-NormBPHProstate
598	472262	2556.F11.GZ43_373674	F	M00073944C:H07	IF97-26811-NormBPHProstate
599	171595	2556.F14.GZ43_373677	F	M00073944D:A07	IF97-26811-NormBPHProstate
600	17855	2556.F15.GZ43_373678	F	M00073944D:E12	IF97-26811-NormBPHProstate

Table 2

SEQ ID	CLUSTER	SEQNAME	ORIENT	CLONE ID	LIBRARY
601	842551	2556.G19.GZ43_373706	F	M00073946D:F07	IF97-26811-NormBPHProstate
602	87051	2556.H15.GZ43_373726	F	M00073947C:B01	IF97-26811-NormBPHProstate
603	297358	2556.H19.GZ43_373730	F	M00073947C:E09	IF97-26811-NormBPHProstate
604	22884	2556.I05.GZ43_373740	F	M00073948A:G05	IF97-26811-NormBPHProstate
605	48896	2556.J03.GZ43_373762	F	M00073949A:C09	IF97-26811-NormBPHProstate
606	9047	2556.J15.GZ43_373774	F	M00073949D:C11	IF97-26811-NormBPHProstate
607	1409	2556.J18.GZ43_373777	F	M00073950C:A05	IF97-26811-NormBPHProstate
608	63551	2556.K03.GZ43_373786	F	M00073950D:H12	IF97-26811-NormBPHProstate
609	13629	2556.K07.GZ43_373790	F	M00073952A:G04	IF97-26811-NormBPHProstate
610	850377	2556.L21.GZ43_373828	F	M00073956D:F02	IF97-26811-NormBPHProstate
611	448319	2556.M11.GZ43_373842	F	M00073960A:B12	IF97-26811-NormBPHProstate
612	582134	2556.M16.GZ43_373847	F	M00073960B:A09	IF97-26811-NormBPHProstate
613	946181	2556.N05.GZ43_373860	F	M00073961B:G01	IF97-26811-NormBPHProstate
614	782981	2556.O05.GZ43_373884	F	M00073962D:E04	IF97-26811-NormBPHProstate
615	43910	2556.O11.GZ43_373890	F	M00073963A:G08	IF97-26811-NormBPHProstate
616	154120	2556.O16.GZ43_373895	F	M00073963B:F04	IF97-26811-NormBPHProstate
617	550104	2556.P03.GZ43_373906	F	M00073964B:H07	IF97-26811-NormBPHProstate
618	471364	2557.B09.GZ43_373960	F	M00073967A:A10	IF97-26811-NormBPHProstate
619	398642	2557.B11.GZ43_373962	F	M00073967C:A01	IF97-26811-NormBPHProstate
620	572170	2557.B22.GZ43_373973	F	M00073968B:B06	IF97-26811-NormBPHProstate
621	780111	2557.C11.GZ43_373986	F	M00073968D:F11	IF97-26811-NormBPHProstate
622	472262	2557.D14.GZ43_374013	F	M00073970B:G01	IF97-26811-NormBPHProstate
623	40330	2557.G10.GZ43_374081	F	M00073977D:B10	IF97-26811-NormBPHProstate
624	218375	2557.G20.GZ43_374091	F	M00073978D:A02	IF97-26811-NormBPHProstate
625	520370	2557.H11.GZ43_374106	F	M00073979C:G07	IF97-26811-NormBPHProstate
626	621573	2557.I17.GZ43_374136	F	M00073981C:F08	IF97-26811-NormBPHProstate
627	551744	2557.J14.GZ43_374157	F	M00073983B:D03	IF97-26811-NormBPHProstate
628	35049	2557.J16.GZ43_374159	F	M00073983C:C07	IF97-26811-NormBPHProstate
629	8268	2557.J21.GZ43_374164	F	M00073984B:D04	IF97-26811-NormBPHProstate
630	697955	2557.J22.GZ43_374165	F	M00073984B:E01	IF97-26811-NormBPHProstate
631	727968	2557.K11.GZ43_374178	F	M00073985C:A05	IF97-26811-NormBPHProstate
632	839437	2557.L12.GZ43_374203	F	M00073987B:A09	IF97-26811-NormBPHProstate
633	533888	2557.L23.GZ43_374214	F	M00073988B:C08	IF97-26811-NormBPHProstate
634	555867	2557.M10.GZ43_374225	F	M00073988D:F09	IF97-26811-NormBPHProstate
635	709796	2557.N14.GZ43_374253	F	M00073993A:A05	IF97-26811-NormBPHProstate
636	736938	2557.A03.GZ43_373930	F	M00073965D:A12	IF97-26811-NormBPHProstate
637	867511	2557.B01.GZ43_373952	F	M00073966C:F08	IF97-26811-NormBPHProstate
638	531505	2557.C04.GZ43_373979	F	M00073968C:C09	IF97-26811-NormBPHProstate
639	401809	2557.C05.GZ43_373980	F	M00073968C:F02	IF97-26811-NormBPHProstate
640	796532	2557.F03.GZ43_374050	F	M00073975A:A12	IF97-26811-NormBPHProstate
641	572170	2557.H03.GZ43_374098	F	M00073979B:B05	IF97-26811-NormBPHProstate
642	644299	2557.H05.GZ43_374100	F	M00073979C:B01	IF97-26811-NormBPHProstate
643	633646	2557.J06.GZ43_374149	F	M00073982B:H01	IF97-26811-NormBPHProstate
644	558581	2557.L01.GZ43_374192	F	M00073986C:D07	IF97-26811-NormBPHProstate
645	558579	2557.M06.GZ43_374221	F	M00073988C:G08	IF97-26811-NormBPHProstate
646	448604	2558.A07.GZ43_374318	F	M00074000C:D06	IF97-26811-NormBPHProstate
647	404482	2558.B13.GZ43_374348	F	M00074003C:H06	IF97-26811-NormBPHProstate
648	847088	2558.B24.GZ43_374359	F	M00074004A:H01	IF97-26811-NormBPHProstate
649	451981	2558.C04.GZ43_374363	F	M00074004C:F03	IF97-26811-NormBPHProstate
650	660842	2558.C18.GZ43_374377	F	M00074006C:B12	IF97-26811-NormBPHProstate

Table 2

SEQ ID	CLUSTER	SEQNAME	ORIENT	CLONE ID	LIBRARY
651	558569	2558.D03.GZ43_374386	F	M00074007B:A02	IF97-26811-NormBPHProstate
652	640319	2558.E21.GZ43_374428	F	M00074010B:D07	IF97-26811-NormBPHProstate
653	556827	2558.E24.GZ43_374431	F	M00074011A:F08	IF97-26811-NormBPHProstate
654	10354	2558.F06.GZ43_374437	F	M00074011D:C05	IF97-26811-NormBPHProstate
655	993554	2558.F19.GZ43_374450	F	M00074013B:F07	IF97-26811-NormBPHProstate
656	643828	2558.F21.GZ43_374452	F	M00074013C:C09	IF97-26811-NormBPHProstate
657	48289	2558.G07.GZ43_374462	F	M00074014A:G03	IF97-26811-NormBPHProstate
658	682	2558.G13.GZ43_374468	F	M00074014D:F04	IF97-26811-NormBPHProstate
659	132559	2558.G17.GZ43_374472	F	M00074015A:C03	IF97-26811-NormBPHProstate
660	23300	2558.H13.GZ43_374492	F	M00074017B:G10	IF97-26811-NormBPHProstate
661	510539	2558.H17.GZ43_374496	F	M00074017D:C01	IF97-26811-NormBPHProstate
662	388450	2558.J01.GZ43_374528	F	M00074019D:H05	IF97-26811-NormBPHProstate
663	50661	2558.J03.GZ43_374530	F	M00074020B:G11	IF97-26811-NormBPHProstate
664	715752	2558.J04.GZ43_374531	F	M00074020C:A05	IF97-26811-NormBPHProstate
665	752831	2558.J09.GZ43_374536	F	M00074020D:G10	IF97-26811-NormBPHProstate
666	505984	2558.K02.GZ43_374553	F	M00074021C:H07	IF97-26811-NormBPHProstate
667	672233	2558.K08.GZ43_374559	F	M00074022A:C06	IF97-26811-NormBPHProstate
668	733132	2558.L15.GZ43_374590	F	M00074024B:G07	IF97-26811-NormBPHProstate
669	1037152	2558.L19.GZ43_374594	F	M00074025A:F06	IF97-26811-NormBPHProstate
670	8268	2558.L21.GZ43_374596	F	M00074025B:A12	IF97-26811-NormBPHProstate
671	918867	2558.M11.GZ43_374610	F	M00074026C:H09	IF97-26811-NormBPHProstate
672	64589	2558.M18.GZ43_374617	F	M00074027D:B03	IF97-26811-NormBPHProstate
673	217122	2558.N22.GZ43_374645	F	M00074030D:A12	IF97-26811-NormBPHProstate
674	559336	2558.O09.GZ43_374656	F	M00074032B:H08	IF97-26811-NormBPHProstate
675	535996	2558.O10.GZ43_374657	F	M00074032C:E02	IF97-26811-NormBPHProstate
676	553342	2558.O11.GZ43_374658	F	M00074032C:H07	IF97-26811-NormBPHProstate
677	404368	2558.P16.GZ43_374687	F	M00074036B:C08	IF97-26811-NormBPHProstate
678	823296	2558.P20.GZ43_374691	F	M00074036D:B05	IF97-26811-NormBPHProstate
679	48738	2559.A01.GZ43_374696	F	M00074037A:B03	IF97-26811-NormBPHProstate
680	948383	2559.A09.GZ43_374704	F	M00074038A:G08	IF97-26811-NormBPHProstate
681	738784	2559.A13.GZ43_374708	F	M00074038C:B08	IF97-26811-NormBPHProstate
682	588996	2559.B05.GZ43_374724	F	M00074040A:B06	IF97-26811-NormBPHProstate
683	5013	2559.D05.GZ43_374772	F	M00074043C:A05	IF97-26811-NormBPHProstate
684	954558	2559.G18.GZ43_374857	F	M00074050B:H07	IF97-26811-NormBPHProstate
685	424776	2559.H08.GZ43_374871	F	M00074051C:F05	IF97-26811-NormBPHProstate
686	519176	2559.H20.GZ43_374883	F	M00074052C:E03	IF97-26811-NormBPHProstate
687	448221	2559.I12.GZ43_374899	F	M00074053C:E05	IF97-26811-NormBPHProstate
688	184489	2559.I13.GZ43_374900	F	M00074053C:G11	IF97-26811-NormBPHProstate
689	404482	2559.I17.GZ43_374904	F	M00074053D:D05	IF97-26811-NormBPHProstate
690	13903	2559.J02.GZ43_374913	F	M00074054C:B04	IF97-26811-NormBPHProstate
691	204255	2559.J13.GZ43_374924	F	M00074055A:G08	IF97-26811-NormBPHProstate
692	551744	2559.K12.GZ43_374947	F	M00074057A:B12	IF97-26811-NormBPHProstate
693	395953	2559.L08.GZ43_374967	F	M00074058A:H02	IF97-26811-NormBPHProstate
694	63891	2559.L09.GZ43_374968	F	M00074058B:A10	IF97-26811-NormBPHProstate
695	406961	2559.M02.GZ43_374985	F	M00074059B:G10	IF97-26811-NormBPHProstate
696	23951	2559.M21.GZ43_375004	F	M00074060D:A10	IF97-26811-NormBPHProstate
697	34391	2559.N05.GZ43_375012	F	M00074061B:E01	IF97-26811-NormBPHProstate
698	16978	2559.N13.GZ43_375020	F	M00074063A:B03	IF97-26811-NormBPHProstate
699	13565	2559.N15.GZ43_375022	F	M00074063A:D09	IF97-26811-NormBPHProstate
700	402267	2559.N18.GZ43_375025	F	M00074063B:B12	IF97-26811-NormBPHProstate

Table 2

SEQ ID	CLUSTER	SEQNAME	ORIENT	CLONE ID	LIBRARY
701	35578	2559.P19.GZ43_375074	F	M00074069D:C11	IF97-26811-NormBPHProstate
702	459865	2560.A08.GZ43_375087	F	M00074070D:G05	IF97-26811-NormBPHProstate
703	37848	2560.B11.GZ43_375114	F	M00074075B:A09	IF97-26811-NormBPHProstate
704	66923	2560.B15.GZ43_375118	F	M00074075C:H04	IF97-26811-NormBPHProstate
705	400258	2560.B20.GZ43_375123	F	M00074076B:F04	IF97-26811-NormBPHProstate
706	404368	2560.C15.GZ43_375142	F	M00074079A:E07	IF97-26811-NormBPHProstate
707	333093	2560.E19.GZ43_375194	F	M00074084C:E01	IF97-26811-NormBPHProstate
708	676448	2560.E22.GZ43_375197	F	M00074084D:B04	IF97-26811-NormBPHProstate
709	554127	2560.F07.GZ43_375206	F	M00074085A:H10	IF97-26811-NormBPHProstate
710	171148	2560.F10.GZ43_375209	F	M00074085B:E06	IF97-26811-NormBPHProstate
711	946181	2560.F16.GZ43_375215	F	M00074085D:E08	IF97-26811-NormBPHProstate
712	697955	2560.G13.GZ43_375236	F	M00074087B:C09	IF97-26811-NormBPHProstate
713	453476	2560.G18.GZ43_375241	F	M00074087C:G05	IF97-26811-NormBPHProstate
714	833580	2560.H01.GZ43_375248	F	M00074088B:A03	IF97-26811-NormBPHProstate
715	531583	2560.H12.GZ43_375259	F	M00074088C:E07	IF97-26811-NormBPHProstate
716	558342	2560.H21.GZ43_375268	F	M00074089A:B09	IF97-26811-NormBPHProstate
717	455862	2560.I09.GZ43_375280	F	M00074089D:E03	IF97-26811-NormBPHProstate
718	19627	2560.I16.GZ43_375287	F	M00074090A:E09	IF97-26811-NormBPHProstate
719	9134	2560.K02.GZ43_375321	F	M00074093A:A06	IF97-26811-NormBPHProstate
720	41346	2560.K08.GZ43_375327	F	M00074093B:A03	IF97-26811-NormBPHProstate
721	756337	2560.K10.GZ43_375329	F	M00074093B:C07	IF97-26811-NormBPHProstate
722	397115	2560.K18.GZ43_375337	F	M00074094B:F10	IF97-26811-NormBPHProstate
723	805118	2560.L14.GZ43_375357	F	M00074096D:G12	IF97-26811-NormBPHProstate
724	456113	2560.L15.GZ43_375358	F	M00074097A:F10	IF97-26811-NormBPHProstate
725	677530	2560.L22.GZ43_375365	F	M00074097C:B09	IF97-26811-NormBPHProstate
726	697955	2560.M11.GZ43_375378	F	M00074098C:B09	IF97-26811-NormBPHProstate
727	493811	2560.M23.GZ43_375390	F	M00074099C:B09	IF97-26811-NormBPHProstate
728	127471	2560.N09.GZ43_375400	F	M00074100B:E01	IF97-26811-NormBPHProstate
729	559267	2560.O08.GZ43_375423	F	M00074101D:D07	IF97-26811-NormBPHProstate
730	691653	2560.O12.GZ43_375427	F	M00074102A:C04	IF97-26811-NormBPHProstate
731	966599	2560.P24.GZ43_375463	F	M00074105A:D02	IF97-26811-NormBPHProstate
732	139979	2561.B03.GZ43_376258	F	M00074106C:E03	IF97-26811-NormBPHProstate
733	668962	2561.B12.GZ43_376267	F	M00074107C:C08	IF97-26811-NormBPHProstate
734	217122	2561.C13.GZ43_376292	F	M00074111C:B02	IF97-26811-NormBPHProstate
735	70908	2561.C15.GZ43_376294	F	M00074111C:G11	IF97-26811-NormBPHProstate
736	557771	2561.D14.GZ43_376317	F	M00074116C:A03	IF97-26811-NormBPHProstate
737	629125	2561.E10.GZ43_376337	F	M00074120A:A12	IF97-26811-NormBPHProstate
738	626993	2561.F09.GZ43_376360	F	M00074123B:A03	IF97-26811-NormBPHProstate
739	69779	2561.F13.GZ43_376364	F	M00074123B:G07	IF97-26811-NormBPHProstate
740	752623	2561.I07.GZ43_376430	F	M00074130B:F06	IF97-26811-NormBPHProstate
741	692282	2561.I11.GZ43_376434	F	M00074131A:H09	IF97-26811-NormBPHProstate
742	685244	2561.J01.GZ43_376448	F	M00074132C:F10	IF97-26811-NormBPHProstate
743	597681	2561.K03.GZ43_376474	F	M00074135A:G09	IF97-26811-NormBPHProstate
744	1037152	2561.K10.GZ43_376481	F	M00074135C:E09	IF97-26811-NormBPHProstate
745	533888	2561.L02.GZ43_376497	F	M00074137C:E05	IF97-26811-NormBPHProstate
746	378561	2561.L13.GZ43_376508	F	M00074138D:A01	IF97-26811-NormBPHProstate
747	415520	2561.L14.GZ43_376509	F	M00074138D:A08	IF97-26811-NormBPHProstate
748	415520	2561.L15.GZ43_376510	F	M00074138D:B07	IF97-26811-NormBPHProstate
749	455254	2561.M03.GZ43_376522	F	M00074142B:C11	IF97-26811-NormBPHProstate
750	315533	2561.M09.GZ43_376528	F	M00074142D:A10	IF97-26811-NormBPHProstate

Table 2

SEQ ID	CLUSTER	SEQNAME	ORIENT	CLONE ID	LIBRARY
751	10585	2561.O10.GZ43_376577	F	M00074148B:D09	IF97-26811-NormBPHProstate
752	20052	2561.B18.GZ43_376273	F	M00074108B:C04	IF97-26811-NormBPHProstate
753	558602	2561.E22.GZ43_376349	F	M00074122A:B02	IF97-26811-NormBPHProstate
754	559336	2561.G20.GZ43_376395	F	M00074126B:E12	IF97-26811-NormBPHProstate
755	163602	2561.H17.GZ43_376416	F	M00074128D:C09	IF97-26811-NormBPHProstate
756	756337	2561.I19.GZ43_376442	F	M00074132A:E11	IF97-26811-NormBPHProstate
757	452194	2561.I24.GZ43_376447	F	M00074132B:B07	IF97-26811-NormBPHProstate
758	31453	2561.J18.GZ43_376465	F	M00074134A:G11	IF97-26811-NormBPHProstate
759	220845	2561.O17.GZ43_376584	F	M00074149A:B10	IF97-26811-NormBPHProstate
760	1022935	2561.O19.GZ43_376586	F	M00074149A:F12	IF97-26811-NormBPHProstate
761	396325	2561.P16.GZ43_376607	F	M00074153A:E07	IF97-26811-NormBPHProstate
762	835488	2561.P19.GZ43_376610	F	M00074153D:A05	IF97-26811-NormBPHProstate
763	119614	2561.P23.GZ43_376614	F	M00074154A:D03	IF97-26811-NormBPHProstate
764	400258	2456.A08.GZ43_355836	F	M00074155B:G09	IF97-26811-NormBPHProstate
765	165378	2456.B09.GZ43_355861	F	M00074157C:G08	IF97-26811-NormBPHProstate
766	641662	2456.B12.GZ43_355864	F	M00074157D:G05	IF97-26811-NormBPHProstate
767	648899	2456.B17.GZ43_355869	F	M00074158C:F12	IF97-26811-NormBPHProstate
768	128596	2456.B18.GZ43_355870	F	M00074158C:H10	IF97-26811-NormBPHProstate
769	452194	2456.C01.GZ43_355877	F	M00074159C:A05	IF97-26811-NormBPHProstate
770	534076	2456.C05.GZ43_355881	F	M00074160A:D12	IF97-26811-NormBPHProstate
771	372750	2456.D04.GZ43_355904	F	M00074161C:F04	IF97-26811-NormBPHProstate
772	391508	2456.D05.GZ43_355905	F	M00074162A:B03	IF97-26811-NormBPHProstate
773	7105	2456.E17.GZ43_355941	F	M00074165D:A11	IF97-26811-NormBPHProstate
774	177808	2456.F16.GZ43_355964	F	M00074170A:D09	IF97-26811-NormBPHProstate
775	516526	2456.F23.GZ43_355971	F	M00074170D:F05	IF97-26811-NormBPHProstate
776	372710	2456.G10.GZ43_355982	F	M00074172B:D12	IF97-26811-NormBPHProstate
777	540142	2456.H02.GZ43_355998	F	M00074174A:C02	IF97-26811-NormBPHProstate
778	1041923	2456.H07.GZ43_356003	F	M00074174C:C03	IF97-26811-NormBPHProstate
779	136276	2456.I05.GZ43_356025	F	M00074175D:E04	IF97-26811-NormBPHProstate
780	568661	2456.I09.GZ43_356029	F	M00074176A:A06	IF97-26811-NormBPHProstate
781	403242	2456.I10.GZ43_356030	F	M00074176A:B10	IF97-26811-NormBPHProstate
782	41455	2456.J06.GZ43_356050	F	M00074177B:H08	IF97-26811-NormBPHProstate
783	853431	2456.J18.GZ43_356062	F	M00074178B:G07	IF97-26811-NormBPHProstate
784	423303	2456.J24.GZ43_356068	F	M00074179A:A01	IF97-26811-NormBPHProstate
785	41455	2456.K07.GZ43_356075	F	M00074179C:B01	IF97-26811-NormBPHProstate
786	568204	2456.M05.GZ43_356121	F	M00074184D:A04	IF97-26811-NormBPHProstate
787	642041	2456.M06.GZ43_356122	F	M00074184D:B01	IF97-26811-NormBPHProstate
788	427449	2456.N23.GZ43_356163	F	M00074190B:F09	IF97-26811-NormBPHProstate
789	565709	2456.O10.GZ43_356174	F	M00074191C:D08	IF97-26811-NormBPHProstate
790	676448	2456.O18.GZ43_356182	F	M00074192C:C10	IF97-26811-NormBPHProstate
791	99399	2456.P23.GZ43_356211	F	M00074195D:B09	IF97-26811-NormBPHProstate
792	222887	2457.A21.GZ43_356233	F	M00074197C:A12	IF97-26811-NormBPHProstate
793	778001	2457.B07.GZ43_356243	F	M00074198C:A12	IF97-26811-NormBPHProstate
794	806992	2457.B10.GZ43_356246	F	M00074198D:D10	IF97-26811-NormBPHProstate
795	217122	2457.B13.GZ43_356249	F	M00074199A:C10	IF97-26811-NormBPHProstate
796	733673	2457.C19.GZ43_356279	F	M00074201A:F03	IF97-26811-NormBPHProstate
797	37375	2457.C23.GZ43_356283	F	M00074201C:E12	IF97-26811-NormBPHProstate
798	41702	2457.D05.GZ43_356289	F	M00074202A:A05	IF97-26811-NormBPHProstate
799	13903	2457.D12.GZ43_356296	F	M00074202B:D03	IF97-26811-NormBPHProstate
800	626993	2457.E05.GZ43_356313	F	M00074203D:F01	IF97-26811-NormBPHProstate

Table 2

SEQ ID	CLUSTER	SEQNAME	ORIENT	CLONE ID	LIBRARY
801	474125	2457.E23.GZ43_356331	F	M00074206A:G02	IF97-26811-NormBPHProstate
802	552374	2457.E24.GZ43_356332	F	M00074206A:H12	IF97-26811-NormBPHProstate
803	220576	2457.F02.GZ43_356334	F	M00074206B:F04	IF97-26811-NormBPHProstate
804	450754	2457.F17.GZ43_356349	F	M00074207D:E07	IF97-26811-NormBPHProstate
805	732950	2457.F20.GZ43_356352	F	M00074208B:B05	IF97-26811-NormBPHProstate
806	948383	2457.F23.GZ43_356355	F	M00074208B:F09	IF97-26811-NormBPHProstate
807	218833	2457.G03.GZ43_356359	F	M00074208D:E08	IF97-26811-NormBPHProstate
808	192830	2457.G13.GZ43_356369	F	M00074209D:H11	IF97-26811-NormBPHProstate
809	1017557	2457.G17.GZ43_356373	F	M00074210B:G12	IF97-26811-NormBPHProstate
810	557507	2457.H17.GZ43_356397	F	M00074213A:C06	IF97-26811-NormBPHProstate
811	551338	2457.I12.GZ43_356416	F	M00074215A:F09	IF97-26811-NormBPHProstate
812	839437	2457.J13.GZ43_356441	F	M00074216C:C11	IF97-26811-NormBPHProstate
813	376516	2457.J23.GZ43_356451	F	M00074216D:H03	IF97-26811-NormBPHProstate
814	397140	2457.K03.GZ43_356455	F	M00074217A:H01	IF97-26811-NormBPHProstate
815	28050	2457.K07.GZ43_356459	F	M00074217C:B04	IF97-26811-NormBPHProstate
816	640582	2457.K08.GZ43_356460	F	M00074217C:C09	IF97-26811-NormBPHProstate
817	993554	2457.L04.GZ43_356480	F	M00074219D:F03	IF97-26811-NormBPHProstate
818	465446	2457.L21.GZ43_356497	F	M00074221B:F12	IF97-26811-NormBPHProstate
819	429609	2457.M11.GZ43_356511	F	M00074223B:D12	IF97-26811-NormBPHProstate
820	449482	2457.M20.GZ43_356520	F	M00074224A:G06	IF97-26811-NormBPHProstate
821	31453	2457.N07.GZ43_356531	F	M00074225A:H12	IF97-26811-NormBPHProstate
822	16641	2457.O02.GZ43_356550	F	M00074226C:E06	IF97-26811-NormBPHProstate
823	130924	2458.A10.GZ43_356618	F	M00074230D:B05	IF97-26811-NormBPHProstate
824	184653	2458.A13.GZ43_356621	F	M00074231A:D10	IF97-26811-NormBPHProstate
825	20858	2458.A24.GZ43_356632	F	M00074231D:G11	IF97-26811-NormBPHProstate
826	140585	2458.B08.GZ43_356640	F	M00074232B:G06	IF97-26811-NormBPHProstate
827	547023	2458.B23.GZ43_356655	F	M00074234A:C05	IF97-26811-NormBPHProstate
828	53675	2458.B24.GZ43_356656	F	M00074234A:E07	IF97-26811-NormBPHProstate
829	498886	2458.C06.GZ43_356662	F	M00074234B:F07	IF97-26811-NormBPHProstate
830	10354	2458.C12.GZ43_356668	F	M00074234D:F12	IF97-26811-NormBPHProstate
831	12906	2458.C23.GZ43_356679	F	M00074235C:D06	IF97-26811-NormBPHProstate
832	184489	2458.D06.GZ43_356686	F	M00074236B:E06	IF97-26811-NormBPHProstate
833	37634	2458.D07.GZ43_356687	F	M00074236C:E11	IF97-26811-NormBPHProstate
834	72628	2458.F01.GZ43_356729	F	M00074242D:F09	IF97-26811-NormBPHProstate
835	23957	2458.F06.GZ43_356734	F	M00074243A:H08	IF97-26811-NormBPHProstate
836	29906	2458.G01.GZ43_356753	F	M00074244C:B11	IF97-26811-NormBPHProstate
837	453526	2458.G20.GZ43_356772	F	M00074247B:G11	IF97-26811-NormBPHProstate
838	18644	2458.G21.GZ43_356773	F	M00074247C:E02	IF97-26811-NormBPHProstate
839	8956	2458.H07.GZ43_356783	F	M00074248C:E12	IF97-26811-NormBPHProstate
840	9710	2458.H16.GZ43_356792	F	M00074249C:B11	IF97-26811-NormBPHProstate
841	390274	2458.H20.GZ43_356796	F	M00074249C:H08	IF97-26811-NormBPHProstate
842	112224	2458.I09.GZ43_356809	F	M00074250D:E06	IF97-26811-NormBPHProstate
843	20915	2458.I10.GZ43_356810	F	M00074250D:F06	IF97-26811-NormBPHProstate
844	77670	2458.I15.GZ43_356815	F	M00074251B:F08	IF97-26811-NormBPHProstate
845	32366	2458.I17.GZ43_356817	F	M00074251C:B06	IF97-26811-NormBPHProstate
846	11031	2458.I20.GZ43_356820	F	M00074251C:E03	IF97-26811-NormBPHProstate
847	112224	2458.I21.GZ43_356821	F	M00074251D:E03	IF97-26811-NormBPHProstate
848	40164	2458.J03.GZ43_356827	F	M00074252C:E02	IF97-26811-NormBPHProstate
849	72825	2458.J21.GZ43_356845	F	M00074253C:F03	IF97-26811-NormBPHProstate
850	36407	2458.K07.GZ43_356855	F	M00074255B:A01	IF97-26811-NormBPHProstate

Table 2

SEQ ID	CLUSTER	SEQNAME	ORIENT	CLONE ID	LIBRARY
851	63902	2458.L06.GZ43_356878	F	M00074258A:H12	IF97-26811-NormBPHProstate
852	954558	2458.L07.GZ43_356879	F	M00074258A:H09	IF97-26811-NormBPHProstate
853	447270	2458.L23.GZ43_356895	F	M00074259C:G08	IF97-26811-NormBPHProstate
854	16174	2458.M05.GZ43_356901	F	M00074260B:A11	IF97-26811-NormBPHProstate
855	139173	2458.N06.GZ43_356926	F	M00074265B:C07	IF97-26811-NormBPHProstate
856	217122	2458.N10.GZ43_356930	F	M00074266A:D01	IF97-26811-NormBPHProstate
857	497138	2458.N19.GZ43_356939	F	M00074267A:B04	IF97-26811-NormBPHProstate
858	559336	2458.O09.GZ43_356953	F	M00074268A:D08	IF97-26811-NormBPHProstate
859	507628	2458.O17.GZ43_356961	F	M00074268C:G03	IF97-26811-NormBPHProstate
860	14453	2458.P06.GZ43_356974	F	M00074270B:A01	IF97-26811-NormBPHProstate
861	858675	2458.P18.GZ43_356986	F	M00074271B:E11	IF97-26811-NormBPHProstate
862	597681	2459.A04.GZ43_356996	F	M00074273B:B03	IF97-26811-NormBPHProstate
863	715752	2459.A24.GZ43_357016	F	M00074275A:B04	IF97-26811-NormBPHProstate
864	14049	2459.B10.GZ43_357026	F	M00074276A:A12	IF97-26811-NormBPHProstate
865	830453	2459.B11.GZ43_357027	F	M00074276A:E02	IF97-26811-NormBPHProstate
866	63551	2459.C05.GZ43_357045	F	M00074278B:D07	IF97-26811-NormBPHProstate
867	456211	2459.C09.GZ43_357049	F	M00074278D:E07	IF97-26811-NormBPHProstate
868	682065	2459.C16.GZ43_357056	F	M00074279C:C11	IF97-26811-NormBPHProstate
869	1049007	2459.D07.GZ43_357071	F	M00074280D:H03	IF97-26811-NormBPHProstate
870	415520	2459.E11.GZ43_357099	F	M00074284B:B03	IF97-26811-NormBPHProstate
871	136276	2459.E16.GZ43_357104	F	M00074284C:B06	IF97-26811-NormBPHProstate
872	532090	2459.E19.GZ43_357107	F	M00074284C:E12	IF97-26811-NormBPHProstate
873	165378	2459.F20.GZ43_357132	F	M00074288A:F11	IF97-26811-NormBPHProstate
874	523261	2459.G01.GZ43_357137	F	M00074290A:G10	IF97-26811-NormBPHProstate
875	22351	2459.G07.GZ43_357143	F	M00074290C:B05	IF97-26811-NormBPHProstate
876	573764	2459.G23.GZ43_357159	F	M00074292D:B04	IF97-26811-NormBPHProstate
877	552996	2459.H09.GZ43_357169	F	M00074293D:B05	IF97-26811-NormBPHProstate
878	923732	2459.H10.GZ43_357170	F	M00074293D:H07	IF97-26811-NormBPHProstate
879	375712	2459.I10.GZ43_357194	F	M00074296C:G09	IF97-26811-NormBPHProstate
880	8342	2459.J12.GZ43_357220	F	M00074299B:F01	IF97-26811-NormBPHProstate
881	446975	2459.K15.GZ43_357247	F	M00074302D:G10	IF97-26811-NormBPHProstate
882	747429	2459.L07.GZ43_357263	F	M00074304B:C09	IF97-26811-NormBPHProstate
883	697955	2459.L13.GZ43_357269	F	M00074304D:D07	IF97-26811-NormBPHProstate
884	2594	2459.L18.GZ43_357274	F	M00074306A:B09	IF97-26811-NormBPHProstate
885	19812	2459.L23.GZ43_357279	F	M00074306B:H01	IF97-26811-NormBPHProstate
886	38435	2459.N09.GZ43_357313	F	M00074310D:D02	IF97-26811-NormBPHProstate
887	4526	2459.O12.GZ43_357340	F	M00074314A:C06	IF97-26811-NormBPHProstate
888	61211	2459.O23.GZ43_357351	F	M00074315B:A03	IF97-26811-NormBPHProstate
889	558789	2459.P24.GZ43_357376	F	M00074317C:C01	IF97-26811-NormBPHProstate
890	676448	2464.B01.GZ43_357705	F	M00074319C:H03	IF97-26811-NormBPHProstate
891	18780	2464.C08.GZ43_357736	F	M00074832B:E05	IF97-26811-NormBPHProstate
892	35553	2464.D18.GZ43_357770	F	M00074835A:H10	IF97-26811-NormBPHProstate
893	797055	2464.D23.GZ43_357775	F	M00074835B:F12	IF97-26811-NormBPHProstate
894	595523	2464.E21.GZ43_357797	F	M00074837A:B06	IF97-26811-NormBPHProstate
895	97523	2464.E23.GZ43_357799	F	M00074837A:E01	IF97-26811-NormBPHProstate
896	22970	2464.F12.GZ43_357812	F	M00074838B:E11	IF97-26811-NormBPHProstate
897	743862	2464.F19.GZ43_357819	F	M00074838D:B06	IF97-26811-NormBPHProstate
898	551338	2464.G18.GZ43_357842	F	M00074843A:C06	IF97-26811-NormBPHProstate
899	524917	2464.H05.GZ43_357853	F	M00074843D:D02	IF97-26811-NormBPHProstate
900	10663	2464.H07.GZ43_357855	F	M00074844B:B02	IF97-26811-NormBPHProstate

Table 2

SEQ ID	CLUSTER	SEQNAME	ORIENT	CLONE ID	LIBRARY
901	453526	2464.H14.GZ43_357862	F	M00074844D:F09	IF97-26811-NormBPHProstate
902	459310	2464.H17.GZ43_357865	F	M00074845A:D12	IF97-26811-NormBPHProstate
903	215935	2464.H22.GZ43_357870	F	M00074845B:F07	IF97-26811-NormBPHProstate
904	158853	2464.I04.GZ43_357876	F	M00074845D:D07	IF97-26811-NormBPHProstate
905	465814	2464.I20.GZ43_357892	F	M00074847B:G03	IF97-26811-NormBPHProstate
906	558463	2464.I23.GZ43_357895	F	M00074847D:E07	IF97-26811-NormBPHProstate
907	323112	2464.J17.GZ43_357913	F	M00074849C:A04	IF97-26811-NormBPHProstate
908	813848	2464.K14.GZ43_357934	F	M00074852A:B01	IF97-26811-NormBPHProstate
909	517954	2464.K18.GZ43_357938	F	M00074852B:A02	IF97-26811-NormBPHProstate
910	532090	2464.L02.GZ43_357946	F	M00074852D:D08	IF97-26811-NormBPHProstate
911	365634	2464.L06.GZ43_357950	F	M00074853A:D05	IF97-26811-NormBPHProstate
912	560612	2464.L15.GZ43_357959	F	M00074854A:C11	IF97-26811-NormBPHProstate
913	419172	2464.M02.GZ43_357970	F	M00074855B:A05	IF97-26811-NormBPHProstate
914	932437	2464.N05.GZ43_357997	F	M00074857D:B02	IF97-26811-NormBPHProstate
915	411524	2464.N06.GZ43_357998	F	M00074858B:E05	IF97-26811-NormBPHProstate
916	558959	2464.O15.GZ43_358031	F	M00074861D:D01	IF97-26811-NormBPHProstate
917	528957	2464.P10.GZ43_358050	F	M00074863D:F07	IF97-26811-NormBPHProstate
918	85702	2464.P17.GZ43_358057	F	M00074864C:B09	IF97-26811-NormBPHProstate
919	88413	2464.A05.GZ43_357685	F	M00074317D:B08	IF97-26811-NormBPHProstate
920	549017	2464.B11.GZ43_357715	F	M00074320C:A06	IF97-26811-NormBPHProstate
921	582134	2465.A03.GZ43_358067	F	M00074865A:F05	IF97-26811-NormBPHProstate
922	482747	2465.B11.GZ43_358099	F	M00074869C:D04	IF97-26811-NormBPHProstate
923	545694	2465.C01.GZ43_358113	F	M00074871C:G05	IF97-26811-NormBPHProstate
924	853085	2465.C24.GZ43_358136	F	M00074874A:G07	IF97-26811-NormBPHProstate
925	146695	2465.D10.GZ43_358146	F	M00074875B:E08	IF97-26811-NormBPHProstate
926	935908	2465.E03.GZ43_358163	F	M00074879A:A02	IF97-26811-NormBPHProstate
927	726585	2465.E08.GZ43_358168	F	M00074879C:D02	IF97-26811-NormBPHProstate
928	647607	2465.F11.GZ43_358195	F	M00074884C:F10	IF97-26811-NormBPHProstate
929	464200	2465.G06.GZ43_358214	F	M00074887A:F03	IF97-26811-NormBPHProstate
930	672079	2465.H11.GZ43_358243	F	M00074890A:E03	IF97-26811-NormBPHProstate
931	498886	2465.I12.GZ43_358268	F	M00074895D:H12	IF97-26811-NormBPHProstate
932	542693	2465.I17.GZ43_358273	F	M00074898B:B01	IF97-26811-NormBPHProstate
933	447795	2465.J11.GZ43_358291	F	M00074900C:E10	IF97-26811-NormBPHProstate
934	725257	2465.J19.GZ43_358299	F	M00074901C:E05	IF97-26811-NormBPHProstate
935	376516	2465.K20.GZ43_358324	F	M00074903D:C04	IF97-26811-NormBPHProstate
936	659483	2465.L02.GZ43_358330	F	M00074904A:E11	IF97-26811-NormBPHProstate
937	41346	2465.L06.GZ43_358334	F	M00074904B:B07	IF97-26811-NormBPHProstate
938	498886	2465.L22.GZ43_358350	F	M00074905D:A01	IF97-26811-NormBPHProstate
939	447525	2465.M11.GZ43_358363	F	M00074906B:H12	IF97-26811-NormBPHProstate
940	672079	2465.M18.GZ43_358370	F	M00074906D:G02	IF97-26811-NormBPHProstate
941	738784	2465.P14.GZ43_358438	F	M00074912B:A10	IF97-26811-NormBPHProstate
942	402167	2466.A02.GZ43_360083	F	M00074912D:H08	IF97-26811-NormBPHProstate
943	11686	2466.B02.GZ43_360107	F	M00074916A:H03	IF97-26811-NormBPHProstate
944	709796	2466.C15.GZ43_360144	F	M00074919C:A08	IF97-26811-NormBPHProstate
945	553629	2466.D19.GZ43_360172	F	M00074921C:E05	IF97-26811-NormBPHProstate
946	627263	2466.D20.GZ43_360173	F	M00074922A:D06	IF97-26811-NormBPHProstate
947	20975	2466.F16.GZ43_360217	F	M00074927A:D02	IF97-26811-NormBPHProstate
948	861172	2466.F19.GZ43_360220	F	M00074927B:G08	IF97-26811-NormBPHProstate
949	588996	2466.G06.GZ43_360231	F	M00074927D:G09	IF97-26811-NormBPHProstate
950	993554	2466.H07.GZ43_360256	F	M00074929D:D04	IF97-26811-NormBPHProstate

Table 2

SEQ ID	CLUSTER	SEQNAME	ORIENT	CLONE ID	LIBRARY
951	652099	2466.H19.GZ43_360268	F	M00074930C:D11	IF97-26811-NormBPHProstate
952	281	2466.I08.GZ43_360281	F	M00074933A:D04	IF97-26811-NormBPHProstate
953	407944	2466.J01.GZ43_360298	F	M00074935A:C01	IF97-26811-NormBPHProstate
954	644299	2466.J24.GZ43_360321	F	M00074936B:E10	IF97-26811-NormBPHProstate
955	374829	2466.L07.GZ43_360352	F	M00074939B:A06	IF97-26811-NormBPHProstate
956	12885	2466.M02.GZ43_360371	F	M00074940C:H08	IF97-26811-NormBPHProstate
957	123563	2466.P11.GZ43_360452	F	M00074950A:D01	IF97-26811-NormBPHProstate
958	540142	2467.B24.GZ43_360513	F	M00074958D:H10	IF97-26811-NormBPHProstate
959	806992	2467.D20.GZ43_360557	F	M00074966D:E08	IF97-26811-NormBPHProstate
960	61211	2467.D23.GZ43_360560	F	M00074967B:A11	IF97-26811-NormBPHProstate
961	682065	2467.E19.GZ43_360580	F	M00074968D:A02	IF97-26811-NormBPHProstate
962	449521	2467.G19.GZ43_360628	F	M00074974C:E11	IF97-26811-NormBPHProstate
963	19342	2467.H18.GZ43_360651	F	M00074980D:E07	IF97-26811-NormBPHProstate
964	373888	2467.A03.GZ43_360468	F	M00074954A:H06	IF97-26811-NormBPHProstate
965	417672	2467.A05.GZ43_360470	F	M00074954B:E03	IF97-26811-NormBPHProstate
966	376630	2467.B11.GZ43_360500	F	M00074957D:F11	IF97-26811-NormBPHProstate
967	733132	2467.D10.GZ43_360547	F	M00074962B:F08	IF97-26811-NormBPHProstate
968	189951	2467.E12.GZ43_360573	F	M00074968A:D09	IF97-26811-NormBPHProstate
969	59884	2467.G01.GZ43_360610	F	M00074973A:H03	IF97-26811-NormBPHProstate
970	16011	2467.K17.GZ43_360722	F	M00072987B:A03	IF97-26811-ProstateCancer3+3
971	2081	2467.N22.GZ43_360799	F	M00072997B:H03	IF97-26811-ProstateCancer3+3
972	377134	2467.I02.GZ43_360659	F	M00072951C:C11	IF97-26811-ProstateCancer3+3
973	3581	2467.I12.GZ43_360669	F	M00072953B:G03	IF97-26811-ProstateCancer3+3
974	21702	2467.J09.GZ43_360690	F	M00072982D:B03	IF97-26811-ProstateCancer3+3
975	1409	2467.K03.GZ43_360708	F	M00072985A:C12	IF97-26811-ProstateCancer3+3
976	36814	2467.K08.GZ43_360713	F	M00072985B:D03	IF97-26811-ProstateCancer3+3
977	448841	2467.K14.GZ43_360719	F	M00072986A:C03	IF97-26811-ProstateCancer3+3
978	568661	2467.M07.GZ43_360760	F	M00072993B:D06	IF97-26811-ProstateCancer3+3
979	388450	2467.N03.GZ43_360780	F	M00072995C:D07	IF97-26811-ProstateCancer3+3
980	129409	2467.N07.GZ43_360784	F	M00072995D:C09	IF97-26811-ProstateCancer3+3
981	14464	2467.N09.GZ43_360786	F	M00072996B:A10	IF97-26811-ProstateCancer3+3
982	1005804	2467.N12.GZ43_360789	F	M00072996C:C04	IF97-26811-ProstateCancer3+3
983	470032	2467.O04.GZ43_360805	F	M00072997D:F08	IF97-26811-ProstateCancer3+3
984	10354	2467.O05.GZ43_360806	F	M00072997D:H06	IF97-26811-ProstateCancer3+3
985	376972	2472.A03.GZ43_360852	F	M00074323D:F09	IF97-26811-ProstateCancer3+3
986	18338	2472.C18.GZ43_360915	F	M00074333D:A11	IF97-26811-ProstateCancer3+3
987	378269	2472.D06.GZ43_360927	F	M00074335A:H08	IF97-26811-ProstateCancer3+3
988	385300	2472.D16.GZ43_360937	F	M00074337A:G08	IF97-26811-ProstateCancer3+3
989	571	2472.E02.GZ43_360947	F	M00074340B:D06	IF97-26811-ProstateCancer3+3
990	377667	2472.E22.GZ43_360967	F	M00074343C:A03	IF97-26811-ProstateCancer3+3
991	450657	2472.F22.GZ43_360991	F	M00074346A:H09	IF97-26811-ProstateCancer3+3
992	15619	2472.G03.GZ43_360996	F	M00074347B:F11	IF97-26811-ProstateCancer3+3
993	185791	2472.G13.GZ43_361006	F	M00074349A:E08	IF97-26811-ProstateCancer3+3
994	193306	2472.I14.GZ43_361055	F	M00074355D:H06	IF97-26811-ProstateCancer3+3
995	377967	2472.K13.GZ43_361102	F	M00074361C:B01	IF97-26811-ProstateCancer3+3
996	373149	2472.L11.GZ43_361124	F	M00074365A:E09	IF97-26811-ProstateCancer3+3
997	612171	2472.L15.GZ43_361128	F	M00074366A:D07	IF97-26811-ProstateCancer3+3
998	560365	2472.L16.GZ43_361129	F	M00074366A:H07	IF97-26811-ProstateCancer3+3
999	217476	2472.M22.GZ43_361159	F	M00074370D:G09	IF97-26811-ProstateCancer3+3
1000	40043	2472.O04.GZ43_361189	F	M00074375D:E05	IF97-26811-ProstateCancer3+3

Table 2

SEQ ID	CLUSTER	SEQNAME	ORIENT	CLONE ID	LIBRARY
1001	374588	2472.P14.GZ43_361223	F	M00074382D:F04	IF97-26811-ProstateCancer3+3
1002	15692	2472.P22.GZ43_361231	F	M00074384D:G07	IF97-26811-ProstateCancer3+3
1003	378507	2473.A01.GZ43_361234	F	M00074388B:E07	IF97-26811-ProstateCancer3+3
1004	374382	2473.C03.GZ43_361284	F	M00074392C:D02	IF97-26811-ProstateCancer3+3
1005	372993	2473.F08.GZ43_361361	F	M00074405B:A04	IF97-26811-ProstateCancer3+3
1006	235268	2473.F14.GZ43_361367	F	M00074417D:F07	IF97-26811-ProstateCancer3+3
1007	387530	2473.G03.GZ43_361380	F	M00074392D:D01	IF97-26811-ProstateCancer3+3
1008	375786	2473.G09.GZ43_361386	F	M00074406B:F10	IF97-26811-ProstateCancer3+3
1009	401120	2473.H18.GZ43_361419	F	M00074430D:G09	IF97-26811-ProstateCancer3+3
1010	4885	2473.I04.GZ43_361429	F	M00074395A:B11	IF97-26811-ProstateCancer3+3
1011	5810	2473.I08.GZ43_361433	F	M00074404B:H01	IF97-26811-ProstateCancer3+3
1012	556192	2473.K02.GZ43_361475	F	M00074391B:D02	IF97-26811-ProstateCancer3+3
1013	392161	2473.L01.GZ43_361498	F	M00074390C:E04	IF97-26811-ProstateCancer3+3
1014	971463	2473.L11.GZ43_361508	F	M00074411B:G07	IF97-26811-ProstateCancer3+3
1015	1338	2473.O13.GZ43_361582	F	M00074415B:A01	IF97-26811-ProstateCancer3+3
1016	470032	2474.C01.GZ43_361666	F	M00074453B:H03	IF97-26811-ProstateCancer3+3
1017	565709	2474.C04.GZ43_361669	F	M00074453C:E09	IF97-26811-ProstateCancer3+3
1018	966482	2474.C08.GZ43_361673	F	M00074454A:D08	IF97-26811-ProstateCancer3+3
1019	549017	2474.E09.GZ43_361722	F	M00074461D:E04	IF97-26811-ProstateCancer3+3
1020	32016	2474.E18.GZ43_361731	F	M00074463B:C03	IF97-26811-ProstateCancer3+3
1021	477010	2474.G17.GZ43_361778	F	M00074468B:C03	IF97-26811-ProstateCancer3+3
1022	837214	2474.I02.GZ43_361811	F	M00074473D:H09	IF97-26811-ProstateCancer3+3
1023	861902	2474.I06.GZ43_361815	F	M00074474B:F02	IF97-26811-ProstateCancer3+3
1024	1084307	2474.J18.GZ43_361851	F	M00074488C:C10	IF97-26811-ProstateCancer3+3
1025	715573	2474.J19.GZ43_361852	F	M00074488C:C08	IF97-26811-ProstateCancer3+3
1026	402167	2474.K20.GZ43_361877	F	M00074492A:F11	IF97-26811-ProstateCancer3+3
1027	287803	2474.M19.GZ43_361924	F	M00074501A:G07	IF97-26811-ProstateCancer3+3
1028	421298	2474.N01.GZ43_361930	F	M00074502C:B08	IF97-26811-ProstateCancer3+3
1029	558463	2474.P19.GZ43_361996	F	M00074515A:E02	IF97-26811-ProstateCancer3+3
1030	187860	2474.P22.GZ43_361999	F	M00074515C:A11	IF97-26811-ProstateCancer3+3
1031	474947	2475.A05.GZ43_362006	F	M00074516B:H03	IF97-26811-ProstateCancer3+3
1032	161012	2475.C18.GZ43_362067	F	M00074525A:B05	IF97-26811-ProstateCancer3+3
1033	823296	2475.E18.GZ43_362115	F	M00074533A:D07	IF97-26811-ProstateCancer3+3
1034	176266	2475.G16.GZ43_362161	F	M00074539D:A10	IF97-26811-ProstateCancer3+3
1035	385843	2475.H06.GZ43_362175	F	M00074540B:H07	IF97-26811-ProstateCancer3+3
1036	1009284	2475.H13.GZ43_362182	F	M00074541D:E07	IF97-26811-ProstateCancer3+3
1037	428883	2475.J15.GZ43_362232	F	M00074549B:A06	IF97-26811-ProstateCancer3+3
1038	732950	2475.L17.GZ43_362282	F	M00074557A:G08	IF97-26811-ProstateCancer3+3
1039	387530	2475.N08.GZ43_362321	F	M00074561D:D12	IF97-26811-ProstateCancer3+3
1040	27991	2475.O11.GZ43_362348	F	M00074566B:A04	IF97-26811-ProstateCancer3+3
1041	485653	2475.P12.GZ43_362373	F	M00074569D:D04	IF97-26811-ProstateCancer3+3
1042	540379	2475.B20.GZ43_362045	F	M00074521D:F01	IF97-26811-ProstateCancer3+3
1043	732950	2475.J19.GZ43_362236	F	M00074549C:H08	IF97-26811-ProstateCancer3+3
1044	187860	2475.K24.GZ43_362265	F	M00074555A:E10	IF97-26811-ProstateCancer3+3
1045	570804	2475.M20.GZ43_362309	F	M00074561A:B09	IF97-26811-ProstateCancer3+3
1046	449889	2475.N21.GZ43_362334	F	M00074565A:D08	IF97-26811-ProstateCancer3+3
1047	724905	2480.A13.GZ43_358516	F	M00074571D:F02	IF97-26811-ProstateCancer3+3
1048	21702	2480.A20.GZ43_358523	F	M00074573A:H02	IF97-26811-ProstateCancer3+3
1049	83576	2480.B22.GZ43_358549	F	M00074577B:B12	IF97-26811-ProstateCancer3+3
1050	649404	2480.C01.GZ43_358552	F	M00074577C:A05	IF97-26811-ProstateCancer3+3

Table 2

SEQ ID	CLUSTER	SEQNAME	ORIENT	CLONE ID	LIBRARY
1051	635332	2480.D13.GZ43_358588	F	M00074582C:C02	IF97-26811-ProstateCancer3+3
1052	805118	2480.D16.GZ43_358591	F	M00074582D:B09	IF97-26811-ProstateCancer3+3
1053	549507	2480.E19.GZ43_358618	F	M00074584D:C01	IF97-26811-ProstateCancer3+3
1054	838155	2480.G04.GZ43_358651	F	M00074588C:H06	IF97-26811-ProstateCancer3+3
1055	529381	2480.G11.GZ43_358658	F	M00074589A:E10	IF97-26811-ProstateCancer3+3
1056	29273	2480.H06.GZ43_358677	F	M00074593A:F05	IF97-26811-ProstateCancer3+3
1057	963580	2480.I08.GZ43_358703	F	M00074596D:B12	IF97-26811-ProstateCancer3+3
1058	104204	2480.K20.GZ43_358763	F	M00074606C:G02	IF97-26811-ProstateCancer3+3
1059	20580	2480.L02.GZ43_358769	F	M00074607D:A12	IF97-26811-ProstateCancer3+3
1060	899126	2480.M15.GZ43_358806	F	M00074613D:F01	IF97-26811-ProstateCancer3+3
1061	14214	2480.M20.GZ43_358811	F	M00074614B:D10	IF97-26811-ProstateCancer3+3
1062	47888	2480.P07.GZ43_358870	F	M00074625A:C12	IF97-26811-ProstateCancer3+3
1063	486512	2480.P22.GZ43_358885	F	M00074628C:C11	IF97-26811-ProstateCancer3+3
1064	597201	2480.P23.GZ43_358886	F	M00074628C:D03	IF97-26811-ProstateCancer3+3
1065	134597	2481.B06.GZ43_358917	F	M00074633A:B09	IF97-26811-ProstateCancer3+3
1066	933128	2481.C22.GZ43_358957	F	M00074636D:C01	IF97-26811-ProstateCancer3+3
1067	8997	2481.D04.GZ43_358963	F	M00074637A:C02	IF97-26811-ProstateCancer3+3
1068	20863	2481.D10.GZ43_358969	F	M00074638D:C12	IF97-26811-ProstateCancer3+3
1069	58496	2481.D13.GZ43_358972	F	M00074639A:C08	IF97-26811-ProstateCancer3+3
1070	372993	2481.E03.GZ43_358986	F	M00074640D:F07	IF97-26811-ProstateCancer3+3
1071	558581	2481.F24.GZ43_359031	F	M00074645C:B07	IF97-26811-ProstateCancer3+3
1072	471364	2481.I05.GZ43_359084	F	M00074654D:B05	IF97-26811-ProstateCancer3+3
1073	234423	2481.J23.GZ43_359126	F	M00074662B:A05	IF97-26811-ProstateCancer3+3
1074	469837	2481.J24.GZ43_359127	F	M00074662D:D01	IF97-26811-ProstateCancer3+3
1075	449749	2481.K12.GZ43_359139	F	M00074664C:G09	IF97-26811-ProstateCancer3+3
1076	35578	2481.L13.GZ43_359164	F	M00074668D:D04	IF97-26811-ProstateCancer3+3
1077	464200	2481.N10.GZ43_359209	F	M00074674D:D02	IF97-26811-ProstateCancer3+3
1078	555867	2481.O05.GZ43_359228	F	M00074676D:H07	IF97-26811-ProstateCancer3+3
1079	218833	2482.A05.GZ43_359276	F	M00074681C:G11	IF97-26811-ProstateCancer3+3
1080	782981	2482.A06.GZ43_359277	F	M00074681D:A02	IF97-26811-ProstateCancer3+3
1081	475054	2482.B22.GZ43_359317	F	M00074687B:E01	IF97-26811-ProstateCancer3+3
1082	468400	2482.E07.GZ43_359374	F	M00074699B:C03	IF97-26811-ProstateCancer3+3
1083	16641	2482.E17.GZ43_359384	F	M00074701D:H09	IF97-26811-ProstateCancer3+3
1084	460493	2482.E20.GZ43_359387	F	M00074702B:F12	IF97-26811-ProstateCancer3+3
1085	922	2482.F01.GZ43_359392	F	M00074702D:H05	IF97-26811-ProstateCancer3+3
1086	1037152	2482.I05.GZ43_359468	F	M00074713B:F02	IF97-26811-ProstateCancer3+3
1087	540379	2482.J06.GZ43_359493	F	M00074716C:H07	IF97-26811-ProstateCancer3+3
1088	475054	2482.L14.GZ43_359549	F	M00074723D:C06	IF97-26811-ProstateCancer3+3
1089	452194	2482.L15.GZ43_359550	F	M00074723D:D05	IF97-26811-ProstateCancer3+3
1090	7292	2482.N01.GZ43_359584	F	M00074728C:B08	IF97-26811-ProstateCancer3+3
1091	375712	2482.N09.GZ43_359592	F	M00074730B:A04	IF97-26811-ProstateCancer3+3
1092	450119	2483.A13.GZ43_359668	F	M00074740B:F06	IF97-26811-ProstateCancer3+3
1093	549507	2483.B23.GZ43_359702	F	M00074744B:B12	IF97-26811-ProstateCancer3+3
1094	448319	2483.D03.GZ43_359730	F	M00074748C:G02	IF97-26811-ProstateCancer3+3
1095	402591	2483.E11.GZ43_359762	F	M00074752A:D08	IF97-26811-ProstateCancer3+3
1096	654181	2483.F04.GZ43_359779	F	M00074753C:E10	IF97-26811-ProstateCancer3+3
1097	379774	2483.F14.GZ43_359789	F	M00074755A:B10	IF97-26811-ProstateCancer3+3
1098	587168	2483.F15.GZ43_359790	F	M00074755A:E07	IF97-26811-ProstateCancer3+3
1099	187860	2483.I21.GZ43_359868	F	M00074765D:F06	IF97-26811-ProstateCancer3+3
1100	437748	2483.J07.GZ43_359878	F	M00074766C:F12	IF97-26811-ProstateCancer3+3

Table 2

SEQ ID	CLUSTER	SEQNAME	ORIENT	CLONE ID	LIBRARY
1101	404081	2483.K02.GZ43_359897	F	M00074768C:A05	IF97-26811-ProstateCancer3+3
1102	545694	2483.L15.GZ43_359934	F	M00074773C:G03	IF97-26811-ProstateCancer3+3
1103	474947	2483.L22.GZ43_359941	F	M00074774A:D03	IF97-26811-ProstateCancer3+3
1104	528957	2483.M09.GZ43_359952	F	M00074777A:E01	IF97-26811-ProstateCancer3+3
1105	597201	2483.N15.GZ43_359982	F	M00074780C:C02	IF97-26811-ProstateCancer3+3
1106	460493	2483.O07.GZ43_359998	F	M00074782A:E04	IF97-26811-ProstateCancer3+3
1107	135899	2488.B07.GZ43_362475	F	M00074808B:H02	IF97-26811-ProstateCancer3+3
1108	839006	2488.C19.GZ43_362511	F	M00074996C:D07	IF97-26811-ProstateCancer3+3
1109	1022081	2488.D15.GZ43_362531	F	M00074981C:C09	IF97-26811-ProstateCancer3+3
1110	423303	2488.E20.GZ43_362560	F	M00075000A:D06	IF97-26811-ProstateCancer3+3
1111	387530	2488.F06.GZ43_362570	F	M00074805A:C12	IF97-26811-ProstateCancer3+3
1112	667872	2488.F15.GZ43_362579	F	M00074981D:A03	IF97-26811-ProstateCancer3+3
1113	22334	2488.G02.GZ43_362590	F	M00074794C:H02	IF97-26811-ProstateCancer3+3
1114	524917	2488.G05.GZ43_362593	F	M00074801C:E06	IF97-26811-ProstateCancer3+3
1115	453981	2488.G12.GZ43_362600	F	M00074821B:B03	IF97-26811-ProstateCancer3+3
1116	423664	2488.H12.GZ43_362624	F	M00074823A:E03	IF97-26811-ProstateCancer3+3
1117	1009284	2488.K04.GZ43_362688	F	M00074800B:H01	IF97-26811-ProstateCancer3+3
1118	1009284	2488.L04.GZ43_362712	F	M00074800D:G09	IF97-26811-ProstateCancer3+3
1119	597201	2488.N08.GZ43_362764	F	M00074812A:F03	IF97-26811-ProstateCancer3+3
1120	724818	2488.N13.GZ43_362769	F	M00074825C:E06	IF97-26811-ProstateCancer3+3
1121	534076	2488.P01.GZ43_362805	F	M00074794A:G10	IF97-26811-ProstateCancer3+3
1122	901160	2489.A03.GZ43_362831	F	M00075018A:G04	IF97-26811-ProstateCancer3+3
1123	448680	2489.A04.GZ43_362832	F	M00075020D:B04	IF97-26811-ProstateCancer3+3
1124	13903	2489.A13.GZ43_362841	F	M00075049A:C09	IF97-26811-ProstateCancer3+3
1125	214762	2489.B07.GZ43_362859	F	M00075032A:F02	IF97-26811-ProstateCancer3+3
1126	21662	2489.D06.GZ43_362906	F	M00075029B:E03	IF97-26811-ProstateCancer3+3
1127	379301	2489.D18.GZ43_362918	F	M00075069C:C01	IF97-26811-ProstateCancer3+3
1128	727966	2489.F09.GZ43_362957	F	M00075039A:E01	IF97-26811-ProstateCancer3+3
1129	13071	2489.G05.GZ43_362977	F	M00075024C:G05	IF97-26811-ProstateCancer3+3
1130	60089	2489.G20.GZ43_362992	F	M00075074D:G11	IF97-26811-ProstateCancer3+3
1131	13091	2489.G24.GZ43_362996	F	M00075011A:C11	IF97-26811-ProstateCancer3+3
1132	32367	2489.H15.GZ43_363011	F	M00075061A:B03	IF97-26811-ProstateCancer3+3
1133	1135	2489.I11.GZ43_363031	F	M00075043B:H05	IF97-26811-ProstateCancer3+3
1134	779428	2489.J08.GZ43_363052	F	M00075035C:C09	IF97-26811-ProstateCancer3+3
1135	560612	2489.J11.GZ43_363055	F	M00075045D:H03	IF97-26811-ProstateCancer3+3
1136	726937	2489.J21.GZ43_363065	F	M00075078C:A07	IF97-26811-ProstateCancer3+3
1137	13182	2489.K20.GZ43_363088	F	M00075075A:D12	IF97-26811-ProstateCancer3+3
1138	1037152	2489.K21.GZ43_363089	F	M00075077C:F09	IF97-26811-ProstateCancer3+3
1139	782981	2489.L05.GZ43_363097	F	M00075026A:D11	IF97-26811-ProstateCancer3+3
1140	20975	2489.M11.GZ43_363127	F	M00075044A:C10	IF97-26811-ProstateCancer3+3
1141	1097678	2489.M20.GZ43_363136	F	M00075075A:E09	IF97-26811-ProstateCancer3+3
1142	22208	2489.N03.GZ43_363143	F	M00075020C:D12	IF97-26811-ProstateCancer3+3
1143	625055	2490.A07.GZ43_363219	F	M00075117B:B06	IF97-26811-ProstateCancer3+3
1144	6544	2490.B06.GZ43_363242	F	M00075114C:G11	IF97-26811-ProstateCancer3+3
1145	19627	2490.B20.GZ43_363256	F	M00075153C:C11	IF97-26811-ProstateCancer3+3
1146	779428	2490.C23.GZ43_363283	F	M00075161A:E05	IF97-26811-ProstateCancer3+3
1147	395603	2490.D10.GZ43_363294	F	M00075126B:A06	IF97-26811-ProstateCancer3+3
1148	43907	2490.E11.GZ43_363319	F	M00075126D:H07	IF97-26811-ProstateCancer3+3
1149	782981	2490.F01.GZ43_363333	F	M00075092C:F04	IF97-26811-ProstateCancer3+3
1150	428699	2490.H05.GZ43_363385	F	M00075110C:B03	IF97-26811-ProstateCancer3+3

Table 2

SEQ ID	CLUSTER	SEQNAME	ORIENT	CLONE ID	LIBRARY
1151	1005804	2490.H12.GZ43_363392	F	M00075132C:A03	IF97-26811-ProstateCancer3+3
1152	72334	2490.I20.GZ43_363424	F	M00075152D:C06	IF97-26811-ProstateCancer3+3
1153	40517	2490.J09.GZ43_363437	F	M00075125B:C07	IF97-26811-ProstateCancer3+3
1154	13495	2490.J12.GZ43_363440	F	M00075132C:E07	IF97-26811-ProstateCancer3+3
1155	1009284	2490.J22.GZ43_363450	F	M00075160A:E04	IF97-26811-ProstateCancer3+3
1156	60866	2490.L17.GZ43_363493	F	M00075149B:A01	IF97-26811-ProstateCancer3+3
1157	14453	2490.M08.GZ43_363508	F	M00075120C:H04	IF97-26811-ProstateCancer3+3
1158	659483	2490.N01.GZ43_363525	F	M00075093B:F10	IF97-26811-ProstateCancer3+3
1159	792	2490.N03.GZ43_363527	F	M00075102A:D02	IF97-26811-ProstateCancer3+3
1160	380136	2490.N24.GZ43_363548	F	M00075090D:B07	IF97-26811-ProstateCancer3+3
1161	62319	2490.O23.GZ43_363571	F	M00075161D:G06	IF97-26811-ProstateCancer3+3
1162	842403	2491.A04.GZ43_363600	F	M00075165B:D04	IF97-26811-ProstateCancer3+3
1163	779428	2491.C13.GZ43_363657	F	M00075174D:D06	IF97-26811-ProstateCancer3+3
1164	697943	2491.D12.GZ43_363680	F	M00075180D:F05	IF97-26811-ProstateCancer3+3
1165	35486	2491.D19.GZ43_363687	F	M00075181D:G10	IF97-26811-ProstateCancer3+3
1166	311745	2491.F16.GZ43_363732	F	M00075189C:G05	IF97-26811-ProstateCancer3+3
1167	640911	2491.H09.GZ43_363773	F	M00075199D:D11	IF97-26811-ProstateCancer3+3
1168	470032	2491.H23.GZ43_363787	F	M00075201D:A05	IF97-26811-ProstateCancer3+3
1169	853371	2491.I06.GZ43_363794	F	M00075203A:G06	IF97-26811-ProstateCancer3+3
1170	56899	2491.J14.GZ43_363826	F	M00075211D:F09	IF97-26811-ProstateCancer3+3
1171	414887	2491.L20.GZ43_363880	F	M00075221C:E02	IF97-26811-ProstateCancer3+3
1172	540379	2491.O02.GZ43_363934	F	M00075228D:G09	IF97-26811-ProstateCancer3+3
1173	558579	2491.P07.GZ43_363963	F	M00075232C:A06	IF97-26811-ProstateCancer3+3
1174	467877	2491.P10.GZ43_363966	F	M00075232D:C06	IF97-26811-ProstateCancer3+3
1175	379077	2491.P20.GZ43_363976	F	M00075234C:E06	IF97-26811-ProstateCancer3+3
1176	209378	2496.B09.GZ43_364116	F	M00075239C:D06	IF97-26811-ProstateCancer3+3
1177	16204	2496.C08.GZ43_364139	F	M00075242A:G04	IF97-26811-ProstateCancer3+3
1178	137552	2496.C18.GZ43_364149	F	M00075243D:F04	IF97-26811-ProstateCancer3+3
1179	625055	2496.D03.GZ43_364158	F	M00075245A:A06	IF97-26811-ProstateCancer3+3
1180	29921	2496.E14.GZ43_364193	F	M00075249A:B08	IF97-26811-ProstateCancer3+3
1181	831469	2496.F14.GZ43_364217	F	M00075252B:F10	IF97-26811-ProstateCancer3+3
1182	649404	2496.G15.GZ43_364242	F	M00075255A:G11	IF97-26811-ProstateCancer3+3
1183	129139	2496.I06.GZ43_364281	F	M00075259C:G02	IF97-26811-ProstateCancer3+3
1184	72712	2496.K15.GZ43_364338	F	M00075270D:A02	IF97-26811-ProstateCancer3+3
1185	83576	2496.L09.GZ43_364356	F	M00075273C:E01	IF97-26811-ProstateCancer3+3
1186	452194	2496.L17.GZ43_364364	F	M00075274B:F06	IF97-26811-ProstateCancer3+3
1187	625055	2496.L22.GZ43_364369	F	M00075275B:H07	IF97-26811-ProstateCancer3+3
1188	400152	2496.M22.GZ43_364393	F	M00075279C:E08	IF97-26811-ProstateCancer3+3
1189	558463	2496.N15.GZ43_364410	F	M00075283A:F04	IF97-26811-ProstateCancer3+3
1190	411524	2497.C11.GZ43_364526	F	M00075302B:C07	IF97-26811-ProstateCancer3+3
1191	715573	2497.D11.GZ43_364550	F	M00075305C:C07	IF97-26811-ProstateCancer3+3
1192	23000	2497.E09.GZ43_364572	F	M00075309C:A06	IF97-26811-ProstateCancer3+3
1193	9386	2497.I15.GZ43_364674	F	M00075323B:B12	IF97-26811-ProstateCancer3+3
1194	61725	2497.I21.GZ43_364680	F	M00075324B:C10	IF97-26811-ProstateCancer3+3
1195	142924	2497.J05.GZ43_364688	F	M00075324D:E02	IF97-26811-ProstateCancer3+3
1196	160424	2497.J23.GZ43_364706	F	M00075326C:B01	IF97-26811-ProstateCancer3+3
1197	741521	2497.K02.GZ43_364709	F	M00075326D:A09	IF97-26811-ProstateCancer3+3
1198	175903	2497.K22.GZ43_364729	F	M00075329B:E10	IF97-26811-ProstateCancer3+3
1199	388450	2497.L05.GZ43_364736	F	M00075330D:F11	IF97-26811-ProstateCancer3+3
1200	31500	2497.L21.GZ43_364752	F	M00075333D:B07	IF97-26811-ProstateCancer3+3

Table 2

SEQ ID	CLUSTER	SEQNAME	ORIENT	CLONE ID	LIBRARY
1201	52245	2497.L22.GZ43_364753	F	M00075333D:D10	IF97-26811-ProstateCancer3+3
1202	18761	2497.M17.GZ43_364772	F	M00075336B:B04	IF97-26811-ProstateCancer3+3
1203	449839	2497.O09.GZ43_364812	F	M00075344D:A08	IF97-26811-ProstateCancer3+3
1204	715573	2497.P04.GZ43_364831	F	M00075347D:D01	IF97-26811-ProstateCancer3+3
1205	212364	2562.B05.GZ43_375492	F	M00075354A:D11	IF97-26811-ProstateCancer3+3
1206	1024470	2562.B06.GZ43_375493	F	M00075354A:G12	IF97-26811-ProstateCancer3+3
1207	40517	2562.B09.GZ43_375496	F	M00075354C:B12	IF97-26811-ProstateCancer3+3
1208	13585	2562.D02.GZ43_375537	F	M00075360D:D04	IF97-26811-ProstateCancer3+3
1209	598388	2562.E03.GZ43_375562	F	M00075365B:B06	IF97-26811-ProstateCancer3+3
1210	185903	2562.I01.GZ43_375656	F	M00075384A:B03	IF97-26811-ProstateCancer3+3
1211	475054	2562.J02.GZ43_375681	F	M00075389B:C06	IF97-26811-ProstateCancer3+3
1212	6136	2562.K03.GZ43_375706	F	M00075391D:D07	IF97-26811-ProstateCancer3+3
1213	60741	2562.N02.GZ43_375777	F	M00075402A:F01	IF97-26811-ProstateCancer3+3
1214	218833	2562.O01.GZ43_375800	F	M00075405B:C07	IF97-26811-ProstateCancer3+3
1215	372710	2562.O06.GZ43_375805	F	M00075405D:A10	IF97-26811-ProstateCancer3+3
1216	465446	2562.E14.GZ43_375573	F	M00075365D:B08	IF97-26811-ProstateCancer3+3
1217	130289	2562.H11.GZ43_375642	F	M00075380D:F06	IF97-26811-ProstateCancer3+3
1218	65337	2562.B24.GZ43_375511	F	M00075356D:C03	IF97-26811-ProstateCancer3+3
1219	743053	2562.A22.GZ43_375485	F	M00075352D:F09	IF97-26811-ProstateCancer3+3
1220	733229	2562.C18.GZ43_375529	F	M00075359D:E09	IF97-26811-ProstateCancer3+3
1221	185886	2562.E16.GZ43_375575	F	M00075365D:H01	IF97-26811-ProstateCancer3+3
1222	11035	2562.F17.GZ43_375600	F	M00075373C:B09	IF97-26811-ProstateCancer3+3
1223	135008	2562.G19.GZ43_375626	F	M00075378B:C07	IF97-26811-ProstateCancer3+3
1224	715573	2562.G21.GZ43_375628	F	M00075379A:E07	IF97-26811-ProstateCancer3+3
1225	376516	2562.H18.GZ43_375649	F	M00075383A:B11	IF97-26811-ProstateCancer3+3
1226	154672	2562.O20.GZ43_375819	F	M00075407A:B05	IF97-26811-ProstateCancer3+3
1227	550132	2562.P16.GZ43_375839	F	M00075409A:E04	IF97-26811-ProstateCancer3+3
1228	452806	2562.P18.GZ43_375841	F	M00075409B:G12	IF97-26811-ProstateCancer3+3
1229	34977	2498.A02.GZ43_364853	F	M00075416C:B02	IF97-26811-ProstateCancer3+3
1230	1759	2498.A19.GZ43_364870	F	M00075458B:F09	IF97-26811-ProstateCancer3+3
1231	743862	2498.B22.GZ43_364897	F	M00075464C:A07	IF97-26811-ProstateCancer3+3
1232	180990	2498.C19.GZ43_364918	F	M00075458C:F01	IF97-26811-ProstateCancer3+3
1233	137835	2498.C22.GZ43_364921	F	M00075463C:E07	IF97-26811-ProstateCancer3+3
1234	396148	2498.D22.GZ43_364945	F	M00075464C:C04	IF97-26811-ProstateCancer3+3
1235	442923	2498.G15.GZ43_365010	F	M00075448B:G11	IF97-26811-ProstateCancer3+3
1236	480410	2498.H08.GZ43_365027	F	M00075434A:D06	IF97-26811-ProstateCancer3+3
1237	395603	2498.H18.GZ43_365037	F	M00075457C:A06	IF97-26811-ProstateCancer3+3
1238	821859	2498.I17.GZ43_365060	F	M00075454C:D06	IF97-26811-ProstateCancer3+3
1239	1082121	2498.K20.GZ43_365111	F	M00075460C:B06	IF97-26811-ProstateCancer3+3
1240	96136	2498.M19.GZ43_365158	F	M00075459A:C02	IF97-26811-ProstateCancer3+3
1241	20460	2498.O01.GZ43_365188	F	M00075414A:D10	IF97-26811-ProstateCancer3+3
1242	6305	2498.P07.GZ43_365218	F	M00075433A:C06	IF97-26811-ProstateCancer3+3
1243	28050	2507.B18.GZ43_366983	F	M00075505B:A04	IF97-26811-ProstateCancer3+3
1244	436755	2507.C03.GZ43_366992	F	M00075474D:B07	IF97-26811-ProstateCancer3+3
1245	691653	2507.C18.GZ43_367007	F	M00075504B:A10	IF97-26811-ProstateCancer3+3
1246	839006	2507.H02.GZ43_367111	F	M00075473C:E08	IF97-26811-ProstateCancer3+3
1247	187223	2507.J14.GZ43_367171	F	M00075499A:H02	IF97-26811-ProstateCancer3+3
1248	966599	2507.L12.GZ43_367217	F	M00075495D:D11	IF97-26811-ProstateCancer3+3
1249	961781	2507.M13.GZ43_367242	F	M00075496D:G05	IF97-26811-ProstateCancer3+3
1250	726937	2507.N22.GZ43_367275	F	M00075514A:G12	IF97-26811-ProstateCancer3+3

Table 2

SEQ ID	CLUSTER	SEQNAME	ORIENT	CLONE ID	LIBRARY
1251	379470	2507.O12.GZ43_367289	F	M00075495B:C12	IF97-26811-ProstateCancer3+3
1252	37881	2507.P13.GZ43_367314	F	M00075497D:H03	IF97-26811-ProstateCancer3+3
1253	855568	2511.A03.GZ43_369412	F	M00075529A:A02	IF97-26811-ProstateCancer3+3
1254	625055	2511.A07.GZ43_369416	F	M00075538C:E03	IF97-26811-ProstateCancer3+3
1255	720671	2511.H08.GZ43_369585	F	M00075544A:C03	IF97-26811-ProstateCancer3+3
1256	375488	2511.D23.GZ43_369504	F	M00075598B:A09	IF97-26811-ProstateCancer3+3
1257	958	2511.D24.GZ43_369505	F	M00075521B:E11	IF97-26811-ProstateCancer3+3
1258	20614	2511.I23.GZ43_369624	F	M00075597C:G01	IF97-26811-ProstateCancer3+3
1259	217230	2511.J18.GZ43_369643	F	M00075584D:B05	IF97-26811-ProstateCancer3+3
1260	51189	2511.N20.GZ43_369741	F	M00075590B:G04	IF97-26811-ProstateCancer3+3
1261	377044	2499.A22.GZ43_365257	F	M00075603D:D09	IF97-26811-ProstateCancer3+3
1262	4655	2499.B16.GZ43_365275	F	M00075607B:D05	IF97-26811-ProstateCancer3+3
1263	395761	2499.C09.GZ43_365292	F	M00075609A:H06	IF97-26811-ProstateCancer3+3
1264	135675	2499.D16.GZ43_365323	F	M00075613D:F01	IF97-26811-ProstateCancer3+3
1265	779428	2499.E18.GZ43_365349	F	M00075619C:D08	IF97-26811-ProstateCancer3+3
1266	224580	2499.F08.GZ43_365363	F	M00075621A:F06	IF97-26811-ProstateCancer3+3
1267	13182	2499.I09.GZ43_365436	F	M00075639A:D12	IF97-26811-ProstateCancer3+3

Table 3

SEQ ID	CONSENSUS SEQ NAME	POLYNTD SEQ NAME
1268	Clu1009284.1	2490.J22.GZ43_363450
1269	Clu1022935.2	2561.O19.GZ43_376586
1270	Clu1037152.1	2558.L19.GZ43_374594
1271	Clu13903.1	2489.A13.GZ43_362841
1272	Clu139979.2	2504.B21.GZ43_365834
1273	Clu163602.2	2561.H17.GZ43_376416
1274	Clu187860.2	2474.P22.GZ43_361999
1275	Clu189993.1	2505.N19.GZ43_366504
1276	Clu20975.1	2466.F16.GZ43_360217
1277	Clu217122.1	2458.N10.GZ43_356930
1278	Clu218833.1	2562.O01.GZ43_375800
1279	Clu244504.2	2367.E23.GZ43_346113
1280	Clu271456.1	2365.G19.GZ43_345389
1281	Clu376516.1	2457.J23.GZ43_356451
1282	Clu376630.1	2467.B11.GZ43_360500
1283	Clu377044.2	2499.A22.GZ43_365257
1284	Clu379689.1	2540.M18.GZ43_372313
1285	Clu380482.2	2542.D09.GZ43_372856
1286	Clu387530.4	2475.N08.GZ43_362321
1287	Clu388450.2	2497.L05.GZ43_364736
1288	Clu396325.1	2561.P16.GZ43_376607
1289	Clu397115.3	2560.K18.GZ43_375337
1290	Clu398642.2	2542.N22.GZ43_373109
1291	Clu400258.1	2504.O12.GZ43_366137
1292	Clu402167.1	2540.C21.GZ43_372076
1293	Clu402591.3	2483.E11.GZ43_359762
1294	Clu402904.1	2504.J02.GZ43_366007
1295	Clu404081.2	2483.K02.GZ43_359897
1296	Clu411524.1	2497.C11.GZ43_364526
1297	Clu41346.1	2560.K08.GZ43_375327
1298	Clu415520.1	2561.L14.GZ43_376509
1299	Clu416124.1	2367.G17.GZ43_346155
1300	Clu417672.1	2367.I09.GZ43_346195
1301	Clu423664.1	2488.H12.GZ43_362624
1302	Clu429609.1	2457.M11.GZ43_356511
1303	Clu442923.3	2498.G15.GZ43_365010
1304	Clu446975.1	2459.K15.GZ43_357247
1305	Clu449839.2	2497.O09.GZ43_364812
1306	Clu449889.1	2475.N21.GZ43_362334
1307	Clu451707.2	2554.P16.GZ43_376223
1308	Clu454509.3	2542.M09.GZ43_373072
1309	Clu454796.1	2540.P02.GZ43_372369
1310	Clu455862.1	2560.I09.GZ43_375280
1311	Clu460493.1	2483.O07.GZ43_359998
1312	Clu464200.1	2465.G06.GZ43_358214
1313	Clu465446.2	2457.L21.GZ43_356497
1314	Clu470032.1	2474.C01.GZ43_361666
1315	Clu474125.1	2457.E23.GZ43_356331
1316	Clu474125.2	2541.A06.GZ43_372397
1317	Clu477271.1	2540.E17.GZ43_372120
1318	Clu480410.1	2498.H08.GZ43_365027
1319	Clu483211.2	2510.J18.GZ43_369259
1320	Clu497138.1	2458.N19.GZ43_356939

Table 3

SEQ ID	CONSENSUS SEQ NAME	POLYNTD SEQ NAME
1321	Clu498886.1	2465.L22.GZ43_358350
1322	Clu498886.2	2541.B15.GZ43_372430
1323	Clu5013.2	2559.D05.GZ43_374772
1324	Clu5105.2	2542.D19.GZ43_372866
1325	Clu510539.2	2558.H17.GZ43_374496
1326	Clu514044.1	2367.F13.GZ43_346127
1327	Clu516526.1	2456.F23.GZ43_355971
1328	Clu519176.2	2559.H20.GZ43_374883
1329	Clu520370.1	2541.N01.GZ43_372704
1330	Clu524917.1	2464.H05.GZ43_357853
1331	Clu528957.1	2540.F15.GZ43_372142
1332	Clu533888.1	2557.L23.GZ43_374214
1333	Clu534076.1	2456.C05.GZ43_355881
1334	Clu540142.2	2456.H02.GZ43_355998
1335	Clu540379.2	2491.O02.GZ43_363934
1336	Clu549507.1	2483.B23.GZ43_359702
1337	Clu551338.3	2457.I12.GZ43_356416
1338	Clu552537.2	2540.C10.GZ43_372065
1339	Clu556827.3	2558.E24.GZ43_374431
1340	Clu558569.2	2558.D03.GZ43_374386
1341	Clu565709.1	2542.P02.GZ43_373137
1342	Clu568204.1	2456.M05.GZ43_356121
1343	Clu570804.1	2475.M20.GZ43_362309
1344	Clu572170.2	2557.H03.GZ43_374098
1345	Clu573764.1	2365.C10.GZ43_345284
1346	Clu587168.1	2483.F15.GZ43_359790
1347	Clu588996.1	2466.G06.GZ43_360231
1348	Clu597681.1	2459.A04.GZ43_356996
1349	Clu598388.1	2562.E03.GZ43_375562
1350	Clu604822.2	2504.F20.GZ43_365929
1351	Clu621573.1	2535.A08.GZ43_370095
1352	Clu625055.1	2511.A07.GZ43_369416
1353	Clu627263.1	2466.D20.GZ43_360173
1354	Clu635332.1	2480.D13.GZ43_358588
1355	Clu640911.2	2541.M24.GZ43_372703
1356	Clu641662.2	2555.D22.GZ43_373253
1357	Clu659483.1	2365.F12.GZ43_345358
1358	Clu6712.1	2535.P14.GZ43_370461
1359	Clu676448.3	2464.B01.GZ43_357705
1360	Clu682065.2	2467.E19.GZ43_360580
1361	Clu685244.2	2561.J01.GZ43_376448
1362	Clu691653.1	2560.O12.GZ43_375427
1363	Clu692282.1	2561.I11.GZ43_376434
1364	Clu697955.1	2557.J22.GZ43_374165
1365	Clu702885.3	2555.H18.GZ43_373345
1366	Clu70908.1	2561.C15.GZ43_376294
1367	Clu709796.2	2542.C20.GZ43_372843
1368	Clu715752.1	2459.A24.GZ43_357016
1369	Clu727966.1	2489.F09.GZ43_362957
1370	Clu732950.2	2475.L17.GZ43_362282
1371	Clu752623.2	2561.I07.GZ43_376430
1372	Clu756337.1	2561.I19.GZ43_376442
1373	Clu782981.1	2489.L05.GZ43_363097

Table 3

SEQ ID	CONSENSUS SEQ NAME	POLYNTD SEQ NAME
1374	Clu805118.3	2480.D16.GZ43_358591
1375	Clu806992.2	2467.D20.GZ43_360557
1376	Clu823296.3	2558.P20.GZ43_374691
1377	Clu830453.2	2540.M22.GZ43_372317
1378	Clu839006.1	2507.H02.GZ43_367111
1379	Clu847088.1	2542.H23.GZ43_372966
1380	Clu853371.2	2491.I06.GZ43_363794
1381	Clu88462.1	2510.K15.GZ43_369280
1382	Clu935908.2	2505.O09.GZ43_366518
1383	Clu948383.1	2541.F05.GZ43_372516
1384	Clu966599.3	2507.L12.GZ43_367217
1385	Clu993554.1	2558.F19.GZ43_374450

Table 4

SEQ ID	cDNA SEQ NAME	POLYNTD SEQ NAME	GENE	CHROM
1386	DTT00087024.1	2467.H18.GZ43_360651	DTG00087008.1	1
1387	DTT00089020.1	2367.I15.GZ43_346201	DTG00089002.1	1
1388	DTT00171014.1	2473.F14.GZ43_361367	DTG00171001.1	1
1389	DTT00514029.1	2488.G02.GZ43_362590	DTG00514005.1	1
1390	DTT00740010.1	2466.I08.GZ43_360281	DTG00740003.1	1
1391	DTT00945030.1	2466.D19.GZ43_360172	DTG00945008.1	1
1392	DTT01169022.1	2464.N05.GZ43_357997	DTG01169003.1	2
1393	DTT01178009.1	2510.O21.GZ43_369382	DTG01178002.1	2
1394	DTT01315010.1	2496.F14.GZ43_364217	DTG01315001.1	2
1395	DTT01503016.1	2538.M17.GZ43_371544	DTG01503005.1	2
1396	DTT01555018.1	2538.C07.GZ43_371294	DTG01555002.1	2
1397	DTT01685047.1	2496.C08.GZ43_364139	DTG01685007.1	2
1398	DTT01764019.1	2535.C23.GZ43_370158	DTG01764003.1	2
1399	DTT01890015.1	2482.J06.GZ43_359493	DTG01890004.1	2
1400	DTT02243008.1	2474.J19.GZ43_361852	DTG02243002.1	3
1401	DTT02367007.1	2366.P08.GZ43_345738	DTG02367002.1	3
1402	DTT02671007.1	2464.H22.GZ43_357870	DTG02671002.1	3
1403	DTT02737017.1	2538.M16.GZ43_371543	DTG02737001.1	3
1404	DTT02850005.1	2472.G03.GZ43_360996	DTG02850001.1	3
1405	DTT02966016.1	2510.M14.GZ43_369327	DTG02966003.1	4
1406	DTT03037029.1	2504.D16.GZ43_365877	DTG03037005.1	4
1407	DTT03150008.1	2491.P10.GZ43_363966	DTG03150002.1	4
1408	DTT03367008.1	2542.P19.GZ43_373154	DTG03367003.1	4
1409	DTT03630013.1	2510.O22.GZ43_369383	DTG03630002.1	4
1410	DTT03881017.1	2507.O12.GZ43_367289	DTG03881007.1	5
1411	DTT03913023.1	2459.P24.GZ43_357376	DTG03913005.1	5
1412	DTT03978010.1	2367.G22.GZ43_346160	DTG03978001.1	5
1413	DTT04070014.1	2540.H07.GZ43_372182	DTG04070007.1	5
1414	DTT04084010.1	2542.D19.GZ43_372866	DTG04084001.1	5
1415	DTT04160007.1	2472.M22.GZ43_361159	DTG04160003.1	5
1416	DTT04302021.1	2483.O07.GZ43_359998	DTG04302002.1	5
1417	DTT04378009.1	2368.O11.GZ43_346725	DTG04378001.1	5
1418	DTT04403013.1	2506.M05.GZ43_366850	DTG04403003.1	5
1419	DTT04414015.1	2368.D20.GZ43_346470	DTG04414005.1	5
1420	DTT04660017.1	2507.C03.GZ43_366992	DTG04660003.1	6
1421	DTT04956054.1	2538.I17.GZ43_371448	DTG04956020.1	6
1422	DTT04970018.1	2365.F24.GZ43_345370	DTG04970007.1	6
1423	DTT05205007.1	2459.J12.GZ43_357220	DTG05205001.1	6
1424	DTT05571010.1	2555.J10.GZ43_373385	DTG05571004.1	7
1425	DTT05650008.1	2557.L01.GZ43_374192	DTG05650003.1	7
1426	DTT05742029.1	2560.K10.GZ43_375329	DTG05742002.1	7
1427	DTT06137030.1	2565.B15.GZ43_398171	DTG06137001.1	8
1428	DTT06161014.1	2367.F06.GZ43_346120	DTG06161007.1	8
1429	DTT06706019.1	2467.D10.GZ43_360547	DTG06706003.1	9
1430	DTT06837021.1	2540.I10.GZ43_372209	DTG06837002.1	9
1431	DTT07040015.1	2504.E23.GZ43_365908	DTG07040006.1	9
1432	DTT07088009.1	2565.H01.GZ43_397953	DTG07088001.1	9
1433	DTT07182014.1	2536.G22.GZ43_370637	DTG07182006.1	10
1434	DTT07405044.1	2560.B11.GZ43_375114	DTG07405010.1	10
1435	DTT07408020.1	2466.M02.GZ43_360371	DTG07408005.1	10
1436	DTT07498014.1	2506.K20.GZ43_366817	DTG07498002.1	10
1437	DTT07600010.1	2464.H17.GZ43_357865	DTG07600001.1	10

Table 4

SEQ ID	cDNA SEQ NAME	POLYNTD SEQ NAME	GENE	CHROM
1438	DTT08005024.1	2475.N21.GZ43_362334	DTG08005009.1	11
1439	DTT08098020.1	2540.M18.GZ43_372313	DTG08098001.1	11
1440	DTT08167018.1	2542.F05.GZ43_372900	DTG08167002.1	11
1441	DTT08249022.1	2498.G15.GZ43_365010	DTG08249008.1	11
1442	DTT08499022.1	2540.A24.GZ43_372031	DTG08499009.1	12
1443	DTT08514022.1	2541.L12.GZ43_372667	DTG08514006.1	12
1444	DTT08527013.1	2489.F09.GZ43_362957	DTG08527005.1	12
1445	DTT08595020.1	2554.N09.GZ43_376168	DTG08595003.1	12
1446	DTT08711019.1	2540.C19.GZ43_372074	DTG08711001.1	12
1447	DTT08773020.1	2559.I12.GZ43_374899	DTG08773008.1	12
1448	DTT08874012.1	2537.P14.GZ43_371229	DTG08874001.1	12
1449	DTT09387018.1	2561.P19.GZ43_376610	DTG09387001.1	14
1450	DTT09396022.1	2489.M11.GZ43_363127	DTG09396001.1	14
1451	DTT09553027.1	2505.J22.GZ43_366411	DTG09553007.1	14
1452	DTT09604016.1	2483.J07.GZ43_359878	DTG09604006.1	14
1453	DTT09705033.1	2536.O22.GZ43_370829	DTG09705006.1	14
1454	DTT09742009.1	2542.N21.GZ43_373108	DTG09742002.1	15
1455	DTT09753017.1	2464.L02.GZ43_357946	DTG09753002.1	15
1456	DTT09793019.1	2464.I04.GZ43_357876	DTG09793004.1	15
1457	DTT09796028.1	2366.L21.GZ43_345942	DTG09796002.1	15
1458	DTT10221016.1	2556.C19.GZ43_373610	DTG10221004.1	16
1459	DTT10360040.1	2475.M20.GZ43_362309	DTG10360016.1	16
1460	DTT10539016.1	2506.J20.GZ43_366793	DTG10539005.1	17
1461	DTT10564022.1	2475.H06.GZ43_362175	DTG10564006.1	17
1462	DTT10683041.1	2542.K21.GZ43_373036	DTG10683007.1	17
1463	DTT10819011.1	2474.I06.GZ43_361815	DTG10819003.1	17
1464	DTT11363027.1	2542.C20.GZ43_372843	DTG11363008.1	19
1465	DTT11479018.1	2506.G24.GZ43_366725	DTG11479007.1	19
1466	DTT11483012.1	2459.H09.GZ43_357169	DTG11483001.1	19
1467	DTT11548015.1	2565.C17.GZ43_398204	DTG11548002.1	19
1468	DTT11730017.1	2535.B09.GZ43_370120	DTG11730004.1	20
1469	DTT11791010.1	2506.E12.GZ43_366665	DTG11791003.1	20
1470	DTT11864036.1	2456.H07.GZ43_356003	DTG11864011.1	21
1471	DTT11902028.1	2490.B06.GZ43_363242	DTG11902009.1	21
1472	DTT11915017.1	2474.G17.GZ43_361778	DTG11915002.1	21
1473	DTT11966040.1	2457.L21.GZ43_356497	DTG11966014.1	22
1474	DTT12042027.1	2459.G01.GZ43_357137	DTG12042005.1	22
1475	DTT12201062.1	2562.B09.GZ43_375496	DTG12201018.1	X
1476	DTT12470020.1	2489.A13.GZ43_362841	DTG12470004.1	X
1477	DTT12550009.1	2504.G01.GZ43_365934	DTG12550003.1	X

Table 5

SEQ ID	PROTEIN SEQ NAME	POLYNTD SEQ NAME	GENE	CHROM	DBL TWIST LOCUS ID
1478	DTP00087033.1	2467.H18.GZ43_360651	DTG00087008.1	1	DTL00087012.1
1479	DTP00089029.1	2367.I15.GZ43_346201	DTG00089002.1	1	DTL00089002.1
1480	DTP00171023.1	2473.F14.GZ43_361367	DTG00171001.1	1	DTL00171013.1
1481	DTP00514038.1	2488.G02.GZ43_362590	DTG00514005.1	1	DTL00514023.1
1482	DTP00740019.1	2466.I08.GZ43_360281	DTG00740003.1	1	DTL00740006.1
1483	DTP00945039.1	2466.D19.GZ43_360172	DTG00945008.1	1	
1484	DTP01169031.1	2464.N05.GZ43_357997	DTG01169003.1	2	DTL01169014.1
1485	DTP01178018.1	2510.O21.GZ43_369382	DTG01178002.1	2	DTL01178007.1
1486	DTP01315019.1	2496.F14.GZ43_364217	DTG01315001.1	2	DTL01315004.1
1487	DTP01503025.1	2538.M17.GZ43_371544	DTG01503005.1	2	DTL01503007.1
1488	DTP01555027.1	2538.C07.GZ43_371294	DTG01555002.1	2	DTL01555003.1
1489	DTP01685056.1	2496.C08.GZ43_364139	DTG01685007.1	2	DTL01685004.1
1490	DTP01764028.1	2535.C23.GZ43_370158	DTG01764003.1	2	DTL01764005.1
1491	DTP01890024.1	2482.J06.GZ43_359493	DTG01890004.1	2	DTL01890001.1
1492	DTP02243017.1	2474.J19.GZ43_361852	DTG02243002.1	3	DTL02243002.1
1493	DTP02367016.1	2366.P08.GZ43_345738	DTG02367002.1	3	DTL02367004.1
1494	DTP02671016.1	2464.H22.GZ43_357870	DTG02671002.1	3	DTL02671002.1
1495	DTP02737026.1	2538.M16.GZ43_371543	DTG02737001.1	3	DTL02737012.1
1496	DTP02850014.1	2472.G03.GZ43_360996	DTG02850001.1	3	DTL02850004.1
1497	DTP02966025.1	2510.M14.GZ43_369327	DTG02966003.1	4	DTL02966001.1
1498	DTP03037038.1	2504.D16.GZ43_365877	DTG03037005.1	4	DTL03037004.1
1499	DTP03150017.1	2491.P10.GZ43_363966	DTG03150002.1	4	DTL03149001.1
1500	DTP03367017.1	2542.P19.GZ43_373154	DTG03367003.1	4	DTL03367005.1
1501	DTP03630022.1	2510.O22.GZ43_369383	DTG03630002.1	4	DTL03630006.1
1502	DTP03881026.1	2507.O12.GZ43_367289	DTG03881007.1	5	DTL03881006.1
1503	DTP03913032.1	2459.P24.GZ43_357376	DTG03913005.1	5	DTL03913012.1
1504	DTP03978019.1	2367.G22.GZ43_346160	DTG03978001.1	5	DTL03978003.1
1505	DTP04070023.1	2540.H07.GZ43_372182	DTG04070007.1	5	
1506	DTP04084019.1	2542.D19.GZ43_372866	DTG04084001.1	5	DTL04084001.1
1507	DTP04160016.1	2472.M22.GZ43_361159	DTG04160003.1	5	DTL04160003.1
1508	DTP04302030.1	2483.O07.GZ43_359998	DTG04302002.1	5	DTL04302006.1
1509	DTP04378018.1	2368.O11.GZ43_346725	DTG04378001.1	5	
1510	DTP04403022.1	2506.M05.GZ43_366850	DTG04403003.1	5	DTL04403004.1
1511	DTP04414024.1	2368.D20.GZ43_346470	DTG04414005.1	5	DTL04414004.1
1512	DTP04660026.1	2507.C03.GZ43_366992	DTG04660003.1	6	DTL04660002.1
1513	DTP04956063.1	2538.I17.GZ43_371448	DTG04956020.1	6	DTL04956028.1
1514	DTP04970027.1	2365.F24.GZ43_345370	DTG04970007.1	6	DTL04970008.1
1515	DTP05205016.1	2459.J12.GZ43_357220	DTG05205001.1	6	DTL05205002.1
1516	DTP05571019.1	2555.J10.GZ43_373385	DTG05571004.1	7	DTL05571003.1
1517	DTP05650017.1	2557.L01.GZ43_374192	DTG05650003.1	7	DTL05650004.1
1518	DTP05742038.1	2560.K10.GZ43_375329	DTG05742002.1	7	DTL05742003.1
1519	DTP06137039.1	2565.B15.GZ43_398171	DTG06137001.1	8	DTL06137003.1
1520	DTP06161023.1	2367.F06.GZ43_346120	DTG06161007.1	8	DTL06161006.1
1521	DTP06706028.1	2467.D10.GZ43_360547	DTG06706003.1	9	DTL06705001.1
1522	DTP06837030.1	2540.I10.GZ43_372209	DTG06837002.1	9	DTL06837010.1
1523	DTP07040024.1	2504.E23.GZ43_365908	DTG07040006.1	9	DTL07040004.1
1524	DTP07088018.1	2565.H01.GZ43_397953	DTG07088001.1	9	DTL07088004.1
1525	DTP07405053.1	2560.B11.GZ43_375114	DTG07405010.1	10	DTL07405034.1
1526	DTP07408029.1	2466.M02.GZ43_360371	DTG07408005.1	10	DTL07408005.1
1527	DTP07498023.1	2506.K20.GZ43_366817	DTG07498002.1	10	DTL07498007.1
1528	DTP07600019.1	2464.H17.GZ43_357865	DTG07600001.1	10	DTL07600004.1
1529	DTP08005033.1	2475.N21.GZ43_362334	DTG08005009.1	11	DTL08005010.1

Table 5

SEQ ID	PROTEIN SEQ NAME	POLYNTD SEQ NAME	GENE	CHROM	DBL TWIST LOCUS ID
1530	DTP08098029.1	2540.M18.GZ43_372313	DTG08098001.1	11	DTL08098013.1
1531	DTP08167027.1	2542.F05.GZ43_372900	DTG08167002.1	11	DTL08167003.1
1532	DTP08249031.1	2498.G15.GZ43_365010	DTG08249008.1	11	DTL08249005.1
1533	DTP08499031.1	2540.A24.GZ43_372031	DTG08499009.1	12	DTL08499012.1
1534	DTP08514031.1	2541.L12.GZ43_372667	DTG08514006.1	12	DTL08514015.1
1535	DTP08527022.1	2489.F09.GZ43_362957	DTG08527005.1	12	DTL08527008.1
1536	DTP08595029.1	2554.N09.GZ43_376168	DTG08595003.1	12	DTL08595002.1
1537	DTP08711028.1	2540.C19.GZ43_372074	DTG08711001.1	12	DTL08710003.1
1538	DTP08773029.1	2559.I12.GZ43_374899	DTG08773008.1	12	DTL08773011.1
1539	DTP08874021.1	2537.P14.GZ43_371229	DTG08874001.1	12	DTL08874009.1
1540	DTP09387027.1	2561.P19.GZ43_376610	DTG09387001.1	14	DTL09387002.1
1541	DTP09396031.1	2489.M11.GZ43_363127	DTG09396001.1	14	DTL09396016.1
1542	DTP09553036.1	2505.J22.GZ43_366411	DTG09553007.1	14	DTL09553018.1
1543	DTP09604025.1	2483.J07.GZ43_359878	DTG09604006.1	14	DTL09604010.1
1544	DTP09705042.1	2536.O22.GZ43_370829	DTG09705006.1	14	DTL09705005.1
1545	DTP09742018.1	2542.N21.GZ43_373108	DTG09742002.1	15	DTL09742007.1
1546	DTP09753026.1	2464.L02.GZ43_357946	DTG09753002.1	15	DTL09753011.1
1547	DTP09793028.1	2464.I04.GZ43_357876	DTG09793004.1	15	DTL09793004.1
1548	DTP09796037.1	2366.L21.GZ43_345942	DTG09796002.1	15	DTL09796021.1
1549	DTP10221025.1	2556.C19.GZ43_373610	DTG10221004.1	16	DTL10221002.1
1550	DTP10360049.1	2475.M20.GZ43_362309	DTG10360016.1	16	DTL10360003.1
1551	DTP10539025.1	2506.J20.GZ43_366793	DTG10539005.1	17	DTL10539004.1
1552	DTP10564031.1	2475.H06.GZ43_362175	DTG10564006.1	17	DTL10564006.1
1553	DTP10683050.1	2542.K21.GZ43_373036	DTG10683007.1	17	DTL10683002.1
1554	DTP10819020.1	2474.I06.GZ43_361815	DTG10819003.1	17	DTL10819002.1
1555	DTP11363036.1	2542.C20.GZ43_372843	DTG11363008.1	19	DTL11363017.1
1556	DTP11479027.1	2506.G24.GZ43_366725	DTG11479007.1	19	DTL11479006.1
1557	DTP11483021.1	2459.H09.GZ43_357169	DTG11483001.1	19	DTL11483006.1
1558	DTP11548024.1	2565.C17.GZ43_398204	DTG11548002.1	19	DTL11548003.1
1559	DTP11730026.1	2535.B09.GZ43_370120	DTG11730004.1	20	DTL11730009.1
1560	DTP11791019.1	2506.E12.GZ43_366665	DTG11791003.1	20	DTL11791005.1
1561	DTP11864045.1	2456.H07.GZ43_356003	DTG11864011.1	21	DTL11864023.1
1562	DTP11902037.1	2490.B06.GZ43_363242	DTG11902009.1	21	DTL11902002.1
1563	DTP11915026.1	2474.G17.GZ43_361778	DTG11915002.1	21	DTL11915001.1
1564	DTP11966049.1	2457.L21.GZ43_356497	DTG11966014.1	22	DTL11966006.1
1565	DTP12042036.1	2459.G01.GZ43_357137	DTG12042005.1	22	DTL12042001.1
1566	DTP12201071.1	2562.B09.GZ43_375496	DTG12201018.1	X	DTL12201023.1
1567	DTP12470029.1	2489.A13.GZ43_362841	DTG12470004.1	X	DTL12470016.1
1568	DTP12550018.1	2504.G01.GZ43_365934	DTG12550003.1	X	DTL12550005.1

Table 6

cDNA SEQ ID	cDNA SEQ NAME	PROTEIN SEQ ID	PROTEIN SEQ NAME	POLYNTD SEQ ID	POLYNTD SEQ NAME
1386	DTT00087024.1	1478	DTP00087033.1	963	2467.H18.GZ43_360651
1386	DTT00087024.1	1478	DTP00087033.1	33	2505.B05.GZ43_366202
1387	DTT00089020.1	1479	DTP00089029.1	213	2367.I15.GZ43_346201
1388	DTT00171014.1	1480	DTP00171023.1	1006	2473.F14.GZ43_361367
1388	DTT00171014.1	1480	DTP00171023.1	1122	2489.A03.GZ43_362831
1389	DTT00514029.1	1481	DTP00514038.1	1113	2488.G02.GZ43_362590
1390	DTT00740010.1	1482	DTP00740019.1	952	2466.I08.GZ43_360281
1391	DTT00945030.1	1483	DTP00945039.1	945	2466.D19.GZ43_360172
1392	DTT01169022.1	1484	DTP01169031.1	482	2540.I17.GZ43_372216
1392	DTT01169022.1	1484	DTP01169031.1	914	2464.N05.GZ43_357997
1393	DTT01178009.1	1485	DTP01178018.1	113	2510.O21.GZ43_369382
1394	DTT01315010.1	1486	DTP01315019.1	1181	2496.F14.GZ43_364217
1395	DTT01503016.1	1487	DTP01503025.1	386	2538.M17.GZ43_371544
1396	DTT01555018.1	1488	DTP01555027.1	366	2538.C07.GZ43_371294
1396	DTT01555018.1	1488	DTP01555027.1	368	2538.D03.GZ43_371314
1396	DTT01555018.1	1488	DTP01555027.1	369	2538.D04.GZ43_371315
1397	DTT01685047.1	1489	DTP01685056.1	1177	2496.C08.GZ43_364139
1398	DTT01764019.1	1490	DTP01764028.1	267	2535.C23.GZ43_370158
1398	DTT01764019.1	1490	DTP01764028.1	771	2456.D04.GZ43_355904
1399	DTT01890015.1	1491	DTP01890024.1	1087	2482.J06.GZ43_359493
1399	DTT01890015.1	1491	DTP01890024.1	1042	2475.B20.GZ43_362045
1399	DTT01890015.1	1491	DTP01890024.1	1200	2497.L21.GZ43_364752
1400	DTT02243008.1	1492	DTP02243017.1	1224	2562.G21.GZ43_375628
1400	DTT02243008.1	1492	DTP02243017.1	1204	2497.P04.GZ43_364831
1400	DTT02243008.1	1492	DTP02243017.1	1025	2474.J19.GZ43_361852
1400	DTT02243008.1	1492	DTP02243017.1	1191	2497.D11.GZ43_364550
1401	DTT02367007.1	1493	DTP02367016.1	174	2366.P08.GZ43_345738
1402	DTT02671007.1	1494	DTP02671016.1	903	2464.H22.GZ43_357870
1402	DTT02671007.1	1494	DTP02671016.1	1055	2480.G11.GZ43_358658
1403	DTT02737017.1	1495	DTP02737026.1	385	2538.M16.GZ43_371543
1404	DTT02850005.1	1496	DTP02850014.1	992	2472.G03.GZ43_360996
1404	DTT02850005.1	1496	DTP02850014.1	1111	2488.F06.GZ43_362570
1404	DTT02850005.1	1496	DTP02850014.1	1039	2475.N08.GZ43_362321
1405	DTT02966016.1	1497	DTP02966025.1	103	2510.M14.GZ43_369327
1406	DTT03037029.1	1498	DTP03037038.1	9	2504.D16.GZ43_365877
1407	DTT03150008.1	1499	DTP03150017.1	428	2565.G20.GZ43_398256
1407	DTT03150008.1	1499	DTP03150017.1	585	2555.I12.GZ43_373363
1407	DTT03150008.1	1499	DTP03150017.1	235	2368.D08.GZ43_346458
1407	DTT03150008.1	1499	DTP03150017.1	1174	2491.P10.GZ43_363966
1408	DTT03367008.1	1500	DTP03367017.1	519	2506.E18.GZ43_366671
1408	DTT03367008.1	1500	DTP03367017.1	557	2542.P19.GZ43_373154
1409	DTT03630013.1	1501	DTP03630022.1	114	2510.O22.GZ43_369383
1410	DTT03881017.1	1502	DTP03881026.1	1251	2507.O12.GZ43_367289
1411	DTT03913023.1	1503	DTP03913032.1	889	2459.P24.GZ43_357376
1412	DTT03978010.1	1504	DTP03978019.1	211	2367.G22.GZ43_346160
1413	DTT04070014.1	1505	DTP04070023.1	423	2565.D06.GZ43_398029
1413	DTT04070014.1	1505	DTP04070023.1	374	2538.F03.GZ43_371362
1413	DTT04070014.1	1505	DTP04070023.1	17	2504.I13.GZ43_365994
1413	DTT04070014.1	1505	DTP04070023.1	692	2559.K12.GZ43_374947
1413	DTT04070014.1	1505	DTP04070023.1	43	2505.E15.GZ43_366284
1413	DTT04070014.1	1505	DTP04070023.1	750	2561.M09.GZ43_376528
1413	DTT04070014.1	1505	DTP04070023.1	463	2540.H07.GZ43_372182

Table 6

cDNA SEQ ID	cDNA SEQ NAME	PROTEIN SEQ ID	PROTEIN SEQ NAME	POLYNTD SEQ ID	POLYNTD SEQ NAME
1413	DTT04070014.1	1505	DTP04070023.1	1069	2481.D13.GZ43_358972
1414	DTT04084010.1	1506	DTP04084019.1	543	2542.D19.GZ43_372866
1415	DTT04160007.1	1507	DTP04160016.1	999	2472.M22.GZ43_361159
1416	DTT04302021.1	1508	DTP04302030.1	1106	2483.O07.GZ43_359998
1417	DTT04378009.1	1509	DTP04378018.1	260	2368.O11.GZ43_346725
1418	DTT04403013.1	1510	DTP04403022.1	531	2506.M05.GZ43_366850
1419	DTT04414015.1	1511	DTP04414024.1	236	2368.D20.GZ43_346470
1420	DTT04660017.1	1512	DTP04660026.1	334	2537.D11.GZ43_370938
1420	DTT04660017.1	1512	DTP04660026.1	1244	2507.C03.GZ43_366992
1421	DTT04956054.1	1513	DTP04956063.1	379	2538.I17.GZ43_371448
1422	DTT04970018.1	1514	DTP04970027.1	363	2538.B03.GZ43_371266
1422	DTT04970018.1	1514	DTP04970027.1	259	2368.O03.GZ43_346717
1422	DTT04970018.1	1514	DTP04970027.1	1101	2483.K02.GZ43_359897
1422	DTT04970018.1	1514	DTP04970027.1	134	2365.F24.GZ43_345370
1423	DTT05205007.1	1515	DTP05205016.1	880	2459.J12.GZ43_357220
1424	DTT05571010.1	1516	DTP05571019.1	586	2555.J10.GZ43_373385
1425	DTT05650008.1	1517	DTP05650017.1	644	2557.L01.GZ43_374192
1426	DTT05742029.1	1518	DTP05742038.1	721	2560.K10.GZ43_375329
1426	DTT05742029.1	1518	DTP05742038.1	126	2365.D10.GZ43_345308
1426	DTT05742029.1	1518	DTP05742038.1	756	2561.I19.GZ43_376442
1427	DTT06137030.1	1519	DTP06137039.1	419	2565.B15.GZ43_398171
1428	DTT06161014.1	1520	DTP06161023.1	205	2367.F06.GZ43_346120
1429	DTT06706019.1	1521	DTP06706028.1	967	2467.D10.GZ43_360547
1430	DTT06837021.1	1522	DTP06837030.1	465	2540.I10.GZ43_372209
1431	DTT07040015.1	1523	DTP07040024.1	10	2504.E23.GZ43_365908
1432	DTT07088009.1	1524	DTP07088018.1	170	2366.J06.GZ43_345700
1432	DTT07088009.1	1524	DTP07088018.1	429	2565.H01.GZ43_397953
1433	DTT07182014.1		DTP07182023.1	306	2536.G22.GZ43_370637
1434	DTT07405044.1	1525	DTP07405053.1	703	2560.B11.GZ43_375114
1435	DTT07408020.1	1526	DTP07408029.1	956	2466.M02.GZ43_360371
1436	DTT07498014.1	1527	DTP07498023.1	529	2506.K20.GZ43_366817
1437	DTT07600010.1	1528	DTP07600019.1	902	2464.H17.GZ43_357865
1438	DTT08005024.1	1529	DTP08005033.1	1046	2475.N21.GZ43_362334
1439	DTT08098020.1	1530	DTP08098029.1	485	2540.M18.GZ43_372313
1440	DTT08167018.1	1531	DTP08167027.1	152	2365.N12.GZ43_345550
1440	DTT08167018.1	1531	DTP08167027.1	544	2542.F05.GZ43_372900
1441	DTT08249022.1	1532	DTP08249031.1	1235	2498.G15.GZ43_365010
1442	DTT08499022.1	1533	DTP08499031.1	452	2540.A24.GZ43_372031
1443	DTT08514022.1	1534	DTP08514031.1	508	2541.L12.GZ43_372667
1444	DTT08527013.1	1535	DTP08527022.1	109	2510.N14.GZ43_369351
1444	DTT08527013.1	1535	DTP08527022.1	394	2554.A16.GZ43_375863
1444	DTT08527013.1	1535	DTP08527022.1	1128	2489.F09.GZ43_362957
1444	DTT08527013.1	1535	DTP08527022.1	569	2555.F16.GZ43_373295
1445	DTT08595020.1	1536	DTP08595029.1	413	2554.N09.GZ43_376168
1446	DTT08711019.1	1537	DTP08711028.1	472	2540.C19.GZ43_372074
1447	DTT08773020.1	1538	DTP08773029.1	687	2559.I12.GZ43_374899
1448	DTT08874012.1	1539	DTP08874021.1	356	2537.P14.GZ43_371229
1449	DTT09387018.1	1540	DTP09387027.1	762	2561.P19.GZ43_376610
1450	DTT09396022.1	1541	DTP09396031.1	1140	2489.M11.GZ43_363127
1451	DTT09553027.1	1542	DTP09553036.1	54	2505.J22.GZ43_366411
1452	DTT09604016.1	1543	DTP09604025.1	1100	2483.J07.GZ43_359878
1453	DTT09705033.1	1544	DTP09705042.1	323	2536.O22.GZ43_370829

Table 6

cDNA SEQ ID	cDNA SEQ NAME	PROTEIN SEQ ID	PROTEIN SEQ NAME	POLYNTD SEQ ID	POLYNTD SEQ NAME
1454	DTT09742009.1	1545	DTP09742018.1	766	2456.B12.GZ43_355864
1454	DTT09742009.1	1545	DTP09742018.1	563	2542.N21.GZ43_373108
1455	DTT09753017.1	1546	DTP09753026.1	910	2464.L02.GZ43_357946
1456	DTT09793019.1	1547	DTP09793028.1	904	2464.I04.GZ43_357876
1457	DTT09796028.1	1548	DTP09796037.1	189	2366.L21.GZ43_345942
1458	DTT10221016.1	1549	DTP10221025.1	592	2556.C19.GZ43_373610
1459	DTT10360040.1	1550	DTP10360049.1	1045	2475.M20.GZ43_362309
1460	DTT10539016.1	1551	DTP10539025.1	527	2506.J20.GZ43_366793
1461	DTT10564022.1	1552	DTP10564031.1	1035	2475.H06.GZ43_362175
1462	DTT10683041.1	1553	DTP10683050.1	561	2542.K21.GZ43_373036
1463	DTT10819011.1	1554	DTP10819020.1	796	2457.C19.GZ43_356279
1463	DTT10819011.1	1554	DTP10819020.1	143	2365.J14.GZ43_345456
1463	DTT10819011.1	1554	DTP10819020.1	1023	2474.I06.GZ43_361815
1464	DTT11363027.1	1555	DTP11363036.1	540	2542.C20.GZ43_372843
1465	DTT11479018.1	1556	DTP11479027.1	521	2506.G24.GZ43_366725
1466	DTT11483012.1	1557	DTP11483021.1	877	2459.H09.GZ43_357169
1467	DTT11548015.1	1558	DTP11548024.1	422	2565.C17.GZ43_398204
1468	DTT11730017.1	1559	DTP11730026.1	264	2535.B09.GZ43_370120
1469	DTT11791010.1	1560	DTP11791019.1	518	2506.E12.GZ43_366665
1470	DTT11864036.1	1561	DTP11864045.1	778	2456.H07.GZ43_356003
1471	DTT11902028.1	1562	DTP11902037.1	1144	2490.B06.GZ43_363242
1472	DTT11915017.1	1563	DTP11915026.1	591	2556.C11.GZ43_373602
1472	DTT11915017.1	1563	DTP11915026.1	1021	2474.G17.GZ43_361778
1472	DTT11915017.1	1563	DTP11915026.1	1163	2491.C13.GZ43_363657
1473	DTT11966040.1	1564	DTP11966049.1	1216	2562.E14.GZ43_375573
1473	DTT11966040.1	1564	DTP11966049.1	818	2457.L21.GZ43_356497
1473	DTT11966040.1	1564	DTP11966049.1	532	2506.M13.GZ43_366858
1474	DTT12042027.1	1565	DTP12042036.1	874	2459.G01.GZ43_357137
1475	DTT12201062.1	1566	DTP12201071.1	759	2561.O17.GZ43_376584
1475	DTT12201062.1	1566	DTP12201071.1	1207	2562.B09.GZ43_375496
1476	DTT12470020.1	1567	DTP12470029.1	1124	2489.A13.GZ43_362841
1476	DTT12470020.1	1567	DTP12470029.1	799	2457.D12.GZ43_356296
1476	DTT12470020.1	1567	DTP12470029.1	690	2559.J02.GZ43_374913
1476	DTT12470020.1	1567	DTP12470029.1	568	2555.E20.GZ43_373275
1477	DTT12550009.1	1568	DTP12550018.1	12	2504.G01.GZ43_365934

Table 7

SEQ ID	SEQ NAME	ACCESSION	GENBANK DESCRIPTION	GENBANK SCORE
6	2504.C08.GZ43_365845	AP000321	gi|4835690|dbj|AP000321.1AP000321 Homo sapiens genomic DNA, chromosome 21q22.1, D21S226-AML region, clone:Q82F5, complete sequence	1.6E-31
7	2504.C11.GZ43_365848	AP002938	gi|16267134|dbj|AP002938.1AP002938 Hoplostethus japonicus mitochondrial DNA, complete genome	4.8E-58
9	2504.D16.GZ43_365877	AK023496	gi|10435445|dbj|AK023496.1AK023496 Homo sapiens cDNA FLJ13434 fis, clone PLACE1002578	0
10	2504.E23.GZ43_365908	M80340	gi|339767|gb|M80340.1HUMTNL12 Human transposon L1.1 with a base deletion relative to L1.2B resulting in a premature stop codon in t	6.1E-182
11	2504.F20.GZ43_365929	AE007289	gi|14524175|gb|AE007289.1AE007289 Sinorhizobium meliloti plasmid pSymA section 95 of 121 of the complete plasmid sequence	2.1E-98
17	2504.I13.GZ43_365994	AJ312523	gi|12830519|emb|AJ312523.1GGO312523 Gorilla gorilla gorilla Xq13.3 chromosome non-coding sequence, isolate G167W	1.1E-44
31	2504.O12.GZ43_366137	AF342020	gi|12961941|gb|AF342020.1AF342020 Sclerotinia sclerotiorum strain LES-1 28S ribosomal RNA gene, partial sequence; intergenic spacer	1.1E-90
33	2505.B05.GZ43_366202	U93571	gi|2072968|gb|U93571.1HSU93571 Human L1 element L1.24 p40 gene, complete cds	1.1E-226
37	2505.C17.GZ43_366238	AJ325713	gi|15870107|emb|AJ325713.1HSA325713 Homo sapiens genomic sequence surrounding NotI site, clone NB1-110S	1.4E-21
40	2505.D03.GZ43_366248	AJ224335	gi|3413799|emb|AJ224335.1HSAJ4335 Homo sapien mRNA for putative secretory protein, hBET3	5.2E-71
43	2505.E15.GZ43_366284	AB030001	gi|7416074|dbj|AB030001.1AB030001 Homo sapiens gene for SGRF, complete cds	8.1E-55
46	2505.G16.GZ43_366333	AE005683	gi|13421186|gb|AE005683.1AE005683 Caulobacter crescentus section 9 of 359 of the complete genome	3.6E-63
48	2505.I04.GZ43_366369	AF255613	gi|8925326|gb|AF255613.1AF255613 Homo sapiens teratoma-associated tyrosine kinase (TAPK) gene, exons 1 through 6 and partial cds	7.9E-73
63	2505.O09.GZ43_366518	AF053644	gi|3598786|gb|AF053644.1HSCSE1G2 Homo sapiens cellular apoptosis susceptibility protein (CSE1) gene, exon 2	9.4E-45
72	2510.C10.GZ43_369083	AB002353	gi|2224650|dbj|AB002353.1AB002353 Human mRNA for KIAA0355 gene, complete cds	1.4E-71

Table 7

SEQ ID	SEQ NAME	ACCES-SION	GENBANK DESCRIPTION	GENBANK SCORE
78	2510.G06.GZ43_369175	AF084935	gi|3603422|gb|AF084935.1AF084935 Homo sapiens galactokinase (GALK1) gene, partial cds	8.9E-24
89	2510.J11.GZ43_369252	AK024617	gi|10436933|dbj|AK024617.1AK024617 Homo sapiens cDNA: FLJ20964 fis, clone ADSH00902	0
102	2510.L21.GZ43_369310	AK023677	gi|10435673|dbj|AK023677.1AK023677 Homo sapiens cDNA FLJ13615 fis, clone PLACE1010896, weakly similar to NUF1 PROTEIN	1.2E-90
109	2510.N14.GZ43_369351	AF271388	gi|8515842|gb|AF271388.1AF271388 Homo sapiens CMP-N-acetylneuraminic acid synthase mRNA, complete cds	0
115	2510.O23.GZ43_369384	AF113169	gi|4164598|gb|AF113169.1AF113169 Homo sapiens glandular kallikrein enhancer region, complete sequence	2.2E-39
124	2365.C20.GZ43_345294	AF069489	gi|3560568|gb|AF069489.1HSPDE4A3 Homo sapiens cAMP specific phosphodiesterase 4A variant pde46 (PDE4A) gene, exons 2 through 13 and	6.6E-24
134	2365.F24.GZ43_345370	AK012908	gi|12849956|dbj|AK012908.1AK012908 Mus musculus 10, 11 days embryo cDNA, RIKEN full-length enriched library, clone:2810046L04, full	2.9E-224
143	2365.J14.GZ43_345456	BC007999	gi|14124949|gb|BC007999.1BC007999 Homo sapiens, hypothetical protein FLJ10759, clone MGC:15757 IMAGE:3357436, mRNA, complete cds	4.4E-56
152	2365.N12.GZ43_345550	U20391	gi|1483626|gb|U20391.1HSU20391 Human folate receptor (FOLR1) gene, complete cds	3.9E-41
162	2366.E03.GZ43_345647	AB025285	gi|5917586|dbj|AB025285.1AB025285 Homo sapiens c-ERBB-2 gene, exons 1', 2', 3', 4'	4.3E-30
163	2366.J03.GZ43_345652	M15885	gi|338414|gb|M15885.1HUMSPP Human prostate secreted seminal plasma protein mRNA, complete cds	1.1E-68
170	2366.J06.GZ43_345700	AF326517	gi|15080738|gb|AF326517.1AF326517 Abies grandis pinene synthase gene, partial cds	0
182	2366.K13.GZ43_345813	U27333	gi|967202|gb|U27333.1HSU27333 Human alpha (1,3) fucosyltransferase (FUT6) mRNA, major transcript I, complete cds	2.5E-44
189	2366.L21.GZ43_345942	AF272390	gi|8705239|gb|AF272390.1AF272390 Homo sapiens myosin 5c (MYO5C) mRNA, complete cds	1.4E-290
195	2367.B10.GZ43_346028	AJ279823	gi|11932035|emb|AJ279823.1ASF279823 Ascovirus SfAV1b partial pol gene for DNA polymerase, Pol2-Pol3-Pol1 fragment	1.4E-231

Table 7

SEQ ID	SEQ NAME	ACCES-SION	GENBANK DESCRIPTION	GENBANK SCORE
198	2367.C12.GZ43_346054	BC014669	gi|15779227|gb|BC014669.1BC014669 Homo sapiens, clone IMAGE:4849317, mRNA, partial cds	2.9E-57
200	2367.D18.GZ43_346084	AE008517	gi|15459138|gb|AE008517.1AE008517 Streptococcus pneumoniae R6 section 133 of 184 of the complete genome	1.4E-34
205	2367.F06.GZ43_346120	AJ330464	gi|15874882|emb|AJ330464.1HSA330464 Homo sapiens genomic sequence surrounding NotI site, clone NR1-IL7C	3.1E-100
206	2367.F13.GZ43_346127	AY035075	gi|14334803|gb|AY035075.1 Arabidopsis thaliana putative H+-transporting ATPase (AT4g30190) mRNA, complete cds	4.1E-229
208	2367.G13.GZ43_346151	AK025355	gi|10437854|dbj|AK025355.1AK025355 Homo sapiens cDNA: FLJ21702 fis, clone COL09874	1.8E-58
209	2367.G17.GZ43_346155	AK000293	gi|7020278|dbj|AK000293.1AK000293 Homo sapiens cDNA FLJ20286 fis, clone HEP04358	4.4E-34
210	2367.G20.GZ43_346158	AL137592	gi|6808332|emb|AL137592.1HSM802347 Homo sapiens mRNA; cDNA DKFZp434L0610 (from clone DKFZp434L0610); partial cds	1.6E-60
211	2367.G22.GZ43_346160	BC015529	gi|15930193|gb|BC015529.1BC015529 Homo sapiens, Similar to ribose 5-phosphate isomerase A, clone MGC:9441 IMAGE:3904718, mRNA, comp	9.7E-60
213	2367.I15.GZ43_346201	AF324172	gi|12958747|gb|AF324172.1AF324172 Dictyophora indusiata strain ASI 32001 internal transcribed spacer 1, partial sequence; 5.8S ribo	4.8E-65
217	2367.K24.GZ43_346258	AF009251	gi|2352833|gb|AF009251.1CLCN6HUM05 Homo sapiens putative chloride channel gene (CLCN6), exon 6	3.8E-62
219	2367.M06.GZ43_346288	AF178322	gi|13344845|gb|AF178322.1AF178322 Schmidtea mediterranea cytochrome oxidase C subunit I (COI) gene, partial cds; mitochondrial gene	1.5E-43
220	2367.M14.GZ43_346296	AK026286	gi|10439097|dbj|AK026286.1AK026286 Homo sapiens cDNA: FLJ22633 fis, clone HSI06502	1E-300
221	2367.M16.GZ43_346298	AF368920	gi|14039926|gb|AF368920.1AF368920 Caenorhabditis elegans voltage-dependent calcium channel alpha13 subunit (cca-1) mRNA, complete c	1.6E-83
224	2367.N16.GZ43_346322	Z78727	gi|1508005|emb|Z78727.1HSPA15B9 H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA15B9	1.3E-37
231	2368.B18.GZ43_346420	AK000293	gi|7020278|dbj|AK000293.1AK000293 Homo sapiens cDNA FLJ20286 fis, clone HEP04358	5E-34

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SEQ ID	SEQ NAME	ACCESSION	GENBANK DESCRIPTION	GENBANK SCORE
235	2368.D08.GZ43_346458	AJ276936	gi|12214232|emb|AJ276936.1NME276936 Neisseria meningitidis partial tbpB gene for transferrin binding protein B subunit, allele 66,	0
245	2368.I04.GZ43_346574	AY042191	gi|15546022|gb|AY042191.1 Mus musculus RF-amide G protein-coupled receptor (MrgA1) mRNA, complete cds	3.1E-26
249	2368.K21.GZ43_346639	AJ310931	gi|15718363|emb|AJ310931.1HSA310931 Homo sapiens mRNA for myosin heavy chain	7E-55
252	2368.M19.GZ43_346685	AK025595	gi|10438161|dbj|AK025595.1AK025595 Homo sapiens cDNA: FLJ21942 fis, clone HEP04527	4.7E-21
257	2368.N15.GZ43_346705	AK014328	gi|12852104|dbj|AK014328.1AK014328 Mus musculus 14, 17 days embryo head cDNA, RIKEN full-length enriched library, clone:3230401M21,	3.1E-103
258	2368.N23.GZ43_346713	AL391428	gi|9864373|emb|AL391428.1AL391428 Human DNA sequence from clone RP11-60P19 on chromosome 1, complete sequence [Homo sapiens]	4.8E-28
259	2368.O03.GZ43_346717	AK012908	gi|12849956|dbj|AK012908.1AK012908 Mus musculus 10, 11 days embryo cDNA, RIKEN full-length enriched library, clone:2810046L04, full	2.1E-227
260	2368.O11.GZ43_346725	AF102129	gi|5922722|gb|AF102129.1AF102129 Rattus norvegicus KPL2 (Kpl2) mRNA, complete cds	2.5E-103
264	2535.B09.GZ43_370120	AF292648	gi|12656358|gb|AF292648.1AF292648 Mus musculus zinc finger 202 m1 (Znf202) mRNA, complete cds	2E-39
267	2535.C23.GZ43_370158	AF307053	gi|12018057|gb|AF307053.1AF307053 Thermococcus litoralis sugar kinase, trehalose/maltose binding protein (malE), trehalose/maltose	0
269	2535.F05.GZ43_370212	AF367433	gi|14486704|gb|AF367433.1AF367433 Lotus japonicus phosphatidylinositol transfer-like protein III (LjPLP-III) mRNA, complete cds	3.8E-38
276	2535.L03.GZ43_370354	AK000099	gi|7019966|dbj|AK000099.1AK000099 Homo sapiens cDNA FLJ20092 fis, clone COL04215	7.1E-52
280	2535.O07.GZ43_370430	BC008425	gi|14250051|gb|BC008425.1BC008425 Homo sapiens, clone MGC:14582 IMAGE:4246114, mRNA, complete cds	3.8E-34
282	2535.P02.GZ43_370449	NM_024074	gi|13129059|ref|NM_024074.1 Homo sapiens hypothetical protein MGC3169 (MGC3169), mRNA	2.4E-23
292	2536.A22.GZ43_370493	AF310311	gi|13517433|gb|AF310311.1AF310311 Homo sapiens isolate Nigeria 9 membrane protein CH1 gene, partial cds	0

Table 7

SEQ ID	SEQ NAME	ACCESSION	GENBANK DESCRIPTION	GENBANK SCORE
297	2536.D17.GZ43_370560	AF015148	gi|2353128|gb|AF015148.1AF015148 Homo sapiens clone HS19.2 Alu-Ya5 sequence	1.6E-46
303	2536.G05.GZ43_370620	AF045605	gi|3228525|gb|AF045605.1AF045605 Homo sapiens germline chromosome 11, 11q13 region	6.2E-77
305	2536.G21.GZ43_370636	AK026490	gi|10439363|dbj|AK026490.1AK026490 Homo sapiens cDNA: FLJ22837 fis, clone KAIA4417	3.5E-143
306	2536.G22.GZ43_370637	NC_002707	gi|13540758|ref|NC_002707.1 Anguilla japonica mitochondrion, complete genome	2.3E-39
309	2536.I05.GZ43_370668	AK000099	gi|7019966|dbj|AK000099.1AK000099 Homo sapiens cDNA FLJ20092 fis, clone COL04215	3.4E-63
310	2536.I15.GZ43_370678	AB013897	gi|6177784|dbj|AB013897.1AB013897 Homo sapiens mRNA for HKR1, partial cds	5.1E-53
313	2536.J11.GZ43_370698	AK023448	gi|10435386|dbj|AK023448.1AK023448 Homo sapiens cDNA FLJ13386 fis, clone PLACE1001104, weakly similar to MYOSIN HEAVY CHAIN, NON-MU	0
314	2536.K12.GZ43_370723	U14573	gi|551542|gb|U14573.1HSU14573 ***ALU WARNING: Human Alu-Sq subfamily consensus sequence	1E-96
319	2536.N05.GZ43_370788	AK001347	gi|7022548|dbj|AK001347.1AK001347 Homo sapiens cDNA FLJ10485 fis, clone NT2RP2000195	6.7E-43
320	2536.N20.GZ43_370803	Y15724	gi|3021395|emb|Y15724.1HSSERCA1 Homo sapiens SERCA3 gene, exons 1-7 (and joined CDS)	1.9E-27
330	2537.B07.GZ43_370886	X69516	gi|288876|emb|X69516.1HSFOLA H.sapiens gene for folate receptor	2.8E-60
334	2537.D11.GZ43_370938	NM_025080	gi|13376633|ref|NM_025080.1 Homo sapiens hypothetical protein FLJ22316 (FLJ22316), mRNA	8.7E-289
338	2537.G05.GZ43_371004	L04193	gi|187144|gb|L04193.1HUMLIMGP Human lens membrane protein (mp19) gene, exon 11	7.4E-52
341	2537.I03.GZ43_371050	Z78727	gi|1508005|emb|Z78727.1HSPA15B9 H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA15B9	1.7E-37
345	2537.K17.GZ43_371112	AL603947	gi|15384818|emb|AL603947.1UMA0006 Ustilago maydis gene for predicted plasmamembrane-ATPase	9.3E-76
350	2537.N23.GZ43_371190	AF242865	gi|9858570|gb|AF242865.1AF242862S4 Homo sapiens coxsackie virus and adenovirus receptor (CXADR) gene, exon 7 and complete cds	2.4E-30
352	2537.O05.GZ43_371196	AB060827	gi|13874462|dbj|AB060827.1AB060827 Macaca fascicularis brain cDNA clone:QtrA-10256, full insert sequence	2.2E-24

Table 7

SEQ ID	SEQ NAME	ACCESSION	GENBANK DESCRIPTION	GENBANK SCORE
356	2537.P14.GZ43_371229	AK026442	gi|10439307|dbj|AK026442.1AK026442 Homo sapiens cDNA: FLJ22789 fis, clone KAIA2171	6.3E-256
361	2538.A10.GZ43_371249	AK001432	gi|7022685|dbj|AK001432.1AK001432 Homo sapiens cDNA FLJ10570 fis, clone NT2RP2003117	1.9E-52
363	2538.B03.GZ43_371266	AK013900	gi|12851449|dbj|AK013900.1AK013900 Mus musculus 12 days embryo head cDNA, RIKEN full-length enriched library, clone:3010026L22, ful	1.2E-201
366	2538.C07.GZ43_371294	AK022973	gi|10434673|dbj|AK022973.1AK022973 Homo sapiens cDNA FLJ12911 fis, clone NT2RP2004425, highly similar to Mus musculus axotrophin mR	0
367	2538.C14.GZ43_371301	M87914	gi|174891|gb|M87914.1HUMALNE461 Human carcinoma cell-derived Alu RNA transcript, clone NE461	2E-89
368	2538.D03.GZ43_371314	AK022973	gi|10434673|dbj|AK022973.1AK022973 Homo sapiens cDNA FLJ12911 fis, clone NT2RP2004425, highly similar to Mus musculus axotrophin mR	4.3E-275
369	2538.D04.GZ43_371315	AK022973	gi|10434673|dbj|AK022973.1AK022973 Homo sapiens cDNA FLJ12911 fis, clone NT2RP2004425, highly similar to Mus musculus axotrophin mR	1.3E-287
371	2538.E01.GZ43_371336	AF074397	gi|3916231|gb|AF074397.1AF074397 Homo sapiens anti-mullerian hormone type II receptor (AMHR2) gene, promoter region and partial cds	4E-40
374	2538.F03.GZ43_371362	L34639	gi|598203|gb|L34639.1HUMPECAM09 Homo sapiens platelet/endothelial cell adhesion molecule-1 (PECAM-1) gene, exon 6	1.5E-43
375	2538.H02.GZ43_371409	AF220173	gi|9651700|gb|AF220173.1AF220172S2 Homo sapiens acid ceramidase (ASAH) gene, exons 2 through 4	2.5E-39
379	2538.I17.GZ43_371448	AF050179	gi|3319283|gb|AF050179.1AF050179 Homo sapiens CENP-C binding protein (DAXX) mRNA, complete cds	4.9E-41
380	2538.J10.GZ43_371465	AY035075	gi|14334803|gb|AY035075.1 Arabidopsis thaliana putative H+-transporting ATPase (AT4g30190) mRNA, complete cds	3.5E-245
381	2538.K17.GZ43_371496	AK022749	gi|10434332|dbj|AK022749.1AK022749 Homo sapiens cDNA FLJ12687 fis, clone NT2RM4002532, weakly similar to PROTEIN HOM1	1.5E-31
385	2538.M16.GZ43_371543	AF375410	gi|14030638|gb|AF375410.1AF375410 Arabidopsis thaliana At2g43970/F6E13.10 gene, complete cds	1.9E-53

Table 7

SEQ ID	SEQ NAME	ACCESSION	GENBANK DESCRIPTION	GENBANK SCORE
386	2538.M17.GZ43_371544	AK025473	gi|10437996|dbj|AK025473.1AK025473 Homo sapiens cDNA: FLJ21820 fis, clone HEP01232	3.2E-282
389	2538.P16.GZ43_371615	AK026286	gi|10439097|dbj|AK026286.1AK026286 Homo sapiens cDNA: FLJ22633 fis, clone HSI06502	0
391	2554.A06.GZ43_375853	AK001324	gi|7022509|dbj|AK001324.1AK001324 Homo sapiens cDNA FLJ10462 fis, clone NT2RP1001494, weakly similar to MALE STERILITY PROTEIN 2	4E-44
394	2554.A16.GZ43_375863	AF271388	gi|8515842|gb|AF271388.1AF271388 Homo sapiens CMP-N-acetylneuraminic acid synthase mRNA, complete cds	0
406	2554.I15.GZ43_376054	AY050376	gi|15215695|gb|AY050376.1 Arabidopsis thaliana AT3g16950/K14A17_7 mRNA, complete cds	8.8E-27
415	2554.P16.GZ43_376223	AK022368	gi|10433751|dbj|AK022368.1AK022368 Homo sapiens cDNA FLJ12306 fis, clone MAMMA1001907	6.7E-46
418	2565.B13.GZ43_398139	AL050012	gi|4884261|emb|AL050012.1HSM800354 Homo sapiens mRNA; cDNA DKFZp564K133 (from clone DKFZp564K133)	1E-44
419	2565.B15.GZ43_398171	AY049285	gi|15146287|gb|AY049285.1 Arabidopsis thaliana AT3g58570/F14P22_160 mRNA, complete cds	2.1E-62
422	2565.C17.GZ43_398204	M24543	gi|341200|gb|M24543.1HUMPSANTIG Human prostate-specific antigen (PA) gene, complete cds	2.5E-49
423	2565.D06.GZ43_398029	AF331321	gi|13095271|gb|AF331321.1AF331321 HIV1 isolate T7C44 from the Netherlands nonfunctional pol polyprotein gene, partial sequence	4.7E-30
428	2565.G20.GZ43_398256	AJ276936	gi|12214232|emb|AJ276936.1NME276936 Neisseria meningitidis partial tbpB gene for transferrin binding protein B subunit, allele 66,	0
429	2565.H01.GZ43_397953	AF326517	gi|15080738|gb|AF326517.1AF326517 Abies grandis pinene synthase gene, partial cds	1E-300
433	2565.I22.GZ43_398290	AK001926	gi|7023492|dbj|AK001926.1AK001926 Homo sapiens cDNA FLJ11064 fis, clone PLACE1004824	8.9E-295
442	2565.M14.GZ43_398166	AF275699	gi|12275949|gb|AF275699.1AF275699 Unidentified Hailaer soda lake bacterium F16 16S ribosomal RNA gene, partial sequence	1.4E-21
447	2565.O07.GZ43_398056	AK024752	gi|10437118|dbj|AK024752.1AK024752 Homo sapiens cDNA: FLJ21099 fis, clone CAS04610	4.3E-51

Table 7

SEQ ID	SEQ NAME	ACCES-SION	GENBANK DESCRIPTION	GENBANK SCORE
452	2540.A24.GZ43_372031	Z69920	gi|1217632|emb|Z69920.1HS91K3D Human DNA sequence from cosmid 91K3, Huntington's Disease Region, chromosome 4p16.3	1.1E-41
463	2540.H07.GZ43_372182	AE008025	gi|15155943|gb|AE008025.1AE008025 Agrobacterium tumefaciens strain C58 circular chromosome, section 83 of 254 of the complete seque	1.7E-40
465	2540.I10.GZ43_372209	AK000658	gi|7020892|dbj|AK000658.1AK000658 Homo sapiens cDNA FLJ20651 fis, clone KAT01814	1.3E-53
468	2540.M22.GZ43_372317	AF375597	gi|14150816|gb|AF375597.1AF375596S2 Mus musculus medium and short chain L-3-hydroxyacyl-Coenzyme A dehydrogenase (Mschad) gene, exo	0
472	2540.C19.GZ43_372074	AB019559	gi|4579750|dbj|AB019559.1AB019559 Sus scrofa mRNA for 130 kDa regulatory subunit of myosin phosphatase, partial cds	3.1E-24
477	2540.F15.GZ43_372142	AY016428	gi|13891961|gb|AY016428.1 Plasmodium falciparum isolate Fas 30-6-7 apical membrane antigen-1 (AMA-1) gene, partial cds	2.2E-33
485	2540.M18.GZ43_372313	AJ331177	gi|15875595|emb|AJ331177.1HSA331177 Homo sapiens genomic sequence surrounding NotI site, clone NL1-ZF18RS	7.7E-237
507	2541.L08.GZ43_372663	BC003673	gi|13277537|gb|BC003673.1BC003673 Homo sapiens, protamine 1, clone MGC:12307 IMAGE:3935638, mRNA, complete cds	2.6E-53
508	2541.L12.GZ43_372667	AJ297708	gi|12055486|emb|AJ297708.1RNO297708 Rattus norvegicus RT6 gene for T cell differentiation marker RT6.2, exons 1-8	9.4E-45
514	2506.C15.GZ43_366620	AE007488	gi|14973493|gb|AE007488.1AE007488 Streptococcus pneumoniae TIGR4 section 171 of 194 of the complete genome	1.4E-287
519	2506.E18.GZ43_366671	AK025164	gi|10437625|dbj|AK025164.1AK025164 Homo sapiens cDNA: FLJ21511 fis, clone COL05748	0
521	2506.G24.GZ43_366725	AY030962	gi|13736961|gb|AY030962.1 HIV-1 isolate NC3964-1999 from USA pol polyprotein (pol) gene, partial cds	9.1E-233
527	2506.J20.GZ43_366793	AF152924	gi|5453323|gb|AF152924.1AF152924 Mus musculus syntaxin4-interacting protein synip mRNA, complete cds	2.3E-79
528	2506.J22.GZ43_366795	AK000169	gi|7020080|dbj|AK000169.1AK000169 Homo sapiens cDNA FLJ20162 fis, clone COL09280	1.8E-99

Table 7

SEQ ID	SEQ NAME	ACCES-SION	GENBANK DESCRIPTION	GENBANK SCORE
531	2506.M05.GZ43_366850	AE007580	gi|15023517|gb|AE007580.1AE007580 Clostridium acetobutylicum ATCC824 section 68 of 356 of the complete genome	2.1E-217
534	2506.P07.GZ43_366924	AF035442	gi|3142369|gb|AF035442.1AF035442 Homo sapiens VAV-like protein mRNA, partial cds	1E-44
540	2542.C20.GZ43_372843	AE007424	gi|14972724|gb|AE007424.1AE007424 Streptococcus pneumoniae TIGR4 section 107 of 194 of the complete genome	2.3E-42
543	2542.D19.GZ43_372866	BC008333	gi|14249906|gb|BC008333.1BC008333 Homo sapiens, clone IMAGE:3506145, mRNA, partial cds	5.3E-284
544	2542.F05.GZ43_372900	AK024179	gi|10436495|dbj|AK024179.1AK024179 Homo sapiens cDNA FLJ14117 fis, clone MAMMA1001785	2.4E-41
553	2542.M09.GZ43_373072	AK022973	gi|10434673|dbj|AK022973.1AK022973 Homo sapiens cDNA FLJ12911 fis, clone NT2RP2004425, highly similar to Mus musculus axotrophin mR	5.8E-243
557	2542.P19.GZ43_373154	AK025164	gi|10437625|dbj|AK025164.1AK025164 Homo sapiens cDNA: FLJ21511 fis, clone COL05748	0
562	2542.M24.GZ43_373087	AK022173	gi|10433509|dbj|AK022173.1AK022173 Homo sapiens cDNA FLJ12111 fis, clone MAMMA1000025	1.2E-284
563	2542.N21.GZ43_373108	AF025409	gi|2582414|gb|AF025409.1AF025409 Homo sapiens zinc transporter 4 (ZNT4) mRNA, complete cds	2E-70
567	2555.D22.GZ43_373253	AL1576971	gi|11121002|emb|AL157697.11AL157697 Human DNA sequence from clone RP5-1092C14 on chromosome 6, complete sequence [Homo sapiens]	1.1E-87
568	2555.E20.GZ43_373275	AK026618	gi|10439509|dbj|AK026618.1AK026618 Homo sapiens cDNA: FLJ22965 fis, clone KAT10418	0
569	2555.F16.GZ43_373295	AF271388	gi|8515842|gb|AF271388.1AF271388 Homo sapiens CMP-N-acetylneuraminic acid synthase mRNA, complete cds	0
574	2555.K17.GZ43_373416	AK026686	gi|10439593|dbj|AK026686.1AK026686 Homo sapiens cDNA: FLJ23033 fis, clone LNG02005	1.8E-23
578	2555.P22.GZ43_373541	AF087913	gi|5081331|gb|AF087913.1AF087913 Human endogenous retrovirus HERV-P-T47D	5.8E-74
579	2555.A11.GZ43_373170	NC_000957	gi|11497445|ref|NC_000957.1 Borrelia burgdorferi plasmid lp5, complete sequence	1.3E-57
585	2555.I12.GZ43_373363	AJ276936	gi|12214232|emb|AJ276936.1NME276936 Neisseria meningitidis partial tbpB gene for transferrin binding protein B subunit, allele 66,	1.6E-237

Table 7

SEQ ID	SEQ NAME	ACCES-SION	GENBANK DESCRIPTION	GENBANK SCORE
589	2556.A02.GZ43_373545	AE007289	gi|14524175|gb|AE007289.1AE007289 Sinorhizobium meliloti plasmid pSymA section 95 of 121 of the complete plasmid sequence	2E-55
591	2556.C11.GZ43_373602	AY039252	gi|15418981|gb|AY039252.1 Macaca mulatta immunoglobulin alpha heavy chain constant region (IgA) gene, IgA-C.II allele, partial cds	3.1E-29
602	2556.H15.GZ43_373726	AK021966	gi|10433275|dbj|AK021966.1AK021966 Homo sapiens cDNA FLJ11904 fis, clone HEMBB1000048	1.6E-70
620	2557.B22.GZ43_373973	AB071392	gi|15721873|dbj|AB071392.1AB071392 Expression vector pAQ-EX1 DNA, complete sequence	1.2E-25
627	2557.J14.GZ43_374157	AK023721	gi|10435737|dbj|AK023721.1AK023721 Homo sapiens cDNA FLJ13659 fis, clone PLACE1011576, moderately similar to Human Kruppel related	1.6E-209
635	2557.N14.GZ43_374253	AB013897	gi|6177784|dbj|AB013897.1AB013897 Homo sapiens mRNA for HKR1, partial cds	1E-44
648	2558.B24.GZ43_374359	AB064318	gi|14595115|dbj|AB064318.1AB064318 Comamonas testosteroni gene for 16S rRNA, partial sequence	4.6E-28
657	2558.G07.GZ43_374462	M92069	gi|337698|gb|M92069.1HUMRTVLC Human retrovirus-like sequence-isoleucine c (RTVL-Ic) gene, Alu repeats	6.7E-46
661	2558.H17.GZ43_374496	AK023812	gi|10435860|dbj|AK023812.1AK023812 Homo sapiens cDNA FLJ13750 fis, clone PLACE3000331	5.2E-31
662	2558.J01.GZ43_374528	AK023448	gi|10435386|dbj|AK023448.1AK023448 Homo sapiens cDNA FLJ13386 fis, clone PLACE1001104, weakly similar to MYOSIN HEAVY CHAIN, NON-MU	4.8E-278
666	2558.K02.GZ43_374553	U14573	gi|551542|gb|U14573.1HSU14573 ***ALU WARNING: Human Alu-Sq subfamily consensus sequence	1.3E-62
683	2559.D05.GZ43_374772	AF338713	gi|14039582|gb|AF338713.1AF338713 Casuarius casuarius mitochondrion, partial genome	4E-297
687	2559.I12.GZ43_374899	AY036096	gi|14486435|gb|AY036096.1 HIV-1 isolate L2Q2P from Belgium reverse transcriptase (pol) gene, partial cds	1.4E-41
690	2559.J02.GZ43_374913	AK026618	gi|10439509|dbj|AK026618.1AK026618 Homo sapiens cDNA: FLJ22965 fis, clone KAT10418	0
692	2559.K12.GZ43_374947	Z96776	gi|2181853|emb|Z96776.1HS9QT023 H.sapiens telomeric DNA sequence, clone 9QTEL023, read 9QTELOO023.seq	5.1E-52

Table 7

SEQ ID	SEQ NAME	ACCES-SION	GENBANK DESCRIPTION	GENBANK SCORE
694	2559.L09.GZ43_374968	AE007426	gi|14972746|gb|AE007426.1AE007426 Streptococcus pneumoniae TIGR4 section 109 of 194 of the complete genome	8.1E-21
696	2559.M21.GZ43_375004	AJ414564	gi|15990852|emb|AJ414564.1HSA414564 Homo sapiens mRNA for connexin40.1 (CX40.1 gene)	9.2E-30
698	2559.N13.GZ43_375020	AL137330	gi|6807822|emb|AL137330.1HSM802010 Homo sapiens mRNA; cDNA DKFZp434F0272 (from clone DKFZp434F0272)	4.1E-47
714	2560.H01.GZ43_375248	U14567	gi|551536|gb|U14567.1HSU14567 ***ALU WARNING: Human Alu-J subfamily consensus sequence	2.7E-42
719	2560.K02.GZ43_375321	AF178754.3	gi|7770069|gb|AF178754.3AF178754 Homo sapiens lithium-sensitive myo-inositol monophosphatase A1 (IMPA1) gene, promoter region and p	3.1E-51
720	2560.K08.GZ43_375327	AK009327	gi|12844057|dbj|AK009327.1AK009327 Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310012P17, full	6.3E-80
721	2560.K10.GZ43_375329	AF344987	gi|13448249|gb|AF344987.1AF344987 Hepatitis C virus isolate RDpostSC1c2 polyprotein gene, partial cds	1E-300
729	2560.O08.GZ43_375423	AY037285	gi|15982643|gb|AY037285.1AY037284S2 HIV-1 from Cameroon vpu protein (vpu) and envelope glycoprotein (env) genes, complete cds; and	5.2E-54
732	2561.B03.GZ43_376258	AF035968.2	gi|8714504|gb|AF035968.2AF035968 Homo sapiens integrin alpha 2 (ITGA2) gene, ITGA2-1 allele, exons 6-9, and partial cds	3.9E-32
733	2561.B12.GZ43_376267	AP000276	gi|4835645|dbj|AP000276.1AP000276 Homo sapiens genomic DNA, chromosome 21q22.1, D21S226-AML region, clone:55A9, complete sequence	1.9E-27
750	2561.M09.GZ43_376528	AF052684	gi|2995716|gb|AF052684.1HSPRCAD2 Homo sapiens protocadherin 43 gene, exon 2	4.1E-41
753	2561.E22.GZ43_376349	AF132952	gi|4680674|gb|AF132952.1AF132952 Homo sapiens CGI-18 protein mRNA, complete cds	3E-41
754	2561.G20.GZ43_376395	U14573	gi|551542|gb|U14573.1HSU14573 ***ALU WARNING: Human Alu-Sq subfamily consensus sequence	1.5E-71
755	2561.H17.GZ43_376416	AF052685	gi|2995717|gb|AF052685.1HSPRCAD3 Homo sapiens protocadherin 43 gene, exon 3, exon 4, and complete cds	2.1E-24
756	2561.I19.GZ43_376442	AF344987	gi|13448249|gb|AF344987.1AF344987 Hepatitis C virus isolate RDpostSC1c2 polyprotein gene, partial cds	3.2E-201

Table 7

SEQ ID	SEQ NAME	ACCESSION	GENBANK DESCRIPTION	GENBANK SCORE
761	2561.P16.GZ43_376607	Z78727	gi|1508005|emb|Z78727.1HSPA15B9 H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA15B9	1.6E-37
762	2561.P19.GZ43_376610	U66535	gi|2270915|gb|U66535.1HSITGBF07 Human beta4-integrin (ITGB4) gene, exons 19,20,21,22,23,24 and 25	8.6E-41
763	2561.P23.GZ43_376614	AF167458	gi|6467463|gb|AF167458.1HSDSRPKR04 Homo sapiens double stranded RNA activated protein kinase (PKR) gene, intron 1	1E-22
771	2456.D04.GZ43_355904	AF307053	gi|12018057|gb|AF307053.1AF307053 Thermococcus litoralis sugar kinase, trehalose/maltose binding protein (malE), trehalose/maltose	0
777	2456.H02.GZ43_355998	AJ005821	gi|3123571|emb|AJ005821.1HSA5821 Homo sapiens mRNA for X-like 1 protein	5.8E-37
788	2456.N23.GZ43_356163	AF188746	gi|6425045|gb|AF188746.1AF188746 Homo sapiens prostrate kallikrein 2 (KLK2) mRNA, complete cds	9.6E-63
796	2457.C19.GZ43_356279	AF368920	gi|14039926|gb|AF368920.1AF368920 Caenorhabditis elegans voltage-dependent calcium channel alpha13 subunit (cca-1) mRNA, complete c	1E-47
799	2457.D12.GZ43_356296	AK026618	gi|10439509|dbj|AK026618.1AK026618 Homo sapiens cDNA: FLJ22965 fis, clone KAT10418	0
810	2457.H17.GZ43_356397	AE007614	gi|15023883|gb|AE007614.1AE007614 Clostridium acetobutylicum ATCC824 section 102 of 356 of the complete genome	9E-63
823	2458.A10.GZ43_356618	AK026920	gi|10439892|dbj|AK026920.1AK026920 Homo sapiens cDNA: FLJ23267 fis, clone COL07266	6.2E-84
827	2458.B23.GZ43_356655	AB050432	gi|10998295|dbj|AB050432.1AB050432 Macaca fascicularis brain cDNA, clone:QnpA-21861	4.3E-129
829	2458.C06.GZ43_356662	U49973	gi|2226003|gb|U49973.1HSU49973 Human Tigger1 transposable element, complete consensus sequence	2E-24
842	2458.I09.GZ43_356809	AK023496	gi|10435445|dbj|AK023496.1AK023496 Homo sapiens cDNA FLJ13434 fis, clone PLACE1002578	2.4E-39
843	2458.I10.GZ43_356810	AF031077	gi|6649934|gb|AF031077.1AF031077 Homo sapiens chromosome X, cosmid LLNLc110C1837, complete sequence	1.3E-52
845	2458.I17.GZ43_356817	AK026569	gi|10439451|dbj|AK026569.1AK026569 Homo sapiens cDNA: FLJ22916 fis, clone KAT06406, highly similar to HSCYCR Human mRNA for T-cell	1.8E-38
846	2458.I20.GZ43_356820	AF184614	gi|6983939|gb|AF184614.1AF184614 Homo sapiens p47-phox (NCF1) gene, complete cds	4.2E-33

Table 7

SEQ ID	SEQ NAME	ACCESSION	GENBANK DESCRIPTION	GENBANK SCORE
855	2458.N06.GZ43_356926	AF367251	gi|14161363|gb|AF367251.1AF367251 Helicobacter pylori strain CAPM N93 cytotoxin associated protein A (cagA) gene, complete cds	2.2E-70
865	2459.B11.GZ43_357027	AF375597	gi|14150816|gb|AF375597.1AF375596S2 Mus musculus medium and short chain L-3-hydroxyacyl-Coenzyme A dehydrogenase (Mschad) gene, exo	0
866	2459.C05.GZ43_357045	X04803.2	gi|6647297|emb|X04803.2HSYUBG1 Homo sapiens ubiquitin gene	6.4E-52
873	2459.F20.GZ43_357132	AK025207	gi|10437672|dbj|AK025207.1AK025207 Homo sapiens cDNA: FLJ21554 fis, clone COL06330	0
877	2459.H09.GZ43_357169	AB046623	gi|9651056|dbj|AB046623.1AB046623 Macaca fascicularis brain cDNA, clone QccE-10576	1.7E-35
888	2459.O23.GZ43_357351	AL049301	gi|4500067|emb|AL049301.1HSM800086 Homo sapiens mRNA; cDNA DKFZp564P073 (from clone DKFZp564P073)	1.3E-31
889	2459.P24.GZ43_357376	AK018110	gi|12857675|dbj|AK018110.1AK018110 Mus musculus adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:633040	1.5E-33
903	2464.H22.GZ43_357870	AB035344	gi|8176599|dbj|AB035344.1AB035344S1 Homo sapiens TCL6 gene, exon 1-10b	1.1E-127
904	2464.I04.GZ43_357876	AK025125	gi|10437578|dbj|AK025125.1AK025125 Homo sapiens cDNA: FLJ21472 fis, clone COL04936	0
905	2464.I20.GZ43_357892	AK025966	gi|10438647|dbj|AK025966.1AK025966 Homo sapiens cDNA: FLJ22313 fis, clone HRC05216	2.8E-61
909	2464.K18.GZ43_357938	AF287938	gi|12656333|gb|AF287938.1AF287938 Guichenotia ledifolia NADH dehydrogenase subunit F (ndhF) gene, partial cds; chloroplast gene for	8.3E-44
912	2464.L15.GZ43_357959	AF141308	gi|5737754|gb|AF141308.1HSPMFG1 Homo sapiens polyamine modulated factor-1 (PMF1) gene, exon 1	9.9E-76
918	2464.P17.GZ43_358057	AF052684	gi|2995716|gb|AF052684.1HSPRCAD2 Homo sapiens protocadherin 43 gene, exon 2	3E-29
934	2465.J19.GZ43_358299	X02571	gi|31870|emb|X02571.1HSGP5MOS Human gene fragment related to oncogene c-mos with Alu repeats (locus gp5, region NV-1)	2.7E-48
935	2465.K20.GZ43_358324	AK019509	gi|12859761|dbj|AK019509.1AK019509 Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched library, clone:4632435C11, full	2.5E-63

Table 7

SEQ ID	SEQ NAME	ACCESSION	GENBANK DESCRIPTION	GENBANK SCORE
937	2465.L06.GZ43_358334	AK009327	gi|12844057|dbj|AK009327.1AK009327 Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310012P17, full	7.9E-73
939	2465.M11.GZ43_358363	AK022253	gi|10433611|dbj|AK022253.1AK022253 Homo sapiens cDNA FLJ12191 fis, clone MAMMA1000843	1.4E-112
943	2466.B02.GZ43_360107	AK023055	gi|10434796|dbj|AK023055.1AK023055 Homo sapiens cDNA FLJ12993 fis, clone NT2RP3000197	7.5E-39
944	2466.C15.GZ43_360144	AB013897	gi|6177784|dbj|AB013897.1AB013897 Homo sapiens mRNA for HKR1, partial cds	4.3E-53
945	2466.D19.GZ43_360172	AL050141	gi|4884352|emb|AL050141.1HSM800441 Homo sapiens mRNA; cDNA DKFZp586O031 (from clone DKFZp586O031)	3.4E-110
952	2466.I08.GZ43_360281	AJ271729	gi|6900103|emb|AJ271729.1HSA271729 Homo sapiens mRNA for glucose-regulated protein (HSPA5 gene)	6.2E-72
953	2466.J01.GZ43_360298	AY058527	gi|16197970|gb|AY058527.1 Drosophila melanogaster LD23445 full length cDNA	9.4E-40
954	2466.J24.GZ43_360321	AF331425	gi|13375486|gb|AF331425.1AF331425 HIV-1 D311 from Australia envelope protein (env) gene, partial cds	1.6E-77
958	2467.B24.GZ43_360513	AJ005821	gi|3123571|emb|AJ005821.1HSA5821 Homo sapiens mRNA for X-like 1 protein	1.4E-34
963	2467.H18.GZ43_360651	AF036235	gi|2695679|gb|AF036235.1AF036235 Gorilla gorilla L1 retrotransposon L1Gg-1A, complete sequence	2E-169
964	2467.A03.GZ43_360468	BC012960	gi|15277963|gb|BC012960.1BC012960 Mus musculus, ring finger protein 12, clone MGC:13712 IMAGE:4193003, mRNA, complete cds	8.7E-36
965	2467.A05.GZ43_360470	BC009113	gi|14318629|gb|BC009113.1BC009113 Homo sapiens, clone MGC:18122 IMAGE:4153377, mRNA, complete cds	4.1E-167
969	2467.G01.GZ43_360610	U14573	gi|551542|gb|U14573.1HSU14573 ***ALU WARNING: Human Alu-Sq subfamily consensus sequence	2E-61
971	2467.N22.GZ43_360799	AF117756	gi|4530440|gb|AF117756.1AF117756 Homo sapiens thyroid hormone receptor-associated protein complex component TRAP150 mRNA, complete	6.8E-77
973	2467.I12.GZ43_360669	AK024049	gi|10436318|dbj|AK024049.1AK024049 Homo sapiens cDNA FLJ13987 fis, clone Y79AA1001963, weakly similar to PUTATIVE PRE-MRNA SPLICING	2.1E-47
977	2467.K14.GZ43_360719	AB030001	gi|7416074|dbj|AB030001.1AB030001 Homo sapiens gene for SGRF, complete cds	7.2E-22

Table 7

SEQ ID	SEQ NAME	ACCES-SION	GENBANK DESCRIPTION	GENBANK SCORE
979	2467.N03.GZ43_360780	AK023448	gi|10435386|dbj|AK023448.1AK023448 Homo sapiens cDNA FLJ13386 fis, clone PLACE1001104, weakly similar to MYOSIN HEAVY CHAIN, NON-MU	0
980	2467.N07.GZ43_360784	AK001931	gi|7023502|dbj|AK001931.1AK001931 Homo sapiens cDNA FLJ11069 fis, clone PLACE1004930, highly similar to Homo sapiens MDC-3.13 isofo	2.3E-54
981	2467.N09.GZ43_360786	AE008338	gi|15159908|gb|AE008338.1AE008338 Agrobacterium tumefaciens strain C58 linear chromosome, section 142 of 187 of the complete sequen	3.7E-50
986	2472.C18.GZ43_360915	K01921	gi|339606|gb|K01921.1HUMTGNB Human Asn-tRNA gene, clone pHt6-2, complete sequence and flanks	3E-29
992	2472.G03.GZ43_360996	AF321082	gi|12958576|gb|AF321082.1AF321082 HIV-1 isolate DGOB from France envelope glycoprotein (env) gene, complete cds	5.1E-28
999	2472.M22.GZ43_361159	AF338299	gi|12958808|gb|AF338299.1AF338299 Amazona ochrocephala auropalliata mitochondrial control region 1, partial sequence	1.4E-145
1002	2472.P22.GZ43_361231	AJ330257	gi|15874675|emb|AJ330257.1HSA330257 Homo sapiens genomic sequence surrounding NotI site, clone NL1-FA14R	1.1E-63
1005	2473.F08.GZ43_361361	AF306355	gi|14573206|gb|AF306355.1AF306355 Homo sapiens clone TF3.19 immunoglobulin heavy chain variable region mRNA, partial cds	3.2E-29
1006	2473.F14.GZ43_361367	AB050477	gi|11034759|dbj|AB050477.1AB050477 Homo sapiens NIBAN mRNA, complete cds	0
1011	2473.I08.GZ43_361433	AF224341	gi|15982934|gb|AF224341.1AF224341 Mus musculus thiamine transporter 1 (Slc19a2) gene, exons 1 through 6 and complete cds	8.7E-67
1015	2473.O13.GZ43_361582	AF203815	gi|6979641|gb|AF203815.1AF203815 Homo sapiens alpha gene sequence	5.4E-44
1018	2474.C08.GZ43_361673	AK000373	gi|7020417|dbj|AK000373.1AK000373 Homo sapiens cDNA FLJ20366 fis, clone HEP18008	5.6E-47
1021	2474.G17.GZ43_361778	U75285	gi|2315862|gb|U75285.1HSU75285 Homo sapiens apoptosis inhibitor survivin gene, complete cds	1.1E-87
1023	2474.I06.GZ43_361815	Z81315	gi|1644298|emb|Z81315.1HSF62D4 Human DNA sequence from fosmid F62D4 on chromosome 22q12-qter	2.1E-67
1024	2474.J18.GZ43_361851	AF029062	gi|3712662|gb|AF029062.1AF029062 Homo sapiens DEAD-box protein (BAT1) gene, partial cds	1.2E-28

Table 7

SEQ ID	SEQ NAME	ACCES-SION	GENBANK DESCRIPTION	GENBANK SCORE
1030	2474.P22.GZ43_361999	AL050204	gi|4884443|emb|AL050204.1HSM800501 Homo sapiens mRNA; cDNA DKFZp586F1223 (from clone DKFZp586F1223)	8.9E-33
1031	2475.A05.GZ43_362006	AL109666	gi|5689800|emb|AL109666.1IRO35907 Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 35907	6.3E-43
1032	2475.C18.GZ43_362067	AK023739	gi|10435762|dbj|AK023739.1AK023739 Homo sapiens cDNA FLJ13677 fis, clone PLACE1011982	2.8E-180
1033	2475.E18.GZ43_362115	AK024206	gi|10436527|dbj|AK024206.1AK024206 Homo sapiens cDNA FLJ14144 fis, clone MAMMA1002909	1.9E-21
1035	2475.H06.GZ43_362175	AF322634	gi|12657820|gb|AF322634.1AF322634S1 Human herpesvirus 3 strain VZV-Iceland glycoprotein B gene, complete cds	1.2E-173
1036	2475.H13.GZ43_362182	AF026853	gi|3882436|gb|AF026853.1HSHADHSC 1 Homo sapiens mitochondrial short-chain L-3-hydroxyacyl-CoA dehydrogenase (HADHSC) gene, nuclear	2.1E-30
1039	2475.N08.GZ43_362321	AK011295	gi|12847322|dbj|AK011295.1AK011295 Mus musculus 10 days embryo cDNA, RIKEN full-length enriched library, clone:2610002L04, full ins	1.1E-84
1045	2475.M20.GZ43_362309	AK023843	gi|10435902|dbj|AK023843.1AK023843 Homo sapiens cDNA FLJ13781 fis, clone PLACE4000465	8.8E-42
1046	2475.N21.GZ43_362334	S45332	gi|255496|gb|S45332.1S45332 erythropoietin receptor [human, placental, Genomic, 8647 nt]	1.4E-101
1055	2480.G11.GZ43_358658	X83497	gi|603558|emb|X83497.1HSLTRERV9 H.sapiens DNA for ZNF80-linked ERV9 long terminal repeat	6.1E-40
1056	2480.H06.GZ43_358677	AB002070	gi|12862447|dbj|AB002070.1AB002070 Aspergillus clavatus gene for 18S rRNA, partial sequence, strain:NRRL 1	5.5E-28
1061	2480.M20.GZ43_358811	AL1576971	gi|11121002|emb|AL157697.11AL157697 Human DNA sequence from clone RP5-1092C14 on chromosome 6, complete sequence [Homo sapiens]	9.3E-36
1064	2480.P23.GZ43_358886	AB037719	gi|7242950|dbj|AB037719.1AB037719 Homo sapiens mRNA for KIAA1298 protein, partial cds	3.6E-35
1065	2481.B06.GZ43_358917	AK023471	gi|10435415|dbj|AK023471.1AK023471 Homo sapiens cDNA FLJ13409 fis, clone PLACE1001716	0
1068	2481.D10.GZ43_358969	AL021306	gi|2808416|emb|AL021306.1HS1109B5 Human DNA sequence from clone CTB-1109B5 on chromosome 22 Contains a GSS, complete sequence [Homo	7E-52

Table 7

SEQ ID	SEQ NAME	ACCES-SION	GENBANK DESCRIPTION	GENBANK SCORE
1069	2481.D13.GZ43_358972	X64467	gi|28579|emb|X64467.1HSALADG H.sapiens ALAD gene for porphobilinogen synthase	4.2E-53
1075	2481.K12.GZ43_359139	AK026901	gi|10439868|dbj|AK026901.1AK026901 Homo sapiens cDNA: FLJ23248 fis, clone COL03555	5.9E-52
1083	2482.E17.GZ43_359384	AK022821	gi|10434440|dbj|AK022821.1AK022821 Homo sapiens cDNA FLJ12759 fis, clone NT2RP2001347	9.4E-35
1084	2482.E20.GZ43_359387	AK014328	gi|12852104|dbj|AK014328.1AK014328 Mus musculus 14, 17 days embryo head cDNA, RIKEN full-length enriched library, clone:3230401M21,	5.2E-99
1091	2482.N09.GZ43_359592	AE008514	gi|15459095|gb|AE008514.1AE008514 Streptococcus pneumoniae R6 section 130 of 184 of the complete genome	6.9E-107
1100	2483.J07.GZ43_359878	AK022722	gi|10434285|dbj|AK022722.1AK022722 Homo sapiens cDNA FLJ12660 fis, clone NT2RM4002174, moderately similar to MRP PROTEIN	1E-300
1101	2483.K02.GZ43_359897	AK012908	gi|12849956|dbj|AK012908.1AK012908 Mus musculus 10, 11 days embryo cDNA, RIKEN full-length enriched library, clone:2810046L04, full	3.7E-189
1106	2483.O07.GZ43_359998	AK014328	gi|12852104|dbj|AK014328.1AK014328 Mus musculus 14, 17 days embryo head cDNA, RIKEN full-length enriched library, clone:3230401M21,	3.2E-103
1108	2488.C19.GZ43_362511	AB023199	gi|4589607|dbj|AB023199.1AB023199 Homo sapiens mRNA for KIAA0982 protein, complete cds	1.1E-50
1110	2488.E20.GZ43_362560	AK001136	gi|7022203|dbj|AK001136.1AK001136 Homo sapiens cDNA FLJ10274 fis, clone HEMBB1001169	1E-35
1111	2488.F06.GZ43_362570	AK011295	gi|12847322|dbj|AK011295.1AK011295 Mus musculus 10 days embryo cDNA, RIKEN full-length enriched library, clone:2610002L04, full ins	8.1E-55
1113	2488.G02.GZ43_362590	X15723	gi|31481|emb|X15723.1HSFURIN Human fur gene, exons 1 through 8	1.8E-85
1117	2488.K04.GZ43_362688	AF026853	gi|3882436|gb|AF026853.1HSHADHSC 1 Homo sapiens mitochondrial short-chain L-3-hydroxyacyl-CoA dehydrogenase (HADHSC) gene, nuclear	2.1E-30
1122	2489.A03.GZ43_362831	AB050477	gi|11034759|dbj|AB050477.1AB050477 Homo sapiens NIBAN mRNA, complete cds	6.7E-46
1124	2489.A13.GZ43_362841	AK026618	gi|10439509|dbj|AK026618.1AK026618 Homo sapiens cDNA: FLJ22965 fis, clone KAT10418	1.8E-178

Table 7

SEQ ID	SEQ NAME	ACCES-SION	GENBANK DESCRIPTION	GENBANK SCORE
1127	2489.D18.GZ43_362918	AF086310	gi|3483655|gb|AF086310.1HUMZD51F08 Homo sapiens full length insert cDNA clone ZD51F08	2.5E-79
1128	2489.F09.GZ43_362957	AF271388	gi|8515842|gb|AF271388.1AF271388 Homo sapiens CMP-N-acetylneuraminic acid synthase mRNA, complete cds	0
1129	2489.G05.GZ43_362977	AK023739	gi|10435762|dbj|AK023739.1AK023739 Homo sapiens cDNA FLJ13677 fis, clone PLACE1011982	6.8E-209
1140	2489.M11.GZ43_363127	AE008029	gi|15155994|gb|AE008029.1AE008029 Agrobacterium tumefaciens strain C58 circular chromosome, section 87 of 254 of the complete seque	4.2E-44
1144	2490.B06.GZ43_363242	AK001915	gi|7023475|dbj|AK001915.1AK001915 Homo sapiens cDNA FLJ11053 fis, clone PLACE1004664	1.7E-43
1155	2490.J22.GZ43_363450	AF026853	gi|3882436|gb|AF026853.1HSHADHSC 1 Homo sapiens mitochondrial short-chain L-3-hydroxyacyl-CoA dehydrogenase (HADHSC) gene, nuclear	2E-30
1160	2490.N24.GZ43_363548	AF167438	gi|9622123|gb|AF167438.1AF167438 Homo sapiens androgen-regulated short-chain dehydrogenase/reductase 1 (ARSDR1) mRNA, complete cds	8.8E-74
1163	2491.C13.GZ43_363657	AK022338	gi|10433714|dbj|AK022338.1AK022338 Homo sapiens cDNA FLJ12276 fis, clone MAMMA1001692	6.2E-30
1174	2491.P10.GZ43_363966	AJ276936	gi|12214232|emb|AJ276936.1NME276936 Neisseria meningitidis partial tbpB gene for transferrin binding protein B subunit, allele 66,	0
1175	2491.P20.GZ43_363976	AY027632	gi|15418751|gb|AY027632.1 Measles virus strain MVs/Masan.KOR/49.00/2 hemagglutinin (H) mRNA, complete cds	7.8E-283
1177	2496.C08.GZ43_364139	U67829	gi|2289943|gb|U67829.1HSU67829 Human primary Alu transcript	3.6E-90
1181	2496.F14.GZ43_364217	X16983	gi|33945|emb|X16983.1HSINTAL4 Human mRNA for integrin alpha-4 subunit	4.7E-53
1183	2496.I06.GZ43_364281	BC004138	gi|13278716|gb|BC004138.1BC004138 Homo sapiens, ribosomal protein L6, clone MGC:1635 IMAGE:2823733, mRNA, complete cds	8.3E-53
1184	2496.K15.GZ43_364338	NM_024711	gi|13376008|ref|NM_024711.1 Homo sapiens hypothetical protein FLJ22690 (FLJ22690), mRNA	1.1E-28
1192	2497.E09.GZ43_364572	AF284421	gi|15088516|gb|AF284421.1AF284421 Homo sapiens complement factor MASP-3 mRNA, complete cds	4.1E-158
1195	2497.J05.GZ43_364688	Z56298	gi|1027529|emb|Z56298.1HS10C4R H.sapiens CpG island DNA genomic Mse1 fragment, clone 10c4, reverse read cpg10c4.rt1a	2.5E-42

Table 7

SEQ ID	SEQ NAME	ACCES-SION	GENBANK DESCRIPTION	GENBANK SCORE
1199	2497.L05.GZ43_364736	AK023448	gi|10435386|dbj|AK023448.1AK023448 Homo sapiens cDNA FLJ13386 fis, clone PLACE1001104, weakly similar to MYOSIN HEAVY CHAIN, NON-MU	0
1207	2562.B09.GZ43_375496	M64241	gi|190813|gb|M64241.1HUMQM Human Wilm's tumor-related protein (QM) mRNA, complete cds	3.2E-52
1210	2562.I01.GZ43_375656	AF083247	gi|5106788|gb|AF083247.1AF083247 Homo sapiens MDG1 mRNA, complete cds	2.4E-48
1214	2562.O01.GZ43_375800	AF223389	gi|11066459|gb|AF223389.1AF223389 Homo sapiens PCGEM1 gene, non-coding mRNA	8.7E-57
1217	2562.H11.GZ43_375642	AK023442	gi|10435378|dbj|AK023442.1AK023442 Homo sapiens cDNA FLJ13380 fis, clone PLACE1001007	1.7E-64
1218	2562.B24.GZ43_375511	AF287932	gi|12656321|gb|AF287932.1AF287932 Rayleya bahiensis NADH dehydrogenase subunit F (ndhF) gene, partial cds; chloroplast gene for chl	1.8E-31
1229	2498.A02.GZ43_364853	AY031766	gi|13738569|gb|AY031766.1 HIV-1 isolate NC5203-1999 from USA pol polyprotein (pol) gene, partial cds	1.3E-29
1230	2498.A19.GZ43_364870	AL122114	gi|6102936|emb|AL122114.1HSM801274 Homo sapiens mRNA; cDNA DKFZp434K0221 (from clone DKFZp434K0221); partial cds	1E-59
1235	2498.G15.GZ43_365010	M86752	gi|184564|gb|M86752.1HUMIEF Human transformation-sensitive protein (IEF SSP 3521) mRNA, complete cds	3.4E-54
1238	2498.I17.GZ43_365060	AJ335654	gi|15880072|emb|AJ335654.1HSA335654 Homo sapiens genomic sequence surrounding NotI site, clone NR5-IJ21R	4.3E-41
1239	2498.K20.GZ43_365111	X15940	gi|36129|emb|X15940.1HSRPL31 Human mRNA for ribosomal protein L31	1.7E-25
1240	2498.M19.GZ43_365158	AF203815	gi|6979641|gb|AF203815.1AF203815 Homo sapiens alpha gene sequence	4E-47
1242	2498.P07.GZ43_365218	AF410975	gi|15553753|gb|AF410975.1AF410975 Measles virus genotype D4 strain MVi/Montreal.CAN/12.89 hemagglutinin gene, complete cds	3.5E-29
1244	2507.C03.GZ43_366992	NM_025080	gi|13376633|ref|NM_025080.1 Homo sapiens hypothetical protein FLJ22316 (FLJ22316), mRNA	1E-232
1259	2511.J18.GZ43_369643	M81806	gi|184406|gb|M81806.1HUMHSKPQZ7 Human housekeeping (Q1Z 7F5) gene, exons 2 through 7, complete cds	4.7E-34
1261	2499.A22.GZ43_365257	AK024860	gi|10437268|dbj|AK024860.1AK024860 Homo sapiens cDNA: FLJ21207 fis, clone COL00362	6.4E-49

Table 7

SEQ ID	SEQ NAME	ACCESSION	GENBANK DESCRIPTION	GENBANK SCORE
1263	2499.C09.GZ43_365292	AJ330464	gi|15874882|emb|AJ330464.1HSA330464 Homo sapiens genomic sequence surrounding NotI site, clone NR1-IL7C	3.3E-100
1268	Clu1009284.1	AF026853	gi|3882436|gb|AF026853.1HSHADHSC 1 Homo sapiens mitochondrial short-chain L-3 hydroxyacyl-CoA dehydrogenase (HADHSC) gene, nuclear	1.3E-30
1269	Clu1022935.2	AL590711.7	gi|16304966|emb|AL590711.7AL590711 Human DNA sequence from clone RP11-284O18 on chromosome 9, complete sequence [Homo sapiens]	3.9E-118
1270	Clu1037152.1	M87652	gi|182743|gb|M87652.1HUMFPRPR Human formylpeptide receptor gene, promoter region	1.1E-21
1271	Clu13903.1	AK026618	gi|10439509|dbj|AK026618.1AK026618 Homo sapiens cDNA: FLJ22965 fis, clone KAT10418	1.5E-293
1272	Clu139979.2	AB056828	gi|13365953|dbj|AB056828.1AB056828 Macaca fascicularis brain cDNA clone:QflA-13447, full insert sequence	1.4E-33
1274	Clu187860.2	AL050204	gi|4884443|emb|AL050204.1HSM800501 Homo sapiens mRNA; cDNA DKFZp586F1223 (from clone DKFZp586F1223)	4.7E-33
1275	Clu189993.1	AB030001	gi|7416074|dbj|AB030001.1AB030001 Homo sapiens gene for SGRF, complete cds	9.6E-87
1276	Clu20975.1	AF039687	gi|3170173|gb|AF039687.1AF039687 Homo sapiens antigen NY-CO-1 (NY-CO-1) mRNA, complete cds	2.7E-190
1278	Clu218833.1	AF223389	gi|11066459|gb|AF223389.1AF223389 Homo sapiens PCGEM1 gene, non-coding mRNA	1E-139
1279	Clu244504.2	Z59663	gi|1031576|emb|Z59663.1HS168F9F H.sapiens CpG island DNA genomic Mse1 fragment, clone 168f9, forward read cpg168f9.ft1a	7.5E-22
1281	Clu376516.1	AK018003	gi|12857525|dbj|AK018003.1AK018003 Mus musculus adult male thymus cDNA, RIKEN full-length enriched library, clone:5830450H20, full	1.7E-63
1282	Clu376630.1	U93571	gi|2072968|gb|U93571.1HSU93571 Human L1 element L1.24 p40 gene, complete cds	8.7E-291
1283	Clu377044.2	AK024860	gi|10437268|dbj|AK024860.1AK024860 Homo sapiens cDNA: FLJ21207 fis, clone COL00362	1.6E-49
1284	Clu379689.1	BC007110	gi|13937991|gb|BC007110.1BC007110 Homo sapiens, clone MGC:14768 IMAGE:4291902, mRNA, complete cds	0

Table 7

SEQ ID	SEQ NAME	ACCESSION	GENBANK DESCRIPTION	GENBANK SCORE
1286	Clu387530.4	AK009770	gi|12844769|dbj|AK009770.1AK009770 Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310043C14, full	1.5E-80
1287	Clu388450.2	AK023448	gi|10435386|dbj|AK023448.1AK023448 Homo sapiens cDNA FLJ13386 fis, clone PLACE1001104, weakly similar to MYOSIN HEAVY CHAIN, NON-MU	0
1288	Clu396325.1	Z78727	gi|1508005|emb|Z78727.1HSPA15B9 H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA15B9	1.2E-38
1291	Clu400258.1	AB038971	gi|12862672|dbj|AB038971.1AB038965S7 Homo sapiens CFLAR gene, exon 10, exon 11	4E-74
1293	Clu402591.3	AF170811	gi|6715105|gb|AF170811.1AF170811 Homo sapiens CaBP2 (CABP2) gene, complete cds	7E-26
1295	Clu404081.2	AK011443	gi|12847570|dbj|AK011443.1AK011443 Mus musculus 10 days embryo cDNA, RIKEN full-length enriched library, clone:2610018B07, full ins	5E-153
1297	Clu41346.1	AB042029	gi|16326128|dbj|AB042029.1AB042029 Homo sapiens DEPC-1 mRNA for prostate cancer antigen-1, complete cds	0
1299	Clu416124.1	AK000293	gi|7020278|dbj|AK000293.1AK000293 Homo sapiens cDNA FLJ20286 fis, clone HEP04358	3.3E-34
1300	Clu417672.1	AK027667	gi|14042514|dbj|AK027667.1AK027667 Homo sapiens cDNA FLJ14761 fis, clone NT2RP3003302	1.6E-183
1301	Clu423664.1	AF287270	gi|9844925|gb|AF287270.1AF287270 Homo sapiens mucolipin (MCOLN1) gene, complete cds	6.3E-34
1303	Clu442923.3	BC014256	gi|15559816|gb|BC014256.1BC014256 Homo sapiens, Similar to guanine nucleotide binding protein (G protein), beta polypeptide 2-like	1.5E-236
1304	Clu446975.1	AL022342.6	gi|7159715|emb|AL022342.6HS29M10 Human DNA sequence from clone RP1-29M10 on chromosome 20, complete sequence [Homo sapiens]	1.8E-74
1305	Clu449839.2	BC001607	gi|12804410|gb|BC001607.1BC001607 Homo sapiens, clone IMAGE:3543874, mRNA, partial cds	1.9E-27
1306	Clu449889.1	S45332	gi|255496|gb|S45332.1S45332 erythropoietin receptor [human, placental, Genomic, 8647 nt]	8E-101
1307	Clu451707.2	AJ004862	gi|4038586|emb|AJ004862.1HSAJ4862 Homo sapiens partial MUC5B gene, exon 1-29	4.7E-49

Table 7

SEQ ID	SEQ NAME	ACCES-SION	GENBANK DESCRIPTION	GENBANK SCORE
1308	Clu454509.3	AK022973	gi|10434673|dbj|AK022973.1AK022973 Homo sapiens cDNA FLJ12911 fis, clone NT2RP2004425, highly similar to Mus musculus axotrophin mR	1.7E-285
1310	Clu455862.1	AK023951	gi|10436049|dbj|AK023951.1AK023951 Homo sapiens cDNA FLJ13889 fis, clone THYRO1001595	3.3E-27
1311	Clu460493.1	AK012865	gi|12849888|dbj|AK012865.1AK012865 Mus musculus 10, 11 days embryo cDNA, RIKEN full-length enriched library, clone:2810036K01, full	1.7E-57
1314	Clu470032.1	AF223389	gi|11066459|gb|AF223389.1AF223389 Homo sapiens PCGEM1 gene, non-coding mRNA	1.2E-116
1317	Clu477271.1	BC007307	gi|13938350|gb|BC007307.1BC007307 Homo sapiens, Similar to zinc finger protein 268, clone IMAGE:3352268, mRNA, partial cds	4.6E-56
1318	Clu480410.1	AK000713	gi|7020973|dbj|AK000713.1AK000713 Homo sapiens cDNA FLJ20706 fis, clone KAIA1273	0
1320	Clu497138.1	AF270579	gi|9755121|gb|AF270579.1AF270579 Homo sapiens clone 18ptel_481c6 sequence	3.8E-29
1321	Clu498886.1	U49973	gi|2226003|gb|U49973.1HSU49973 Human Tigger1 transposable element, complete consensus sequence	1.4E-24
1323	Clu5013.2	BC007458	gi|13938610|gb|BC007458.1BC007458 Homo sapiens, clone MGC:12217 IMAGE:3828631, mRNA, complete cds	0
1324	Clu5105.2	AL512712	gi|12224956|emb|AL512712.1HSM802915 Homo sapiens mRNA; cDNA DKFZp761J139 (from clone DKFZp761J139)	0
1325	Clu510539.2	AK023812	gi|10435860|dbj|AK023812.1AK023812 Homo sapiens cDNA FLJ13750 fis, clone PLACE3000331	1.4E-32
1326	Clu514044.1	AJ403947	gi|14270388|emb|AJ403947.1HSA403947 Homo sapiens partial SLC22A3 gene for organic cation transporter 3, exon 2	4.4E-295
1329	Clu520370.1	AF093016	gi|5579305|gb|AF093016.1AF093016 Homo sapiens 22k48 gene, 5'UTR	7.3E-67
1330	Clu524917.1	AL1573620	gi|15028613|emb|AL157362.10AL157362 Human DNA sequence from clone RP11-142D16 on chromosome 13q14.3-21.31, complete sequence [Homo	4.9E-23
1331	Clu528957.1	AB060919	gi|13874604|dbj|AB060919.1AB060919 Macaca fascicularis brain cDNA clone:QtrA-14728, full insert sequence	1.5E-31
1334	Clu540142.2	AJ005821	gi|3123571|emb|AJ005821.1HSA5821 Homo sapiens mRNA for X-like 1 protein	3.5E-36

Table 7

SEQ ID	SEQ NAME	ACCES-SION	GENBANK DESCRIPTION	GENBANK SCORE
1335	Clu540379.2	AF088011	gi|3523217|gb|AF088011.1HUMYY75G10 Homo sapiens full length insert cDNA clone YY75G10	2.4E-49
1336	Clu549507.1	U14571	gi|551540|gb|U14571.1HSU14571 ***ALU WARNING: Human Alu-Sc subfamily consensus sequence	1.6E-48
1339	Clu556827.3	AB038163	gi|10280537|dbj|AB038163.1AB038163 Homo sapiens NDUFV3 gene for mitochondrial NADH-Ubiquinone oxidoreductase, complete cds	9.7E-22
1340	Clu558569.2	AF061258	gi|3108092|gb|AF061258.1AF061258 Homo sapiens LIM protein mRNA, complete cds	1E-300
1343	Clu570804.1	AK023843	gi|10435902|dbj|AK023843.1AK023843 Homo sapiens cDNA FLJ13781 fis, clone PLACE4000465	4.4E-42
1344	Clu572170.2	U18271	gi|885681|gb|U18271.1HSTMPO6 Human thymopoietin (TMPO) gene, partial exon 6, complete exon 7, partial exon 8, and partial cds for t	4.9E-57
1346	Clu587168.1	AJ276804	gi|10803412|emb|AJ276804.1HSA276804 Homo sapiens mRNA for protocadherin (PCDHX gene)	5.8E-69
1347	Clu588996.1	U73166	gi|1613889|gb|U73166.1U73166 Homo sapiens cosmid clone LUCA15 from 3p21.3, complete sequence	9.3E-22
1349	Clu598388.1	AF327178	gi|11878341|gb|AF327178.1AF327178 Homo sapiens clone 20ptel_cA35_21t7 sequence	1.1E-26
1350	Clu604822.2	AB063021	gi|14388457|dbj|AB063021.1AB063021 Macaca fascicularis brain cDNA clone:QmoA-11389, full insert sequence	2.6E-65
1353	Clu627263.1	AK021759	gi|10433005|dbj|AK021759.1AK021759 Homo sapiens cDNA FLJ11697 fis, clone HEMBA1005035	5.7E-30
1356	Clu641662.2	AL1576971	gi|11121002|emb|AL157697.11AL157697 Human DNA sequence from clone RP5-1092C14 on chromosome 6, complete sequence [Homo sapiens]	7E-84
1358	Clu6712.1	AK024029	gi|10436287|dbj|AK024029.1AK024029 Homo sapiens cDNA FLJ13967 fis, clone Y79AA1001402, weakly similar to Homo sapiens paraneoplasti	0
1361	Clu685244.2	S56773	gi|298606|gb|S56773.1S56773 putative serine-threonine protein kinase {3' UTR, Alu repeats} [human, Genomic, 1470 nt]	1.1E-35
1362	Clu691653.1	D28126	gi|559316|dbj|D28126.1HUMATPSAS Human gene for ATP synthase alpha subunit, complete cds (exon 1 to 12)	6.3E-37
1367	Clu709796.2	AB070013	gi|15207866|dbj|AB070013.1AB070013 Macaca fascicularis testis cDNA clone:QtsA-11243, full insert sequence	8.4E-118

Table 7

SEQ ID	SEQ NAME	ACCES-SION	GENBANK DESCRIPTION	GENBANK SCORE
1369	Clu727966.1	AF271388	gi|8515842|gb|AF271388.1AF271388 Homo sapiens CMP-N-acetylneuraminic acid synthase mRNA, complete cds	0
1372	Clu756337.1	BC004923	gi|13436241|gb|BC004923.1BC004923 Homo sapiens, clone IMAGE:3605104, mRNA, partial cds	4.1E-250
1376	Clu823296.3	AK023179	gi|10434987|dbj|AK023179.1AK023179 Homo sapiens cDNA FLJ13117 fis, clone NT2RP3002660	6.4E-33
1377	Clu830453.2	AK027301	gi|14041890|dbj|AK027301.1AK027301 Homo sapiens cDNA FLJ14395 fis, clone HEMBA1003250, weakly similar to PROTEIN KINASE APK1A (EC 2	0
1378	Clu839006.1	AB023199	gi|4589607|dbj|AB023199.1AB023199 Homo sapiens mRNA for KIAA0982 protein, complete cds	3.3E-51
1379	Clu847088.1	AL078632.6	gi|6002309|emb|AL078632.6HSA255N20 Human DNA sequence from clone 255N20 on chromosome 22, complete sequence [Homo sapiens]	4.2E-40
1380	Clu853371.2	S79349	gi|1110571|gb|S79349.1S79349 Homo sapiens type 1 iodothyronine deiodinase (hdiol) gene, partial cds	1.6E-48
1381	Clu88462.1	AF026855	gi|3882438|gb|AF026855.1HSHADHSC 3 Homo sapiens mitochondrial short-chain L-3 hydroxyacyl-CoA dehydrogenase (HADHSC) gene, nuclear	1.1E-65
1382	Clu935908.2	AK025271	gi|10437753|dbj|AK025271.1AK025271 Homo sapiens cDNA: FLJ21618 fis, clone COL07487	8.2E-54
1386	DTT00087024.1	AF036235	gi|2695679|gb|AF036235.1AF036235 Gorilla gorilla L1 retrotransposon L1Gg-1A, complete sequence	0
1387	DTT00089020.1	AF324172	gi|12958747|gb|AF324172.1AF324172 Dictyophora indusiata strain ASI 32001 internal transcribed spacer 1, partial sequence; 5.8S ribo	1.1E-142
1388	DTT00171014.1	AB050477	gi|11034759|dbj|AB050477.1AB050477 Homo sapiens NIBAN mRNA, complete cds	0
1389	DTT00514029.1	BC001978	gi|12805042|gb|BC001978.1BC001978 Homo sapiens, clone IMAGE:3461487, mRNA, partial cds	6E-284
1390	DTT00740010.1	AF216292	gi|7229461|gb|AF216292.1AF216292 Homo sapiens endoplasmic reticulum lumenal Ca2+ binding protein grp78 mRNA, complete cds	9.5E-229
1391	DTT00945030.1	AL117237	gi|5834563|emb|AL117237.1HS328E191 Novel human gene mapping to chomosome 1	0
1394	DTT01315010.1	X16983	gi|33945|emb|X16983.1HSINTAL4 Human mRNA for integrin alpha-4 subunit	0

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SEQ ID	SEQ NAME	ACCESSION	GENBANK DESCRIPTION	GENBANK SCORE
1395	DTT01503016.1	AK025473	gi|10437996|dbj|AK025473.1AK025473 Homo sapiens cDNA: FLJ21820 fis, clone HEP01232	0
1396	DTT01555018.1	AE007613	gi|15023874|gb|AE007613.1AE007613 Clostridium acetobutylicum ATCC824 section 101 of 356 of the complete genome	0
1397	DTT01685047.1	M54985	gi|177005|gb|M54985.1GIBBGLOETA H.lar psi-eta beta-like globin pseudogene, exon 1,2,3	6.8E-107
1398	DTT01764019.1	AF307053	gi|12018057|gb|AF307053.1AF307053 Thermococcus litoralis sugar kinase, trehalose/maltose binding protein (malE), trehalose/maltose	0
1401	DTT02367007.1	AK001580	gi|7022920|dbj|AK001580.1AK001580 Homo sapiens cDNA FLJ10718 fis, clone NT2RP3001096, weakly similar to Rattus norvegicus leprecan	0
1402	DTT02671007.1	AF384048	gi|14488027|gb|AF384048.1AF384048 Homo sapiens interferon kappa precursor gene, complete cds	1.8E-170
1403	DTT02737017.1	AF182418	gi|10197635|gb|AF182418.1AF182418 Homo sapiens MDS017 (MDS017) mRNA, complete cds	9E-207
1404	DTT02850005.1	AK011295	gi|12847322|dbj|AK011295.1AK011295 Mus musculus 10 days embryo cDNA, RIKEN full-length enriched library, clone:2610002L04, full ins	2.5E-141
1406	DTT03037029.1	AE006916	gi|13879055|gb|AE006916.1AE006916 Mycobacterium tuberculosis CDC1551, section 2 of 280 of the complete genome	2.1E-129
1407	DTT03150008.1	M83822	gi|1580780|gb|M83822.1HUMCDC4REL Human beige-like protein (BGL) mRNA, partial cds	0
1408	DTT03367008.1	NM_012090.2	gi|15011903|ref|NM_012090.2 Homo sapiens actin cross-linking factor (ACF7), transcript variant 1, mRNA	0
1411	DTT03913023.1	AK018110	gi|12857675|dbj|AK018110.1AK018110 Mus musculus adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:633040	2E-214
1412	DTT03978010.1	BC015529	gi|15930193|gb|BC015529.1BC015529 Homo sapiens, Similar to ribose 5-phosphate isomerase A, clone MGC:9441 IMAGE:3904718, mRNA, comp	0
1413	DTT04070014.1	L43411	gi|893273|gb|L43411.1HUM25DC1Z Homo sapiens (subclone 5_g5 from P1 H25) DNA sequence	4E-102
1414	DTT04084010.1	AF259790	gi|12240019|gb|AF259790.1AF259790 Desulfitobacterium sp. PCE-1 o-chlorophenol reductive dehalogenase (cprA) gene, complete cds	2.2E-288

Table 7

SEQ ID	SEQ NAME	ACCES-SION	GENBANK DESCRIPTION	GENBANK SCORE
1415	DTT04160007.1	AF338299	gi|12958808|gb|AF338299.1AF338299 Amazona ochrocephala auropalliata mitochondrial control region 1, partial sequence	1.4E-181
1417	DTT04378009.1	AF102129	gi|5922722|gb|AF102129.1AF102129 Rattus norvegicus KPL2 (Kpl2) mRNA, complete cds	4.7E-146
1418	DTT04403013.1	AE007580	gi|15023517|gb|AE007580.1AE007580 Clostridium acetobutylicum ATCC824 section 68 of 356 of the complete genome	1.5E-199
1420	DTT04660017.1	NM_025079	gi|13376631|ref|NM_025079.1 Homo sapiens hypothetical protein FLJ23231 (FLJ23231), mRNA	0
1421	DTT04956054.1	AF050179	gi|3319283|gb|AF050179.1AF050179 Homo sapiens CENP-C binding protein (DAXX) mRNA, complete cds	0
1422	DTT04970018.1	AK015635	gi|12854041|dbj|AK015635.1AK015635 Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930486L24, full	1.4E-84
1424	DTT05571010.1	AB014533	gi|3327079|dbj|AB014533.1AB014533 Homo sapiens mRNA for KIAA0633 protein, partial cds	1.8E-53
1426	DTT05742029.1	AF344987	gi|13448249|gb|AF344987.1AF344987 Hepatitis C virus isolate RDpostSC1c2 polyprotein gene, partial cds	0
1427	DTT06137030.1	AY049285	gi|15146287|gb|AY049285.1 Arabidopsis thaliana AT3g58570/F14P22_160 mRNA, complete cds	2.2E-143
1428	DTT06161014.1	AJ330465	gi|15874883|emb|AJ330465.1HSA330465 Homo sapiens genomic sequence surrounding NotI site, clone NR1-IM15C	2.5E-28
1429	DTT06706019.1	AF226787	gi|12407487|gb|AF226787.1AF226787 Syrrhopodon confertus ribulose-1,5-bisphosphate carboxylase large subunit (rbcL) gene, partial cd	0
1430	DTT06837021.1	AK000658	gi|7020892|dbj|AK000658.1AK000658 Homo sapiens cDNA FLJ20651 fis, clone KAT01814	0
1431	DTT07040015.1	AF047347	gi|3005557|gb|AF047347.1AF047347 Homo sapiens adaptor protein X11alpha mRNA, complete cds	0
1432	DTT07088009.1	AF326517	gi|15080738|gb|AF326517.1AF326517 Abies grandis pinene synthase gene, partial cds	0
1433	DTT07182014.1	AB035187	gi|9955412|dbj|AB035187.1AB035187 Homo sapiens RHD gene, intron 1, complete sequence	3.1E-84
1434	DTT07405044.1	AP002946	gi|16267254|dbj|AP002946.1AP002946 Mastacembelus favus mitochondrial DNA, complete genome	0

Table 7

SEQ ID	SEQ NAME	ACCES-SION	GENBANK DESCRIPTION	GENBANK SCORE
1435	DTT07408020.1	AE008061	gi|15156405|gb|AE008061.1AE008061 Agrobacterium tumefaciens strain C58 circular chromosome, section 119 of 254 of the complete sequ	6.9E-245
1438	DTT08005024.1	U18270	gi|885679|gb|U18270.1HSTMPO4 Human thymopoietin (TMPO) gene, exons 4 and 5, and complete cds for thymopoietin alpha	5.1E-108
1439	DTT08098020.1	AF387946	gi|15021617|gb|AF387946.1AF387946 Homo sapiens clone J102 melanocortin 1 receptor gene, promoter region	0
1440	DTT08167018.1	NM_020642	gi|11034852|ref|NM_020642.1 Homo sapiens chromosome 11 open reading frame 17 (C11orf17), mRNA	1E-183
1441	DTT08249022.1	M86752	gi|184564|gb|M86752.1HUMIEF Human transformation-sensitive protein (IEF SSP 3521) mRNA, complete cds	0
1443	DTT08514022.1	AK001927	gi|7023494|dbj|AK001927.1AK001927 Homo sapiens cDNA FLJ11065 fis, clone PLACE1004868, weakly similar to MALE STERILITY PROTEIN 2	0
1444	DTT08527013.1	AF271388	gi|8515842|gb|AF271388.1AF271388 Homo sapiens CMP-N-acetylneuraminic acid synthase mRNA, complete cds	0
1445	DTT08595020.1	L07758	gi|177764|gb|L07758.1HUM56KDAPR Human IEF SSP 9502 mRNA, complete cds	0
1446	DTT08711019.1	D87930	gi|2443337|dbj|D87930.1D87930 Homo sapiens mRNA for myosin phosphatase target subunit 1 (MYPT1)	0
1447	DTT08773020.1	X15187	gi|37260|emb|X15187.1HSTRA1 Human tra1 mRNA for human homologue of murine tumor rejection antigen gp96	6.8E-298
1448	DTT08874012.1	AK026442	gi|10439307|dbj|AK026442.1AK026442 Homo sapiens cDNA: FLJ22789 fis, clone KAIA2171	0
1449	DTT09387018.1	AF273672	gi|15186755|gb|AF273672.1AF273672 Mus musculus RANBP9 isoform 1 (Ranbp9) mRNA, complete cds	0
1450	DTT09396022.1	AK000913	gi|7021874|dbj|AK000913.1AK000913 Homo sapiens cDNA FLJ10051 fis, clone HEMBA1001281	0
1452	DTT09604016.1	AK022722	gi|10434285|dbj|AK022722.1AK022722 Homo sapiens cDNA FLJ12660 fis, clone NT2RM4002174, moderately similar to MRP PROTEIN	2.2E-198
1454	DTT09742009.1	AF025409	gi|2582414|gb|AF025409.1AF025409 Homo sapiens zinc transporter 4 (ZNT4) mRNA, complete cds	0
1455	DTT09753017.1	L03532	gi|187280|gb|L03532.1HUMM4PRO Human M4 protein mRNA, complete cds	5.7E-58

Table 7

SEQ ID	SEQ NAME	ACCES-SION	GENBANK DESCRIPTION	GENBANK SCORE
1456	DTT09793019.1	AK025125	gi|10437578|dbj|AK025125.1AK025125 Homo sapiens cDNA: FLJ21472 fis, clone COL04936	0
1457	DTT09796028.1	AF272390	gi|8705239|gb|AF272390.1AF272390 Homo sapiens myosin 5c (MYO5C) mRNA, complete cds	0
1459	DTT10360040.1	AJ133798	gi|6453351|emb|AJ133798.1HSA133798 Homo sapiens mRNA for copine VI protein	0
1460	DTT10539016.1	AF152924	gi|5453323|gb|AF152924.1AF152924 Mus musculus syntaxin4-interacting protein synip mRNA, complete cds	2.6E-70
1461	DTT10564022.1	AF322634	gi|12657820|gb|AF322634.1AF322634S1 Human herpesvirus 3 strain VZV-Iceland glycoprotein B gene, complete cds	0
1462	DTT10683041.1	X69392	gi|36114|emb|X69392.1HSRP26AA H.sapiens mRNA for ribosomal protein L26	3E-250
1463	DTT10819011.1	U14568	gi|551537|gb|U14568.1HSU14568 ***ALU WARNING: Human Alu-Sb subfamily consensus sequence	2.6E-93
1465	DTT11479018.1	AF309561	gi|10954043|gb|AF309561.1AF309561 Homo sapiens KRAB zinc finger protein ZFQR mRNA, complete cds	0
1466	DTT11483012.1	U57053	gi|1616674|gb|U57053.1HSU57053 Human unconventional myosin-ID (MYO1F) gene, partial cds	3.1E-245
1467	DTT11548015.1	X05332	gi|35740|emb|X05332.1HSPSAR Human mRNA for prostate specific antigen	0
1468	DTT11730017.1	U14572	gi|551541|gb|U14572.1HSU14572 ***ALU WARNING: Human Alu-Sp subfamily consensus sequence	4.7E-90
1471	DTT11902028.1	AK001915	gi|7023475|dbj|AK001915.1AK001915 Homo sapiens cDNA FLJ11053 fis, clone PLACE1004664	0
1472	DTT11915017.1	U66062	gi|1724068|gb|U66062.1HSU66062 Human glp-1 receptor gene, promoter region and partial cds	5.9E-111
1475	DTT12201062.1	M73791	gi|189265|gb|M73791.1HUMNOVGENE Human novel gene mRNA, complete cds	0
1476	DTT12470020.1	AK026618	gi|10439509|dbj|AK026618.1AK026618 Homo sapiens cDNA: FLJ22965 fis, clone KAT10418	0

Table 8

SEQ ID	SEQ NAME	PFAM ID	PFAM DESCRIPTION	SCORE	START	END
7	2504.C11.GZ43_365848	PF00179	Ubiquitin-conjugating enzyme	92.64	4	159
10	2504.E23.GZ43_365908	PF01260	AP endonuclease family 1	88.28	222	481
46	2505.G16.GZ43_366333	PF02594	Uncharacterized ACR, YggU family COG1872	77.64	263	495
109	2510.N14.GZ43_369351	PF02348	Cytidylyltransferase	187.84	357	675
126	2365.D10.GZ43_345308	PF01018	GTP1/OBG family	96.12	50	507
134	2365.F24.GZ43_345370	PF00160	Cyclophilin type peptidyl-prolyl cis-trans isomerase	120.2	251	522
189	2366.L21.GZ43_345942	PF00612	IQ calmodulin-binding motif	33.96	415	477
	2366.L21.GZ43_345942	PF00063	Myosin head (motor domain)	207.12	8	369
259	2368.O03.GZ43_346717	PF00160	Cyclophilin type peptidyl-prolyl cis-trans isomerase	120.2	242	513
267	2535.C23.GZ43_370158	PF02114	Phosducin	32	152	589
334	2537.D11.GZ43_370938	PF00083	Sugar (and other) transporter	122.88	4	288
335	2537.D20.GZ43_370947	PF00131	Metallothionein	48.56	563	665
349	2537.N12.GZ43_371179	PF01352	KRAB box	123.24	313	498
363	2538.B03.GZ43_371266	PF00160	Cyclophilin type peptidyl-prolyl cis-trans isomerase	117.68	320	591
391	2554.A06.GZ43_375853	PF03015	Male sterility protein	44.96	605	749
394	2554.A16.GZ43_375863	PF02348	Cytidylyltransferase	195.48	397	650
405	2554.I10.GZ43_376049	PF03041	lef-2	31.88	479	536
419	2565.B15.GZ43_398171	PF02271	Ubiquinol-cytochrome C reductase complex 14kD subunit	70.76	29	188
422	2565.C17.GZ43_398204	PF00089	Trypsin	45.28	5	110
482	2540.I17.GZ43_372216	PF00023	Ank repeat	75.44	444	542
507	2541.L08.GZ43_372663	PF00499	NADH-ubiquinone/plastoquinone oxidoreductase chain 6	54.72	89	237
514	2506.C15.GZ43_366620	PF00076	RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	44.44	70	276
521	2506.G24.GZ43_366725	PF00096	Zinc finger, C2H2 type	46.68	156	224
527	2506.J20.GZ43_366793	PF00595	PDZ domain (Also known as DHR or GLGF).	34.16	290	502
543	2542.D19.GZ43_372866	PF00098	Zinc knuckle	46.68	224	276
563	2542.N21.GZ43_373108	PF01545	Cation efflux family	42.24	191	325
569	2555.F16.GZ43_373295	PF02348	Cytidylyltransferase	215.04	357	713
716	2560.H21.GZ43_375268	PF00510	Cytochrome c oxidase subunit III	37.28	224	436
721	2560.K10.GZ43_375329	PF01018	GTP1/OBG family	104.56	50	573
759	2561.O17.GZ43_376584	PF00826	Ribosomal L10	79.88	46	180
766	2456.B12.GZ43_355864	PF01545	Cation efflux family	34.16	102	236
771	2456.D04.GZ43_355904	PF02114	Phosducin	30.52	139	576
813	2457.J23.GZ43_356451	PF02594	Uncharacterized ACR, YggU family COG1872	77.64	189	421
818	2457.L21.GZ43_356497	PF00023	Ank repeat	38	208	306

Table 8

SEQ ID	SEQ NAME	PFAM ID	PFAM DESCRIPTION	SCORE	START	END
910	2464.L02.GZ43_357946	PF00076	RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	34.84	244	350
914	2464.N05.GZ43_357997	PF00023	Ank repeat	128.28	491	589
935	2465.K20.GZ43_358324	PF02594	Uncharacterized ACR, YggU family COG1872	77.64	210	442
952	2466.I08.GZ43_360281	PF00012	Hsp70 protein	120.92	16	208
967	2467.D10.GZ43_360547	PF00008	EGF-like domain	31.04	63	113
1002	2472.P22.GZ43_361231	PF00499	NADH-ubiquinone/plastoquinone oxidoreductase chain 6	64.72	81	209
1011	2473.I08.GZ43_361433	PF00895	ATP synthase protein 8	66.88	5	148
1039	2475.N08.GZ43_362321	PF00804	Syntaxin	53.08	226	601
1051	2480.D13.GZ43_358588	PF03025	Papillomavirus E5	33.56	583	749
1065	2481.B06.GZ43_358917	PF00098	Zinc knuckle	35.88	79	133
1100	2483.J07.GZ43_359878	PF00142	4Fe-4S iron sulfur cluster binding proteins, NifH/frxC family	32.8	211	288
1101	2483.K02.GZ43_359897	PF00160	Cyclophilin type peptidyl-prolyl cis-trans isomerase	117.52	244	516
1107	2488.B07.GZ43_362475	PF01260	AP endonuclease family 1	79.88	251	614
1128	2489.F09.GZ43_362957	PF02348	Cytidylyltransferase	174.36	347	591
1183	2496.I06.GZ43_364281	PF02790	Cytochrome C oxidase subunit II, transmembrane domain	45.8	131	242
1207	2562.B09.GZ43_375496	PF00826	Ribosomal L10	106.28	49	341
1216	2562.E14.GZ43_375573	PF00023	Ank repeat	87.04	230	328
1225	2562.H18.GZ43_375649	PF02594	Uncharacterized ACR, YggU family COG1872	65.44	206	437
1244	2507.C03.GZ43_366992	PF00083	Sugar (and other) transporter	95.52	107	355
1267	2499.I09.GZ43_365436	PF00160	Cyclophilin type peptidyl-prolyl cis-trans isomerase	43.24	139	238

Table 9

SEQ ID	PROTEIN SEQ NAME	PFAM ID	PFAM DESCRIPTION	SCORE	START	END
1481	DTP00514038.1	PF00587	tRNA synthetase class II core domain (G, H, P, S and T)	33.42	1	116
1482	DTP00740019.1	PF00012	Hsp70 protein	948.22	27	564
1484	DTP01169031.1	PF00023	Ank repeat	159.66	82	114
1484	DTP01169031.1	PF00023	Ank repeat	159.66	181	213
1484	DTP01169031.1	PF00023	Ank repeat	159.66	148	180
1484	DTP01169031.1	PF00023	Ank repeat	159.66	115	147
1484	DTP01169031.1	PF00023	Ank repeat	159.66	82	114
1484	DTP01169031.1	PF00023	Ank repeat	159.66	49	81
1484	DTP01169031.1	PF00023	Ank repeat	159.66	16	48
1484	DTP01169031.1	PF00023	Ank repeat	159.66	181	213
1484	DTP01169031.1	PF00023	Ank repeat	159.66	115	147
1484	DTP01169031.1	PF00023	Ank repeat	159.66	49	81
1484	DTP01169031.1	PF00023	Ank repeat	159.66	16	48
1484	DTP01169031.1	PF00023	Ank repeat	159.66	148	180
1486	DTP01315019.1	PF01839	FG-GAP repeat	255.09	427	479
1486	DTP01315019.1	PF01839	FG-GAP repeat	255.09	49	111
1486	DTP01315019.1	PF01839	FG-GAP repeat	255.09	248	300
1486	DTP01315019.1	PF01839	FG-GAP repeat	255.09	303	362
1486	DTP01315019.1	PF01839	FG-GAP repeat	255.09	365	424
1495	DTP02737026.1	PF01423	Sm protein	31.6	19	66
1496	DTP02850014.1	PF00804	Syntaxin	156.59	1	292
1496	DTP02850014.1	PF00804	Syntaxin	156.59	1	292
1496	DTP02850014.1	PF00804	Syntaxin	156.59	1	292
1510	DTP04403022.1	PF00400	WD domain, G-beta repeat	35.93	80	116
1510	DTP04403022.1	PF00400	WD domain, G-beta repeat	35.93	38	74
1510	DTP04403022.1	PF00400	WD domain, G-beta repeat	35.93	1	33
1512	DTP04660026.1	PF00083	Sugar (and other) transporter	234.43	1	484
1512	DTP04660026.1	PF00083	Sugar (and other) transporter	234.43	1	484
1518	DTP05742038.1	PF01018	GTP1/OBG family	133.76	105	208
1518	DTP05742038.1	PF01018	GTP1/OBG family	133.76	7	97
1518	DTP05742038.1	PF01018	GTP1/OBG family	133.76	105	208
1518	DTP05742038.1	PF01018	GTP1/OBG family	133.76	7	97
1518	DTP05742038.1	PF01018	GTP1/OBG family	133.76	105	208
1518	DTP05742038.1	PF01018	GTP1/OBG family	133.76	7	97
1519	DTP06137039.1	PF02271	Ubiquinol-cytochrome C reductase complex 14kD subunit	141.38	4	154
1521	DTP06706028.1	PF00054	Laminin G domain	63.34	56	178
1521	DTP06706028.1	PF00054	Laminin G domain	63.34	281	292
1523	DTP07040024.1	PF00640	Phosphotyrosine interaction domain (PTB/PID).	233.89	461	618
1523	DTP07040024.1	PF00595	PDZ domain (Also known as DHR or GLGF).	85.47	656	742
1532	DTP08249031.1	PF00515	TPR Domain	115	4	37
1532	DTP08249031.1	PF00515	TPR Domain	115	72	105
1532	DTP08249031.1	PF00515	TPR Domain	115	38	71
1532	DTP08249031.1	PF00515	TPR Domain	115	259	292
1532	DTP08249031.1	PF00515	TPR Domain	115	300	333
1532	DTP08249031.1	PF00515	TPR Domain	115	225	258
1535	DTP08527022.1	PF02348	Cytidylyltransferase	48.59	1	166

Table 9

SEQ ID	PROTEIN SEQ NAME	PFAM ID	PFAM DESCRIPTION	SCORE	START	END
1535	DTP08527022.1	PF02348	Cytidylyltransferase	48.59	1	166
1535	DTP08527022.1	PF02348	Cytidylyltransferase	48.59	1	166
1535	DTP08527022.1	PF02348	Cytidylyltransferase	48.59	1	166
1536	DTP08595029.1	PF00400	WD domain, G-beta repeat	80.04	183	221
1536	DTP08595029.1	PF00400	WD domain, G-beta repeat	80.04	236	273
1536	DTP08595029.1	PF00400	WD domain, G-beta repeat	80.04	365	402
1536	DTP08595029.1	PF00400	WD domain, G-beta repeat	80.04	279	316
1536	DTP08595029.1	PF00400	WD domain, G-beta repeat	80.04	325	357
1537	DTP08711028.1	PF00023	Ank repeat	81.96	22	54
1537	DTP08711028.1	PF00023	Ank repeat	81.96	55	87
1538	DTP08773029.1	PF00183	Hsp90 protein	100.71	104	173
1540	DTP09387027.1	PF00069	Protein kinase domain	224.56	76	342
1545	DTP09742018.1	PF01545	Cation efflux family	368.71	114	418
1545	DTP09742018.1	PF01545	Cation efflux family	368.71	114	418
1548	DTP09796037.1	PF00612	IQ calmodulin-binding motif	87.63	879	899
1548	DTP09796037.1	PF00612	IQ calmodulin-binding motif	87.63	856	876
1548	DTP09796037.1	PF00612	IQ calmodulin-binding motif	87.63	831	851
1548	DTP09796037.1	PF00612	IQ calmodulin-binding motif	87.63	808	828
1548	DTP09796037.1	PF00612	IQ calmodulin-binding motif	87.63	780	800
1548	DTP09796037.1	PF00612	IQ calmodulin-binding motif	87.63	757	777
1548	DTP09796037.1	PF01843	DIL domain	125.23	1574	1679
1548	DTP09796037.1	PF00063	Myosin head (motor domain)	1228.24	69	741
1550	DTP10360049.1	PF00168	C2 domain	50.07	26	114
1550	DTP10360049.1	PF00168	C2 domain	50.07	228	315
1551	DTP10539025.1	PF00595	PDZ domain (Also known as DHR or GLGF).	32.34	5	84
1553	DTP10683050.1	PF00467	KOW motif	89.22	49	107
1556	DTP11479027.1	PF00096	Zinc finger, C2H2 type	209.31	402	424
1556	DTP11479027.1	PF01352	KRAB box	134.58	8	70
1556	DTP11479027.1	PF00096	Zinc finger, C2H2 type	209.31	374	396
1556	DTP11479027.1	PF00096	Zinc finger, C2H2 type	209.31	346	368
1556	DTP11479027.1	PF00096	Zinc finger, C2H2 type	209.31	318	340
1556	DTP11479027.1	PF00096	Zinc finger, C2H2 type	209.31	290	312
1556	DTP11479027.1	PF00096	Zinc finger, C2H2 type	209.31	262	284
1556	DTP11479027.1	PF00096	Zinc finger, C2H2 type	209.31	234	256
1556	DTP11479027.1	PF00096	Zinc finger, C2H2 type	209.31	206	228
1557	DTP11483021.1	PF00063	Myosin head (motor domain)	339.24	117	271
1557	DTP11483021.1	PF00063	Myosin head (motor domain)	339.24	34	115
1558	DTP11548024.1	PF00089	Trypsin	272.53	25	253
1564	DTP11966049.1	PF00023	Ank repeat	165.68	49	81
1564	DTP11966049.1	PF00023	Ank repeat	165.68	148	180
1564	DTP11966049.1	PF00023	Ank repeat	165.68	181	214
1564	DTP11966049.1	PF00023	Ank repeat	165.68	148	180
1564	DTP11966049.1	PF00023	Ank repeat	165.68	115	147
1564	DTP11966049.1	PF00023	Ank repeat	165.68	82	114
1564	DTP11966049.1	PF00023	Ank repeat	165.68	49	81
1564	DTP11966049.1	PF00023	Ank repeat	165.68	181	214
1564	DTP11966049.1	PF00023	Ank repeat	165.68	181	214
1564	DTP11966049.1	PF00023	Ank repeat	165.68	16	48
1564	DTP11966049.1	PF00023	Ank repeat	165.68	115	147
1564	DTP11966049.1	PF00023	Ank repeat	165.68	82	114
1564	DTP11966049.1	PF00023	Ank repeat	165.68	16	48

Table 9

SEQ ID	PROTEIN SEQ NAME	PFAM ID	PFAM DESCRIPTION	SCORE	START	END
1564	DTP11966049.1	PF00023	Ank repeat	165.68	148	180
1564	DTP11966049.1	PF00023	Ank repeat	165.68	115	147
1564	DTP11966049.1	PF00023	Ank repeat	165.68	82	114
1564	DTP11966049.1	PF00023	Ank repeat	165.68	49	81
1564	DTP11966049.1	PF00023	Ank repeat	165.68	16	48
1566	DTP12201071.1	PF00826	Ribosomal L10	467.36	1	176
1566	DTP12201071.1	PF00826	Ribosomal L10	467.36	1	176

Table 10

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

Table 10

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
128	147	III	Transverse colon	5.0	T3	G2	Invasion of muscularis propria into percolonic fat	Pos	1/5	N1	Neg	M0	
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.

Table 10

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
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
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	

Table 10

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
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..
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	Rectosigm oid	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 inva sive	T3	G2	Invasion through muscularis propria to involve pericolonic fat. Arising from villous adenoma.	Neg	0/4	N0	Neg	MX	

Table 10

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
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.
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.

Table 10

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
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
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	

Table 10

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
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
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

Table 10

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
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.
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

Table 10

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
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.
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.

Table 10

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
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 adenocarcinoma arising from tubulovillous adenoma.

Table 13

SEQ ID	CLONE ID	BREAST PATIENTS >=2x	BREAST PATIENTS <=halfx	COLON PATIENTS >=2x	COLON PATIENTS <=halfx	PROSTATE PATIENTS >=2x	PROSTATE PATIENTS <=halfx
4	M00072944A:C07				35		
8	M00072947B:G04				32.5		
9	M00072947D:G05				27.5		
15	M00072963B:G11				40		
16	M00072967A:G07				25		
18	M00072968A:F08				22.5		
20	M00072968D:E05				32.5		
21	M00072970C:B07				25		
24	M00072971C:B07				22.5		
28	M00072975A:D11	23.5					
34	M00073001A:F07				27.5		
38	M00073003A:E06				42.5		
39	M00073003B:E10				27.5		
42	M00073006A:H08	23.5					
43	M00073006C:D07				27.5		
45	M00073009B:C08				32.5		52.4
48	M00073013A:D10				32.5		
49	M00073013A:F10				20		
50	M00073013C:B10				32.5		
52	M00073014D:F01				40		
54	M00073015A:H06				47.5		
61	M00073020C:F07				32.5		
62	M00073020D:C06			37.5			
63	M00073021C:E04				30		
71	M00073030B:C02				22.5		
72	M00073030C:A02				20		
73	M00073036C:H10				25		
86	M00073043D:H09				32.5		
90	M00073044C:G12				32.5		
94	M00073045C:E06				22.5		
96	M00073045D:B04				30		
105	M00073048C:B01				20		
107	M00073049A:H04				27.5		49.2
108	M00073049B:B03		23.5		40		31.7
109	M00073049B:B06				20		
110	M00073049C:C09				20		
136	M00073066C:D02				27.5		
142	M00073070B:B06				32.5		
146	M00073074D:A04				20		
153	M00073086D:B05				30		
156	M00073091B:C04				20		
163	M00073424D:C03	52.9					
171	M00073403C:C10				30		
173	M00073403C:E11	29.4			52.5		
176	M00073412C:E07				30		
177	M00073435C:E06				27.5		
178	M00073412D:B07		35.3	42.5			
189	M00073430C:B02				32.5		
196	M00073442A:F07				25		
197	M00073442B:D12				27.5		20.6
199	M00073446C:A03				22.5		

Table 13

SEQ ID	CLONE ID	BREAST PATIENTS >=2x	BREAST PATIENTS <=halfx	COLON PATIENTS >=2x	COLON PATIENTS <=halfx	PROSTATE PATIENTS >=2x	PROSTATE PATIENTS <=halfx
201	M00073447D:F01				45		38.1
204	M00073453C:C09	41.2					
212	M00073469B:A09				27.5		36.5
216	M00073474C:F08				30		22.2
220	M00073484B:A05		23.5		30		22.2
228	M00073497C:D03		29.4	30			
233	M00073513A:G07	23.5				25.4	
236	M00073517A:A06				32.5		
241	M00073529A:F03				20		
242	M00073530B:A02				20		54.0
243	M00073531B:H02						50.8
246	M00073539C:H05				27.5		
247	M00073541B:C10				30		
248	M00073547B:F04				22.5		
249	M00073547C:D02				35		
256	M00073554B:D11				37.5		
264	M00073568A:G06				32.5		
265	M00073568C:G07				25		
269	M00073576B:E03				22.5		
270	M00073576C:C11				20		
273	M00073580A:D08				32.5		
280	M00073598D:E11				40		
284	M00073601D:D08				32.5		
286	M00073603B:C03			30			
288	M00073603C:C02		76.5		67.5		
290	M00073604B:B07				30		
294	M00073605B:F11		58.8				
299	M00073614C:F06			60			
300	M00073615D:E03				82.5		
301	M00073616A:F06				32.5		28.6
304	M00073621D:A04				27.5		
316	M00073633D:A04		23.5	52.5			
318	M00073634C:H08	23.5			85	39.7	
319	M00073635D:C10		35.3				
323	M00073638A:A12			47.5			
325	M00073639A:G08				27.5		
340	M00073651C:F06	29.4			27.5		36.5
342	M00073652D:B11		64.7		70		
343	M00073655B:A04			37.5			
353	M00073669A:F04				20		
354	M00073669B:E12	23.5		27.5			
357	M00073687A:D11			50		22.2	
361	M00073672D:E09				35		42.9
367	M00073677B:F01				32.5		
369	M00073678B:H02			35			
372	M00073681A:F12		29.4				25.4
377	M00073689C:C09						41.3
382	M00073696C:D11		35.3				
384	M00073697C:F11		29.4				34.9
388	M00073700B:D12				30		
390	M00073708D:E10						23.8

Table 13

SEQ ID	CLONE ID	BREAST PATIENTS >=2x	BREAST PATIENTS <=halfx	COLON PATIENTS >=2x	COLON PATIENTS <=halfx	PROSTATE PATIENTS >=2x	PROSTATE PATIENTS <=halfx
392	M00073709B:F01				25		
394	M00073709C:A02				22.5		
398	M00073713D:E07				27.5		
399	M00073715A:F05				20		31.7
400	M00073715B:B06				37.5		27.0
401	M00073717C:A12				37.5		
403	M00073720D:H11				27.5		20.6
408	M00073735C:E04						23.8
413	M00073743C:F03				25		
417	M00073748B:F07				35		
424	M00073754B:D05				37.5		
436	M00073765A:E02				32.5		
439	M00073766B:B07				22.5		
442	M00073772B:E07						22.2
450	M00073779B:B11				32.5		
462	M00073798A:H03				35		
464	M00073801B:A10				35		
467	M00073809C:E09		23.5	45		25.4	
469	M00073813D:B06						27.0
470	M00073814C:B04						71.4
473	M00073790A:A12						36.5
480	M00073799A:G02				37.5		
481	M00073799D:G04				30		
486	M00073813A:E06				32.5		
487	M00073813B:A01				30		
493	M00073822C:E02				35		
494	M00073824A:C04						38.1
497	M00073832A:A06				20		20.6
500	M00073834A:H10				35		
502	M00073834D:H06				25		31.7
503	M00073836D:E05					23.8	
506	M00073838B:F09				25		
509	M00073839A:D05		23.5		47.5		41.3
513	M00073850A:H09						54.0
532	M00073867D:F10						36.5
533	M00073871B:C12				32.5		
534	M00073872C:B09				22.5		
535	M00073872D:B01				32.5		
536	M00073872D:E10				22.5		
544	M00073883B:D03				22.5		
550	M00073892B:F12				32.5		
555	M00073905B:A03						55.6
562	M00073897B:B11				30		
564	M00073899A:D06				32.5		
565	M00073911B:G10						23.8
567	M00073916A:B07				42.5		23.8
572	M00073923C:A04	29.4			22.5		
575	M00073931D:E02				27.5		
577	M00073936D:E05				25		
579	M00073908C:D09				40		27.0
599	M00073944D:A07				27.5		

Table 13

SEQ ID	CLONE ID	BREAST PATIENTS >=2x	BREAST PATIENTS <=halfx	COLON PATIENTS >=2x	COLON PATIENTS <=halfx	PROSTATE PATIENTS >=2x	PROSTATE PATIENTS <=halfx
620	M00073968B:B06				27.5		57.1
625	M00073979C:G07				37.5		44.4
634	M00073988D:F09						38.1
641	M00073979B:B05				27.5		66.7
645	M00073988C:G08				40		
654	M00074011D:C05				42.5		
656	M00074013C:C09				20		
659	M00074015A:C03				22.5		
665	M00074020D:G10				40		
669	M00074025A:F06				25		36.5
670	M00074025B:A12						20.6
671	M00074026C:H09				32.5		
687	M00074053C:E05	25.0		30			
695	M00074059B:G10				27.5		
703	M00074075B:A09			27.5			
706	M00074079A:E07				42.5		31.7
708	M00074084D:B04						33.3
710	M00074085B:E06						23.8
712	M00074087B:C09						28.6
713	M00074087C:G05						23.8
717	M00074089D:E03				20		54.0
720	M00074093B:A03		23.5	27.5			
722	M00074094B:F10						52.4
723	M00074096D:G12						25.4
726	M00074098C:B09						23.8
727	M00074099C:B09				20		
729	M00074101D:D07			35			
730	M00074102A:C04				37.5		
733	M00074107C:C08				35		
741	M00074131A:H09				37.5		27.0
742	M00074132C:F10				32.5		22.2
747	M00074138D:A08				45		22.2
749	M00074142B:C11				32.5		
750	M00074142D:A10				22.5		
753	M00074122A:B02				37.5		
756	M00074132A:E11			22.5			
757	M00074132B:B07				35		20.6
758	M00074134A:G11				27.5		
759	M00074149A:B10		41.2	47.5			
762	M00074153D:A05				37.5		
765	M00074157C:G08				25		
767	M00074158C:F12				37.5		
769	M00074159C:A05				25		
777	M00074174A:C02				27.5		27.0
782	M00074177B:H08				35		
785	M00074179C:B01				27.5		28.6
787	M00074184D:B01				37.5		28.6
789	M00074191C:D08						57.1
790	M00074192C:C10						33.3
793	M00074198C:A12	29.4			45		31.7
794	M00074198D:D10						36.5

Table 13

SEQ ID	CLONE ID	BREAST PATIENTS >=2x	BREAST PATIENTS <=halfx	COLON PATIENTS >=2x	COLON PATIENTS <=halfx	PROSTATE PATIENTS >=2x	PROSTATE PATIENTS <=halfx
800	M00074203D:F01				40		
802	M00074206A:H12				40		22.2
806	M00074208B:F09				22.5		41.3
811	M00074215A:F09				42.5		
813	M00074216D:H03				35		
819	M00074223B:D12				30		
821	M00074225A:H12				25		
827	M00074234A:C05				30		
830	M00074234D:F12				37.5		
834	M00074242D:F09				25		
837	M00074247B:G11				27.5		
839	M00074248C:E12					25.4	
840	M00074249C:B11				27.5		
846	M00074251C:E03				35		
849	M00074253C:F03				32.5		
850	M00074255B:A01				20		
851	M00074258A:H12				32.5		
861	M00074271B:E11				25		
869	M00074280D:H03				20		31.7
870	M00074284B:B03				27.5		25.4
873	M00074288A:F11				45		20.6
874	M00074290A:G10				37.5		
875	M00074290C:B05						20.6
877	M00074293D:B05				20		
878	M00074293D:H07				32.5		
882	M00074304B:C09				22.5		39.7
883	M00074304D:D07						36.5
884	M00074306A:B09				27.5		
886	M00074310D:D02				35		25.4
888	M00074315B:A03				22.5		
892	M00074835A:H10				40		
893	M00074835B:F12				22.5		
895	M00074837A:E01				35		
899	M00074843D:D02				25		65.1
900	M00074844B:B02		58.8	20			
901	M00074844D:F09				30		20.6
905	M00074847B:G03				30		
909	M00074852B:A02			37.5			
912	M00074854A:C11				40		
913	M00074855B:A05				27.5		
917	M00074863D:F07				27.5		
919	M00074317D:B08						20.6
920	M00074320C:A06						54.0
921	M00074865A:F05				20		50.8
923	M00074871C:G05				20		
926	M00074879A:A02				35		22.2
930	M00074890A:E03				20		20.6
931	M00074895D:H12						20.6
934	M00074901C:E05				27.5		
938	M00074905D:A01				35		30.2
941	M00074912B:A10						65.1

Table 13

SEQ ID	CLONE ID	BREAST PATIENTS >=2x	BREAST PATIENTS <=halfx	COLON PATIENTS >=2x	COLON PATIENTS <=halfx	PROSTATE PATIENTS >=2x	PROSTATE PATIENTS <=halfx
943	M00074916A:H03				30		
949	M00074927D:G09				22.5		
954	M00074936B:E10				37.5		
955	M00074939B:A06				32.5		
959	M00074966D:E08						34.9
962	M00074974C:E11						22.2
964	M00074954A:H06				20		
975	M00072985A:C12				20		
981	M00072996B:A10				27.5		20.6
984	M00072997D:H06				40		20.6
986	M00074333D:A11		41.2	47.5			
990	M00074343C:A03				30		
998	M00074366A:H07				27.5		42.9
1004	M00074392C:D02				32.5		
1006	M00074417D:F07		23.5	67.5			
1008	M00074406B:F10				27.5		
1012	M00074391B:D02			27.5			
1019	M00074461D:E04				47.5		25.4
1025	M00074488C:C08				32.5		
1027	M00074501A:G07						49.2
1029	M00074515A:E02					25.4	
1030	M00074515C:A11				32.5		
1031	M00074516B:H03						23.8
1032	M00074525A:B05						20.6
1039	M00074561D:D12				30	28.6	
1040	M00074566B:A04				35		
1044	M00074555A:E10				27.5		
1045	M00074561A:B09				40		
1052	M00074582D:B09						25.4
1057	M00074596D:B12				20		22.2
1058	M00074606C:G02	29.4					
1064	M00074628C:D03				37.5		
1067	M00074637A:C02				20		
1068	M00074638D:C12	29.4			35		
1069	M00074639A:C08				30		
1073	M00074662B:A05		35.3				
1078	M00074676D:H07				22.5		
1080	M00074681D:A02				32.5		
1082	M00074699B:C03				32.5		
1083	M00074701D:H09				25		
1086	M00074713B:F02				20		39.7
1089	M00074723D:D05				27.5		
1092	M00074740B:F06				27.5		
1095	M00074752A:D08				32.5		20.6
1099	M00074765D:F06				40		
1102	M00074773C:G03				20		
1103	M00074774A:D03						31.7
1105	M00074780C:C02				20		
1110	M00075000A:D06				32.5		
1117	M00074800B:H01				35		
1120	M00074825C:E06				30		

Table 13

SEQ ID	CLONE ID	BREAST PATIENTS >=2x	BREAST PATIENTS <=halfx	COLON PATIENTS >=2x	COLON PATIENTS <=halfx	PROSTATE PATIENTS >=2x	PROSTATE PATIENTS <=halfx
1122	M00075018A:G04				30		
1134	M00075035C:C09				32.5		
1135	M00075045D:H03				25		
1145	M00075153C:C11				22.5		
1146	M00075161A:E05				30		
1152	M00075152D:C06				30		
1155	M00075160A:E04				42.5		
1163	M00075174D:D06				27.5		
1167	M00075199D:D11		29.4				36.5
1168	M00075201D:A05				30		
1169	M00075203A:G06				35		20.6
1179	M00075245A:A06		41.2	37.5		28.6	
1189	M00075283A:F04					34.9	
1198	M00075329B:E10		25.0	62.5			
1203	M00075344D:A08				22.5		
1224	M00075379A:E07				27.5		
1225	M00075383A:B11				25		
1227	M00075409A:E04				25		
1235	M00075448B:G11				35		20.6
1239	M00075460C:B06		35.3	62.5		20.6	
1245	M00075504B:A10				32.5		
1250	M00075514A:G12				32.5		
1266	M00075621A:F06				20		20.6
1386		23.5					
1387				34.3			
1388			23.5	67.5			
1390		35.3		26.1			
1400					32.5		
1402							41.3
1403							
1404					30.0	28.6	
1426				36.6			
1427					42.9		38.2
1429					31.6		
1434				55.0			
1438					21.3		21.5
1439					30.0		
1444							
1445				27.5			
1447		29.4		32.6			
1449		35.3		60.9			
1461			29.4				
1462			41.2	36.2			
1463					27.5		
1472					23.4		
1474					37.5		
1475			35.3	54.3			

Table 15 ES No.	CLONE ID	ATCC#	ES No.	CLONE ID	ATCC#
ES 210	M00073054A:A06	PTA-2376	ES 213	M00074100B:E01	PTA-2379
ES 210	M00073054A:C10	PTA-2376	ES 213	M00074101D:D07	PTA-2379
ES 210	M00073054B:E07	PTA-2376	ES 213	M00074102A:C04	PTA-2379
ES 210	M00073054C:E02	PTA-2376	ES 213	M00074105A:D02	PTA-2379
ES 210	M00073055D:E11	PTA-2376	ES 213	M00074106C:E03	PTA-2379
ES 210	M00073056C:A09	PTA-2376	ES 213	M00074107C:C08	PTA-2379
ES 210	M00073056C:C12	PTA-2376	ES 213	M00074111C:B02	PTA-2379
ES 210	M00073057A:F09	PTA-2376	ES 213	M00074111C:G11	PTA-2379
ES 210	M00073057D:A12	PTA-2376	ES 213	M00074116C:A03	PTA-2379
ES 210	M00073060B:C06	PTA-2376	ES 213	M00074120A:A12	PTA-2379
ES 210	M00073061B:F10	PTA-2376	ES 213	M00074123B:A03	PTA-2379
ES 210	M00073061C:G08	PTA-2376	ES 213	M00074123B:G07	PTA-2379
ES 210	M00073062B:D09	PTA-2376	ES 213	M00074130B:F06	PTA-2379
ES 210	M00073062C:D09	PTA-2376	ES 213	M00074131A:H09	PTA-2379
ES 210	M00073064C:A11	PTA-2376	ES 213	M00074132C:F10	PTA-2379
ES 210	M00073064C:H09	PTA-2376	ES 213	M00074135A:G09	PTA-2379
ES 210	M00073064D:B11	PTA-2376	ES 213	M00074135C:E09	PTA-2379
ES 210	M00073065D:D11	PTA-2376	ES 213	M00074137C:E05	PTA-2379
ES 210	M00073066B:G03	PTA-2376	ES 213	M0Q074138D:A01	PTA-2379
ES 210	M00073066C:D02	PTA-2376	ES 213	M00074138D:A08	PTA-2379
ES 210	M00073067A:E09	PTA-2376	ES 213	M00074138D:B07	PTA-2379
ES 210	M00073067B:D04	PTA-2376	ES 213	M00074142B:C11	PTA-2379
ES 210	M00073067D:B02	PTA-2376	ES 213	M00074142D:A10	PTA-2379
ES 210	M00073069D:G03	PTA-2376	ES 213	M00074148B:D09	PTA-2379
ES 210	M00073070A:B12	PTA-2376	ES 213	M00074108B:C04	PTA-2379
ES 210	M00073070B:B06	PTA-2376	ES 213	M00074122A:B02	PTA-2379
ES 210	M00073071D:D02	PTA-2376	ES 213	M00074126B:E12	PTA-2379
ES 210	M00073072A:A10	PTA-2376	ES 213	M00074128D:C09	PTA-2379
ES 210	M00073074B:G04	PTA-2376	ES 213	M00074132A:E11	PTA-2379
ES 210	M00073074D:A04	PTA-2376	ES 213	M00074132B:B07	PTA-2379
ES 210	M00073078B:F08	PTA-2376	ES 213	M00074134A:G11	PTA-2379
ES 210	M00073080B:A07	PTA-2376	ES 213	M00074149A:B10	PTA-2379
ES 210	M00073081A:F08	PTA-2376	ES 213	M00074149A:F12	PTA-2379
ES 210	M00073081D:C07	PTA-2376	ES 213	M00074153A:E07	PTA-2379
ES 210	M00073084C:E02	PTA-2376	ES 213	M00074153D:A05	PTA-2379
ES 210	M00073085D:B01	PTA-2376	ES 213	M00074154A:D03	PTA-2379
ES 210	M00073086D:B05	PTA-2376	ES 213	M00074155B:G09	PTA-2379
ES 210	M00073088C:B04	PTA-2376	ES 213	M00074157C:G08	PTA-2379
ES 210	M00073088D:F07	PTA-2376	ES 213	M00074157D:G05	PTA-2379
ES 210	M00073091B:C04	PTA-2376	ES 213	M00074158C:F12	PTA-2379
ES 210	M00073091D:B06	PTA-2376	ES 213	M00074158C:H10	PTA-2379
ES 210	M00073092A:D03	PTA-2376	ES 213	M00074159C:A05	PTA-2379
ES 210	M00073092D:B03	PTA-2376	ES 213	M00074160A:D12	PTA-2379
ES 210	M00073094B:A01	PTA-2376	ES 213	M00074161C:F04	PTA-2379
ES 210	M00073412A:C03	PTA-2376	ES 213	M00074162A:B03	PTA-2379
ES 210	M00073408C:F06	PTA-2376	ES 213	M00074165D:A11	PTA-2379

Table 15 ES No.	CLONE ID	ATCC#	ES No.	CLONE ID	ATCC#
ES 210	M00073424D:C03	PTA-2376	ES 213	M00074170A:D09	PTA-2379
ES 210	M00073403B:F06	PTA-2376	ES 213	M00074170D:F05	PTA-2379
ES 210	M00073407A:E12	PTA-2376	ES 213	M00074172B:D12	PTA-2379
ES 210	M00073412A:H09	PTA-2376	ES 213	M00074174A:C02	PTA-2379
ES 210	M00073421C:B07	PTA-2376	ES 213	M00074174C:C03	PTA-2379
ES 210	M00073416B:F01	PTA-2376	ES 213	M00074175D:E04	PTA-2379
ES 210	M00073425A:G10	PTA-2376	ES 213	M00074176A:A06	PTA-2379
ES 210	M00073425A:H12	PTA-2376	ES 213	M00074176A:B10	PTA-2379
ES 210	M00073403C:C10	PTA-2376	ES 213	M00074177B:H08	PTA-2379
ES 210	M00073428D:H03	PTA-2376	ES 213	M00074178B:G07	PTA-2379
ES 210	M00073403C:E11	PTA-2376	ES 213	M00074179A:A01	PTA-2379
ES 210	M00073435B:E11	PTA-2376	ES 213	M00074179C:B01	PTA-2379
ES 210	M00073431A:G02	PTA-2376	ES 213	M00074184D:A04	PTA-2379
ES 210	M00073412C:E07	PTA-2376	ES 213	M00074184D:B01	PTA-2379
ES 210	M00073435C:E06	PTA-2376	ES 213	M00074190B:F09	PTA-2379
ES 210	M00073412D:B07	PTA-2376	ES 213	M00074191C:D08	PTA-2379
ES 210	M00073429B:H10	PTA-2376	ES 213	M00074192C:C10	PTA-2379
ES 210	M00073403C:H09	PTA-2376	ES 213	M00074195D:B09	PTA-2379
ES 210	M00073412D:E02	PTA-2376	ES 213	M00074197C:A12	PTA-2379
ES 210	M00073427B:C08	PTA-2376	ES 213	M00074198C:A12	PTA-2379
ES 210	M00073423C:E01	PTA-2376	ES 213	M00074198D:D10	PTA-2379
ES 210	M00073427B:E04	PTA-2376	ES 213	M00074199A:C10	PTA-2379
ES 210	M00073425D:F08	PTA-2376	ES 213	M00074201A:F03	PTA-2379
ES 210	M00073096B:A12	PTA-2376	ES 213	M00074201C:E12	PTA-2379
ES 210	M00073430C:A01	PTA-2376	ES 213	M00074202A:A05	PTA-2379
ES 210	M00073418B:B09	PTA-2376	ES 213	M00074202B:D03	PTA-2379
ES 210	M00073430C:B02	PTA-2376	ES 213	M00074203D:F01	PTA-2379
ES 210	M00073097C:A03	PTA-2376	ES 213	M00074206A:G02	PTA-2379
ES 210	M00073418B:H09	PTA-2376	ES 213	M00074206A:H12	PTA-2379
ES 210	M00073408A:D06	PTA-2376	ES 213	M00074206B:F04	PTA-2379
ES 210	M00073438A:A08	PTA-2376	ES 213	M00074207D:E07	PTA-2379
ES 210	M00073438A:B02	PTA-2376	ES 213	M00074208B:B05	PTA-2379
ES 210	M00073438D:G05	PTA-2376	ES 213	M00074208B:F09	PTA-2379
ES 210	M00073442A:F07	PTA-2376	ES 213	M00074208D:E08	PTA-2379
ES 210	M00073442B:D12	PTA-2376	ES 213	M00074209D:H11	PTA-2379
ES 210	M00073442D:E11	PTA-2376	ES 213	M00074210B:G12	PTA-2379
ES 210	M00073446C:A03	PTA-2376	ES 213	M00074213A:C06	PTA-2379
ES 210	M00073447B:A03	PTA-2376	ES 213	M00074215A:F09	PTA-2379
ES 210	M00073447D:F01	PTA-2376	ES 213	M00074216C:C11	PTA-2379
ES 210	M00073448B:F11	PTA-2376	ES 213	M00074216D:H03	PTA-2379
ES 210	M00073448B:F07	PTA-2376	ES 213	M00074217A:H01	PTA-2379
ES 210	M00073453C:C09	PTA-2376	ES 213	M00074217C:B04	PTA-2379
ES 210	M00073455C:G09	PTA-2376	ES 213	M00074217C:C09	PTA-2379
ES 210	M00073457A:G09	PTA-2376	ES 213	M00074219D:F03	PTA-2379
ES 210	M00073462C:H12	PTA-2376	ES 213	M00074221B:F12	PTA-2379
ES 210	M00073462D:D12	PTA-2376	ES 213	M00074223B:D12	PTA-2379

Table 15 ES No.	CLONE ID	ATCC#	ES No.	CLONE ID	ATCC#
ES 210	M00073464B:E01	PTA-2376	ES 213	M00074224A:G06	PTA-2379
ES 210	M00073464D:G12	PTA-2376	ES 213	M00074225A:H12	PTA-2379
ES 210	M00073465A:H08	PTA-2376	ES 213	M00074226C:E06	PTA-2379
ES 210	M00073469B:A09	PTA-2376	ES 213	M00074230D:B05	PTA-2379
ES 210	M00073469D:A06	PTA-2376	ES 213	M00074231A:D10	PTA-2379
ES 210	M00073470D:A01	PTA-2376	ES 213	M00074231D:G11	PTA-2379
ES 210	M00073474A:G11	PTA-2376	ES 213	M00074232B:G06	PTA-2379
ES 210	M00073474C:F08	PTA-2376	ES 213	M00074234A:C05	PTA-2379
ES 210	M00073475D:E05	PTA-2376	ES 213	M00074234A:E07	PTA-2379
ES 210	M00073478C:A07	PTA-2376	ES 213	M00074234B:F07	PTA-2379
ES 210	M00073483B:C07	PTA-2376	ES 213	M00074234D:F12	PTA-2379
ES 210	M00073484B:A05	PTA-2376	ES 213	M00074235C:D06	PTA-2379
ES 210	M00073484C:B04	PTA-2376	ES 213	M00074236B:E06	PTA-2379
ES 210	M00073486A:A12	PTA-2376	ES 213	M00074236C:E11	PTA-2379
ES 210	M00073487A:C07	PTA-2376	ES 213	M00074242D:F09	PTA-2379
ES 210	M00073489B:A07	PTA-2376	ES 213	M00074243A:H08	PTA-2379
ES 210	M00073493A:E12	PTA-2376	ES 213	M00074243C:B06	PTA-2379
ES 210	M00073493D:F05	PTA-2376	ES 213	M00074244C:B11	PTA-2379
ES 210	M00073495B:G11	PTA-2376	ES 213	M00074247B:G11	PTA-2379
ES 210	M00073497C:D03	PTA-2376	ES 213	M00074247C:E02	PTA-2379
ES 210	M00073504D:F03	PTA-2376	ES 213	M00074248C:E12	PTA-2379
ES 210	M00073505D:F01	PTA-2376	ES 213	M00074249C:B11	PTA-2379
ES 210	M00073509B:B11	PTA-2376	ES 213	M00074249C:H08	PTA-2379
ES 210	M00073509B:E03	PTA-2376	ES 213	M00074250D:E06	PTA-2379
ES 210	M00073513A:G07	PTA-2376	ES 213	M00074250D:F06	PTA-2379
ES 210	M00073513D:A11	PTA-2376	ES 213	M00074251B:F08	PTA-2379
ES 210	M00073515A:F09	PTA-2376	ES 213	M00074251C:B06	PTA-2379
ES 210	M00073517A:A06	PTA-2376	ES 213	M00074251C:E03	PTA-2379
ES 210	M00073517D:F11	PTA-2376	ES 213	M00074251D:E03	PTA-2379
ES 210	M00073520D:A04	PTA-2376	ES 213	M00074252C:E02	PTA-2379
ES 210	M00073524A:A03	PTA-2376	ES 213	M00074253C:F03	PTA-2379
ES 210	M00073524A:G05	PTA-2376	ES 213	M00074255B:A01	PTA-2379
ES 210	M00073529A:F03	PTA-2376	ES 213	M00074258A:H12	PTA-2379
ES 210	M00073530B:A02	PTA-2376	ES 213	M00074258A:H09	PTA-2379
ES 210	M00073531B:H02	PTA-2376	ES 213	M00074259C:G08	PTA-2379
ES 210	M00073531C:F12	PTA-2376	ES 213	M00074260B:A11	PTA-2379
ES 210	M00073537B:A12	PTA-2376	ES 213	M00074265B:C07	PTA-2379
ES 210	M00073539C:H05	PTA-2376	ES 213	M00074266A:D01	PTA-2379
ES 210	M00073541B:C10	PTA-2376	ES 213	M00074267A:B04	PTA-2379
ES 210	M00073547B:F04	PTA-2376	ES 213	M00074268A:D08	PTA-2379
ES 210	M00073547C:D02	PTA-2376	ES 213	M00074268C:G03	PTA-2379
ES 210	M00073549B:B03	PTA-2376	ES 213	M00074270B:A01	PTA-2379
ES 210	M00073551B:E10	PTA-2376	ES 213	M00074271B:E11	PTA-2379
ES 210	M00073552A:F06	PTA-2376	ES 214	M00072971A:E04	PTA-2380
ES 210	M00073554A:C01	PTA-2376	ES 214	M00072971A:F11	PTA-2380
ES 210	M00073554A:G04	PTA-2376	ES 214	M00072971C:B07	PTA-2380

Table 15 ES No.	CLONE ID	ATCC#	ES No.	CLONE ID	ATCC#
ES 210	M00073554B:A08	PTA-2376	ES 214	M00072972A:C03	PTA-2380
ES 210	M00073554B:D11	PTA-2376	ES 214	M00072974A:A11	PTA-2380
ES 210	M00073555A:B09	PTA-2376	ES 214	M00072974D:B04	PTA-2380
ES 210	M00073555D:B04	PTA-2376	ES 214	M00072975A:D11	PTA-2380
ES 210	M00073557A:A05	PTA-2376	ES 214	M00072975A:E02	PTA-2380
ES 210	M00073558A:A02	PTA-2376	ES 214	M00072977A:F06	PTA-2380
ES 210	M00073561C:A04	PTA-2376	ES 214	M00072977B:C05	PTA-2380
ES 210	M00073565D:E05	PTA-2376	ES 214	M00072980B:C05	PTA-2380
ES 210	M00073566A:G01	PTA-2376	ES 214	M00072980B:G01	PTA-2380
ES 210	M00073568A:G06	PTA-2376	ES 214	M00073001A:F07	PTA-2380
ES 210	M00073568C:G07	PTA-2376	ES 214	M00073001B:E07	PTA-2380
ES 210	M00073569A:H02	PTA-2376	ES 214	M00073002B:B12	PTA-2380
ES 210	M00073571A:F12	PTA-2376	ES 214	M00073002D:B08	PTA-2380
ES 210	M00073575B:H12	PTA-2376	ES 214	M00073003A:E06	PTA-2380
ES 210	M00073576B:E03	PTA-2376	ES 214	M00073003B:E10	PTA-2380
ES 210	M00073576C:C11	PTA-2376	ES 214	M00073003B:H01	PTA-2380
ES 210	M00073577B:D12	PTA-2376	ES 214	M00073003C:C05	PTA-2380
ES 210	M00073579B:A04	PTA-2376	ES 214	M00073006A:H08	PTA-2380
ES 210	M00073580A:D08	PTA-2376	ES 214	M00073006C:D07	PTA-2380
ES 210	M00073587D:E12	PTA-2376	ES 214	M00073007D:E05	PTA-2380
ES 210	M00073588B:H07	PTA-2376	ES 214	M00073009B:C08	PTA-2380
ES 210	M00073590C:F07	PTA-2376	ES 214	M00073009D:A02	PTA-2380
ES 210	M00073592B:D09	PTA-2376	ES 214	M00073012A:C11	PTA-2380
ES 210	M00073594B:B11	PTA-2376	ES 214	M00073013A:D10	PTA-2380
ES 210	M00073595D:A11	PTA-2376	ES 214	M00073013A:F10	PTA-2380
ES 210	M00073598D:E11	PTA-2376	ES 214	M00073013C:B10	PTA-2380
ES 210	M00073599C:E08	PTA-2376	ES 214	M00073013C:G05	PTA-2380
ES 210	M00073601A:B06	PTA-2376	ES 214	M00073014D:F01	PTA-2380
ES 210	M00073601A:F07	PTA-2376	ES 214	M00073015A:E12	PTA-2380
ES 210	M00073601D:D08	PTA-2376	ES 214	M00073015A:H06	PTA-2380
ES 210	M00073603A:F04	PTA-2376	ES 214	M00073015B:A05	PTA-2380
ES 210	M00073603B:C03	PTA-2376	ES 214	M00073015C:E10	PTA-2380
ES 210	M00073603C:A11	PTA-2376	ES 214	M00073017A:D06	PTA-2380
ES 210	M00073603C:C02	PTA-2376	ES 214	M00073017A:F03	PTA-2380
ES 210	M00073603D:E07	PTA-2376	ES 214	M00073019A:H12	PTA-2380
ES 210	M00073604B:B07	PTA-2376	ES 214	M00073019B:B12	PTA-2380
ES 210	M00073604B:H06	PTA-2376	ES 214	M00073020C:F07	PTA-2380
ES 210	M00073604C:H09	PTA-2376	ES 214	M00073020D:C06	PTA-2380
ES 210	M00073605B:F10	PTA-2376	ES 214	M00073021C:E04	PTA-2380
ES 210	M00073605B:F11	PTA-2376	ES 214	M00073021D:C03	PTA-2380
ES 210	M00073606D:F12	PTA-2376	ES 214	M00073023A:D10	PTA-2380
ES 210	M00073610A:F06	PTA-2376	ES 214	M00073025A:E11	PTA-2380
ES 210	M00073614B:A12	PTA-2376	ES 214	M00073026B:F01	PTA-2380
ES 210	M00073614B:G09	PTA-2376	ES 214	M00073026D:G04	PTA-2380
ES 210	M00073614C:F06	PTA-2376	ES 214	M00073027B:H12	PTA-2380
ES 210	M00073615D:E03	PTA-2376	ES 214	M00073030A:G05	PTA-2380

Table 15 ES No.	CLONE ID	ATCC#	ES No.	CLONE ID	ATCC#
ES 210	M00073616A:F06	PTA-2376	ES 214	M00073030B:C02	PTA-2380
ES 210	M00073617A:H04	PTA-2376	ES 214	M00073030C:A02	PTA-2380
ES 210	M00073620A:G05	PTA-2376	ES 214	M00073036C:H10	PTA-2380
ES 210	M00073621D:A04	PTA-2376	ES 214	M00073037A:C06	PTA-2380
ES 210	M00073621D:D02	PTA-2376	ES 214	M00073037D:H02	PTA-2380
ES 210	M00073621D:H05	PTA-2376	ES 214	M00073038C:C07	PTA-2380
ES 210	M00073623D:H10	PTA-2376	ES 214	M00073038D:D12	PTA-2380
ES 210	M00073625C:D09	PTA-2376	ES 214	M00073038D:F10	PTA-2380
ES 211	M00073626D:A01	PTA-2377	ES 214	M00073039A:D09	PTA-2380
ES 211	M00073628A:E03	PTA-2377	ES 214	M00073039C:B10	PTA-2380
ES 211	M00073630A:C03	PTA-2377	ES 214	M00073040A:B02	PTA-2380
ES 211	M00073630B:E09	PTA-2377	ES 214	M00073040D:F05	PTA-2380
ES 211	M00073630C:D02	PTA-2377	ES 214	M00073043B:C10	PTA-2380
ES 211	M00073632A:B12	PTA-2377	ES 214	M00073043B:E08	PTA-2380
ES 211	M00073632C:A03	PTA-2377	ES 214	M00073043C:F04	PTA-2380
ES 211	M00073633D:A04	PTA-2377	ES 214	M00073043D:H09	PTA-2380
ES 211	M00073633D:G04	PTA-2377	ES 214	M00073044B:F08	PTA-2380
ES 211	M00073634C:H08	PTA-2377	ES 214	M00073044C:C12	PTA-2380
ES 211	M00073635D:C10	PTA-2377	ES 214	M00073044C:D08	PTA-2380
ES 211	M00073636C:F03	PTA-2377	ES 214	M00073044C:G12	PTA-2380
ES 211	M00073637C:B01	PTA-2377	ES 214	M00073044D:F08	PTA-2380
ES 211	M00073637C:E04	PTA-2377	ES 214	M00073045B:A03	PTA-2380
ES 211	M00073638A:A12	PTA-2377	ES 214	M00073045B:D06	PTA-2380
ES 211	M00073638D:D10	PTA-2377	ES 214	M00073045C:E06	PTA-2380
ES 211	M00073639A:G08	PTA-2377	ES 214	M00073045C:E07	PTA-2380
ES 211	M00073639B:F02	PTA-2377	ES 214	M00073045D:B04	PTA-2380
ES 211	M00073634B:C12	PTA-2377	ES 214	M00073046A:A05	PTA-2380
ES 211	M00073640B:G08	PTA-2377	ES 214	M00073046A:A06	PTA-2380
ES 211	M00073640C:A03	PTA-2377	ES 214	M00073046B:A12	PTA-2380
ES 211	M00073640D:A11	PTA-2377	ES 214	M00073046D:F04	PTA-2380
ES 211	M00073640D:G07	PTA-2377	ES 214	M00073047B:E10	PTA-2380
ES 211	M00073641B:G07	PTA-2377	ES 214	M00073047C:G01	PTA-2380
ES 211	M00073641C:E04	PTA-2377	ES 214	M00073048A:H05	PTA-2380
ES 211	M00073643B:E11	PTA-2377	ES 214	M00073048C:A11	PTA-2380
ES 211	M00073644A:G12	PTA-2377	ES 214	M00073048C:B01	PTA-2380
ES 211	M00073646A:C01	PTA-2377	ES 214	M00073048C:E11	PTA-2380
ES 211	M00073647B:H07	PTA-2377	ES 214	M00073049A:H04	PTA-2380
ES 211	M00073649A:A03	PTA-2377	ES 214	M00073049B:B03	PTA-2380
ES 211	M00073649A:G08	PTA-2377	ES 214	M00073049B:B06	PTA-2380
ES 211	M00073651C:F06	PTA-2377	ES 214	M00073049C:C09	PTA-2380
ES 211	M00073651C:H07	PTA-2377	ES 214	M00073049C:H07	PTA-2380
ES 211	M00073652D:B11	PTA-2377	ES 214	M00073050A:D09	PTA-2380
ES 211	M00073655B:A04	PTA-2377	ES 214	M00073051A:D07	PTA-2380
ES 211	M00073657B:D05	PTA-2377	ES 214	M00073051A:F12	PTA-2380
ES 211	M00073659C:D03	PTA-2377	ES 214	M00073051A:F07	PTA-2380
ES 211	M00073663A:E02	PTA-2377	ES 214	M00073052B:H12	PTA-2380

Table 15 ES No.	CLONE ID	ATCC#	ES No.	CLONE ID	ATCC#
ES 211	M00073663D:G06	PTA-2377	ES 214	M00074273B:B03	PTA-2380
ES 211	M00073664A:E03	PTA-2377	ES 214	M00074275A:B04	PTA-2380
ES 211	M00073666B:B01	PTA-2377	ES 214	M00074276A:A12	PTA-2380
ES 211	M00073668A:H03	PTA-2377	ES 214	M00074276A:E02	PTA-2380
ES 211	M00073668B:A08	PTA-2377	ES 214	M00074278B:D07	PTA-2380
ES 211	M00073668D:D10	PTA-2377	ES 214	M00074278D:E07	PTA-2380
ES 211	M00073669A:F04	PTA-2377	ES 214	M00074279C:C11	PTA-2380
ES 211	M00073669B:E12	PTA-2377	ES 214	M00074280D:H03	PTA-2380
ES 211	M00073669D:G10	PTA-2377	ES 214	M00074284B:B03	PTA-2380
ES 211	M00073671B:D09	PTA-2377	ES 214	M00074284C:B06	PTA-2380
ES 211	M00073687A:D11	PTA-2377	ES 214	M00074284C:E12	PTA-2380
ES 211	M00073699C:E02	PTA-2377	ES 214	M00074288A:F11	PTA-2380
ES 211	M00073701D:G10	PTA-2377	ES 214	M00074290A:G10	PTA-2380
ES 211	M00073672D:B07	PTA-2377	ES 214	M00074290C:B05	PTA-2380
ES 211	M00073672D:E09	PTA-2377	ES 214	M00074292D:B04	PTA-2380
ES 211	M00073673A:D11	PTA-2377	ES 214	M00074293D:B05	PTA-2380
ES 211	M00073673D:H03	PTA-2377	ES 214	M00074293D:H07	PTA-2380
ES 211	M00073674D:F10	PTA-2377	ES 214	M00074296C:G09	PTA-2380
ES 211	M00073676A:G08	PTA-2377	ES 214	M00074299B:F01	PTA-2380
ES 211	M00073676D:H04	PTA-2377	ES 214	M00074302D:G10	PTA-2380
ES 211	M00073677B:F01	PTA-2377	ES 214	M00074304B:C09	PTA-2380
ES 211	M00073678B:E08	PTA-2377	ES 214	M00074304D:D07	PTA-2380
ES 211	M00073678B:H02	PTA-2377	ES 214	M00074306A:B09	PTA-2380
ES 211	M00073679A:D06	PTA-2377	ES 214	M00074306B:H01	PTA-2380
ES 211	M00073680D:F11	PTA-2377	ES 214	M00074310D:D02	PTA-2380
ES 211	M00073681A:F12	PTA-2377	ES 214	M00074314A:C06	PTA-2380
ES 211	M00073684B:F10	PTA-2377	ES 214	M00074315B:A03	PTA-2380
ES 211	M00073685A:F07	PTA-2377	ES 214	M00074317C:C01	PTA-2380
ES 211	M00073688C:A12	PTA-2377	ES 214	M00074319C:H03	PTA-2380
ES 211	M00073688D:C11	PTA-2377	ES 214	M00074320C:B07	PTA-2380
ES 211	M00073689C:C09	PTA-2377	ES 214	M00074832B:E05	PTA-2380
ES 211	M00073690B:G04	PTA-2377	ES 214	M00074835A:H10	PTA-2380
ES 211	M00073691A:G02	PTA-2377	ES 214	M00074835B:F12	PTA-2380
ES 211	M00073692D:H02	PTA-2377	ES 214	M00074837A:B06	PTA-2380
ES 211	M00073695C:D11	PTA-2377	ES 214	M00074837A:E01	PTA-2380
ES 211	M00073696C:D11	PTA-2377	ES 214	M00074838B:E11	PTA-2380
ES 211	M00073696D:A08	PTA-2377	ES 214	M00074838D:B06	PTA-2380
ES 211	M00073697C:F11	PTA-2377	ES 214	M00074843A:C06	PTA-2380
ES 211	M00073699B:D02	PTA-2377	ES 214	M00074843A:F11	PTA-2380
ES 211	M00073699B:D09	PTA-2377	ES 214	M00074843D:D02	PTA-2380
ES 211	M00073700A:C09	PTA-2377	ES 214	M00074844B:B02	PTA-2380
ES 211	M00073700B:D12	PTA-2377	ES 214	M00074844D:F09	PTA-2380
ES 211	M00073707B:G08	PTA-2377	ES 214	M00074845A:D12	PTA-2380
ES 211	M00073708D:E10	PTA-2377	ES 214	M00074845B:F07	PTA-2380
ES 211	M00073708D:F03	PTA-2377	ES 214	M00074845D:D07	PTA-2380
ES 211	M00073709B:F01	PTA-2377	ES 214	M00074847B:G03	PTA-2380

Table 15 ES No.	CLONE ID	ATCC#	ES No.	CLONE ID	ATCC#
ES 211	M00073709C:A01	PTA-2377	ES 214	M00074847D:E07	PTA-2380
ES 211	M00073709C:A02	PTA-2377	ES 214	M00074849C:A04	PTA-2380
ES 211	M00073710B:A09	PTA-2377	ES 214	M00074852A:B01	PTA-2380
ES 211	M00073710D:G06	PTA-2377	ES 214	M00074852B:A02	PTA-2380
ES 211	M00073711C:E12	PTA-2377	ES 214	M00074852D:D08	PTA-2380
ES 211	M00073713D:E07	PTA-2377	ES 214	M00074853A:D05	PTA-2380
ES 211	M00073715A:F05	PTA-2377	ES 214	M00074854A:C11	PTA-2380
ES 211	M00073715B:B06	PTA-2377	ES 214	M00074855B:A05	PTA-2380
ES 211	M00073717C:A12	PTA-2377	ES 214	M00074857D:B02	PTA-2380
ES 211	M00073718A:F11	PTA-2377	ES 214	M00074858B:E05	PTA-2380
ES 211	M00073720D:H11	PTA-2377	ES 214	M00074861D:D01	PTA-2380
ES 211	M00073724D:F04	PTA-2377	ES 214	M00074863D:F07	PTA-2380
ES 211	M00073732C:B09	PTA-2377	ES 214	M00074864C:B09	PTA-2380
ES 211	M00073733A:A05	PTA-2377	ES 214	M00074317D:B08	PTA-2380
ES 211	M00073733A:E03	PTA-2377	ES 214	M00074320C:A06	PTA-2380
ES 211	M00073735C:E04	PTA-2377	ES 214	M00074865A:F05	PTA-2380
ES 211	M00073737A:C12	PTA-2377	ES 214	M00074869C:D04	PTA-2380
ES 211	M00073739D:B04	PTA-2377	ES 214	M00074871C:G05	PTA-2380
ES 211	M00073740B:F08	PTA-2377	ES 214	M00074874A:G07	PTA-2380
ES 211	M00073741A:B01	PTA-2377	ES 214	M00074875B:E08	PTA-2380
ES 211	M00073741C:D05	PTA-2377	ES 214	M00074879A:A02	PTA-2380
ES 211	M00073743C:F03	PTA-2377	ES 214	M00074879C:D02	PTA-2380
ES 211	M00073746A:H03	PTA-2377	ES 214	M00074884C:F10	PTA-2380
ES 211	M00073748A:F09	PTA-2377	ES 214	M00074887A:F03	PTA-2380
ES 211	M00073748B:A12	PTA-2377	ES 214	M00074890A:E03	PTA-2380
ES 211	M00073748B:F07	PTA-2377	ES 214	M00074895D:H12	PTA-2380
ES 211	M00073750A:E08	PTA-2377	ES 214	M00074898B:B01	PTA-2380
ES 211	M00073750A:H08	PTA-2377	ES 214	M00074900C:E10	PTA-2380
ES 211	M00073750B:D05	PTA-2377	ES 214	M00074901C:E05	PTA-2380
ES 211	M00073750C:G06	PTA-2377	ES 214	M00074903D:C04	PTA-2380
ES 211	M00073751D:A06	PTA-2377	ES 214	M00074904A:E11	PTA-2380
ES 211	M00073753B:B05	PTA-2377	ES 214	M00074904B:B07	PTA-2380
ES 211	M00073754B:D05	PTA-2377	ES 214	M00074905D:A01	PTA-2380
ES 211	M00073754B:H02	PTA-2377	ES 214	M00074906B:H12	PTA-2380
ES 211	M00073754C:C01	PTA-2377	ES 214	M00074906D:G02	PTA-2380
ES 211	M00073758C:G03	PTA-2377	ES 214	M00074912B:A10	PTA-2380
ES 211	M00073760B:B11	PTA-2377	ES 214	M00074912D:H08	PTA-2380
ES 211	M00073760D:F04	PTA-2377	ES 214	M00074916A:H03	PTA-2380
ES 211	M00073762A:B09	PTA-2377	ES 214	M00074919C:A08	PTA-2380
ES 211	M00073762D:C02	PTA-2377	ES 214	M00074921C:E05	PTA-2380
ES 211	M00073763A:D06	PTA-2377	ES 214	M00074922A:D06	PTA-2380
ES 211	M00073764B:B09	PTA-2377	ES 214	M00074927A:D02	PTA-2380
ES 211	M00073764D:A07	PTA-2377	ES 214	M00074927B:G08	PTA-2380
ES 211	M00073764D:B12	PTA-2377	ES 214	M00074927D:G09	PTA-2380
ES 211	M00073765A:E02	PTA-2377	ES 214	M00074929D:D04	PTA-2380
ES 211	M00073765C:B01	PTA-2377	ES 214	M00074930C:D11	PTA-2380

Table 15 ES No.	CLONE ID	ATCC#	ES No.	CLONE ID	ATCC#
ES 211	M00073766A:B07	PTA-2377	ES 214	M00074933A:D04	PTA-2380
ES 211	M00073766B:B07	PTA-2377	ES 214	M00074935A:C01	PTA-2380
ES 211	M00073766B:C04	PTA-2377	ES 214	M00074936B:E10	PTA-2380
ES 211	M00073769D:G10	PTA-2377	ES 214	M00074939B:A06	PTA-2380
ES 211	M00073772B:E07	PTA-2377	ES 214	M00074940C:H08	PTA-2380
ES 211	M00073773A:F05	PTA-2377	ES 215	M00074950A:D01	PTA-2381
ES 211	M00073773A:G04	PTA-2377	ES 215	M00074958D:H10	PTA-2381
ES 211	M00073773B:A09	PTA-2377	ES 215	M00074966D:E08	PTA-2381
ES 211	M00073774C:G12	PTA-2377	ES 215	M00074967B:A11	PTA-2381
ES 211	M00073776C:F11	PTA-2377	ES 215	M00074968D:A02	PTA-2381
ES 211	M00073777A:A01	PTA-2377	ES 215	M00074974C:E11	PTA-2381
ES 211	M00073777A:H03	PTA-2377	ES 215	M00074980D:E07	PTA-2381
ES 211	M00073779B:B11	PTA-2377	ES 215	M00074954A:H06	PTA-2381
ES 211	M00073784A:A12	PTA-2377	ES 215	M00074954B:E03	PTA-2381
ES 211	M00073785C:A05	PTA-2377	ES 215	M00074957D:F11	PTA-2381
ES 211	M00073785D:D01	PTA-2377	ES 215	M00074962B:F08	PTA-2381
ES 211	M00073787D:H12	PTA-2377	ES 215	M00074968A:D09	PTA-2381
ES 211	M00073788C:A10	PTA-2377	ES 215	M00074973A:H03	PTA-2381
ES 211	M00073790C:E07	PTA-2377	ES 215	M00072987B:A03	PTA-2381
ES 211	M00073793C:E09	PTA-2377	ES 215	M00072997B:H03	PTA-2381
ES 211	M00073795A:F03	PTA-2377	ES 215	M00072951C:C11	PTA-2381
ES 211	M00073795B:B05	PTA-2377	ES 215	M00072953B:G03	PTA-2381
ES 211	M00073795B:B09	PTA-2377	ES 215	M00072982D:B03	PTA-2381
ES 211	M00073796A:C03	PTA-2377	ES 215	M00072985A:C12	PTA-2381
ES 211	M00073798A:H03	PTA-2377	ES 215	M00072985B:D03	PTA-2381
ES 211	M00073800D:F08	PTA-2377	ES 215	M00072986A:C03	PTA-2381
ES 211	M00073801B:A10	PTA-2377	ES 215	M00072993B:D06	PTA-2381
ES 211	M00073802D:B11	PTA-2377	ES 215	M00072995C:D07	PTA-2381
ES 211	M00073806D:C09	PTA-2377	ES 215	M00072995D:C09	PTA-2381
ES 211	M00073809C:E09	PTA-2377	ES 215	M00072996B:A10	PTA-2381
ES 211	M00073810C:F05	PTA-2377	ES 215	M00072996C:C04	PTA-2381
ES 211	M00073813D:B06	PTA-2377	ES 215	M00072997D:F08	PTA-2381
ES 211	M00073814C:B04	PTA-2377	ES 215	M00072997D:H06	PTA-2381
ES 211	M00073786D:B03	PTA-2377	ES 215	M00074323D:F09	PTA-2381
ES 211	M00073789C:B06	PTA-2377	ES 215	M00074333D:A11	PTA-2381
ES 211	M00073790A:A12	PTA-2377	ES 215	M00074335A:H08	PTA-2381
ES 211	M00073792B:A03	PTA-2377	ES 215	M00074337A:G08	PTA-2381
ES 211	M00073794B:G09	PTA-2377	ES 215	M00074340B:D06	PTA-2381
ES 211	M00073794D:G07	PTA-2377	ES 215	M00074343C:A03	PTA-2381
ES 211	M00073796A:D08	PTA-2377	ES 215	M00074346A:H09	PTA-2381
ES 211	M00073796B:A03	PTA-2377	ES 215	M00074347B:F11	PTA-2381
ES 211	M00073799A:A09	PTA-2377	ES 215	M00074349A:E08	PTA-2381
ES 211	M00073799A:G02	PTA-2377	ES 215	M00074355D:H06	PTA-2381
ES 211	M00073799D:G04	PTA-2377	ES 215	M00074361C:B01	PTA-2381
ES 211	M00073803B:B03	PTA-2377	ES 215	M00074365A:E09	PTA-2381
ES 211	M00073803B:C06	PTA-2377	ES 215	M00074366A:D07	PTA-2381

Table 15 ES No.	CLONE ID	ATCC#	ES No.	CLONE ID	ATCC#
ES 211	M00073810B:G10	PTA-2377	ES 215	M00074366A:H07	PTA-2381
ES 211	M00073810C:A06	PTA-2377	ES 215	M00074370D:G09	PTA-2381
ES 211	M00073813A:E06	PTA-2377	ES 215	M00074375D:E05	PTA-2381
ES 211	M00073813B:A01	PTA-2377	ES 215	M00074382D:F04	PTA-2381
ES 211	M00073815D:E02	PTA-2377	ES 215	M00074384D:G07	PTA-2381
ES 211	M00073818A:A06	PTA-2377	ES 215	M00074388B:E07	PTA-2381
ES 211	M00073819D:C11	PTA-2377	ES 215	M00074392C:D02	PTA-2381
ES 211	M00073821A:B10	PTA-2377	ES 215	M00074405B:A04	PTA-2381
ES 211	M00073821B:H03	PTA-2377	ES 215	M00074417D:F07	PTA-2381
ES 211	M00073822C:E02	PTA-2377	ES 215	M00074392D:D01	PTA-2381
ES 211	M00073824A:C04	PTA-2377	ES 215	M00074406B:F10	PTA-2381
ES 211	M00073826B:C01	PTA-2377	ES 215	M00074430D:G09	PTA-2381
ES 211	M00073831B:H09	PTA-2377	ES 215	M00074395A:B11	PTA-2381
ES 211	M00073832A:A06	PTA-2377	ES 215	M00074404B:H01	PTA-2381
ES 211	M00073832A:G01	PTA-2377	ES 215	M00074391B:D02	PTA-2381
ES 211	M00073832B:B05	PTA-2377	ES 215	M00074390C:E04	PTA-2381
ES 212	M00073834A:H10	PTA-2378	ES 215	M00074411B:G07	PTA-2381
ES 212	M00073834D:E07	PTA-2378	ES 215	M00074415B:A01	PTA-2381
ES 212	M00073834D:H06	PTA-2378	ES 215	M00074453B:H03	PTA-2381
ES 212	M00073836D:E05	PTA-2378	ES 215	M00074453C:E09	PTA-2381
ES 212	M00073837B:D12	PTA-2378	ES 215	M00074454A:D08	PTA-2381
ES 212	M00073838A:H07	PTA-2378	ES 215	M00074461D:E04	PTA-2381
ES 212	M00073838B:F09	PTA-2378	ES 215	M00074463B:C03	PTA-2381
ES 212	M00073838B:H06	PTA-2378	ES 215	M00074468B:C03	PTA-2381
ES 212	M00073838D:E01	PTA-2378	ES 215	M00074473D:H09	PTA-2381
ES 212	M00073839A:D05	PTA-2378	ES 215	M00074474B:F02	PTA-2381
ES 212	M00073840D:C08	PTA-2378	ES 215	M00074488C:C10	PTA-2381
ES 212	M00073841A:A03	PTA-2378	ES 215	M00074488C:C08	PTA-2381
ES 212	M00073845D:F05	PTA-2378	ES 215	M00074492A:F11	PTA-2381
ES 212	M00073850A:H09	PTA-2378	ES 215	M00074501A:G07	PTA-2381
ES 212	M00073850D:G04	PTA-2378	ES 215	M00074502C:B08	PTA-2381
ES 212	M00073851A:C05	PTA-2378	ES 215	M00074515A:E02	PTA-2381
ES 212	M00073851A:E04	PTA-2378	ES 215	M00074515C:A11	PTA-2381
ES 212	M00073853C:A01	PTA-2378	ES 215	M00074516B:H03	PTA-2381
ES 212	M00073854B:B04	PTA-2378	ES 215	M00074525A:B05	PTA-2381
ES 212	M00073854C:F08	PTA-2378	ES 215	M00074533A:D07	PTA-2381
ES 212	M00073857A:B12	PTA-2378	ES 215	M00074539D:A10	PTA-2381
ES 212	M00073859A:C09	PTA-2378	ES 215	M00074540B:H07	PTA-2381
ES 212	M00073860B:F12	PTA-2378	ES 215	M00074541D:E07	PTA-2381
ES 212	M00073861D:A09	PTA-2378	ES 215	M00074549B:A06	PTA-2381
ES 212	M00073861D:D08	PTA-2378	ES 215	M00074557A:G08	PTA-2381
ES 212	M00073862B:D11	PTA-2378	ES 215	M00074561D:D12	PTA-2381
ES 212	M00073862D:F06	PTA-2378	ES 215	M00074566B:A04	PTA-2381
ES 212	M00073863B:G09	PTA-2378	ES 215	M00074569D:D04	PTA-2381
ES 212	M00073863C:D04	PTA-2378	ES 215	M00074521D:F01	PTA-2381
ES 212	M00073865B:G04	PTA-2378	ES 215	M00074549C:H08	PTA-2381

Table 15 ES No.	CLONE ID	ATCC#	ES No.	CLONE ID	ATCC#
ES 212	M00073866A:G07	PTA-2378	ES 215	M00074555A:E10	PTA-2381
ES 212	M00073867B:E01	PTA-2378	ES 215	M00074561A:B09	PTA-2381
ES 212	M00073867D:F10	PTA-2378	ES 215	M00074565A:D08	PTA-2381
ES 212	M00073871B:C12	PTA-2378	ES 215	M00074571D:F02	PTA-2381
ES 212	M00073872C:B09	PTA-2378	ES 215	M00074573A:H02	PTA-2381
ES 212	M00073872D:B01	PTA-2378	ES 215	M00074577B:B12	PTA-2381
ES 212	M00073872D:E10	PTA-2378	ES 215	M00074577C:A05	PTA-2381
ES 212	M00073873C:A06	PTA-2378	ES 215	M00074582C:C02	PTA-2381
ES 212	M00073875A:B03	PTA-2378	ES 215	M00074582D:B09	PTA-2381
ES 212	M00073875C:G02	PTA-2378	ES 215	M00074584D:C01	PTA-2381
ES 212	M00073878C:A03	PTA-2378	ES 215	M00074588C:H06	PTA-2381
ES 212	M00073879D:B08	PTA-2378	ES 215	M00074589A:E10	PTA-2381
ES 212	M00073880B:B02	PTA-2378	ES 215	M00074593A:F05	PTA-2381
ES 212	M00073880B:B09	PTA-2378	ES 215	M00074596D:B12	PTA-2381
ES 212	M00073883B:D03	PTA-2378	ES 215	M00074606C:G02	PTA-2381
ES 212	M00073883B:H03	PTA-2378	ES 215	M00074607D:A12	PTA-2381
ES 212	M00073886C:C12	PTA-2378	ES 215	M00074613D:F01	PTA-2381
ES 212	M00073889B:G08	PTA-2378	ES 215	M00074614B:D10	PTA-2381
ES 212	M00073891A:A06	PTA-2378	ES 215	M00074625A:C12	PTA-2381
ES 212	M00073892A:E02	PTA-2378	ES 215	M00074628C:C11	PTA-2381
ES 212	M00073892B:F12	PTA-2378	ES 215	M00074628C:D03	PTA-2381
ES 212	M00073893D:A04	PTA-2378	ES 215	M00074633A:B09	PTA-2381
ES 212	M00073895C:F02	PTA-2378	ES 215	M00074636D:C01	PTA-2381
ES 212	M00073896A:F07	PTA-2378	ES 215	M00074637A:C02	PTA-2381
ES 212	M00073899C:E12	PTA-2378	ES 215	M00074638D:C12	PTA-2381
ES 212	M00073905B:A03	PTA-2378	ES 215	M00074639A:C08	PTA-2381
ES 212	M00073905D:C11	PTA-2378	ES 215	M00074640D:F07	PTA-2381
ES 212	M00073907B:B06	PTA-2378	ES 215	M00074645C:B07	PTA-2381
ES 212	M00073884D:B06	PTA-2378	ES 215	M00074654D:B05	PTA-2381
ES 212	M00073888C:C10	PTA-2378	ES 215	M00074662B:A05	PTA-2381
ES 212	M00073891C:A12	PTA-2378	ES 215	M00074662D:D01	PTA-2381
ES 212	M00073893B:C08	PTA-2378	ES 215	M00074664C:G09	PTA-2381
ES 212	M00073897B:B11	PTA-2378	ES 215	M00074668D:D04	PTA-2381
ES 212	M00073899A:C02	PTA-2378	ES 215	M00074674D:D02	PTA-2381
ES 212	M00073899A:D06	PTA-2378	ES 215	M00074676D:H07	PTA-2381
ES 212	M00073911B:G10	PTA-2378	ES 215	M00074681C:G11	PTA-2381
ES 212	M00073912B:C04	PTA-2378	ES 215	M00074681D:A02	PTA-2381
ES 212	M00073916A:B07	PTA-2378	ES 215	M00074687B:E01	PTA-2381
ES 212	M00073917B:B07	PTA-2378	ES 215	M00074699B:C03	PTA-2381
ES 212	M00073918C:B03	PTA-2378	ES 215	M00074701D:H09	PTA-2381
ES 212	M00073921B:H12	PTA-2378	ES 215	M00074702B:F12	PTA-2381
ES 212	M00073922C:E02	PTA-2378	ES 215	M00074702D:H05	PTA-2381
ES 212	M00073923C:A04	PTA-2378	ES 215	M00074713B:F02	PTA-2381
ES 212	M00073924B:H03	PTA-2378	ES 215	M00074716C:H07	PTA-2381
ES 212	M00073927D:E09	PTA-2378	ES 215	M00074723D:C06	PTA-2381
ES 212	M00073931D:E02	PTA-2378	ES 215	M00074723D:D05	PTA-2381

Table 15 ES No.	CLONE ID	ATCC#	ES No.	CLONE ID	ATCC#
ES 212	M00073932D:G05	PTA-2378	ES 215	M00074728C:B08	PTA-2381
ES 212	M00073936D:E05	PTA-2378	ES 215	M00074730B:A04	PTA-2381
ES 212	M00073938B:D11	PTA-2378	ES 215	M00074740B:F06	PTA-2381
ES 212	M00073908C:D09	PTA-2378	ES 215	M00074744B:B12	PTA-2381
ES 212	M00073916C:H11	PTA-2378	ES 215	M00074748C:G02	PTA-2381
ES 212	M00073918A:F07	PTA-2378	ES 215	M00074752A:D08	PTA-2381
ES 212	M00073918A:G12	PTA-2378	ES 215	M00074753C:E10	PTA-2381
ES 212	M00073919C:B04	PTA-2378	ES 215	M00074755A:B10	PTA-2381
ES 212	M00073920D:F08	PTA-2378	ES 215	M00074755A:E07	PTA-2381
ES 212	M00073922D:G04	PTA-2378	ES 215	M00074765D:F06	PTA-2381
ES 212	M00073924C:G05	PTA-2378	ES 215	M00074766C:F12	PTA-2381
ES 212	M00073927C:B07	PTA-2378	ES 215	M00074768C:A05	PTA-2381
ES 212	M00073933B:B12	PTA-2378	ES 215	M00074773C:G03	PTA-2381
ES 212	M00073938B:F09	PTA-2378	ES 215	M00074774A:D03	PTA-2381
ES 212	M00073941B:A06	PTA-2378	ES 215	M00074777A:E01	PTA-2381
ES 212	M00073941D:H09	PTA-2378	ES 215	M00074780C:C02	PTA-2381
ES 212	M00073942B:C01	PTA-2378	ES 215	M00074782A:E04	PTA-2381
ES 212	M00073942C:E04	PTA-2378	ES 215	M00074808B:H02	PTA-2381
ES 212	M00073942D:D09	PTA-2378	ES 215	M00074996C:D07	PTA-2381
ES 212	M00073942D:G05	PTA-2378	ES 215	M00074981C:C09	PTA-2381
ES 212	M00073944A:E10	PTA-2378	ES 215	M00075000A:D06	PTA-2381
ES 212	M00073944A:H05	PTA-2378	ES 215	M00074805A:C12	PTA-2381
ES 212	M00073944C:H07	PTA-2378	ES 215	M00074981D:A03	PTA-2381
ES 212	M00073944D:A07	PTA-2378	ES 215	M00074794C:H02	PTA-2381
ES 212	M00073944D:E12	PTA-2378	ES 215	M00074801C:E06	PTA-2381
ES 212	M00073946D:F07	PTA-2378	ES 215	M00074821B:B03	PTA-2381
ES 212	M00073947C:B01	PTA-2378	ES 215	M00074823A:E03	PTA-2381
ES 212	M00073947C:E09	PTA-2378	ES 215	M00074800B:H01	PTA-2381
ES 212	M00073948A:G05	PTA-2378	ES 215	M00074800D:G09	PTA-2381
ES 212	M00073949A:C09	PTA-2378	ES 215	M00074812A:F03	PTA-2381
ES 212	M00073949D:C11	PTA-2378	ES 215	M00074825C:E06	PTA-2381
ES 212	M00073950C:A05	PTA-2378	ES 215	M00074794A:G10	PTA-2381
ES 212	M00073950D:H12	PTA-2378	ES 215	M00075018A:G04	PTA-2381
ES 212	M00073952A:G04	PTA-2378	ES 215	M00075020D:B04	PTA-2381
ES 212	M00073956D:F02	PTA-2378	ES 215	M00075049A:C09	PTA-2381
ES 212	M00073960A:B12	PTA-2378	ES 215	M00075032A:F02	PTA-2381
ES 212	M00073960B:A09	PTA-2378	ES 215	M00075029B:E03	PTA-2381
ES 212	M00073961B:G01	PTA-2378	ES 215	M00075069C:C01	PTA-2381
ES 212	M00073962D:E04	PTA-2378	ES 215	M00075039A:E01	PTA-2381
ES 212	M00073963A:G08	PTA-2378	ES 215	M00075024C:G05	PTA-2381
ES 212	M00073963B:F04	PTA-2378	ES 215	M00075074D:G11	PTA-2381
ES 212	M00073964B:H07	PTA-2378	ES 215	M00075011A:C11	PTA-2381
ES 212	M00073967A:A10	PTA-2378	ES 215	M00075061A:B03	PTA-2381
ES 212	M00073967C:A01	PTA-2378	ES 215	M00075043B:H05	PTA-2381
ES 212	M00073968B:B06	PTA-2378	ES 215	M00075035C:C09	PTA-2381
ES 212	M00073968D:F11	PTA-2378	ES 215	M00075045D:H03	PTA-2381

Table 15 ES No.	CLONE ID	ATCC#	ES No.	CLONE ID	ATCC#
ES 212	M00073970B:G01	PTA-2378	ES 215	M00075078C:A07	PTA-2381
ES 212	M00073977D:B10	PTA-2378	ES 215	M00075075A:D12	PTA-2381
ES 212	M00073978D:A02	PTA-2378	ES 215	M00075077C:F09	PTA-2381
ES 212	M00073979C:G07	PTA-2378	ES 215	M00075026A:D11	PTA-2381
ES 212	M00073981C:F08	PTA-2378	ES 215	M00075044A:C10	PTA-2381
ES 212	M00073983B:D03	PTA-2378	ES 215	M00075075A:E09	PTA-2381
ES 212	M00073983C:C07	PTA-2378	ES 215	M00075020C:D12	PTA-2381
ES 212	M00073984B:D04	PTA-2378	ES 215	M00075117B:B06	PTA-2381
ES 212	M00073984B:E01	PTA-2378	ES 215	M00075114C:G11	PTA-2381
ES 212	M00073985C:A05	PTA-2378	ES 215	M00075153C:C11	PTA-2381
ES 212	M00073987B:A09	PTA-2378	ES 215	M00075161A:E05	PTA-2381
ES 212	M00073988B:C08	PTA-2378	ES 215	M00075126B:A06	PTA-2381
ES 212	M00073988D:F09	PTA-2378	ES 215	M00075126D:H07	PTA-2381
ES 212	M00073993A:A05	PTA-2378	ES 216	M00075092C:F04	PTA-2382
ES 212	M00073965D:A12	PTA-2378	ES 216	M00075110C:B03	PTA-2382
ES 212	M00073966C:F08	PTA-2378	ES 216	M00075132C:A03	PTA-2382
ES 212	M00073968C:C09	PTA-2378	ES 216	M00075152D:C06	PTA-2382
ES 212	M00073968C:F02	PTA-2378	ES 216	M00075125B:C07	PTA-2382
ES 212	M00073975A:A12	PTA-2378	ES 216	M00075132C:E07	PTA-2382
ES 212	M00073979B:B05	PTA-2378	ES 216	M00075160A:E04	PTA-2382
ES 212	M00073979C:B01	PTA-2378	ES 216	M00075149B:A01	PTA-2382
ES 212	M00073982B:H01	PTA-2378	ES 216	M00075120C:H04	PTA-2382
ES 212	M00073986C:D07	PTA-2378	ES 216	M00075093B:F10	PTA-2382
ES 212	M00073988C:G08	PTA-2378	ES 216	M00075102A:D02	PTA-2382
ES 212	M00074000C:D06	PTA-2378	ES 216	M00075090D:B07	PTA-2382
ES 212	M00074003C:H06	PTA-2378	ES 216	M00075161D:G06	PTA-2382
ES 212	M00074004A:H01	PTA-2378	ES 216	M00075165B:D04	PTA-2382
ES 212	M00074004C:F03	PTA-2378	ES 216	M00075174D:D06	PTA-2382
ES 212	M00074006C:B12	PTA-2378	ES 216	M00075180D:F05	PTA-2382
ES 212	M00074007B:A02	PTA-2378	ES 216	M00075181D:G10	PTA-2382
ES 212	M00074010B:D07	PTA-2378	ES 216	M00075189C:G05	PTA-2382
ES 212	M00074011A:F08	PTA-2378	ES 216	M00075199D:D11	PTA-2382
ES 212	M00074011D:C05	PTA-2378	ES 216	M00075201D:A05	PTA-2382
ES 212	M00074013B:F07	PTA-2378	ES 216	M00075203A:G06	PTA-2382
ES 212	M00074013C:C09	PTA-2378	ES 216	M00075211D:F09	PTA-2382
ES 212	M00074014A:G03	PTA-2378	ES 216	M00075221C:E02	PTA-2382
ES 212	M00074014D:F04	PTA-2378	ES 216	M00075228D:G09	PTA-2382
ES 212	M00074015A:C03	PTA-2378	ES 216	M00075232C:A06	PTA-2382
ES 212	M00074017B:G10	PTA-2378	ES 216	M00075232D:C06	PTA-2382
ES 212	M00074017D:C01	PTA-2378	ES 216	M00075234C:E06	PTA-2382
ES 212	M00074019D:H05	PTA-2378	ES 216	M00075239C:D06	PTA-2382
ES 212	M00074020B:G11	PTA-2378	ES 216	M00075242A:G04	PTA-2382
ES 212	M00074020C:A05	PTA-2378	ES 216	M00075243D:F04	PTA-2382
ES 212	M00074020D:G10	PTA-2378	ES 216	M00075245A:A06	PTA-2382
ES 212	M00074021C:H07	PTA-2378	ES 216	M00075249A:B08	PTA-2382
ES 212	M00074022A:C06	PTA-2378	ES 216	M00075252B:F10	PTA-2382

Table 15 ES No.	CLONE ID	ATCC#	ES No.	CLONE ID	ATCC#
ES 212	M00074024B:G07	PTA-2378	ES 216	M00075255A:G11	PTA-2382
ES 212	M00074025A:F06	PTA-2378	ES 216	M00075259C:G02	PTA-2382
ES 212	M00074025B:A12	PTA-2378	ES 216	M00075270D:A02	PTA-2382
ES 212	M00074026C:H09	PTA-2378	ES 216	M00075273C:E01	PTA-2382
ES 212	M00074027D:B03	PTA-2378	ES 216	M00075274B:F06	PTA-2382
ES 212	M00074030D:A12	PTA-2378	ES 216	M00075275B:H07	PTA-2382
ES 212	M00074032B:H08	PTA-2378	ES 216	M00075279C:E08	PTA-2382
ES 212	M00074032C:E02	PTA-2378	ES 216	M00075283A:F04	PTA-2382
ES 212	M00074032C:H07	PTA-2378	ES 216	M00075302B:C07	PTA-2382
ES 212	M00074036B:C08	PTA-2378	ES 216	M00075305C:C07	PTA-2382
ES 212	M00074036D:B05	PTA-2378	ES 216	M00075309C:A06	PTA-2382
ES 212	M00074037A:B03	PTA-2378	ES 216	M00075323B:B12	PTA-2382
ES 212	M00074038A:G08	PTA-2378	ES 216	M00075324B:C10	PTA-2382
ES 212	M00074038C:B08	PTA-2378	ES 216	M00075324D:E02	PTA-2382
ES 212	M00074040A:B06	PTA-2378	ES 216	M00075326C:B01	PTA-2382
ES 212	M00074043C:A05	PTA-2378	ES 216	M00075326D:A09	PTA-2382
ES 212	M00074050B:H07	PTA-2378	ES 216	M00075329B:E10	PTA-2382
ES 212	M00074051C:F05	PTA-2378	ES 216	M00075330D:F11	PTA-2382
ES 212	M00074052C:E03	PTA-2378	ES 216	M00075333D:B07	PTA-2382
ES 212	M00074053C:E05	PTA-2378	ES 216	M00075333D:D10	PTA-2382
ES 212	M00074053C:G11	PTA-2378	ES 216	M00075336B:B04	PTA-2382
ES 212	M00074053D:D05	PTA-2378	ES 216	M00075344D:A08	PTA-2382
ES 212	M00074054C:B04	PTA-2378	ES 216	M00075347D:D01	PTA-2382
ES 212	M00074055A:G08	PTA-2378	ES 216	M00075354A:D11	PTA-2382
ES 213	M00072942B:E02	PTA-2379	ES 216	M00075354A:G12	PTA-2382
ES 213	M00072942D:F07	PTA-2379	ES 216	M00075354C:B12	PTA-2382
ES 213	M00072943B:E04	PTA-2379	ES 216	M00075360D:D04	PTA-2382
ES 213	M00072944A:C07	PTA-2379	ES 216	M00075365B:B06	PTA-2382
ES 213	M00072944A:E06	PTA-2379	ES 216	M00075384A:B03	PTA-2382
ES 213	M00072944C:C02	PTA-2379	ES 216	M00075389B:C06	PTA-2382
ES 213	M00072944D:C08	PTA-2379	ES 216	M00075391D:D07	PTA-2382
ES 213	M00072947B:G04	PTA-2379	ES 216	M00075402A:F01	PTA-2382
ES 213	M00072947D:G05	PTA-2379	ES 216	M00075405B:C07	PTA-2382
ES 213	M00072950A:A06	PTA-2379	ES 216	M00075405D:A10	PTA-2382
ES 213	M00072961A:G04	PTA-2379	ES 216	M00075365D:B08	PTA-2382
ES 213	M00072961B:G10	PTA-2379	ES 216	M00075380D:F06	PTA-2382
ES 213	M00072961C:B06	PTA-2379	ES 216	M00075356D:C03	PTA-2382
ES 213	M00072962A:B05	PTA-2379	ES 216	M00075352D:F09	PTA-2382
ES 213	M00072963B:G11	PTA-2379	ES 216	M00075359D:E09	PTA-2382
ES 213	M00072967A:G07	PTA-2379	ES 216	M00075365D:H01	PTA-2382
ES 213	M00072967B:G06	PTA-2379	ES 216	M00075373C:B09	PTA-2382
ES 213	M00072968A:F08	PTA-2379	ES 216	M00075378B:C07	PTA-2382
ES 213	M00072968D:A06	PTA-2379	ES 216	M00075379A:E07	PTA-2382
ES 213	M00072968D:E05	PTA-2379	ES 216	M00075383A:B11	PTA-2382
ES 213	M00072970C:B07	PTA-2379	ES 216	M00075407A:B05	PTA-2382
ES 213	M00074057A:B12	PTA-2379	ES 216	M00075409A:E04	PTA-2382

Table 15 ES No.	CLONE ID	ATCC#	ES No.	CLONE ID	ATCC#
ES 213	M00074058A:H02	PTA-2379	ES 216	M00075409B:G12	PTA-2382
ES 213	M00074058B:A10	PTA-2379	ES 216	M00075416C:B02	PTA-2382
ES 213	M00074059B:G10	PTA-2379	ES 216	M00075458B:F09	PTA-2382
ES 213	M00074060D:A10	PTA-2379	ES 216	M00075464C:A07	PTA-2382
ES 213	M00074061B:E01	PTA-2379	ES 216	M00075458C:F01	PTA-2382
ES 213	M00074063A:B03	PTA-2379	ES 216	M00075463C:E07	PTA-2382
ES 213	M00074063A:D09	PTA-2379	ES 216	M00075464C:C04	PTA-2382
ES 213	M00074063B:B12	PTA-2379	ES 216	M00075448B:G11	PTA-2382
ES 213	M00074069D:C11	PTA-2379	ES 216	M00075434A:D06	PTA-2382
ES 213	M00074070D:G05	PTA-2379	ES 216	M00075457C:A06	PTA-2382
ES 213	M00074075B:A09	PTA-2379	ES 216	M00075454C:D06	PTA-2382
ES 213	M00074075C:H04	PTA-2379	ES 216	M00075460C:B06	PTA-2382
ES 213	M00074076B:F04	PTA-2379	ES 216	M00075459A:C02	PTA-2382
ES 213	M00074079A:E07	PTA-2379	ES 216	M00075414A:D10	PTA-2382
ES 213	M00074084C:E01	PTA-2379	ES 216	M00075433A:C06	PTA-2382
ES 213	M00074084D:B04	PTA-2379	ES 216	M00075505B:A04	PTA-2382
ES 213	M00074085A:H10	PTA-2379	ES 216	M00075474D:B07	PTA-2382
ES 213	M00074085B:E06	PTA-2379	ES 216	M00075504B:A10	PTA-2382
ES 213	M00074085D:E08	PTA-2379	ES 216	M00075473C:E08	PTA-2382
ES 213	M00074087B:C09	PTA-2379	ES 216	M00075499A:H02	PTA-2382
ES 213	M00074087C:G05	PTA-2379	ES 216	M00075495D:D11	PTA-2382
ES 213	M00074088B:A03	PTA-2379	ES 216	M00075496D:G05	PTA-2382
ES 213	M00074088C:E07	PTA-2379	ES 216	M00075514A:G12	PTA-2382
ES 213	M00074089A:B09	PTA-2379	ES 216	M00075495B:C12	PTA-2382
ES 213	M00074089D:E03	PTA-2379	ES 216	M00075497D:H03	PTA-2382
ES 213	M00074090A:E09	PTA-2379	ES 216	M00075529A:A02	PTA-2382
ES 213	M00074093A:A06	PTA-2379	ES 216	M00075538C:E03	PTA-2382
ES 213	M00074093B:A03	PTA-2379	ES 216	M00075544A:C03	PTA-2382
ES 213	M00074093B:C07	PTA-2379	ES 216	M00075598B:A09	PTA-2382
ES 213	M00074094B:F10	PTA-2379	ES 216	M00075521B:E11	PTA-2382
ES 213	M00074096D:G12	PTA-2379	ES 216	M00075597C:G01	PTA-2382
ES 213	M00074097A:F10	PTA-2379	ES 216	M00075584D:B05	PTA-2382
ES 213	M00074097C:B09	PTA-2379	ES 216	M00075590B:G04	PTA-2382
ES 213	M00074098C:B09	PTA-2379	ES 216	M00075603D:D09	PTA-2382
ES 213	M00074099C:B09	PTA-2379	ES 216	M00075607B:D05	PTA-2382
			ES 216	M00075609A:H06	PTA-2382
			ES 216	M00075613D:F01	PTA-2382
			ES 216	M00075619C:D08	PTA-2382
			ES 216	M00075621A:F06	PTA-2382
			ES 216	M00075639A:D12	PTA-2382

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: 1-1477.

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:1-1477, a degenerate variant of SEQ ID NOS:1-1477, an antisense of SEQ ID NOS:1-1477, and a complement of SEQ ID NOS:1-1477.

3. An isolated polynucleotide comprising at least 15 contiguous nucleotides of a nucleotide sequence selected from the group consisting of: SEQ ID NOS:1-1477, a degenerate variant of SEQ ID NOS:1-1477, an antisense of SEQ ID NOS:1-1477, and a complement of SEQ ID NOS:1-1477.

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:1-1477, a degenerate variant of SEQ ID NOS:1-1477, an antisense of SEQ ID NOS:1-1477, and a complement of SEQ ID NOS:1-1477.

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-2918.

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:1-1477.

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 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 1, 2, 3, 6, 9, or 10., said culturing being under conditions suitable for the expression of an encoded polypeptide; and

recovering the polypeptide from the host cell culture.

17. An isolated polypeptide encoded by the polynucleotide according to claims 1, 2, 3, 6, 9, or 10.

18. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOS:1478-1568.

19. An antibody that specifically binds the polypeptide of claim 17 or 18.

20. 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:1-1477;

wherein detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived.

21. 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 comprises an amino acid sequence selected from the group consisting of SEQ ID NOS:1478-1568;

wherein detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived.

22. 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.

23. The library of claim 22, wherein the library is provided on a nucleic acid array.

24. The library of claim 22, wherein the library is provided in a computer-readable format.

25. 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:1-1477.

26. A method of inhibiting tumor growth by modulating expression of a gene product, the gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOS:1478-1568.