Novel Compounds

Field of Invention

This invention relates to newly identified polypeptides and polynucleotides encoding such polypeptides, to their use in diagnosis and in identifying compounds that may be agonists, antagonists that are potentially useful in therapy, and to production of such polypeptides and polynucleotides. The polynucleotides and polypeptides of the present invention also relate to proteins with signal sequences which allow them to be secreted extracellularly or membrane-associated (hereinafter often referred collectively as secreted proteins or secreted polypeptides).

Background of the Invention

The drug discovery process is currently undergoing a fundamental revolution as it embraces "functional genomics", that is, high throughput genome- or gene-based biology. This approach as a means to identify genes and gene products as therapeutic targets is rapidly superseding earlier approaches based on "positional cloning". A phenotype, that is a biological function or genetic disease, would be identified and this would then be tracked back to the responsible gene, based on its genetic map position.

Functional genomics relies heavily on high-throughput DNA sequencing technologies and the various tools of bioinformatics to identify gene sequences of potential interest from the many molecular biology databases now available. There is a continuing need to identify and characterise further genes and their related polypeptides/proteins, as targets for drug discovery.

Proteins and polypeptides that are naturally secreted into blood, lymph and other body fluids, or secreted into the cellular membrane are of primary interest for pharmaceutical research and development. The reason for this interest is the relative ease to target protein therapeutics into their place of action (body fluids or the cellular membrane). The natural pathway for protein secretion into extracellular space is the endoplasmic reticulum in eukaryotes and the inner membrane in prokaryotes (Palade, 1975, Science, 189, 347; Milstein, Brownlee, Harrison, and Mathews, 1972, Nature New Biol., 239, 117; Blobel, and Dobberstein, 1975, J. Cell. Biol., 67, 835). On the other hand, there is no known natural pathway for exporting a protein from the exterior of the cells into the cytosol (with the exception of pinocytosis, a mechanism of snake venom toxin intrusion into cells). Therefore targeting protein therapeutics into cells poses extreme difficulties.

The secreted and membrane-associated proteins include but are not limited

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to all peptide hormones and their receptors (including but not limited to insulin, growth hormones, chemokines, cytokines, neuropeptides, integrins, kallikreins, lamins, melanins, natriuretic hormones, neuropsin, neurotropins, pituitiary hormones, pleiotropins, prostaglandins, secretogranins, selectins, thromboglobulins, thymosins), the breast and colon cancer gene products, leptin, the obesity gene protein and its receptors, serum albumin, superoxide dismutase, spliceosome proteins, 7TM (transmembrane) proteins also called as G-protein coupled receptors, immunoglobulins, several families of serine proteinases (including but not limited to proteins of the blood coagulation cascade, digestive enzymes), deoxyribonuclease I, etc.

Therapeutics based on secreted or membrane-associated proteins approved by FDA or foreign agencies include but are not limited to insulin, glucagon, growth hormone, chorionic gonadotropin, follicle stimulating hormone, luteinizing hormone, calcitonin, adrenocorticotropic hormone (ACTH), vasopressin, interleukines, interferones, immunoglobulins, lactoferrin (diverse products marketed by several companies), tissue-type plasminogen activator (Alteplase by Genentech), hyaulorindase (Wydase by Wyeth-Ayerst), dornase alpha (Pulmozyme\ by Genentech), Chymodiactin (chymopapain by Knoll), alglucerase (Ceredase by Genzyme), streptokinase (Kabikinase by Pharmacia) (Streptase by Astra), etc. This indicates that secreted and membrane-associated proteins have an established, proven history as therapeutic targets. Clearly, there is a need for identification and characterization of further secreted and membrane-associated proteins which can play a role in preventing, ameliorating or correcting dysfunction or disease, including but not limited to diabetes, breast-, prostate-, colon cancer and other malignant tumors, hyper- and hypotension, obesity, bulimia, anorexia, growth abnormalities, asthma, manic depression, dementia, delirium, mental retardation, Huntington's disease, Tourette's syndrome, schizophrenia, growth, mental or sexual development disorders, and dysfunctions of the blood cascade system including those leading to stroke. The proteins of the present invention which include the signal sequences are also useful to further elucidate the mechanism of protein transport which at present is not entirely understood, and thus can be used as research tools.

Summary of the Invention

The present invention relates to particular polypeptides and polynucleotides of the genes set forth in Table I, including recombinant materials and methods for their production. Such polypeptides and polynucleotides are of interest in relation to methods of treatment of

certain diseases, including, but not limited to, the diseases set forth in Tables III and V, hereinafter referred to as "diseases of the invention". In a further aspect, the invention relates to methods for identifying agonists and antagonists (*e.g.*, inhibitors) using the materials provided by the invention, and treating conditions associated with imbalance of polypeptides and/or polynucleotides of the genes set forth in Table I with the identified compounds. In still a further aspect, the invention relates to diagnostic assays for detecting diseases associated with inappropriate activity or levels the genes set forth in Table I. Another aspect of the invention concerns a polynucleotide comprising any of the nucleotide sequences set forth in the Sequence Listing and a polypeptide comprising a polypeptide encoded by the nucleotide sequence. In another aspect, the invention relates to a polypeptide comprising any of the polypeptide sequences set forth in the Sequence Listing and recombinant materials and methods for their production. Another aspect of the invention relates to methods for using such polypeptides and polynucleotides. Such uses include the treatment of diseases, abnormalities and disorders (hereinafter simply referred to as diseases) caused by abnormal expression, production, function and or metabolism of the genes of this invention, and such diseases are readily apparent by those skilled in the art from the homology to other proteins disclosed for each attached sequence. In still another aspect, the invention relates to methods to identify agonists and antagonists using the materials provided by the invention, and treating conditions associated with the imbalance with the identified compounds. Yet another aspect of the invention relates to diagnostic assays for detecting diseases associated with inappropriate activity or levels of the secreted proteins of the present invention.

Description of the Invention

In a first aspect, the present invention relates to polypeptides the genes set forth in Table I. Such polypeptides include:

(a) an isolated polypeptide encoded by a polynucleotide comprising a sequence set forth in the Sequence Listing, herein when referring to polynucleotides or polypeptides of the Sequence Listing, a reference is also made to the Sequence Listing referred to in the Sequence Listing;

(b) an isolated polypeptide comprising a polypeptide sequence having at least 95%, 96%, 97%, 98%, or 99% identity to a polypeptide sequence set forth in the Sequence Listing;

(c) an isolated polypeptide comprising a polypeptide sequence set forth in the Sequence Listing;

(d) an isolated polypeptide having at least 95%, 96%, 97%, 98%, or 99% identity to a polypeptide sequence set forth in the Sequence Listing;

(e) a polypeptide sequence set forth in the Sequence Listing; and

(f) an isolated polypeptide having or comprising a polypeptide sequence that has an Identity Index of 0.95, 0.96, 0.97, 0.98, or 0.99 compared to a polypeptide sequence set forth in the Sequence Listing;

(g) fragments and variants of such polypeptides in (a) to (f).

Polypeptides of the present invention are believed to be members of the gene families set forth in Table II . They are therefore of therapeutic and diagnostic interest for the reasons set forth in Tables III and V. The biological properties of the polypeptides and polynucleotides of the genes set forth in Table I are hereinafter referred to as "the biological activity" of polypeptides and polynucleotides of the genes set forth in Table I. Preferably, a polypeptide of the present invention exhibits at least one biological activity of the genes set forth in Table I.

Polypeptides of the present invention also include variants of the aforementioned polypeptides, including all allelic forms and splice variants. Such polypeptides vary from the reference polypeptide by insertions, deletions, and substitutions that may be conservative or non-conservative, or any combination thereof. Particularly preferred variants are those in which several, for instance from 50 to 30, from 30 to 20, from 20 to 10, from 10 to 5, from 5 to 3, from 3 to 2, from 2 to 1 or 1 amino acids are inserted, substituted, or deleted, in any combination.

Preferred fragments of polypeptides of the present invention include an isolated polypeptide comprising an amino acid sequence having at least 30, 50 or 100 contiguous amino acids from an amino acid sequence set forth in the Sequence Listing, or an isolated polypeptide comprising an amino acid sequence having at least 30, 50 or 100 contiguous amino acids truncated or deleted from an amino acid sequence set forth in the Sequence Listing. Preferred fragments are biologically active fragments that mediate the biological activity of polypeptides and polynucleotides of the genes set forth in Table I, including those with a similar activity or an improved activity, or with a decreased undesirable activity. Also preferred are those fragments that are antigenic or immunogenic in an animal, especially in a human.

Fragments of a polypeptide of the invention may be employed for producing the corresponding full-length polypeptide by peptide synthesis; therefore, these variants may be employed as intermediates for producing the full-length polypeptides of the invention. A polypeptide of the present invention may be in the form of the "mature" protein or may be a

part of a larger protein such as a precursor or a fusion protein. It is often advantageous to include an additional amino acid sequence that contains secretory or leader sequences, pro-sequences, sequences that aid in purification, for instance multiple histidine residues, or an additional sequence for stability during recombinant production.

Polypeptides of the present invention can be prepared in any suitable manner, for instance by isolation form naturally occurring sources, from genetically engineered host cells comprising expression systems (*vide infra*) or by chemical synthesis, using for instance automated peptide synthesizers, or a combination of such methods. Means for preparing such polypeptides are well understood in the art.

In a further aspect, the present invention relates to polynucleotides of the genes set forth in Table I. Such polynucleotides include:

(a) an isolated polynucleotide comprising a polynucleotide sequence having at least 95%, 96%, 97%, 98%, or 99% identity to a polynucleotide sequence set forth in the Sequence Listing;

(b) an isolated polynucleotide comprising a polynucleotide set forth in the Sequence Listing;

(c) an isolated polynucleotide having at least 95%, 96%, 97%, 98%, or 99% identity to a polynucleotide set forth in the Sequence Listing;

(d) an isolated polynucleotide set forth in the Sequence Listing;

(e) an isolated polynucleotide comprising a polynucleotide sequence encoding a polypeptide sequence having at least 95%, 96%, 97%, 98%, or 99% identity to a polypeptide sequence set forth in the Sequence Listing;

(f) an isolated polynucleotide comprising a polynucleotide sequence encoding a polypeptide set forth in the Sequence Listing;

(g) an isolated polynucleotide having a polynucleotide sequence encoding a polypeptide sequence having at least 95%, 96%, 97%, 98%, or 99% identity to a polypeptide sequence set forth in the Sequence Listing;

(h) an isolated polynucleotide encoding a polypeptide set forth in the Sequence Listing;

(i) an isolated polynucleotide having or comprising a polynucleotide sequence that has an Identity Index of 0.95, 0.96, 0.97, 0.98, or 0.99 compared to a polynucleotide sequence set forth in the Sequence Listing;

(j) an isolated polynucleotide having or comprising a polynucleotide sequence encoding a polypeptide sequence that has an Identity Index of 0.95, 0.96, 0.97, 0.98, or 0.99 compared to a polypeptide sequence set forth in the Sequence Listing; and

polynucleotides that are fragments and variants of the above mentioned polynucleotides or that are complementary to above mentioned polynucleotides, over the entire length thereof.

Preferred fragments of polynucleotides of the present invention include an isolated polynucleotide comprising an nucleotide sequence having at least 15, 30, 50 or 100 contiguous nucleotides from a sequence set forth in the Sequence Listing, or an isolated polynucleotide comprising a sequence having at least 30, 50 or 100 contiguous nucleotides truncated or deleted from a sequence set forth in the Sequence Listing.

Preferred variants of polynucleotides of the present invention include splice variants, allelic variants, and polymorphisms, including polynucleotides having one or more single nucleotide polymorphisms (SNPs).

Polynucleotides of the present invention also include polynucleotides encoding polypeptide variants that comprise an amino acid sequence set forth in the Sequence Listing and in which several, for instance from 50 to 30, from 30 to 20, from 20 to 10, from 10 to 5, from 5 to 3, from 3 to 2, from 2 to 1 or 1 amino acid residues are substituted, deleted or added, in any combination.

In a further aspect, the present invention provides polynucleotides that are RNA transcripts of the DNA sequences of the present invention. Accordingly, there is provided an RNA polynucleotide that:

(a) comprises an RNA transcript of the DNA sequence encoding a polypeptide set forth in the Sequence Listing;

(b) is a RNA transcript of a DNA sequence encoding a polypeptide set forth in the Sequence Listing;

(c) comprises an RNA transcript of a DNA sequence set forth in the Sequence Listing; or

(d) is a RNA transcript of a DNA sequence set forth in the Sequence Listing; and RNA polynucleotides that are complementary thereto.

The polynucleotide sequences set forth in the Sequence Listing show homology with the polynucleotide sequences set forth in Table II. A polynucleotide sequence set forth in the Sequence Listing is a cDNA sequence that encodes a polypeptide set forth in the Sequence Listing. A polynucleotide sequence encoding a polypeptide set forth in the Sequence Listing may be identical to a polypeptide encoding a sequence set forth in the Sequence Listing or it may be a sequence other than a sequence set forth in the Sequence Listing, which, as a result of the redundancy (degeneracy) of the genetic code, also encodes a polypeptide set forth in the Sequence Listing. A polypeptide of a sequence set forth in the Sequence Listingis related to other proteins of the gene families set forth in Table II, having

homology and/or structural similarity with the polypeptides set forth in Table II. Preferred polypeptides and polynucleotides of the present invention are expected to have, *inter alia*, similar biological functions/properties to their homologous polypeptides and polynucleotides. Furthermore, preferred polypeptides and polynucleotides of the present invention have at least one activity of the genes set forth in Table I.

Polynucleotides of the present invention may be obtained using standard cloning and screening techniques from a cDNA library derived from mRNA from the tissues set forth in Table IV (see for instance, Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1989)). Polynucleotides of the invention can also be obtained from natural sources such as genomic DNA libraries or can be synthesized using well known and commercially available techniques.

When polynucleotides of the present invention are used for the recombinant production of polypeptides of the present invention, the polynucleotide may include the coding sequence for the mature polypeptide, by itself, or the coding sequence for the mature polypeptide in reading frame with other coding sequences, such as those encoding a leader or secretory sequence, a pre-, or pro- or prepro- protein sequence, or other fusion peptide portions. For example, a marker sequence that facilitates purification of the fused polypeptide can be encoded. In certain preferred embodiments of this aspect of the invention, the marker sequence is a hexa-histidine peptide, as provided in the pQE vector (Qiagen, Inc.) and described in Gentz *et al.*, Proc Natl Acad Sci USA (1989) 86:821-824, or is an HA tag. A polynucleotide may also contain non-coding 5' and 3' sequences, such as transcribed, non-translated sequences, splicing and polyadenylation signals, ribosome binding sites and sequences that stabilize mRNA.

Polynucleotides that are identical, or have sufficient identity to a polynucleotide sequence set forth in the Sequence Listing, may be used as hybridization probes for cDNA and genomic DNA or as primers for a nucleic acid amplification reaction (for instance, PCR). Such probes and primers may be used to isolate full-length cDNAs and genomic clones encoding polypeptides of the present invention and to isolate cDNA and genomic clones of other genes (including genes encoding paralogs from human sources and orthologs and paralogs from other species) that have a high sequence similarity to sequences set forth in the Sequence Listing, typically at least 95% identity. Preferred probes and primers will generally comprise at least 15 nucleotides, preferably, at least 30 nucleotides and may have at least 50, if not at least 100 nucleotides. Particularly preferred probes will have between

30 and 50 nucleotides. Particularly preferred primers will have between 20 and 25 nucleotides.

A polynucleotide encoding a polypeptide of the present invention, including homologs from other species, may be obtained by a process comprising the steps of screening a library under stringent hybridization conditions with a labeled probe having a sequence set forth in the Sequence Listing or a fragment thereof, preferably of at least 15 nucleotides; and isolating full-length cDNA and genomic clones containing the polynucleotide sequence set forth in the Sequence Listing. Such hybridization techniques are well known to the skilled artisan. Preferred stringent hybridization conditions include overnight incubation at 42°C in a solution comprising: 50% formamide, 5xSSC (150mM NaCl, 15mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10 % dextran sulfate, and 20 microgram/ml denatured, sheared salmon sperm DNA; followed by washing the filters in 0.1x SSC at about 65°C. Thus the present invention also includes isolated polynucleotides, preferably with a nucleotide sequence of at least 100, obtained by screening a library under stringent hybridization conditions with a labeled probe having the sequence set forth in the Sequence Listing or a fragment thereof, preferably of at least 15 nucleotides.

The skilled artisan will appreciate that, in many cases, an isolated cDNA sequence will be incomplete, in that the region coding for the polypeptide does not extend all the way through to the 5' terminus. This is a consequence of reverse transcriptase, an enzyme with inherently low "processivity" (a measure of the ability of the enzyme to remain attached to the template during the polymerisation reaction), failing to complete a DNA copy of the mRNA template during first strand cDNA synthesis.

There are several methods available and well known to those skilled in the art to obtain full-length cDNAs, or extend short cDNAs, for example those based on the method of Rapid Amplification of cDNA ends (RACE) (see, for example, Frohman et al., Proc Nat Acad Sci USA 85, 8998-9002, 1988). Recent modifications of the technique, exemplified by the Marathon (trade mark) technology (Clontech Laboratories Inc.) for example, have significantly simplified the search for longer cDNAs. In the Marathon (trade mark) technology, cDNAs have been prepared from mRNA extracted from a chosen tissue and an 'adaptor' sequence ligated onto each end. Nucleic acid amplification (PCR) is then carried out to amplify the "missing" 5' end of the cDNA using a combination of gene specific and adaptor specific oligonucleotide primers. The PCR reaction is then repeated using 'nested' primers, that is, primers designed to anneal within the amplified product (typically an adapter specific primer that anneals further 3' in the adaptor sequence and a gene specific

primer that anneals further 5' in the known gene sequence). The products of this reaction can then be analyzed by DNA sequencing and a full-length cDNA constructed either by joining the product directly to the existing cDNA to give a complete sequence, or carrying out a separate full-length PCR using the new sequence information for the design of the 5' primer.

Recombinant polypeptides of the present invention may be prepared by processes well known in the art from genetically engineered host cells comprising expression systems. Accordingly, in a further aspect, the present invention relates to expression systems comprising a polynucleotide or polynucleotides of the present invention, to host cells which are genetically engineered with such expression systems and to the production of polypeptides of the invention by recombinant techniques. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention.

For recombinant production, host cells can be genetically engineered to incorporate expression systems or portions thereof for polynucleotides of the present invention. Polynucleotides may be introduced into host cells by methods described in many standard laboratory manuals, such as Davis et al., Basic Methods in Molecular Biology (1986) and Sambrook *et al.*(*ibid*). Preferred methods of introducing polynucleotides into host cells include, for instance, calcium phosphate transfection, DEAE-dextran mediated transfection, transvection, micro-injection, cationic lipid-mediated transfection, electroporation, transduction, scrape loading, ballistic introduction or infection.

Representative examples of appropriate hosts include bacterial cells, such as *Streptococci*, *Staphylococci*, *E. coli*, *Streptomyces* and *Bacillus subtilis* cells; fungal cells, such as yeast cells and *Aspergillus* cells; insect cells such as *Drosophila* S2 and *Spodoptera* Sf9 cells; animal cells such as CHO, COS, HeLa, C127, 3T3, BHK, HEK 293 and Bowes melanoma cells; and plant cells.

A great variety of expression systems can be used, for instance, chromosomal, episomal and virus-derived systems, *e.g.*, vectors derived from bacterial plasmids, from bacteriophage, from transposons, from yeast episomes, from insertion elements, from yeast chromosomal elements, from viruses such as baculoviruses, papova viruses, such as SV40, vaccinia viruses, adenoviruses, fowl pox viruses, pseudorabies viruses and retroviruses, and vectors derived from combinations thereof, such as those derived from plasmid and bacteriophage genetic elements, such as cosmids and phagemids. The expression systems may contain control regions that regulate as well as engender expression. Generally, any system or vector that is able to maintain, propagate or express a polynucleotide to produce a

polypeptide in a host may be used. The appropriate polynucleotide sequence may be inserted into an expression system by any of a variety of well-known and routine techniques, such as, for example, those set forth in Sambrook *et al.*, (*ibid*). Appropriate secretion signals may be incorporated into the desired polypeptide to allow secretion of the translated protein into the lumen of the endoplasmic reticulum, the periplasmic space or the extracellular environment. These signals may be endogenous to the polypeptide or they may be heterologous signals.

If a polypeptide of the present invention is to be expressed for use in screening assays, it is generally preferred that the polypeptide be produced at the surface of the cell. In this event, the cells may be harvested prior to use in the screening assay. If the polypeptide is secreted into the medium, the medium can be recovered in order to recover and purify the polypeptide. If produced intracellularly, the cells must first be lysed before the polypeptide is recovered.

Polypeptides of the present invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Most preferably, high performance liquid chromatography is employed for purification. Well known techniques for refolding proteins may be employed to regenerate active conformation when the polypeptide is denatured during intracellular synthesis, isolation and/or purification.

Polynucleotides of the present invention may be used as diagnostic reagents, through detecting mutations in the associated gene. Detection of a mutated form of a gene is characterized by the polynucleotides set forth in the Sequence Listing in the cDNA or genomic sequence and which is associated with a dysfunction. Will provide a diagnostic tool that can add to, or define, a diagnosis of a disease, or susceptibility to a disease, which results from under-expression, over-expression or altered spatial or temporal expression of the gene. Individuals carrying mutations in the gene may be detected at the DNA level by a variety of techniques well known in the art.

Nucleic acids for diagnosis may be obtained from a subject's cells, such as from blood, urine, saliva, tissue biopsy or autopsy material. The genomic DNA may be used directly for detection or it may be amplified enzymatically by using PCR, preferably RT-PCR, or other amplification techniques prior to analysis. RNA or cDNA may also be used in similar fashion. Deletions and insertions can be detected by a change in size of the amplified product in comparison to the normal genotype. Point mutations can be identified

by hybridizing amplified DNA to labeled nucleotide sequences of the genes set forth in Table I. Perfectly matched sequences can be distinguished from mismatched duplexes by RNase digestion or by differences in melting temperatures. DNA sequence difference may also be detected by alterations in the electrophoretic mobility of DNA fragments in gels, with or without denaturing agents, or by direct DNA sequencing (see, for instance, Myers *et al.*, Science (1985) 230:1242). Sequence changes at specific locations may also be revealed by nuclease protection assays, such as RNase and S1 protection or the chemical cleavage method (see Cotton *et al.*, Proc Natl Acad Sci USA (1985) 85: 4397-4401).

An array of oligonucleotides probes comprising polynucleotide sequences or fragments thereof of the genes set forth in Table I can be constructed to conduct efficient screening of *e.g.*, genetic mutations. Such arrays are preferably high density arrays or grids. Array technology methods are well known and have general applicability and can be used to address a variety of questions in molecular genetics including gene expression, genetic linkage, and genetic variability, see, for example, M. Chee et al., Science, 274, 610-613 (1996) and other references cited therein.

Detection of abnormally decreased or increased levels of polypeptide or mRNA expression may also be used for diagnosing or determining susceptibility of a subject to a disease of the invention. Decreased or increased expression can be measured at the RNA level using any of the methods well known in the art for the quantitation of polynucleotides, such as, for example, nucleic acid amplification, for instance PCR, RT-PCR, RNase protection, Northern blotting and other hybridization methods. Assay techniques that can be used to determine levels of a protein, such as a polypeptide of the present invention, in a sample derived from a host are well-known to those of skill in the art. Such assay methods include radio-immunoassays, competitive-binding assays, Western Blot analysis and ELISA assays.

Thus in another aspect, the present invention relates to a diagnostic kit comprising:
(a) a polynucleotide of the present invention, preferably the nucleotide sequence set forth in the Sequence Listing , or a fragment or an RNA transcript thereof;
(b) a nucleotide sequence complementary to that of (a);
(c) a polypeptide of the present invention, preferably the polypeptide set forth in the Sequence Listing or a fragment thereof; or
(d) an antibody to a polypeptide of the present invention, preferably to the polypeptide set forth in the Sequence Listing .

It will be appreciated that in any such kit, (a), (b), (c) or (d) may comprise a substantial component. Such a kit will be of use in diagnosing a disease or susceptibility to a disease, particularly diseases of the invention, amongst others.

The polynucleotide sequences of the present invention are valuable for chromosome localisation studies. The sequences set forth in the Sequence Listing are specifically targeted to, and can hybridize with, a particular location on an individual human chromosome. The mapping of relevant sequences to chromosomes according to the present invention is an important first step in correlating those sequences with gene associated disease. Once a sequence has been mapped to a precise chromosomal location, the physical position of the sequence on the chromosome can be correlated with genetic map data. Such data are found in, for example, V. McKusick, Mendelian Inheritance in Man (available on-line through Johns Hopkins University Welch Medical Library). The relationship between genes and diseases that have been mapped to the same chromosomal region are then identified through linkage analysis (co-inheritance of physically adjacent genes). Precise human chromosomal localisations for a genomic sequence (gene fragment etc.) can be determined using Radiation Hybrid (RH) Mapping (Walter, M. Spillett, D., Thomas, P., Weissenbach, J., and Goodfellow, P., (1994) A method for constructing radiation hybrid maps of whole genomes, Nature Genetics 7, 22-28). A number of RH panels are available from Research Genetics (Huntsville, AL, USA) e.g. the GeneBridge4 RH panel (Hum Mol Genet 1996 Mar;5(3):339-46 A radiation hybrid map of the human genome. Gyapay G, Schmitt K, Fizames C, Jones H, Vega-Czarny N, Spillett D, Muselet D, Prud'Homme JF, Dib C, Auffray C, Morissette J, Weissenbach J, Goodfellow PN). To determine the chromosomal location of a gene using this panel, 93 PCRs are performed using primers designed from the gene of interest on RH DNAs. Each of these DNAs contains random human genomic fragments maintained in a hamster background (human / hamster hybrid cell lines). These PCRs result in 93 scores indicating the presence or absence of the PCR product of the gene of interest. These scores are compared with scores created using PCR products from genomic sequences of known location. This comparison is conducted at http://www.genome.wi.mit.edu/.

The polynucleotide sequences of the present invention are also valuable tools for tissue expression studies. Such studies allow the determination of expression patterns of polynucleotides of the present invention which may give an indication as to the expression patterns of the encoded polypeptides in tissues, by detecting the mRNAs that encode them. The techniques used are well known in the art and include in situ hydridization techniques to clones arrayed on a grid, such as cDNA microarray hybridization (Schena *et al*, Science, 270, 467-470, 1995 and Shalon *et al*, Genome Res, 6, 639-645, 1996) and nucleotide amplification techniques such as PCR. A preferred method uses the TAQMAN (Trade mark) technology available from Perkin Elmer. Results from these studies can provide an

indication of the normal function of the polypeptide in the organism. In addition, comparative studies of the normal expression pattern of mRNAs with that of mRNAs encoded by an alternative form of the same gene (for example, one having an alteration in polypeptide coding potential or a regulatory mutation) can provide valuable insights into the role of the polypeptides of the present invention, or that of inappropriate expression thereof in disease. Such inappropriate expression may be of a temporal, spatial or simply quantitative nature.

A further aspect of the present invention relates to antibodies. The polypeptides of the invention or their fragments, or cells expressing them, can be used as immunogens to produce antibodies that are immunospecific for polypeptides of the present invention. The term "immunospecific" means that the antibodies have substantially greater affinity for the polypeptides of the invention than their affinity for other related polypeptides in the prior art.

Antibodies generated against polypeptides of the present invention may be obtained by administering the polypeptides or epitope-bearing fragments, or cells to an animal, preferably a non-human animal, using routine protocols. For preparation of monoclonal antibodies, any technique which provides antibodies produced by continuous cell line cultures can be used. Examples include the hybridoma technique (Kohler, G. and Milstein, C., Nature (1975) 256:495-497), the trioma technique, the human B-cell hybridoma technique (Kozbor *et al.*, Immunology Today (1983) 4:72) and the EBV-hybridoma technique (Cole *et al.*, Monoclonal Antibodies and Cancer Therapy, 77-96, Alan R. Liss, Inc., 1985).

Techniques for the production of single chain antibodies, such as those described in U.S. Patent No. 4,946,778, can also be adapted to produce single chain antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms, including other mammals, may be used to express humanized antibodies.

The above-described antibodies may be employed to isolate or to identify clones expressing the polypeptide or to purify the polypeptides by affinity chromatography. Antibodies against polypeptides of the present invention may also be employed to treat diseases of the invention, amongst others.

Polypeptides and polynucleotides of the present invention may also be used as vaccines. Accordingly, in a further aspect, the present invention relates to a method for inducing an immunological response in a mammal that comprises inoculating the mammal with a polypeptide of the present invention, adequate to produce antibody and/or T cell immune response, including, for example, cytokine-producing T cells or cytotoxic T cells,

to protect said animal from disease, whether that disease is already established within the individual or not. An immunological response in a mammal may also be induced by a method comprises delivering a polypeptide of the present invention *via* a vector directing expression of the polynucleotide and coding for the polypeptide *in vivo* in order to induce such an immunological response to produce antibody to protect said animal from diseases of the invention. One way of administering the vector is by accelerating it into the desired cells as a coating on particles or otherwise. Such nucleic acid vector may comprise DNA, RNA, a modified nucleic acid, or a DNA/RNA hybrid. For use a vaccine, a polypeptide or a nucleic acid vector will be normally provided as a vaccine formulation (composition). The formulation may further comprise a suitable carrier. Since a polypeptide may be broken down in the stomach, it is preferably administered parenterally (for instance, subcutaneous, intra-muscular, intravenous, or intra-dermal injection). Formulations suitable for parenteral administration include aqueous and non-aqueous sterile injection solutions that may contain anti-oxidants, buffers, bacteriostats and solutes that render the formulation instonic with the blood of the recipient; and aqueous and non-aqueous sterile suspensions that may include suspending agents or thickening agents. The formulations may be presented in unit-dose or multi-dose containers, for example, sealed ampoules and vials and may be stored in a freeze-dried condition requiring only the addition of the sterile liquid carrier immediately prior to use. The vaccine formulation may also include adjuvant systems for enhancing the immunogenicity of the formulation, such as oil-in water systems and other systems known in the art. The dosage will depend on the specific activity of the vaccine and can be readily determined by routine experimentation.

Polypeptides of the present invention have one or more biological functions that are of relevance in one or more disease states, in particular the diseases of the invention hereinbefore mentioned. It is therefore useful to identify compounds that stimulate or inhibit the function or level of the polypeptide. Accordingly, in a further aspect, the present invention provides for a method of screening compounds to identify those that stimulate or inhibit the function or level of the polypeptide. Such methods identify agonists or antagonists that may be employed for therapeutic and prophylactic purposes for such diseases of the invention as hereinbefore mentioned. Compounds may be identified from a variety of sources, for example, cells, cell-free preparations, chemical libraries, collections of chemical compounds, and natural product mixtures. Such agonists or antagonists so-identified may be natural or modified substrates, ligands, receptors, enzymes, etc., as the case may be, of the polypeptide; a structural or functional mimetic thereof (see Coligan *et al.*, Current Protocols in Immunology 1(2):Chapter 5 (1991)) or a small molecule. Such

small molecules preferably have a molecular weight below 2,000 daltons, more preferably between 300 and 1,000 daltons, and most preferably between 400 and 700 daltons. It is preferred that these small molecules are organic molecules.

The screening method may simply measure the binding of a candidate compound to the polypeptide, or to cells or membranes bearing the polypeptide, or a fusion protein thereof, by means of a label directly or indirectly associated with the candidate compound. Alternatively, the screening method may involve measuring or detecting (qualitatively or quantitatively) the competitive binding of a candidate compound to the polypeptide against a labeled competitor (*e.g.* agonist or antagonist). Further, these screening methods may test whether the candidate compound results in a signal generated by activation or inhibition of the polypeptide, using detection systems appropriate to the cells bearing the polypeptide. Inhibitors of activation are generally assayed in the presence of a known agonist and the effect on activation by the agonist by the presence of the candidate compound is observed. Further, the screening methods may simply comprise the steps of mixing a candidate compound with a solution containing a polypeptide of the present invention, to form a mixture, measuring an activity of the genes set forth in Table I in the mixture, and comparing activity of the mixture of the genes set forth in Table I to a control mixture which contains no candidate compound.

Polypeptides of the present invention may be employed in conventional low capacity screening methods and also in high-throughput screening (HTS) formats. Such HTS formats include not only the well-established use of 96- and, more recently, 384-well micotiter plates but also emerging methods such as the nanowell method described by Schullek et al, Anal Biochem., 246, 20-29, (1997).

Fusion proteins, such as those made from Fc portion and polypeptide of the genes set forth in Table I, as hereinbefore described, can also be used for high-throughput screening assays to identify antagonists for the polypeptide of the present invention (see D. Bennett *et al.*, J Mol Recognition, 8:52-58 (1995); and K. Johanson *et al.*, J Biol Chem, 270(16):9459-9471 (1995)).

The polynucleotides, polypeptides and antibodies to the polypeptide of the present invention may also be used to configure screening methods for detecting the effect of added compounds on the production of mRNA and polypeptide in cells. For example, an ELISA assay may be constructed for measuring secreted or cell associated levels of polypeptide using monoclonal and polyclonal antibodies by standard methods known in the art. This can be used to discover agents that may inhibit or enhance the production of polypeptide (also called antagonist or agonist, respectively) from suitably manipulated cells or tissues.

A polypeptide of the present invention may be used to identify membrane bound or soluble receptors, if any, through standard receptor binding techniques known in the art. These include, but are not limited to, ligand binding and crosslinking assays in which the polypeptide is labeled with a radioactive isotope (for instance, ^{125}I), chemically modified (for instance, biotinylated), or fused to a peptide sequence suitable for detection or purification, and incubated with a source of the putative receptor (cells, cell membranes, cell supernatants, tissue extracts, bodily fluids). Other methods include biophysical techniques such as surface plasmon resonance and spectroscopy. These screening methods may also be used to identify agonists and antagonists of the polypeptide that compete with the binding of the polypeptide to its receptors, if any. Standard methods for conducting such assays are well understood in the art.

Examples of antagonists of polypeptides of the present invention include antibodies or, in some cases, oligonucleotides or proteins that are closely related to the ligands, substrates, receptors, enzymes, etc., as the case may be, of the polypeptide, *e.g.*, a fragment of the ligands, substrates, receptors, enzymes, etc.; or a small molecule that bind to the polypeptide of the present invention but do not elicit a response, so that the activity of the polypeptide is prevented.

Screening methods may also involve the use of transgenic technology and the genes set forth in Table I. The art of constructing transgenic animals is well established. For example, the genes set forth in Table I may be introduced through microinjection into the male pronucleus of fertilized oocytes, retroviral transfer into pre- or post-implantation *embryos, or injection of genetically modified, such as by electroporation, embryonic stem* cells into host blastocysts. Particularly useful transgenic animals are so-called "knock-in" animals in which an animal gene is replaced by the human equivalent within the genome of that animal. Knock-in transgenic animals are useful in the drug discovery process, for target validation, where the compound is specific for the human target. Other useful transgenic animals are so-called "knock-out" animals in which the expression of the animal ortholog of a polypeptide of the present invention and encoded by an endogenous DNA sequence in a cell is partially or completely annulled. The gene knock-out may be targeted to specific cells or tissues, may occur only in certain cells or tissues as a consequence of the limitations of the technology, or may occur in all, or substantially all, cells in the animal. Transgenic animal technology also offers a whole animal expression-cloning system in which introduced genes are expressed to give large amounts of polypeptides of the present invention

Screening kits for use in the above described methods form a further aspect of the present invention. Such screening kits comprise:

(a) a polypeptide of the present invention;

(b) a recombinant cell expressing a polypeptide of the present invention;

(c) a cell membrane expressing a polypeptide of the present invention; or

(d) an antibody to a polypeptide of the present invention;

which polypeptide is preferably that set forth in the Sequence Listing.

It will be appreciated that in any such kit, (a), (b), (c) or (d) may comprise a substantial component.

Glossary

The following definitions are provided to facilitate understanding of certain terms used frequently hereinbefore.

"Antibodies" as used herein includes polyclonal and monoclonal antibodies, chimeric, single chain, and humanized antibodies, as well as Fab fragments, including the products of an

Fab or other immunoglobulin expression library.

"Isolated" means altered "by the hand of man" from its natural state, *i.e.*, if it occurs in nature, it has been changed or removed from its original environment, or both. For example, a polynucleotide or a polypeptide naturally present in a living organism is not "isolated," but the same polynucleotide or polypeptide separated from the coexisting materials of its natural state is "isolated", as the term is employed herein. Moreover, a polynucleotide or polypeptide that is introduced into an organism by transformation, genetic manipulation or by any other recombinant method is "isolated" even if it is still present in said organism, which organism may be living or non-living.

"Secreted protein activity or secreted polypeptide activity" or "biological activity of the secreted protein or secreted polypeptide" refers to the metabolic or physiologic function of said secreted protein including similar activities or improved activities or these activities with decreased undesirable side-effects. Also included are antigenic and immunogenic activities of said secreted protein.

"Secreted protein gene" refers to a polynucleotide comprising any of the attached nucleotide sequences or allelic variants thereof and/or their complements.

"Polynucleotide" generally refers to any polyribonucleotide (RNA) or polydeoxribonucleotide (DNA), which may be unmodified or modified RNA or DNA. "Polynucleotides" include, without limitation, single- and double-stranded DNA, DNA that

is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, "polynucleotide" refers to triple-stranded regions comprising RNA or DNA or both RNA and DNA. The term "polynucleotide" also includes DNAs or RNAs containing one or more modified bases and DNAs or RNAs with backbones modified for stability or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications may be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically or metabolically modified forms of polynucleotides as typically found in nature, as well as the chemical forms of DNA and RNA characteristic of viruses and cells. "Polynucleotide" also embraces relatively short polynucleotides, often referred to as oligonucleotides.

"Polypeptide" refers to any polypeptide comprising two or more amino acids joined to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres. "Polypeptide" refers to both short chains, commonly referred to as peptides, oligopeptides or oligomers, and to longer chains, generally referred to as proteins. Polypeptides may contain amino acids other than the 20 gene-encoded amino acids. "Polypeptides" include amino acid sequences modified either by natural processes, such as post-translational processing, or by chemical modification techniques that are well known in the art. Such modifications are well described in basic texts and in more detailed monographs, as well as in a voluminous research literature. Modifications may occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present to the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be branched as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched and branched cyclic polypeptides may result from post-translation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, biotinylation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphotidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cystine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation,

myristoylation, oxidation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination (see, for instance, Proteins - Structure and Molecular Properties, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York, 1993; Wold, F., Post-translational Protein Modifications: Perspectives and Prospects, 1-12, in Post-translational Covalent Modification of Proteins, B. C. Johnson, Ed., Academic Press, New York, 1983; Seifter *et al.*, "Analysis for protein modifications and nonprotein cofactors", Meth Enzymol, 182, 626-646, 1990, and Rattan *et al.*, "Protein Synthesis: Post-translational Modifications and Aging", Ann NY Acad Sci, 663, 48-62, 1992).

"Fragment" of a polypeptide sequence refers to a polypeptide sequence that is shorter than the reference sequence but that retains essentially the same biological function or activity as the reference polypeptide. "Fragment" of a polynucleotide sequence refers to a polynucleotide sequence that is shorter than the reference sequence set forth in the Sequence Listing.

"Variant" refers to a polynucleotide or polypeptide that differs from a reference polynucleotide or polypeptide, but retains the essential properties thereof. A typical variant of a polynucleotide differs in nucleotide sequence from the reference polynucleotide. Changes in the nucleotide sequence of the variant may or may not alter the amino acid sequence of a polypeptide encoded by the reference polynucleotide. Nucleotide changes may result in amino acid substitutions, additions, deletions, fusions and truncations in the polypeptide encoded by the reference sequence, as discussed below. A typical variant of a polypeptide differs in amino acid sequence from the reference polypeptide. Generally, alterations are limited so that the sequences of the reference polypeptide and the variant are closely similar overall and, in many regions, identical. A variant and reference polypeptide may differ in amino acid sequence by one or more substitutions, insertions, deletions in any combination. A substituted or inserted amino acid residue may or may not be one encoded by the genetic code. Typical conservative substitutions include Gly, Ala; Val, Ile, Leu; Asp, Glu; Asn, Gln; Ser, Thr; Lys, Arg; and Phe and Tyr. A variant of a polynucleotide or polypeptide may be naturally occurring such as an allele, or it may be a variant that is not known to occur naturally. Non-naturally occurring variants of polynucleotides and polypeptides may be made by mutagenesis techniques or by direct synthesis. Also included as variants are polypeptides having one or more post-translational modifications, for instance glycosylation, phosphorylation, methylation, ADP ribosylation and the like. Embodiments include methylation of the N-terminal amino acid, phosphorylations of serines and threonines and modification of C-terminal glycines.

"Allele" refers to one of two or more alternative forms of a gene occurring at a given locus in the genome.

"Polymorphism" refers to a variation in nucleotide sequence (and encoded polypeptide sequence, if relevant) at a given position in the genome within a population.

"Single Nucleotide Polymorphism" (SNP) refers to the occurrence of nucleotide variability at a single nucleotide position in the genome, within a population. An SNP may occur within a gene or within intergenic regions of the genome. SNPs can be assayed using Allele Specific Amplification (ASA). For the process at least 3 primers are required. A common primer is used in reverse complement to the polymorphism being assayed. This common primer can be between 50 and 1500 bps from the polymorphic base. The other two (or more) primers are identical to each other except that the final 3' base wobbles to match one of the two (or more) alleles that make up the polymorphism. Two (or more) PCR reactions are then conducted on sample DNA, each using the common primer and one of the Allele Specific Primers.

"Splice Variant" as used herein refers to cDNA molecules produced from RNA molecules initially transcribed from the same genomic DNA sequence but which have undergone alternative RNA splicing. Alternative RNA splicing occurs when a primary RNA transcript undergoes splicing, generally for the removal of introns, which results in the production of more than one mRNA molecule each of that may encode different amino acid sequences. The term splice variant also refers to the proteins encoded by the above cDNA molecules.

"Identity" reflects a relationship between two or more polypeptide sequences or two or more polynucleotide sequences, determined by comparing the sequences. In general, identity refers to an exact nucleotide to nucleotide or amino acid to amino acid correspondence of the two polynucleotide or two polypeptide sequences, respectively, over the length of the sequences being compared.

"% Identity" - For sequences where there is not an exact correspondence, a "% identity" may be determined. In general, the two sequences to be compared are aligned to give a maximum correlation between the sequences. This may include inserting "gaps" in either one or both sequences, to enhance the degree of alignment. A % identity may be determined over the whole length of each of the sequences being compared (so-called global alignment), that is particularly suitable for sequences of the same or very similar length, or over shorter, defined lengths (so-called local alignment), that is more suitable for sequences of unequal length.

"Similarity" is a further, more sophisticated measure of the relationship between two polypeptide sequences. In general, "similarity" means a comparison between the amino acids of two polypeptide chains, on a residue by residue basis, taking into account not only exact correspondences between a between pairs of residues, one from each of the sequences being compared (as for identity) but also, where there is not an exact correspondence, whether, on an evolutionary basis, one residue is a likely substitute for the other. This likelihood has an associated "score" from which the "% similarity" of the two sequences can then be determined.

Methods for comparing the identity and similarity of two or more sequences are well known in the art. Thus for instance, programs available in the Wisconsin Sequence Analysis Package, version 9.1 (Devereux J et al, Nucleic Acids Res, 12, 387-395, 1984, available from Genetics Computer Group, Madison, Wisconsin, USA), for example the programs BESTFIT and GAP, may be used to determine the % identity between two polynucleotides and the % identity and the % similarity between two polypeptide sequences. BESTFIT uses the "local homology" algorithm of Smith and Waterman (J Mol Biol, 147,195-197, 1981, Advances in Applied Mathematics, 2, 482-489, 1981) and finds the best single region of similarity between two sequences. BESTFIT is more suited to comparing two polynucleotide or two polypeptide sequences that are dissimilar in length, the program assuming that the shorter sequence represents a portion of the longer. In comparison, GAP aligns two sequences, finding a "maximum similarity", according to the algorithm of Neddleman and Wunsch (J Mol Biol, 48, 443-453, 1970). GAP is more suited to comparing sequences that are approximately the same length and an alignment is expected over the entire length. Preferably, the parameters "Gap Weight" and "Length Weight" used in each program are 50 and 3, for polynucleotide sequences and 12 and 4 for polypeptide sequences, respectively. Preferably, % identities and similarities are determined when the two sequences being compared are optimally aligned.

Other programs for determining identity and/or similarity between sequences are also known in the art, for instance the BLAST family of programs (Altschul S F et al, J Mol Biol, 215, 403-410, 1990, Altschul S F et al, Nucleic Acids Res., 25:389-3402, 1997, available from the National Center for Biotechnology Information (NCBI), Bethesda, Maryland, USA and accessible through the home page of the NCBI at www.ncbi.nlm.nih.gov) and FASTA (Pearson W R, Methods in Enzymology, 183, 63-99, 1990; Pearson W R and Lipman D J, Proc Nat Acad Sci USA, 85, 2444-2448,1988, available as part of the Wisconsin Sequence Analysis Package).

Preferably, the BLOSUM62 amino acid substitution matrix (Henikoff S and Henikoff J G, Proc. Nat. Acad Sci. USA, 89, 10915-10919, 1992) is used in polypeptide sequence comparisons including where nucleotide sequences are first translated into amino acid sequences before comparison.

Preferably, the program BESTFIT is used to determine the % identity of a query polynucleotide or a polypeptide sequence with respect to a reference polynucleotide or a polypeptide sequence, the query and the reference sequence being optimally aligned and the parameters of the program set at the default value, as hereinbefore described.

"Identity Index" is a measure of sequence relatedness which may be used to compare a candidate sequence (polynucleotide or polypeptide) and a reference sequence. Thus, for instance, a candidate polynucleotide sequence having, for example, an Identity Index of 0.95 compared to a reference polynucleotide sequence is identical to the reference sequence except that the candidate polynucleotide sequence may include on average up to five differences per each 100 nucleotides of the reference sequence. Such differences are selected from the group consisting of at least one nucleotide deletion, substitution, including transition and transversion, or insertion. These differences may occur at the 5' or 3' terminal positions of the reference polynucleotide sequence or anywhere between these terminal positions, interspersed either individually among the nucleotides in the reference sequence or in one or more contiguous groups within the reference sequence. In other words, to obtain a polynucleotide sequence having an Identity Index of 0.95 compared to a reference polynucleotide sequence, an average of up to 5 in every 100 of the nucleotides of the in the reference sequence may be deleted, substituted or inserted, or any combination thereof, as hereinbefore described. The same applies *mutatis mutandis* for other values of the Identity Index, for instance 0.96, 0.97, 0.98 and 0.99.

Similarly, for a polypeptide, a candidate polypeptide sequence having, for example, an Identity Index of 0.95 compared to a reference polypeptide sequence is identical to the reference sequence except that the polypeptide sequence may include an average of up to five differences per each 100 amino acids of the reference sequence. Such differences are selected from the group consisting of at least one amino acid deletion, substitution, including conservative and non-conservative substitution, or insertion. These differences may occur at the amino- or carboxy-terminal positions of the reference polypeptide sequence or anywhere between these terminal positions, interspersed either individually among the amino acids in the reference sequence or in one or more contiguous groups within the reference sequence. In other words, to obtain a polypeptide sequence having an Identity Index of 0.95 compared to a reference polypeptide sequence, an average of up to 5

in every 100 of the amino acids in the reference sequence may be deleted, substituted or inserted, or any combination thereof, as hereinbefore described. The same applies *mutatis mutandis* for other values of the Identity Index, for instance 0.96, 0.97, 0.98 and 0.99.

The relationship between the number of nucleotide or amino acid differences and the Identity Index may be expressed in the following equation:

$$n_a \leq x_a - (x_a \bullet I),$$

in which:

n_a is the number of nucleotide or amino acid differences,

x_a is the total number of nucleotides or amino acids in a sequence set forth in the Sequence Listing,

I is the Identity Index,

• is the symbol for the multiplication operator, and

in which any non-integer product of x_a and I is rounded down to the nearest integer prior to subtracting it from x_a.

"Homolog" is a generic term used in the art to indicate a polynucleotide or polypeptide sequence possessing a high degree of sequence relatedness to a reference sequence. Such relatedness may be quantified by determining the degree of identity and/or similarity between the two sequences as hereinbefore defined. Falling within this generic term are the terms "ortholog", and "paralog". "Ortholog" refers to a polynucleotide or polypeptide that is the functional equivalent of the polynucleotide or polypeptide in another species. "Paralog" refers to a polynucleotideor polypeptide that within the same species which is functionally similar.

"Fusion protein" refers to a protein encoded by two, often unrelated, fused genes or fragments thereof. In one example, EP-A-0 464 533-A discloses fusion proteins comprising various portions of constant region of immunoglobulin molecules together with another human protein or part thereof. In many cases, employing an immunoglobulin Fc region as a part of a fusion protein is advantageous for use in therapy and diagnosis resulting in, for example, improved pharmacokinetic properties [see, *e.g.*, EP-A 0232 262]. On the other hand, for some uses it would be desirable to be able to delete the Fc part after the fusion protein has been expressed, detected and purified.

All publications and references, including but not limited to patents and patent applications, cited in this specification are herein incorporated by reference in their entirety as if each individual publication or reference were specifically and individually indicated to be incorporated by reference herein as being fully set forth. Any patent application to which

this application claims priority is also incorporated by reference herein in its entirety in the manner described above for publications and references.

Table I.

Gene Name	GSK Gene ID	Nucleic Acid SEQ ID NO's	Corresponding Protein SEQ ID NO's
sbg960509cbrecpt	960509	SEQ ID NO:1	SEQ ID NO:45
sbg614126complfH	614126	SEQ ID NO:2 SEQ ID NO:3	SEQ ID NO:46 SEQ ID NO:47
sbg120703RNase	120703	SEQ ID NO:4	SEQ ID NO:48
sbg98530TS	98530	SEQ ID NO:5 SEQ ID NO:6	SEQ ID NO:49 SEQ ID NO:50
sbg563917RDP	63917	SEQ ID NO:7 SEQ ID NO:8	SEQ ID NO:51 SEQ ID NO:52
sbg618069LRR	618069	SEQ ID NO:9 SEQ ID NO:10	SEQ ID NO:53 SEQ ID NO:54
sbg934114Relaxin	934114	SEQ ID NO:11	SEQ ID NO:55
sbg99174LOX-like	99174	SEQ ID NO:12	SEQ ID NO:56
sbg995002PIGR	995002	SEQ ID NO:13	SEQ ID NO:57
sbg1033026C1q	1033026	SEQ ID NO.14 SEQ ID NO:15	SEQ ID NO:58 SEQ ID NO:59
sbg1003675RNase	1003675	SEQ ID NO:16	SEQ ID NO:60
sbg1015258PLM	1015258	SEQ ID NO:17	SEQ ID NO:61
sbg1003328IG	1003328	SEQ ID NO:18 SEQ ID NO:19	SEQ ID NO:62 SEQ ID NO:63
sbg1020829SGLT	1020829	SEQ ID NO:20	SEQ ID NO.64
sbg1005450UDPGT	1005450	SEQ ID NO:21 SEQ ID NO:22	SEQ ID NO:65 SEQ ID NO:66
sbg1002620TIa	1002620	SEQ ID NO:23 SEQ ID NO:24	SEQ ID NO:67 SEQ ID NO:68
sbg1002620TIb	1002620	SEQ ID NO:25	SEQ ID NO:69
sbg102200MCTa	102200	SEQ ID NO:26 SEQ ID NO:27	SEQ ID NO:70 SEQ ID NO:71
sbg102200MCTb	102200	SEQ ID NO:28	SEQ ID NO:72
sbg1020380LYG	1020380	SEQ ID NO:29 SEQ ID NO:30	SEQ ID NO:73 SEQ ID NO:74
sbg1007026SGLT	1007026	SEQ ID NO:31	SEQ ID NO:75
sbg1012732GLUT	1012732	SEQ ID NO:32 SEQ ID NO:33	SEQ ID NO:76 SEQ ID NO:77
sbg1012732GLUTb	1012732	SEQ ID NO:34	SEQ ID NO:78
sbg1018172CSP	1018172	SEQ ID NO:35 SEQ ID NO:36	SEQ ID NO:79 SEQ ID NO:80
sbg1004570ERGIC	1004570	SEQ ID NO:37 SEQ ID NO:38	SEQ ID NO:81 SEQ ID NO:82
sbg1016995IGBrecpt	1016995	SEQ ID NO:39 SEQ ID NO:40	SEQ ID NO:83 SEQ ID NO:84
sbg1151bSREC	1151	SEQ ID NO:41 SEQ ID NO:42	SEQ ID NO:85 SEQ ID NO:86
sbg1399854ANK	1399854	SEQ ID NO:43 SEQ ID NO:44	SEQ ID NO:87 SEQ ID NO:88

Table II

Gene Name	Gene Family	Closest Polynucleotide by homology	Closest Polypeptide by homology	Cell Localization (by homology)
sbg960509 cbrecpt	Carbohydrate-binding receptor	GB:AC007395 Direct submitted (25-APR-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA	Mouse Kupffer cell c-type lectin receptor, gi: 7949066 Submitted (25-OCT-1996) to the DDBJ/EMBL/GenBank databases.	Membrane-bound
sbg614126 complfH	Complement factor H	SC:AL353809 Submitted (20-JAN-2001) by Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK.	Human H-factor like 1, gi:11321587 Estaller,C., Koistinen,V., Schwaeble,W., Dierich,M.P., and Weiss,E.H. J. Immunol. 146, 3190-3196 (1991)	Secreted
sbg120703 RNase	RNase	GB:AL157687 Direct Submitted (24-MAY-2000) to the EMBL/GenBank/DDBJ databases by Genoscope.	Human keratinocyte-derived RNase-like protein, geneseqp: Y44192 Submitted by INNOGENETICS NV Application number and publication date: EP-943679-A1, 22-SEP-99	Secreted
sbg98530TS	Thrombospondin type I	GB:AC027307 Submitted (30-MAR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA	Mouse RIKEN cDNA 2010109H09 gene, gi:13385092 The RIKEN Genome Exploration Research Group Phase II Team and FANTOM Consortium. Nature 409, 685-690 (2001)	Secreted
sbg563917 RDP	Renal dipeptidase	GB:AC009077 Directly submitted (03-AUG-1999) by Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA	Human putative metallopeptidase (family M19) gi:11641273 Chen,J.M., Fortunato,M. and Barrett, A.J. Submitted (02-NOV-2000) Chen J.M., MRC Molecular Enzymology Laboratory, The Babraham Institute, Babraham, Cambridge, CB2 4AT, UK	Secreted

Table II (cont).

Gene Name	Gene Family	Closest Polynucleotide by homology	Closest Polypeptide by homology	Cell Localization (by homology)
sbg618069 LRR	Leucine-rich repeat	GB:AL589765 Submitted (16-MAR-2001) by Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK.	Macaca fascicularis brain protein, gi: 9651088 Submitted (28-JUL-2000) to the DDBJ/EMBL/GenBank databases. Katsuyuki Hashimoto, National Institute of Infectious Diseases, Division of Genetic Resources; 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan	Membrane-bound
sbg934114 Relaxin	Insulin	JGI:CIT978SKB_55O6 Found at Joint Genome Institute DoE/LLNL/LBNL/LANL.	Mouse insulin-like peptide (relaxin/insulin-like protein), gi:7387805 Conklin D, Lofton-Day CE, Haldeman BA, Ching A, Whitmore TE, Lok S, Jaspers S. 1999. Genomics 60:50-56.	Secreted
sbg99174L OX-like	C-type lectin	GB:AL137062 Direct submitted (09-AUG-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK.	Mouse putative protien, gi: 12855891 The RIKEN Genome Exploration Research Group Phase II Team and FANTOM Consortium. Nature 409, 685-690 (2001)	Membrane-bound
sbg995002 PIGR	Polymeric - immublob ulin receptor (PIGR)	GB.AC027192 Direct submitted (28-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA.	Human TANGO 354 protein, geneseqp: B66271 Submitted by (MILL-) MILLENNIUM PHARM INC Application number and publication date: WO200100673-A1, 04-JAN-01	Membrane-bound
sbg103302 6C1q	C1q	GB:AL359736 Direct submitted (22-AUG-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK.	Human adipocyte-specific secretory protein, gi: 4757760 Maeda,K., Okubo,K., Shimomura,I., Funahashi,T., Matsuzawa,Y. and Matsubara,K. Biochem. Biophys. Res. Commun. 221 (2), 286-289 (1996)	Secreted

Table II (cont).

Gene Name	Gene Family	Closest Polynucleotide by homology	Closest Polypeptide by homology	Cell Localization (by homology)
sbg100367 5RNase	RNase	EMBL:CNS01RIH Found at European Molecular Biology Laboratory.	Chinchilla brevicaudata pancreatic ribonuclease, gi:133205 Van Den Berg A, Van Den Hende-Timmer L, Beintema JJ. 1976. Biochim Biophys Acta 453:400-9.	Secreted
sbg101525 8PLM	Phospholemman (PLM)	GB:AL022345 Direct submitted (10-DEC-1999) by Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK.	Human phospholemman-like protein, geneseqp:W51104 Submitted by (HUMA-) HUMAN GENOME SCI INC Application number and publication date: WO9839448-A2, 11-SEP-98	Membrane-bound
sbg100332 8IG	Immunoglobulin	EMBL:HSBA536C5 Found at European Molecular Biology Laboratory.	Human immune system molecule, geneseqp:B15536 Submitted by (INCY-) INCYTE PHARM INC Application number and publication date. WO200060080-A2, 12-OCT-00	Membrane-bound
sbg102082 9SGLT	Na+/glucose cotransporter	GB:AJ009617 Directly submitted (17-JUL-1998) by MPIMG, Abt.Lehrach, Max Planck Institut fuer Molekulare Genetik, Ihnestrasse 73, Berlin, 14195, Germany.	Oryctolagus cuniculus Na/glucose cotransporters, gi:520469 Pajor,A.M. 1994 Biochim. Biophys. Acta 1194 (2), 349-51.	Membrane-bound
sbg100545 0UDPGT	UDP-glucuronosyltransferase(UDPGT)	GB:AC016612 Submitted (04-DEC-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA	Human PRO1780 protein , geneseqp: B24025 Submitted by GENENTECH INC Application number and publication date: WO200053750-A1, 14-SEP-00	Membrane-bound
sbg100262 0TIa	Cysteine-rich secretory protein (CRISP) trypsin inhibitor	GB:AC025280 Submitted (08-MAR-2000) by Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA	Human hypothetical protein DKFZp434B044, gi: 13899332 Wiemann,S., Weil,B. et al. Genome Res. 11 (3), 422-435 (2001)	Secreted

Table II (cont).

Gene Name	Gene Family	Closest Polynucleotide by homology	Closest Polypeptide by homology	Cell Localization (by homology)
sbg100262 0TIb	Cysteine-rich secretory protein (CRISP) trypsin inhibitor	GB:AC025280 Submitted (08-MAR-2000) by Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA	Rat late gestation lung protein 1 , gi:4324682 Kaplan,F., Ledoux,P., Kassamali,F.Q., Gagnon,S., Post,M., Koehler,D., Deimling,J. and Sweezey,N.B. Am. J. Physiol. 276 (6), L1027-L1036 (1999)	Secreted
sbg102200 MCTa	Monocarboxylate cotransporter (MCT1)	GB: AC015918 Directly submitted (17-NOV-1999) by Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA.	Mouse unnamed protein product, gi:7670446 Submitted (12-APR-2000) to the DDBJ/EMBL/GenBank databases by Katsuyuki Hashimoto, National Institute of Infectious Diseases, Division of Genetic Resources; 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan	Membrane-bound
sbg102200 MCTb	Monocarboxylate cotransporter (MCT1)	GB: AC015918 Directly submitted (17-NOV-1999) by Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA.	Human solute carrier 16 (monocarboxylic acid transporters), member 8, gi:13655082 Submitted (17-APR-2001) by National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA	Membrane-bound
sbg102038 0LYG	Goose-type lysozyme G	GB:AC023965 Directly submitted (20-FEB-2000) by Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA	Lysozyme G (1,4-beta-N-acetylmuramidas E) (Goose-type lysozyme). gi:126634 Schoentgen, F., Jolles,J. and Jolles, P. Eur. J. Biochem. 123 (3), 489-497 (1982)	Secreted
sbg100702 6SGLT	Sodium-glucose cotransporter	GB:AC046167 Direct submitted (13-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141.	Human transport protein TPPT-13, geneseqp: B60093 Submitted by INCYTE GENOMICS INC Application number and publication date: WO200078953-A2, 28-DEC-00	Membrane-bound

Table II (cont).

Gene Name	Gene Family	Closest Polynucleotide by homology	Closest Polypeptide by homology	Cell Localization (by homology)
sbg101273 2GLUT	Glucose transporte r	GB:AP000350 Direct submitted (10-JUN-1999) to the DDBJ/EMBL/GenBank databases. Nobuyoshi Shimizu, Keio university, school of medicine, Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo 160-0016, Japan.	Human glucose transporter GLUT10, gi:13540598 Submitted (10-FEB-2000) Joost H.G., Institute of Pharmacology and Toxicology, Medical Faculty, Technical University of Aachen, Wendlingweg 2, Aachen, D-52057, GERMANY	Membrane-bound
sbg101273 2GLUTb	Glucose transporte r	GB:AP000350 Direct submitted (10-JUN-1999) to the DDBJ/EMBL/GenBank databases. Nobuyoshi Shimizu, Keio university, school of medicine, Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo 160-0016, Japan.	Human glucose transporter GLUT10, gi.13540598 Submitted (10-FEB-2000) Joost H.G., Institute of Pharmacology and Toxicology, Medical Faculty, Technical University of Aachen, Wendlingweg 2, Aachen, D-52057, GERMANY	Membrane-bound
sbg101817 2CSP	Chondroit in sulfate proteoglyc an	EMBL:AL354819, and SC:AL590007. Submitted (30-APR-2001 and 04-MAY-2001) by Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. EMBL:AC017111, Submitted (09-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA	Lytechinus variegatus embryonic blastocoelar extracellular matrix protein , gi:9837426 Submitted (14-JUL-2000) Biological Sciences, Carnegie Mellon University, 4400 Fifth Ave, Pittsburgh, PA 15213, USA	Secreted
sbg100457 0ERGIC	ER-Golgi intermedia te compartm ent protein	GB:AC020705 Submitted (08-JAN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA	Human ERGL protein, gi:11141891 Submitted (06-SEP-2000) Laboratory of Molecular Biology, NCI, NIH, 37 Convent Dr., Bldg. 37, Rm. 4B20, Bethesda, MD 20892, USA	Membrane-bound

Table II (cont).

Gene Name	Gene Family	Closest Polynucleotide by homology	Closest Polypeptide by homology	Cell Localization (by homology)
sbg101699 5IGBrecpt	Immunoglobulin receptor	GB:AL353721 Submitted (07-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK.	Human immunoglobulin superfamily receptor translocation associated 1, gi:14550416 Hatzivassiliou,G., Miller,I.J., Takizawa,J., et al. Immunity 14 (3), 277-289 (2001)	Membrane-bound
sbg1151bS REC	EGF-like LDL receltor protein	GB:AC005500 Chen,F., D,L., Do,T., Dumanski,J.P. and Roe,B.A. Direct submission (31-MAY-01) Department Of Chemistry and Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA	Human nurse cell receptor B6TNC#10b, geneseqp: B60395 Submitted by (SHIO) SHIONOGI & CO LTD Application number and publication date: JP2000308492-A, 07-NOV-00	Membrane-bound
sbg139985 4ANK	The ankyrin repeat family	GB: AC020658 Direct submitted (08-JAN-2000) Multimegabase Sequencing Center, University of Washington, PO BOX 357730, Seattle, WA 98195, USA	Human KIAA1223 protein, gi:6330617 Nagase T, Ishikawa K, Kikuno R, Hirosawa M, Nomura N, and Ohara O; 1999 DNA Res 6:337-45.	Cytosolic

Table III

Gene Name	Uses	Associated Diseases
sbg960509 cbrecpt	An embodiment of the invention is the use of sbg960509cbrecpt in the treatment or diagnosis of cancer. A close homologue of sbg960509cbrecpt is Langerin. Langerin was a type II Ca2+-dependent lectin, an endocytic receptor and expressed by Langerhans cells (LC). Transfection of Langerin cDNA into fibroblasts created a compact network of membrane structures with typical features of Birbeck granules(BG). It was proposed that induction of BG was a consequence of the antigen-capture function of Langerin, allowing routing into these organelles and providing access to a nonclassical antigen-processing pathway (Valladeau J, Ravel O, Dezutter-Dambuyant C, Moore K, Kleijmeer M, Liu Y, Duvert-Frances V, Vincent C, Schmitt D, Davoust J, Caux C, Lebecque S, Saeland S. 2000. Immunity Jan;12(1):71-81). A striking incongruity was found between variably spliced transcripts for the second asialoglycoprotein receptor polypeptide, H2, in normal and transformed human liver cells (Paietta E, Stockert RJ, Racevskis J. 1992. Hepatology Mar;15(3):395-402). Human macrophage cell surface C-type lectin was demonstrated to recognize Tn Ag, a well-known human carcinoma-associated epitope (Suzuki N, Yamamoto K, Toyoshima S, Osawa T, Irimura T.1996. J Immunol Jan 1;156(1):128-35).	Autoimmune disorder and cancer
sbg614126 complfH	An embodiment of the invention is the use of sbg614126complfH in the diagnosis or treatment of cancer, Alzheimer disease, and/or tumor cell evasion. A close homologue of sbg614126complfH is Human complement factor H. Human complement factor H was detected by the AM34 antibody in the cerebrospinal fluid from an Alzheimer's disease patient. It was recently found that AM34 was capable of staining senile plaques positively and factor H was associated with senile plaques in the human brain (Honda S, Itoh F, Yoshimoto M, Ohno S, Hinoda Y, Imai K. 2000. J Gerontol A Biol Sci Med Sci. May;55(5):M265-9). It was also suggested that exceptional resistance of human H2 glioblastoma cells to complement-mediated killing was due to the production and binding of factor H and factor H-like protein 1 (Junnikkala S, Jokiranta TS, Friese MA, Jarva H, Zipfel PF, Meri S. 2000. J Immunol. Jun 1;164(11):6075-81). Moreover, factor H was shown to bind to bone sialoprotein and osteopontin and enable tumor cell evasion of complement-mediated attack (Fedarko NS, Fohr B, Robey PG, Young MF, Fisher LW. 2000. J Biol Chem. Jun 2;275(22):16666-72). Finally, complement factor H gene mutation was associated with autosomal recessive atypical hemolytic uremic syndrome (Ying L, Katz Y, Schlesinger M, Carmi R, Shalev H, Haider N, Beck G, Sheffield VC, Landau D. 1999. Am J Hum Genet Dec;65(6):1538-46).	Alzheimer's disease, cancer, tumor metastasis and autosomal recessive atypical hemolytic uremic syndrome

Table III (cont).

Gene Name	Uses	Associated Diseases
sbg120703 RNase	An embodiment of the invention is the use of sbg120703Rnase as a tool for anticancer therapy, and treating apoptosis-related disorders. It has been shown that a genetic-engineered pancreatic RNase has cytotoxic action on mouse and human tumor cells, but lacks any appreciable toxicity on human and mouse normal cells. This variant of human pancreatic RNase selectively sensitized cells derived from a human thyroid tumor to apoptotic death. Because of its selectivity for tumor cells, and because of its human origin, this protein is thought to represent a promising tool for anticancer therapy (Piccoli R, Di Gaetano S, De Lorenzo C, Grauso M, Monaco C, Spalletti-Cernia D, Laccetti P, Cinatl J, Matousek J, D'Alessio G. 1999. Proc Natl Acad Sci U S A 96:7768-73). In addition, RNase itself can be used to treat an RNA viral infection, and its antagonist may be useful in treating apoptosis-related disorders.	Cancer and infection
sbg98530TS	An embodiment of the invention is the use of sbg98530TS in the wound healing processes, development of the nervous system, and affecting cell migration, survival, or angiogenesis. Close homologues of sbg98530TS are thrombospondins. The thrombospondins are a family of proteins found widely in the embryonic extracellular matrix, and the expression patterns and in vitro properties of many thrombospondins suggest potential roles in the guidance of cell and growth cone migration, especially during the development of the nervous system (Adams JC, 2000. Tucker RP Dev Dyn 218:280-99). Cell interactions with extracellular matrices are important to pathological changes that occur during cell transformation and tumorigenesis. The thrombospondin-1 has been suggested to modulate tumor phenotype by affecting cell migration, survival, or angiogenesis (Liaw L, Crawford HC. 1999. Braz J Med Biol Res 32:805-12). In addition, thrombospondin-1 is also a transient component of extracellular matrix in developing and repairing tissues (Adams JC. 1997. Int J Biochem Cell Biol 29:861-5).	Cancer, wound healing disorders
sbg563917 RDP	An embodiment of the invention is the use of sbg563917RDP in treatment or diagnosis of chronic renal failure and aged eye lenses and cataracts. Close homologues of sbg563917RDP are renal and lens dipeptidases. It has been reported that the renal dipeptidase activity was significantly lower in the chronic renal failure group (Fukumura Y, Kera Y, Oshitani S, Ushijima Y, Kobayashi I, LiuZ, Watanabe T, Yamada R, Kikuchi H, Kawazu S and Yabuuchi M. 1999 Ann Clin Biochem Mar;36 (Pt 2):221-5). In contrast, increased lens dipeptidase activity was detected in aging and cataracts (Sulochana KN, Ramakrishnan S and Punitham R.1999 Br J Ophthalmol Jul;83(7):885).	Renal diseases, aging, cataract, cancer, and Alzheimer disease

Table III (cont).

Gene Name	Uses	Associated Diseases
sbg618069 LRR	An embodiment of the invention is the use of sbg618069LRR in treatment or diagnosis of neural development and the adult nervous system disorders. Close homologues of sbg618069LRR are Leucine-rich repeat proteins. Leucine-rich repeat protein, the spineless-aristapedia, has been shown to interact with tango bHLH-PAS proteins for controlling antennal and tarsal development in Drosophila (Emmons RB, Duncan D, Estes PA, Kiefel P, Mosher JT, Sonnenfeld M, Ward MP, Duncan I and Crews ST. 1999. Development Sep;126(17):3937-45). In mouse, neuronal Leucine-Rich Repeat NLRR-1 and NLRR-2 mRNAs were expressed primarily in the central nervous system and may play significant but distinct roles in neural development and in the adult nervous system (Taguchi A, Wanaka A, Mori T, Matsumoto K, Imai Y, Tagaki T and Tohyama M. 1996. Brain Res Mol Brain Res Jan;35(1-2):31-40). Furthermore, a new member of the leucine-rich repeat superfamily GAC1 was amplified and overexpressed in malignant gliomas (Almeida A, Zhu XX, Vogt N, Tyagi R, Muleris M, Dutrillaux AM, Dutrillaux B, Ross D, Malfoy B and Hanash S. 1998. Oncogene Jun 11;16(23):2997-3002).	Tango-associated diseases, disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions, Parkinson's disease, Alzheimer's disease, ALS, neuropathies, cancer, wound healing and tissue repair
sbg934114 Relaxin	An embodiment of the invention is the use of sbg934114Relaxin in treatment or diagnosis of collagen remodeling, breast cancer, and uterine contractile disorders. A close homologue of sbg934114Relaxin is Relaxin. Relaxin has various biologic activities, including the induction of collagen remodeling and consequent softening of the tissues of the birth canal during delivery, the inhibition of uterine contractile activity, and the stimulation of growth and differentiation of the mammary gland (Bani D. 1997. Gen Pharmacol 28:13-22). Relaxin belongs to the insulin superfamily, and is produced primarily by the corpus luteum in both pregnant and nonpregnant females. In males, relaxin is synthesized in the prostate and released in the seminal fluid (Goldsmith LT, Weiss G, Steinetz BG. 1995. Endocrinol Metab Clin North Am 24:171-86). It has been further demonstrated that relaxin regulates growth and differentiation of breast cancer cells in culture, promotes dilation of blood vessels in several organs, including the uterus, the mammary gland, the lung and the heart, has a chronotropic action on the heart, inhibits the release of histamine by mast cells, depresses aggregation of platelets and their release by megakaryocytes, and influences the secretion of hormones by the pituitary gland (Bani D. 1997. Gen Pharmacol 28:13-22). In addition, some reports have shown that relaxin is effective in decreasing skin involvement in systemic sclerosis (Furst DE. 1998. Curr Opin Rheumatol 10:123-8).	Cancer, rheumatic diseases, heart diseases, systemic sclerosis (scleroderma), and preterm birth

Table III (cont).

Gene Name	Uses	Associated Diseases
sbg99174LOX-like	An embodiment of the invention is the use of sbg99174LOX-like in treatment or diagnosis of endothelial function or atherosclerosis. A close homologue of sbg99174LOX-like is oxidized low-density lipoprotein receptor 1. sbg99174LOX-like as well as oxidized low-density lipoprotein receptor 1, contain a C-type lectin domain (CTL) (Colonna M, Samaridis J, Angman L. 2000. Eur J Immunol 30:697-704). Evidence suggests that oxidized low-density lipoprotein (OxLDL) plays a critical role in the changes in endothelial function. Lectin-like OxLDL receptor-1 (LOX-1) is the major endothelial OxLDL receptor. Functional changes of endothelial cells are implicated in the earliest stage of the pathogenesis of atherosclerosis (Aoyama T, Sawamura T, Furutani Y, Matsuoka R, Yoshida MC, Fujiwara H, Masaki T. Biochem J. 1999 339 (Pt 1):177-84).	Cardiovascular disorders (e.g. atherosclerosis, hypertension, stroke),
sbg995002PIGR	An embodiment of the invention is the use of sbg995002PIGR to actively transport IgA and IgM to the apical surface of epithelia. A close homologue of sbg995002PIGR is polymeric-immunoglobulin receptor. The polymeric-immunoglobulin receptor binds polymeric IgA and IgM at the basolateral surface of epithelial cells. PIGR knockout mice completely lack active external IgA and IgM translocation, but remain normal and fertile (Johansen FE, Pekna M, Norderhaug IN, Haneberg B, Hietala MA, Krajci P, Betsholtz C, Brandtzaeg P. 1999. J Exp Med 190:915-22). In addition, it has been reported that PIGR can be upregulated by tumor necrosis factor (TNF)-alpha (Takenouchi-Ohkubo N, Takahashi T, Tsuchiya M, Mestecky J, Moldoveanu Z, Moro I; 2000. Immunogenetics 51:289-95).	Infection and inflammation such as inflammatory bowel disease, gluten-sensitive enteropathy, and urinary tract infection)
sbg1033026C1q	An embodiment of the invention is the use of sbg1033026C1q to regulate central nervous system functions. A close homologue of sbg1033026C1q is C1q-related factor. C1q is a subunit of the C1 enzyme complex that activates the serum complement system. It has been shown that human C1q-related factor (CRF) transcript is expressed at highest levels in the brain, particularly in the brainstem. Similarly, in mouse brain CRF transcripts are most abundant in areas of the nervous system involved in motor function (Berube NG, Swanson XH, Bertram MJ, Kittle JD, Didenko V, Baskin DS, Smith JR, and Pereira-Smith OM., 1999, Brain Res. Mol. Brain Res. 63:233-240). Moreover, ACRP30 is structurally similar to complement factor C1q, and it forms large homo-oligomers that undergo a series of post-translational modifications. ACRP30 proteins may be a factor that participates in the complex balanced system of energy homeostasis involving food intake, carbohydrate catabolism, and lipid catabolism (Scherer PE, Williams S, Fogliano M, Baldini G, Lodish HF; 1995; J Biol Chem 270:26746-9).	Central nervous system disorder
sbg1003675RNase	An embodiment of the invention is the use of sbg1003675RNase as a promising tool for anticancer therapy, and apoptosis-related disorders. A close homologue of sbg1003675RNase is RNase. It has been shown that a genetic-engineered pancreatic RNase has cytotoxic action on mouse and human tumor cells, but lacks any appreciable	Viral infection, and tumor

	toxicity on human and mouse normal cells. This variant of human pancreatic RNase selectively sensitized cells derived from a human thyroid tumor to apoptotic death. Because of its selectivity for tumor cells, and because of its human origin, this protein was thought to represent a promising tool for anticancer therapy (Piccoli R, Di Gaetano S, De Lorenzo C, Grauso M, Monaco C, Spalletti-Cernia D, Laccetti P, Cinatl J, Matousek J, D'Alessio G. 1999. Proc Natl Acad Sci U S A 96:7768-73). Moreover, RNase itself can be used to treat an RNA viral infection, and its antagonist of this RNase may be useful in treating apoptosis-related disorders.	
sbg1015258PLM	An embodiment of the invention is the use of sbg1015258PLM to regulate skeletal and cardiac muscle disorders. A close homologue of sbg1015258PLM is phospholemman. The phospholemman (PLM) is enriched in skeletal muscle and the heart, and is a major substrate phosphorylated in response to insulin and adrenergic stimulation. All phospholemman proteins are small and have a single transmembrane domain (Chen LS, Lo CF, Numann R, Cuddy M. 1997. Genomics 41:435-4). Phospholemman can be phosphorylated by protein kinases A and C to induce a hyperpolarization-activated chloride current, and therefore may play a role in muscle contraction. Recently phospholemman was shown to be a substrate for myotonic dystrophy protein kinase, and therefore is associated with the disease, an autosomal dominant-inherited disorder with prominent effects on skeletal and cardiac muscle (Mounsey JP, John JE 3rd, Helmke SM, Bush EW, Gilbert J, Roses AD, Perryman MB, Jones LR, Moorman JR. 2000. J Biol Chem ;275:23362-7).	Myotonic muscular dystrophy
sbg1003328IG	An embodiment of the invention is the use of sbg1003328IG to generate immunosuppressants to suppress immune responses. A close homologue of sbg1003328IG is V7, a human leukocyte surface protein (Stockinger H, Gadd SJ, Eher R, Majdic O, Schreiber W, Kasinrerk W, Strass B, Schnabl E, Knapp W. 1990. J Immunol 145:3889-97). sbg1003328IG is an immunoglobulin (Ig)-like membrane protein containing three potential Ig domains, and it has an overall strong sequence similarity to V7.	Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders, and inflammation
sbg1020829SGLT	An embodiment of the invention is the use of sbg1020829SGLT to regulate Na(+)-dependent glucose transport. A close homologue of sbg1020829SGLT is Na+/glucose cotransporters. The human intestinal Na+/glucose cotransporter (SGLT1) was cloned and sequenced. Close homology was observed between the human and rabbit intestinal Na+/glucose cotransporters, and a significant homology was found between these and the Escherichia coli Na+/proline cotransporter (putP) indicating that the mammalian Na+/glucose and prokaryote Na+/proline cotransporters sharing a common ancestral gene (Hediger MA, Turk E, Wright EM. 1989 Proc Natl Acad Sci U S A Aug;86(15):5748-52). In addition, study of intestinal biopsies of glucose/galactose malabsorption (GCM) patients has revealed a specific defect in Na(+)-dependent absorption of glucose in the brush border. A single missense mutation was found in SGLT1 amplified from the genomic DNA derived from members of a family affected with GGM. This mutated SGLT1 cosegregated with the GGM	Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders, inflammation and glucose/galactose malabsorption

	phenotype and resulted in a complete loss of Na(+)-dependent glucose transport in Xenopus oocytes injected with this complementary RNA (Turk E, Zabel B, Mundlos S, Dyer J, Wright EM. 1991 Nature Mar 28;350(6316):354-6).	
sbg100545 0UDPGT	An embodiment of the invention is the use of sbg1005450UDPGT to regulate estrogen and androgen catabolism in peripheral steroid target tissues. A close homologue of sbg1005450UDPGT is UDP-glucuronosyltransferase (UDPGT) gene. Mutations had been found in the promoter and coding regions of UDP-glucuronosyltransferase (UDPGT) gene in seven patients with Crigler-Najjar syndrome type II caused by reduction in hepatic bilirubin UDPGT activity (Yamamoto K, Soeda Y, Kamisako T, Hosaka H, Fukano M, Sato H, Fujiyama Y, Adachi Y, Satoh Y, Bamba T. 1998. J Hum Genet 43(2):111-4). A case of Gilbert syndrome caused by a homozygous missense mutation of the bilirubin UDPGT gene was also reported (Maruo Y, Sato H, Yamano T, Doida Y, Shimada M. 1998. J Pediatr Jun;132(6):1045-7). In addition, monkey UDPGT UGT1A9 had been cloned and the mRNA was expressed in extrahepatic estrogen-responsive tissues indicating its potential role in estrogen metabolism (Albert C, Vallee M, Beaudry G, Belanger A, Hum DW. 1999. Endocrinology Jul;140(7):3292-302). Human UDPGT UGT2B23 transcript was also expressed in extrahepatic tissues including prostate, mammary gland, epididymis, testis, and ovary. The activity of UGT2B23 was tested with 62 potential endogenous substrates and was demonstrated to be active on 6 steroids and the bile acid, hyodeoxycholic acid suggesting that UGT2B23 might play an important role in estrogen and androgen catabolism in peripheral steroid target tissues (Barbier O, Levesque E, Belanger A, Hum DW. 1999. Endocrinology Dec;140(12):5538-48).	Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders, inflammation Gilbert syndrome, Crigler-Najjar syndrome (CN) type II, and steroid hormone catabolism malfunction
sbg100262 0TIa	An embodiment of the invention is the use of sbg1002620TIa to regulate human tumor cells. A close homologue of sbg1002620TIa is human hypothetical protein DKFZp434B044. This gene is also similar to trypsin inhibitor which contains Sc7 family of extracellular domains at its N-ternimal region (Genome Res. 11 (3), 422-435 (2001)). Trypsin inhibitor P25TI sequence had similarity to CRISP family proteins including insect venom allergens, mammalian testis-specific proteins and plant pathogenesis-related proteins. mRNA encoding P25TI and another two glioma pathogenesis-related protein GliPR and RTVP-1, which were also shown to be structurally similar to CRISP family proteins was frequently expressed in human tumor tissues but not detected in normal human tissue cell lines (Yamakawa T, Miyata S, Ogawa N, Koshikawa N, Yasumitsu H, Kanamori T, Miyazaki K 1998. Biochim Biophys Acta Jan 21; 1395(2):202-8., Murphy EV, Zhang Y, Zhu W, Biggs J. 1995. Gene Jun 14;159(1):131-5., Rich T, Chen P, Furman F, Huynh N, Israel MA.1996. Gene Nov 21;180(1-2):125-30).	Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders, inflammation, blood coagulation disorders, cellular adhesion disorders, pancreatitis, shock, multi-organ failure, and gastrointestinal ulceration
sbg100262 0TIb	An embodiment of the invention is the use of sbg1002620TIb as a marker for some nervous system tumors, and to regulate expression of human neuroblastoma and glioblastoma. A close homologue of sbg1002620TIb is late-gestation lung 1 (LGL1) protein. Late-gestation lung 1 (LGL1) protein showed 81% homology to P25TI, the trypsin	Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders,

	inhibitor purified from the culture medium of human glioblastoma cells (Kaplan F, Ledoux P, Kassamali FQ, Gagnon S, Post M, Koehler D, Deimling J, Sweezey NB. 1999. Am J Physiol Jun;276(6 Pt 1):L1027-36; Koshikawa N, Nakamura T, Tsuchiya N, Isaji M, Yasumitsu H, Umeda M, Miyazaki K. 1996. J Biochem (Tokyo) Feb;119(2):334-9). The cDNA encoding P25TI was isolated and the sequence had similarity to CRISP family proteins including insect venom allergens, mammalian testis-specific proteins and plant pathogenesis-related proteins. P25TI mRNA was frequently expressed in human neuroblastoma and glioblastoma but not detected in normal human tissues cell lines (Yamakawa T, Miyata S, Ogawa N, Koshikawa N, Yasumitsu H, Kanamori T, Miyazaki K 1998. Biochim Biophys Acta Jan 21; 1395(2):202-8). Another two glioma pathogenesis-related protein GliPR and RTVP-1 were also shown to be structurally similar to CRISP family proteins. The GLIPR gene was highly expressed in the human brain tumor, glioblastoma multiforme/astrocytoma, but neither in normal fetal or adult brain tissue, nor in other nervous system tumors (Murphy EV, Zhang Y, Zhu W, Biggs J. 1995. Gene Jun 14;159(1):131-5). Multiple RTVP-1 mRNA species were highly expressed in a panel of cell lines from nervous system tumors arising from glia, in contrast, the expression of these RNAs was low or absent in nonglial-derived nervous system tumor cell lines (Rich T, Chen P, Furman F, Huynh N, Israel MA.1996. Gene Nov 21;180(1-2):125-30).	inflammation, blood coagulation disorders, cellular adhesion disorders, pancreatitis, shock, multi-organ failure, and gastrointestinal ulceration
sbg102200 MCTa	An embodiment of the invention is the use of sbg102200MCTa in regulating cancer cells, including the hematopoietic lineages, Burkitt's lymphoma, and solid tumor cells. A close homologue of sbg102200MCTa is MCT1 from Chinese hamster and mouse. Mouse H+-monocarboxylate cotransporter (MCT1) was cloned and sequenced from Ehrlich Lettre tumour cells, the sequence of MCT1 is 93% and 87% homologous to MCT1 from Chinese hamster and human, respectively. N-glycanase-F treatment and an in vitro translation experiments demonstrated that glycosylation was not required for MCT1 function (Carpenter L, Poole RC, Halestrap AP. 1996. Biochim Biophys Acta Mar 13;1279(2):157-63). Chick monocarboxylate transporter MCT3 cloned from retinal pigment epithelium (RPE) cDNA library was found only expressed in RPE cells. A rat thyroid epithelial cell line FRTL transfected with pCl-neo/MCT3 showed enhanced pyruvate uptake suggesting that MCT3 may regulate lactate levels in the interphotoreceptor space (Yoon H, Fanelli A, Grollman EF, Philp NJ. 1997. Biochem Biophys Res Commun May 8;234(1):90-4). In human, MCT2 had been implicated as a primary pyruvate transporter in man. The mRNAs of MCT1 and MCT2 were found co-expressed in various human cancer cell lines, including the hematopoietic lineages HL60, K562, MOLT-4, Burkitt's lymphoma Raji, and solid tumor cells such as SW480, A549, and G361. These findings suggested that human MCT1 and MCT2 may have distinct biological roles (Lin RY, Vera JC, Chaganti RS, Golde DW. 1998. J Biol Chem Oct 30;273(44):28959-65).	Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders, and inflammation
sbg102200 MCTb	An embodiment of the invention is the use of sbg102200MCTb in regulating cancer cells, including the hematopoietic lineages, Burkitt's lymphoma, and solid tumor	Cancer, infection, autoimmune disorder,

	cells. A close homologue of sbg102200MCTb is MCT1 from Chinese hamster and mouse. Mouse H+-monocarboxylate cotransporter (MCT1) was cloned and sequenced from Ehrlich Lettre tumour cells, the sequence of MCT1 is 93% and 87% homologous to MCT1 from Chinese hamster and human, respectively. N-glycanase-F treatment and an in vitro translation experiments demonstrated that glycosylation was not required for MCT1 function (Carpenter L, Poole RC, Halestrap AP. 1996. Biochim Biophys Acta Mar 13;1279(2):157-63). Chick monocarboxylate transporter MCT3 cloned from retinal pigment epithelium (RPE) cDNA library was found only expressed in RPE cells. A rat thyroid epithelial cell line FRTL transfected with pCl-neo/MCT3 showed enhanced pyruvate uptake suggesting that MCT3 may regulate lactate levels in the interphotoreceptor space (Yoon H, Fanelli A, Grollman EF, Philp NJ. 1997. Biochem Biophys Res Commun May 8;234(1):90-4). In human, MCT2 had been implicated as a primary pyruvate transporter in man. The mRNAs of MCT1 and MCT2 were found co-expressed in various human cancer cell lines, including the hematopoietic lineages HL60, K562, MOLT-4, Burkitt's lymphoma Raji, and solid tumor cells such as SW480, A549, and G361. These findings suggested that human MCT1 and MCT2 may have distinct biological roles (Lin RY, Vera JC, Chaganti RS, Golde DW. 1998. J Biol Chem Oct 30;273(44):28959-65).	hematopoietic disorder, wound healing disorders, and inflammation
sbg102038 0LYG	An embodiment of the invention is the use of sbg1020380LYG in the immune system and enhance the activity of immunoagents and may serve as biomarkers of periodontal disease activity. Close homologues of sbg1020380LYG are lysozymes. Lysozymes are bacteriolytic defensive agents and have been adapted to serve a digestive function (Qasba PK, Kumar S, 1997, Crit Rev Biochem Mol Biol 32:255-306). Those in tissue and body fluids are involved in the immune system and enhance the activity of immunoagents. Llysozymes may serve as biomarkers of periodontal disease activity from inflammatory cell origin (Eley BM, and Cox SW, 1998, Br Dent J 184:323-8).	Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders, and inflammation
sbg100702 6SGLT	An embodiment of the invention is the use of sbg1007026SGLT, a human sodium-glucose cotransporter, in regulation of Glucose/galactose malabsorption (GGM), familial renal glycosuria, and diabetic renal disorders. Close homologues of sbg1007026SGLT are other sodium-glucose cotransporters from humans and rabbits. Human sodium-glucose cotransporters are responsible for the active accumulation of glucose in cells (Hediger MA, Turk E, Wright EM. 1989. Proc Natl Acad Sci U S A 86:5748-52). The renal sodium-glucose cotrnasporter may be related to the pathophysiology of renal diseases such as familial renal glycosuria and diabetic renal disorders (Kanai Y, Lee WS, You G, Brown D, Hediger MA. 1994. J Clin Invest 93:397-404). In addition, study of glucose/galactose malabsorption (GGM) patients has revealed a specific defect in sodium-dependent absorption of glucose in the brush border, and the consequent severe diarrhea and dehydration caused by glucose/galactose malabsorption are usually lethal unless these sugars are eliminated from the diet (Turk E, Zabel B, Mundlos S, Dyer J, Wright EM. 1991 Nature 350:354-6).	Glucose/galactos e malabsorption (GGM), familial renal glycosuria, and diabetic renal disorders

sbg101273 2GLUT	An embodiment of the invention is the use of sbg1012732GLUT, in the maintenance of cellular homeostasis and metabolism. Close homologues of sbg1012732GLUT are transmembrane glucose transporters (gluts). Glucose uptake is achieved by transmembrane glucose transporters (gluts), and the transport of glucose across plasma membranes is important for the maintenance of cellular homeostasis and metabolism. Glucose is taken up by cells and then phosphorylated to glucose-6-phosphate, and lucose utilization by cancer cells is greatly enhanced when compared with that by normal tissue. Tumor tissue is frequently associated with the abnormal and/or over-expression of glucose transporters, especially glut1 (Smith TA. 1999. Br J Biomed Sci 56:285-92). Increased utilization of glucose in glomerular cells cause the increased expression and activity of aldose reductase, protein kinase C and TGF-beta, which have been implicated in excessive extracellular matrix accumulation in diabetic nephropathy (Z Katedry i Zakladu Patofizjologii, Akaemii Medycznej w Poznaniu. 1999. Przegl Lek 56:793-9). Changes in endothelial glucose transport and GLUT1 abundance in the barriers of the brain and retina may severely affect glucose delivery to these tissues and major implications in the development of two major diabetic complications, insulin-induced hypoglycemia and diabetic retinopathy (Kumagai AK. 1999. Diabetes Metab Res Rev 15:261-73).	Tumor, diabetic nephropathy, and insulin-induced hypoglycemia
sbg101273 2GLUTb	An embodiment of the invention is the use of sbg1012732GLUTb, in the maintenance of cellular homeostasis and metabolism. Close homologues of sbg1012732GLUTb are transmembrane glucose transporters (gluts). Glucose uptake is achieved by transmembrane glucose transporters (gluts), and the transport of glucose across plasma membranes is important for the maintenance of cellular homeostasis and metabolism. Glucose is taken up by cells and then phosphorylated to glucose-6-phosphate, and lucose utilization by cancer cells is greatly enhanced when compared with that by normal tissue. Tumor tissue is frequently associated with the abnormal and/or over-expression of glucose transporters, especially glut1 (Smith TA. 1999. Br J Biomed Sci 56:285-92). Increased utilization of glucose in glomerular cells cause the increased expression and activity of aldose reductase, protein kinase C and TGF-beta, which have been implicated in excessive extracellular matrix accumulation in diabetic nephropathy (Z Katedry i Zakladu Patofizjologii, Akaemii Medycznej w Poznaniu. 1999. Przegl Lek 56:793-9). Changes in endothelial glucose transport and GLUT1 abundance in the barriers of the brain and retina may severely affect glucose delivery to these tissues and major implications in the development of two major diabetic complications, insulin-induced hypoglycemia and diabetic retinopathy (Kumagai AK. 1999. Diabetes Metab Res Rev 15:261-73).	Tumor, diabetic nephropathy, and insulin-induced hypoglycemia
sbg101817 2CSP	An embodiment of the invention is the use of sbg1018172CSP in regulation of melanoma, autoimmune disorders, hematopoietic disorder, wound healing, and inflammation. A close homologue of sbg1018172CSP is melanoma-associated chondroitin sulfate proteoglycan	Melanoma, infection, autoimmune disorder, hematopoietic

	(MCSP) core protein NG2. The MCSP core protein NG2 can act as a coreceptor for spreading and focal contact formation in association with alpha 4 beta 1 integrin in melanoma cells (Iida J, Meijne AM, Spiro RC, Roos E, Furcht LT, McCarthy JB. 1995. Cancer Res Mar 15;55(10):2177-85). Cloning of MCSP recognized by mAb 9.2.27 showed that the core protein contained an open reading frame of 2322 AAs, encompassing a large extracellular domain, a hydrophobic transmembrane region, and a relatively short cytoplasmic tail. MCSP RNA was detected in human melanoma cell lines and in biopsies prepared from melanoma skin metastases but not in other human cancer cells or a variety of human fetal and adult tissues (Pluschke G, Vanek M, Evans A, Dittmar T, Schmid P, Itin P, Filardo EJ, Reisfeld RA. 1996. Proc Natl Acad Sci U S A Sep 3;93(18):9710-5).	disorder, wound healing, and inflammation
sbg100457 0ERGIC	An embodiment of the invention is the use of sbg1004570ERGIC as a probe for studying protein trafficking in the secretory pathway which is crucial for the elucidation and treatment of many inherited and acquired diseases, such as cystic fibrosis, Alzheimer's disease and viral infectionsin regulation of melanoma, autoimmune disorders, hematopoietic disorder, wound healing, and inflammation. A close homologue of sbg1004570ERGIC is ERGIC-53, an ER-Golgi intermediate compartment (ERGIC) protein. A ERGIC protein was elevated more than two fold in HT-29 colon adenocarcinoma cells resistant to the the antitumor drug KRN5500. Together with other information, the cellular secretory pathway was suggested a primary determinant of sensitivity to KRN550 (Kamishohara M, Kenney S, Domergue R, Vistica DT, Sausville EA. 2000 Exp Cell Res May 1;256(2):468-79). Mutations in ERGIC-53 was shown to cause combined deficiency of coagulation factors V and VIII and it was suggested that ERGIC-53 might function as a molecular chaperone for the transport from ER to Golgi of a specific subset of secreted proteins, including coagulation factors V and VII (Nichols WC, Seligsohn U, Zivelin A, Terry VH, Hertel CE, Wheatley MA, Moussalli MJ, Hauri HP, Ciavarella N, Kaufman RJ, Ginsburg D. 1998. Cell Apr 3;93(1):61-70). In addition, ERGIC-53 was reviewed as an attractive probe for studying numerous aspects of protein trafficking in the secretory pathway which is crucial for the elucidation and treatment of many inherited and acquired diseases, such as cystic fibrosis, Alzheimer's disease and viral infections (Hauri HP, Kappeler F, Andersson H, Appenzeller C. 2000 J Cell Sci Feb;113 (Pt 4):587-96).	Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders, inflammation, and Alzheimer's disease
sbg101699 5IGBrecpt	An embodiment of the invention is the use of sbg1016995IGBrecpt in the clearance of circulating autoantibodies and immune complexes. A close homologue of sbg1016995IGBrecpt is guinea pig Fc receptor for immunoglobulin (Tominaga M, Sakata A, Ohmura T, Yamashita T, Koyama J, Onoue K, 1990. Biochem Biophys Res Commun Apr 30;168(2):683-9). IgG Fc-receptor polymorphisms have been reported recently in patients with guillain-Barre syndrome indicating the role of IgG Fc-receptor in the clearance of circulating autoantibodies and immune complexes (Vedeler CA, Raknes G, Myhr KM, Nyland H. 2000 Neurology Sep 12;55(5):705-7).	Auto-immune diseases, allergy, and guillain-Barre syndrom

sbg1151bSREC	An embodiment of the invention is the use of sbg1151bSREC, a scavenger receptor, in the regulation of pathogenesis in atherosclerosis and the formation of foam cells in atherosclerotic lesions. A close homologue of sbg1151bSREC is scavenger receptor class A type I and type II. Most of the scavenger receptors interacted with several structurally different ligands such as oxidized low density lipoprotein (Ox-LDL) and acetyl LDL. Several studies showed Ox-LDL was involved in the pathogenesis of atherosclerosis (Steinbrecher UP. 1999 Biochim Biophys Acta Jan 4;1436(3):279-98). In macrophages scattered in aortic walls without atherosclerotic lesions, scavenger receptor class A type I and type II (SRA) was detected weakly but consistently. In contrast, in atherosclerotic lesions, macrophages around the core region showed a strong immunoreactivity to SRA indicating the involvement of SRA in the formation of foam cells in atherosclerotic lesions (Nakata A, Nakagawa Y, Nishida M, Nozaki S, Miyagawa J, Nakagawa T, Tamura R, Matsumoto K, Kameda-Takemura K, Yamashita S and Matsuzawa Y. Arterioscler Thromb Vasc Biol 1999 May;19(5):1333-9).	Atherosclerosis disease
sbg1399854ANK	An embodiment of the invention is the use of sbg1399854ANK in protein-protein interactions and it may act by inhibiting protein of cyclin dependent kinase. The present invention contains both death domain and ankyrin repeat region. The death domain is involved in cell death signaling (Cleveland J. and Ihle J.N. 1995. Cell 81:479-482). Ankyrin repeats (ANK) are tandem repeat modules of about 33 amino acids. Many ankyrin repeat regions are known to be involved in protein-protein interaction (Svetlana Gorina and Nikola P. Pavletich; 1996 Science 274:1001-1005).	Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders, and inflammation

Table IV. Quantitative, Tissue-specific mRNA expression detected using SybrMan

Quantitative, tissue-specific, mRNA expression patterns of the genes were measured using SYBR-Green Quantitative PCR (Applied Biosystems, Foster City, CA; see Schmittgen T.D. et al., Analytical Biochemistry 285:194-204, 2000) and human cDNAs prepared from various human tissues. Gene-specific PCR primers were designed using the first nucleic acid sequence listed in the Sequence List for each gene. The threshold cycle (C_t) is defined as the fractional cycle number at which the reporter fluorescence generated by cleavage of the probe reaches a threshold defined as 10 times the background. In cases sequence detection system software predicted more than one PCR product, Taqman was used for the specific PCR amplification as indicated under the specific genes.

In each gene's first subset table, two replicate measurements of gene of identification (GOI) mRNA were measured from various human tissues (column 3 and 4). The average GOI mRNA copies of the two replicates were made from each tissue RNA (column 5). The average amount of 18S rRNA from each tissue RNA was measured (column 6) and used for normalization. To make each tissue with the same amount of 50 ng of 18S rRNA, the normalization factor (column 7) was calculated by dividing 50 ng with the amount of 18S rRNA measured from each tissue (column 6). The mRNA copies per 50 ng of total RNA were obtained by multipling each GOI normalization factor and the average mRNA copies (column8).

Fold changes shown in each gene's second subset table were only calculated for disease tissues which have a normal counterpart. There are blanks in the fold change column for all samples that do not have counterparts. In addition, the fold change calculations are the fold change in the disease sample as compared to the normal sample. Accordingly, there will not be a fold change calculation next to any of the normal samples. For patient matched cancer pairs (colon, lung, and breast), each tumor is compared to its specific normal counterpart. When patient-matched normal/disease pairs do not exist, each disease sample was compared back to the average of all the normal samples of that same tissue type. For example, normal brain from the same patient that provided Alzheimer's brain is not applicable . Three normal brain samples and 4 Alzheimer's brain samples are used in the fold change. Three normal samples were averaged, and each of the Alzheimer's samples was compared back to that average.

Abbreviations

ALZ Alzheimer's Disease
CT CLONTECH (1020 East Meadow Circle Palo Alto, CA 94303-4230, USA)
KC Sample prepared by GSK investigator
COPD chronic obstructive pulmonary disease
endo endothelial
VEGF vascular endothelial growth factor
bFGF basic fibroblast growth factor
BM bone marrow
osteo osteoblast
OA osteoarthritis
RA rheumatoid arthritis
PBL peripheral blood lymphocytes
PBMNC peripheral blood mononuclear cells
HIV human immunodeficiency virus
HSV Herpes simplex virus
HPV human papilloma virus

Gene Name sbg960509cbrecpt

Lowest overall expression in normal and disease samples. Highest normal expression in the whole brain, fetal liver, and uterus. Highest disease expression in 2 of the lung tumor samples, one of the breast tumor samples, and one of the normal breast samples. Downregulation in 1 of 4 colon tumors implies an involvement in cancer of the colon. Downregulation in 2 of 4 AD brain samples as well as high expression in whole brain suggests an involvement in Alzheimer's disease. Downregulation in 3 of 3 COPD lung samples and downregulation in 4 of 4 asthmatic lung samples implicates this gene in COPD and asthma. Upregulation in 2 of 3 heart samples proposes roles in non-obstructive and obstructive DCM. Patterns difficult to interpret due to Cts > 35. Moderate to low expression in immune cells. Moderate expression in OA and RA synovium.

Sample sbg960509cbrecpt	**Ct (sample 1 and 2)**	**Mean GOI copies (sample 1)**	**Mean GOI copies (sample 2)**	**Average GOI Copies**	**18S rRNA (ng)**	**50 ng/18S rRNA (ng)**	**copies of mRNA detected/50 ng total RNA**
Subcutaneous Adipocytes Zenbio	40, 40	0	0	0.00	3.06	16.34	0.00
Subcutaneous Adipose Zenbio	40, 40	0	0	0.00	0.96	52.36	0.00
Adrenal Gland Clontech	40, 40	0	0	0.00	0.61	81.97	0.00
Whole Brain Clontech	33.26, 32.07	24.63	48.4	36.52	7.24	6.91	252.18
Fetal Brain Clontech	40, 40	0	0	0.00	0.48	103.95	0.00
Cerebellum Clontech	40, 40	0	0	0.00	2.17	23.04	0.00
Cervix	40, 40	0	0	0.00	2.42	20.66	0.00
Colon	40, 40	0	0	0.00	2.71	18.45	0.00
Endometrium	40, 40	0.81	0	0.41	0.73	68.21	27.63
Esophagus	40, 40	0	0	0.00	1.37	36.50	0.00
Heart Clontech	40, 40	0	0	0.00	1.32	37.88	0.00
Hypothalamus	40, 40	0	0	0.00	0.32	155.28	0.00
Ileum	40, 40	0	0	0.00	2.58	19.38	0.00
Jejunum	35.56, 34.42	6.66	12.71	9.69	6.60	7.58	73.37
Kidney	40, 40	0	0	0.00	2.12	23.58	0.00
Liver	40, 40	0	0	0.00	1.50	33.33	0.00
Fetal Liver Clontech	33.46, 34.83	14.95	27.51	21.23	10.40	4.81	102.07
Lung	40, 40	0	0	0.00	2.57	19.46	0.00
Mammary Gland Clontech	40, 40	21.94	10.06	16.00	13.00	3.85	61.54
Myometrium	40, 40	0	0	0.00	2.34	21.37	0.00
Omentum	40, 40	0	0	0.00	3.94	12.69	0.00
Ovary	40, 40	0	0	0.00	4.34	11.52	0.00
Pancreas	40, 40	0	0	0.00	0.81	61.80	0.00
Head of Pancreas	40, 40	0	0	0.00	1.57	31.85	0.00
Parotid Gland	40, 40	0	0	0.00	5.48	9.12	0.00
Placenta Clontech	40, 40	0.39	0	0.20	5.26	9.51	1.85
Prostate	40, 40	0	0	0.00	3.00	16.67	0.00
Rectum	40, 40	0	0	0.00	1.23	40.65	0.00
Salivary Gland	34.79, 40	10.31	0	5.16	7.31	6.84	35.26

Clontech							
Skeletal Muscle Clontech	40, 40	0	0	0.00	1.26	39.68	0.00
Skin	40, 40	0	0	0.00	1.21	41.32	0.00
Small Intestine Clontech	40, 40	0	0	0.00	0.98	51.07	0.00
Spleen	40, 40	0	0	0.00	4.92	10.16	0.00
Stomach	35.8, 38.29	5.82	1.41	3.62	2.73	18.32	66.21
Testis Clontech	40, 40	0	0	0.00	0.57	87.87	0.00
Thymus Clontech	35.13, 35.08	8.48	8.75	8.62	9.89	5.06	43.55
Thyroid	40, 40	0	0	0.00	2.77	18.05	0.00
Trachea Clontech	35.26, ND	7.9	ND	7.90	9.71	5.15	40.68
Urinary Bladder	40, ND	0	ND	0.00	5.47	9.14	0.00
Uterus	35.09, 33.87	8.67	17.4	13.04	5.34	9.36	122.05
genomic	26.62	1067.33					
b-actin	27.44	670.43					
1.00E+05	19.22	100000					
1.00E+05	19.38	100000					
1.00E+04	22.78	10000					
1.00E+04	20.52	10000					
1.00E+03	26.45	1000					
1.00E+03	27.03	1000					
1.00E+02	30.99	100					
1.00E+02	31.26	100					
1.00E+01	40	0					
1.00E+01	40	0					
1.00E-00	40	0					
1.00E-00	40	0					
NTC	40	0					
NTC	40	0					

Sample sbg960509cbrecpt	**Reg number (GSK identifier)**	**Ct**	**Mean GOI copies**	**copies of mRNA detected/50 ng total RNA**	**Sample**	**Fold Change in Disease Population**
colon normal GW98-167	21941	29.42		332.32	colon normal	
colon tumor GW98-166	21940	30.95	66.31	132.62	colon tumor	-2.51
colon normal GW98-178	22080	31.32	53.01	106.02	colon normal	
colon tumor GW98-177	22060	30.57	83.1	166.20	colon tumor	1.57
colon normal GW98-561	23514	31.44	49.16	98.32	colon normal	
colon tumor GW98-560	23513	31.81	39.47	78.94	colon tumor	-1.25
colon normal GW98-894	24691	29.44	164.69	329.38	colon normal	
colon tumor GW98-893	24690	34.42	8.18	16.36	colon tumor	-20.13
lung normal GW98-3	20742	28.04	383.11	766.22	lung normal	

lung tumor GW98-2	20741	34.22	9.19	18.38	lung tumor	-41.69
lung normal GW97-179	20677	30.93	66.74	133.48	lung normal	
lung tumor GW97-178	20676	27.11	667.61	1335.22	lung tumor	10.00
lung normal GW98-165	21922	28.31	323.99	647.98	lung normal	
lung tumor GW98-164	21921	30.92	67.22	134.44	lung tumor	-4.82
lung normal GW98-282	22584	31.76	40.67	81.34	lung normal	
lung tumor GW98-281	22583	29.61	148.67	297.34	lung tumor	3.66
breast normal GW00-392	28750	27.64	487.44	487.44	breast normal	
breast tumor GW00-391	28746	27.47	539.99	1079.98	breast tumor	2.22
breast normal GW00-413	28798	33.36	15.44	15.44	breast normal	
breast tumor GW00-412	28797	30.88	68.84	137.68	breast tumor	8.92
breast normal GW00-235:238	27592-95	34.74	6.73	6.73	breast normal	
breast tumor GW00-231:234	27588-91	33.73	12.41	12.41	breast tumor	1.84
breast normal GW98-621	23656	27.7	469.27	938.54	breast normal	
breast tumor GW98-620	23655	33.1	18.13	36.26	breast tumor	-25.88
brain normal BB99-542	25507	31.46	48.61	97.22	brain normal	
brain normal BB99-406	25509	34.17	9.52	19.04	brain normal	
brain normal BB99-904	25546	35.69	3.79	7.58	brain normal	
brain stage 5 ALZ BB99-874	25502	40	0	0.00	brain stage 5 ALZ	-41.28
brain stage 5 ALZ BB99-887	25503	34.96	5.91	11.82	brain stage 5 ALZ	-3.49
brain stage 5 ALZ BB99-862	25504	33.13	17.82	35.64	brain stage 5 ALZ	-1.16
brain stage 5 ALZ BB99-927	25542	40	0	0.00	brain stage 5 ALZ	-41.28
CT lung KC	normal	29.53	155.88	311.76	CT lung	
lung 26 KC	normal				lung 26	
lung 27 KC	normal	39.2	0.46	0.46	lung 27	
lung 24 KC	COPD	40	0	0.00	lung 24	-104.07
lung 28 KC	COPD	40	0	0.00	lung 28	-104.07
lung 23 KC	COPD	34.81	6.44	6.44	lung 23	-16.16
lung 25 KC	normal	40	0	0.00	lung 25	
asthmatic lung ODO3112	29321	38.99	0.52	0.52	asthmatic lung	-200.14
asthmatic lung ODO3433	29323	33.69	12.65	25.30	asthmatic lung	-4.11
asthmatic lung ODO3397	29322	33.53	13.98	27.96	asthmatic lung	-3.72
asthmatic lung ODO4928	29325	34.27	8.96	17.92	asthmatic lung	-5.81
endo cells KC	control	40	0	0.00	endo cells	
endo VEGF KC		40	0	0.00	endo VEGF	0.00
endo bFGF KC		40	0	0.00	endo bFGF	0.00
heart Clontech	normal	35.53	4.19	8.38	heart	
heart (T-1) ischemic	29417	34	10.5	21.00	heart T-1	2.51
heart (T-14) non-obstructive DCM	29422	31.16	58.24	116.48	heart T-14	13.90
heart (T-3399) DCM	29426	28.35	317.67	635.34	heart T-3399	75.82

adenoid GW99-269	26162	31.52	46.93	93.86	adenoid	
tonsil GW98-280	22582	30.82	71.35	142.70	tonsil	
T cells PC00314	28453	34.36	8.47	16.94	T cells	
PBMNC		40	0	0.00	PBMNC	
monocyte		40	0	0.00	monocyte	
B cells PC00665	28455	40	0	0.00	B cells	
dendritic cells 28441		31.52	47.02	94.04	dendritic cells	
neutrophils	28440	36.13	2.91	2.91	neutrophils	
eosinophils	28446	40	0	0.00	eosinophils	
BM unstim		40	0	0.00	BM unstim	
BM stim		40	0	0.00	BM stim	0.00
osteo dif		40	0	0.00	osteo dif	0.00
osteo undif		40	0	0.00	osteo undif	
chondrocytes		40	0	0.00	chondrocytes	
OA Synovium IP12/01	29462	32.08	33.47	33.47	OA Synovium	
OA Synovium NP10/01	29461	31.43	49.5	99.00	OA Synovium	
OA Synovium NP57/00	28464	30.42	91.04	182.08	OA Synovium	
RA Synovium NP03/01	28466	32.11	32.84	65.68	RA Synovium	
RA Synovium NP71/00	28467	31.07	61.51	123.02	RA Synovium	
RA Synovium NP45/00	28475	36.21	2.78	5.56	RA Synovium	
OA bone (biobank)	29217	31.49	47.85	47.85	OA bone (biobank)	
OA bone Sample 1	J. Emory	30.11	109.44	218.88	OA bone	
OA bone Sample 2	J. Emory	32.6	24.52	49.04	OA bone	
Cartilage (pool)	Normal	32.09	33.26	66.52	Cartilage (pool)	
Cartilage (pool)	OA	33.1	18.07	36.14	Cartilage (pool)	-1.84
PBL unifected	28441	27.68	474.91	949.82	PBL unifected	
PBL HIV IIIB	28442	31.76	40.5	81.00	PBL HIV IIIB	-11.73
MRC5 uninfected (100%)	29158	40	0	0.00	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	34.15	9.61	19.22	MRC5 HSV strain F	19.22
W12 cells	29179	40	0	0.00	W12 cells	
Keratinocytes	29180	38.16	0.85	1.70	Keratinocytes	
B-actin control		27.02	707.5			
genomic		26.1	1232.73			
1.00E+05		18.64	100000			
1.00E+05		18.95	100000			
1.00E+04		22.4	10000			
1.00E+04		22.17	10000			
1.00E+03		26.34	1000			
1.00E+03		25.94	1000			
1.00E+02		31.03	100			
1.00E+02		32.83	100			
1.00E+01		33.21	10			
1.00E+01		32.93	10			
1.00E-00		40	0			
1.00E-00		40	0			
NTC		40	0			

Gene Name sbg960509cbrecpt

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	-2.51
colon tumor	1.57
colon tumor	-1.25
colon tumor	-20.13
lung tumor	-41.69
lung tumor	10.00
lung tumor	-4.82
lung tumor	3.66
breast tumor	2.22
breast tumor	8.92
breast tumor	1.84
breast tumor	-25.88
brain stage 5 ALZ	-41.28
brain stage 5 ALZ	-3.49
brain stage 5 ALZ	-1.16
brain stage 5 ALZ	-41.28
lung 24	-104.07
lung 28	-104.07
lung 23	-16.16
asthmatic lung	-200.14
asthmatic lung	-4.11
asthmatic lung	-3.72
asthmatic lung	-5.81
endo VEGF	0.00
endo bFGF	0.00
heart T-1	2.51
heart T-14	13.90
heart T-3399	75.82
BM stim	0.00
osteo undif	0.00
Cartilage (pool)	-1.84
PBL HIV IIIB	-11.73
MRC5 HSV strain F	19.22

Gene Name sbg614126complfH

Moderate to low overall expression in normal and disease samples. Highest normal expression in liver and fetal liver. Lower (but still significant expression) is seen in the whole brain, ovary, and uterus. Highest disease expression in 2 of the breast tumor samples, one of the normal brain samples, one of the normal lungs, one of the OA synovium samples, and the HSV-infected MRC5 cells. Upregulation in 1 of 4 colon tumors suggests a role in cancer of the colon. Downregulation in 2 of 4 lung tumors and upregulation in 1 of 4 breast tumors suggest roles in cancers of the lung and breast. Downregulation in 3 of 3 COPD lung samples as well as downregulation in 4 of 4 asthmatic lungs implies an involvement in chronic obstructive pulmonary disease and asthma. Upregulation in 1 of 3 heart samples suggests a role in DCM. Upregulation in HSV implicates involvement in herpes simplex virus as a potential host factor. Moderate to low expression in immune cells, RA and OA synovium bone, and chondrocytes.

Sample sbg614126complfH	Ct (sample 1	Mean GOI	Mean GOI	Average GOI	18S rRNA	50 ng/18S	copies of

	and 2)	copies (sample 1)	copies (sample 2)	Copies	(ng)	rRNA (ng)	mRNA detected/50 ng total RNA
Subcutaneous Adipocytes Zenbio	40, 40	0	0	0.00	3.06	16.34	0.00
Subcutaneous Adipose Zenbio	40, 40	0	0	0.00	0.96	52.36	0.00
Adrenal Gland Clontech	40, 40	0	0	0.00	0.61	81.97	0.00
Whole Brain Clontech	32.34, 31.88	46.5	61.71	54.11	7.24	6.91	373.65
Fetal Brain Clontech	40, 40	0	0	0.00	0.48	103.95	0.00
Cerebellum Clontech	40, 40	0	0	0.00	2.17	23.04	0.00
Cervix	40, 35.04	0	8.88	4.44	2.42	20.66	91.74
Colon	40, 40	0	0	0.00	2.71	18.45	0.00
Endometrium	40, 40	0	0	0.00	0.73	68.21	0.00
Esophagus	40, 40	0	0	0.00	1.37	36.50	0.00
Heart Clontech	40, 40	0	0	0.00	1.32	37.88	0.00
Hypothalamus	40, 39.79	0	0.48	0.24	0.32	155.28	37.27
Ileum	40, 36.32	0	4.04	2.02	2.58	19.38	39.15
Jejunum	33.25, 34.19	26.6	14.98	20.79	6.60	7.58	157.50
Kidney	40, 40	0	0	0.00	2.12	23.58	0.00
Liver	28.77, 28.81	417.4	407.38	412.39	1.50	33.33	13746.33
Fetal Liver Clontech	29.63, 29.5	246.38	266.67	256.53	10.40	4.81	1233.29
Lung	40, 40	0	0	0.00	2.57	19.46	0.00
Mammary Gland Clontech	34.19, 40	14.9	0	7.45	13.00	3.85	28.65
Myometrium	35.76, 40	5.7	0	2.85	2.34	21.37	60.90
Omentum	36.04, 33.62	4.81	21.16	12.99	3.94	12.69	164.78
Ovary	34.29, 32.95	14.02	31.93	22.98	4.34	11 52	264.69
Pancreas	40, 40	0	0	0.00	0.81	61.80	0.00
Head of Pancreas	38.98, 35.35	0.79	7.32	4.06	1.57	31.85	129.14
Parotid Gland	34.58, 33.83	11.74	18.68	15.21	5.48	9.12	138.78
Placenta Clontech	35.73, 35.66	5.82	6.06	5.94	5.26	9.51	56.46
Prostate	40, 40	0	0	0.00	3.00	16.67	0.00
Rectum	40, 40	0.38	0	0.19	1.23	40.65	7.72
Salivary Gland Clontech	40, 40	0.3	0	0.15	7.31	6.84	1.03
Skeletal Muscle Clontech	40, 40	0	0.28	0.14	1.26	39.68	5.56
Skin	40, 40	0	0.33	0.17	1.21	41.32	6.82
Small Intestine Clontech	40, 40	0	0	0.00	0.98	51.07	0.00
Spleen	40, 40	0	0	0.00	4.92	10.16	0.00
Stomach	40, 36	0	4.92	2.46	2.73	18.32	45.05
Testis Clontech	40, 40	0	0	0.00	0.57	87.87	0.00

Thymus Clontech	40, 37.06	0	2.56	1.28	9.89	5.06	6.47
Thyroid	40, 40	0	0.31	0.16	2.77	18.05	2.80
Trachea Clontech	40, 40	0.28	0	0.14	9.71	5.15	0.72
Urinary Bladder	40, 34.13	0	15.53	7.77	5.47	9.14	70.98
Uterus	33.21, 32.79	27.27	35.32	31.30	5.34	9.36	293.02
genomic	26.93	1288.98					
b-actin	27.55	878.74					
1.00E+05	20.07	100000					
1.00E+05	20.14	100000					
1.00E+04	23.43	10000					
1.00E+04	23.34	10000					
1.00E+03	26.84	1000					
1.00E+03	27.02	1000					
1.00E+02	31.72	100					
1.00E+02	31.32	100					
1.00E+01	33.78	10					
1.00E+01	35.79	10					
1.00E-00	40	0					
1.00E-00	40	0					
NTC	40	0					
NTC	40	0					

Sample sbg614126complfH	**Reg number (GSK identifier)**	**Ct**	**Mean GOI copies**	**copies of mRNA detected/50 ng total RNA**	**Sample**	**Fold Change in Disease Population**
colon normal GW98-167	21941	34.6	13.63	27.26	colon normal	
colon tumor GW98-166	21940	35.71	7.35	14.70	colon tumor	-1.85
colon normal GW98-178	22080	40	0	0.00	colon normal	
colon tumor GW98-177	22060	39.81	0.75	1.50	colon tumor	1.50
colon normal GW98-561	23514	38.61	1.45	2.90	colon normal	
colon tumor GW98-560	23513	34.84	11.95	23.90	colon tumor	8.24
colon normal GW98-894	24691	39.05	1.14	2.28	colon normal	
colon tumor GW98-893	24690	40	0	0.00	colon tumor	-2.28
lung normal GW98-3	20742	35.78	7.04	14.08	lung normal	
lung tumor GW98-2	20741	40	0	0.00	lung tumor	-14.08
lung normal GW97-179	20677	33.99	19.21	38.42	lung normal	
lung tumor GW97-178	20676	40	0.49	0.98	lung tumor	-39.20
lung normal GW98-165	21922	39.63	0.82	1.64	lung normal	
lung tumor GW98-164	21921	38.89	1.24	2.48	lung tumor	1.51
lung normal GW98-282	22584	40	0	0.00	lung normal	
lung tumor GW98-281	22583	40	0	0.00	lung tumor	0.00

breast normal GW00-392	28750	32.71	39.28	39.28	breast normal	
breast tumor GW00-391	28746	31.65	70.89	141.78	breast tumor	3.61
breast normal GW00-413	28798	35.83	6.88	6.88	breast normal	
breast tumor GW00-412	28797	33.17	30.3	60.60	breast tumor	8.81
breast normal GW00-235:238	27592-95	36.73	4.16	4.16	breast normal	
breast tumor GW00-231:234	27588-91	35.98	6.33	6.33	breast tumor	1.52
breast normal GW98-621	23656	37.38	2.89	5.78	breast normal	
breast tumor GW98-620	23655	34.95	11.23	22.46	breast tumor	3.89
brain normal BB99-542	25507	32.26	50.34	100.68	brain normal	
brain normal BB99-406	25509	40	0.57	1.14	brain normal	
brain normal BB99-904	25546	34.68	13.04	26.08	brain normal	
brain stage 5 ALZ BB99-874	25502	40	0	0.00	brain stage 5 ALZ	-42.63
brain stage 5 ALZ BB99-887	25503	35.87	6.73	13.46	brain stage 5 ALZ	-3.17
brain stage 5 ALZ BB99-862	25504	39.2	1.05	2.10	brain stage 5 ALZ	-20.30
brain stage 5 ALZ BB99-927	25542	40	0	0.00	brain stage 5 ALZ	-42.63
CT lung KC	normal	39.4	0.93	1.86	CT lung	
lung 26 KC	normal				lung 26	
lung 27 KC	normal	40	0	0.00	lung 27	
lung 24 KC	COPD	40	0	0.00	lung 24	-0.62
lung 28 KC	COPD	40	0	0.00	lung 28	-0.62
lung 23 KC	COPD	40	0	0.00	lung 23	-0.62
lung 25 KC	normal	40	0	0.00	lung 25	
asthmatic lung ODO3112	29321	36.52	4.68	4.68	asthmatic lung	7.55
asthmatic lung ODO3433	29323	40	0	0.00	asthmatic lung	-0.62
asthmatic lung ODO3397	29322	40	0	0.00	asthmatic lung	-0.62
asthmatic lung ODO4928	29325	38.18	1.85	3.70	asthmatic lung	5.97
endo cells KC	control	40	0	0.00	endo cells	
endo VEGF KC		40	0	0.00	endo VEGF	0.00
endo bFGF KC		40	0	0.00	endo bFGF	0.00
heart Clontech	normal	40	0	0.00	heart	
heart (T-1) ischemic	29417	40	0	0.00	heart T-1	0.00
heart (T-14) non-obstructive DCM	29422	40	0	0.00	heart T-14	0.00
heart (T-3399) DCM	29426	36.03	6.13	12.26	heart T-3399	12.26
adenoid GW99-269	26162	34.08	18.19	36.38	adenoid	
tonsil GW98-280	22582	37.46	2.77	5.54	tonsil	
T cells PC00314	28453	40	0	0.00	T cells	
PBMNC		40	0	0.00	PBMNC	
monocyte		40	0	0.00	monocyte	

B cells PC00665	28455	34.56	13.99	27.98	B cells	
dendritic cells 28441		40	0	0.00	dendritic cells	
neutrophils	28440	33.76	21.85	21.85	neutrophils	
eosinophils	28446	40	0	0.00	eosinophils	
BM unstim		40	0	0.00	BM unstim	
BM stim		40	0	0.00	BM stim	0.00
osteo dif		40	0	0.00	osteo dif	0.00
osteo undif		40	0	0.00	osteo undif	
chondrocytes		34.25	16.55	41.38	chondrocytes	
OA Synovium IP12/01	29462	40	0	0.00	OA Synovium	
OA Synovium NP10/01	29461	40	0	0.00	OA Synovium	
OA Synovium NP57/00	28464	33.1	31.54	63.08	OA Synovium	
RA Synovium NP03/01	28466	40	0	0.00	RA Synovium	
RA Synovium NP71/00	28467	40	0	0.00	RA Synovium	
RA Synovium NP45/00	28475	40	0	0.00	RA Synovium	
OA bone (biobank)	29217	40	0	0.00	OA bone (biobank)	
OA bone Sample 1	J. Emory	40	0	0.00	OA bone	
OA bone Sample 2	J. Emory	40	0	0.00	OA bone	
Cartilage (pool)	Normal	40	0	0.00	Cartilage (pool)	
Cartilage (pool)	OA	40	0	0.00	Cartilage (pool)	0.00
PBL unifected	28441	36.12	5.84	11.68	PBL unifected	
PBL HIV IIIB	28442	36.1	5.9	11.80	PBL HIV IIIB	1.01
MRC5 uninfected (100%)	29158	40	0	0.00	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	31.83	64.08	128.16	MRC5 HSV strain F	128.16
W12 cells	29179	40	0	0.00	W12 cells	
Keratinocytes	29180	40	0	0.00	Keratinocytes	
B-actin control		27.26	820.77			
genomic		26.18	1496.25			
1 00E+05		19.13	100000			
1.00E+05		19.38	100000			
1.00E+04		22.56	10000			
1.00E+04		22.67	10000			
1.00E+03		26.01	1000			
1.00E+03		26.44	1000			
1.00E+02		30.93	100			
1.00E+02		30.1	100			
1.00E+01		38.59	10			
1.00E+01		33.26	10			
1.00E-00		40	0			
1.00E-00		40	0			
NTC		40	0			

Gene Name sbg614126complfH

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	-1.85
colon tumor	1.50
colon tumor	8.24
colon tumor	-2.28
lung tumor	-14.08
lung tumor	-39.20
lung tumor	1.51
lung tumor	0.00
breast tumor	3.61
breast tumor	8.81
breast tumor	1.52
breast tumor	3.89
brain stage 5 ALZ	-42.63
brain stage 5 ALZ	-3.17
brain stage 5 ALZ	-20.30
brain stage 5 ALZ	-42.63
lung 24	-0.62
lung 28	-0.62
lung 23	-0.62
asthmatic lung	7.55
asthmatic lung	-0.62
asthmatic lung	-0.62
asthmatic lung	5.97
endo VEGF	0.00
endo bFGF	0.00
heart T-1	0.00
heart T-14	0.00
heart T-3399	12.26
BM stim	0.00
osteo undif	0.00
Cartilage (pool)	0.00
PBL HIV IIIB	1.01
MRC5 HSV strain F	128.16

Gene Name sbg120703RNase

Moderate to low overall expression in normal and disease samples. Highest normal expression in whole brain and salivary gland. Moderate expression in the fetal liver and the thymus. Highest disease expression in 2 of the normal lung samples, one of the lung tumor samples, the normal cartilage pool, and the HSV-infected MRC5 cells. Upregulation in 1 of 4 colon tumors suggests a role in cancer of the colon. Downregulation in 2 of 4 lung tumor samples suggests possible implication in lung cancer. Upregulation in 2 of 4 breast tumors implies an involvement in cancers of the breast. Downregulation in 3 of 3 COPD lung samples implies an involvement in COPD. Upregulation in 3 of 3 heart samples implicates this gene in diseases of the heart such as DCM and ischemia. High expression in the OA and RA synovium and the OA bone samples suggests a possible involvement in osteoarthritis and rheumatoid arthritis. Upregulation in HSV implicates this gene in herpes simplex virus as a potential host factor. Moderate to low expression in immune cells.

Sample sbg120703RNase	Ct (sample 1 and 2)	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detected/50 ng total RNA
Subcutaneous Adipocytes Zenbio	40, 36.24	0	2.54	1.27	3.06	16.34	20.75
Subcutaneous Adipose Zenbio	36.58, 40	2.07	0	1.04	0.96	52.36	54.19
Adrenal Gland Clontech	40, 40	0.22	0	0.11	0.61	81.97	9.02
Whole Brain Clontech	28.62, 28.6	245.21	247.41	246.31	7.24	6.91	1701.04
Fetal Brain Clontech	40, 40	0.3	0	0.15	0.48	103.95	15.59
Cerebellum Clontech	40, 40	0.29	0	0.15	2.17	23.04	3.34
Cervix	35.3, 40	4.45	0	2.23	2.42	20.66	45.97
Colon	40, 40	0.26	0	0.13	2.71	18.45	2.40
Endometrium	40, 38.38	0	0.7	0.35	0.73	68.21	23.87
Esophagus	36.11, 37.01	2.74	1.6	2.17	1.37	36.50	79.20
Heart Clontech	40, 40	0	0	0.00	1.32	37.88	0.00
Hypothalamus	40, 40	0	0	0.00	0.32	155.28	0.00
Ileum	39.31, 36.07	0.4	2.8	1.60	2.58	19.38	31.01
Jejunum	34.13, 39.51	8.98	0.36	4.67	6.60	7.58	35.38
Kidney	40, 40	0.48	0	0.24	2.12	23.58	5.66
Liver	34.4, 36.04	7.64	2.86	5.25	1.50	33.33	175.00
Fetal Liver Clontech	31.46, 31.39	44.65	46.4	45.53	10.40	4.81	218.87
Lung	34.21, 35.61	8.59	3.71	6.15	2.57	19.46	119.65
Mammary Gland Clontech	34.9, 35.65	5.67	3.6	4.64	13.00	3.85	17.83
Myometrium	40, 38.99	0	0.49	0.25	2.34	21.37	5.24
Omentum	38.39, 34.35	0.7	7.89	4.30	3.94	12.69	54.51
Ovary	35, 33.21	5.34	15.64	10.49	4.34	11.52	120 85
Pancreas	40	0	0	0.00	0.81	61.80	0.00
Head of Pancreas	40	0	0	0.00	1.57	31.85	0.00
Parotid Gland	32.22, 33.49	28.28	13.18	20.73	5.48	9.12	189.14
Placenta Clontech	37, 39.59	1.6	0.34	0.97	5.26	9.51	9.22
Prostate	35.03, 35.75	5.23	3.4	4.32	3.00	16.67	71.92
Rectum	38.25, 40	0.76	0.21	0.49	1.23	40.65	19.72
Salivary Gland Clontech	30.01, 29.73	106.25	125.78	116.02	7.31	6.84	793.54
Skeletal Muscle Clontech	40, 39.16	0.41	0.44	0.43	1.26	39.68	16.87
Skin	37.21, 35.01	1.42	5.31	3.37	1.21	41.32	139.05
Small Intestine Clontech	40, 40	0	0.19	0.10	0.98	51.07	4.85
Spleen	35.4, 35.9	4.2	3.11	3.66	4.92	10.16	37.14
Stomach	36.12, 40	2.73	0.21	1.47	2.73	18.32	26.92
Testis Clontech	40, 40	0	0	0.00	0.57	87.87	0.00

Thymus Clontech	31.88, 31.42	34.61	45.62	40.12	9.89	5.06	202.81
Thyroid	40, 35.22	0	4.67	2.34	2.77	18.05	42.15
Trachea Clontech	35.38, 37.52	4.26	1.17	2.72	9.71	5.15	13.98
Urinary Bladder	38.77, 40	0.56	0.31	0.44	5.47	9.14	3.98
Uterus	33.66, 37.55	11.93	1.16	6.55	5.34	9.36	61.28
genomic	25.78	1342.66					
b-actin	27.27	551.42					
1.00E+05	19.03	100000					
1.00E+05	19.08	100000					
1.00E+04	22.28	10000					
1.00E+04	22.27	10000					
1.00E+03	25.85	1000					
1.00E+03	25.6	1000					
1.00E+02	30.44	100					
1.00E+02	29.33	100					
1.00E+01	34.4	10					
1.00E+01	34.48	10					
1.00E-00							
1.00E-00							
NTC	40	-1					
NTC	40	0					

Sample sbg120703RNase	**Reg number (GSK identifier)**	**Ct**	**Mean GOI copies**	**copies of mRNA detected/ 50 ng total RNA**	**Sample**	**Fold Change in Disease Population**
colon normal GW98-167	21941	29.03	142.85	285.70	colon normal	
colon tumor GW98-166	21940	28.31	226.87	453.74	colon tumor	1.59
colon normal GW98-178	22080	33.08	10.78	21.56	colon normal	
colon tumor GW98-177	22060	29.33	118.09	236.18	colon tumor	10.95
colon normal GW98-561	23514	30.02	76.09	152.18	colon normal	
colon tumor GW98-560	23513	30.42	58.89	117.78	colon tumor	-1.29
colon normal GW98-894	24691	29.07	139.29	278.58	colon normal	
colon tumor GW98-893	24690	30.3	63.5	127.00	colon tumor	-2.19
lung normal GW98-3	20742	26.86	574.4	1148.80	lung normal	
lung tumor GW98-2	20741	30.07	73.89	147.78	lung tumor	-7.77
lung normal GW97-179	20677	29.74	90.79	181.58	lung normal	
lung tumor GW97-178	20676	27.63	351.24	702.48	lung tumor	3.87
lung normal GW98-165	21922	26.63	663.94	1327.88	lung normal	
lung tumor GW98-164	21921	29.38	114.52	229.04	lung tumor	-5.80
lung normal GW98-282	22584	30	77.02	154.04	lung normal	
lung tumor GW98-281	22583	29.64	97.04	194.08	lung tumor	1.26
breast normal GW00-392	28750	29.08	138.57	138.57	breast normal	
breast tumor GW00-391	28746	28.77	169.53	339.06	breast tumor	2.45
breast normal GW00-413	28798	32.72	13.55	13.55	breast normal	
breast tumor GW00-412	28797	31.01	40.4	80.80	breast tumor	5.96

breast normal GW00-235:238	27592-95	34.39	4.68	4.68	breast normal	
breast tumor GW00-231:234	27588-91	31.4	31.48	31.48	breast tumor	6.73
breast normal GW98-621	23656	28.54	195.6	391.20	breast normal	
breast tumor GW98-620	23655	30.37	60.84	121.68	breast tumor	-3.21
brain normal BB99-542	25507	32.94	11.79	23.58	brain normal	
brain normal BB99-406	25509	32.22	18.66	37.32	brain normal	
brain normal BB99-904	25546	32.3	17.71	35.42	brain normal	
brain stage 5 ALZ BB99-874	25502	32.82	12.76	25.52	brain stage 5 ALZ	-1.26
brain stage 5 ALZ BB99-887	25503	30.31	63.18	126.36	brain stage 5 ALZ	3.94
brain stage 5 ALZ BB99-862	25504	31.42	31.08	62.16	brain stage 5 ALZ	1.94
brain stage 5 ALZ BB99-927	25542	33.35	9.08	18.16	brain stage 5 ALZ	-1.77
CT lung KC	normal	30.41	59.49	118.98	CT lung	
lung 26 KC	normal				lung 26	
lung 27 KC	normal	37.69	0.57	0.57	lung 27	
lung 24 KC	COPD	40	0	0.00	lung 24	-40.17
lung 28 KC	COPD	40	0	0.00	lung 28	-40 17
lung 23 KC	COPD	40	0	0.00	lung 23	-40.17
lung 25 KC	normal	36.86	0.97	0.97	lung 25	
asthmatic lung ODO3112	29321	33.08	10.79	10.79	asthmatic lung	-3.72
asthmatic lung ODO3433	29323	29.94	80.31	160.62	asthmatic lung	4.00
asthmatic lung ODO3397	29322	29.79	87.94	175.88	asthmatic lung	4.38
asthmatic lung ODO4928	29325	30.08	73.39	146.78	asthmatic lung	3.65
endo cells KC	control	40	0.13	0.13	endo cells	
endo VEGF KC		40	0	0.00	endo VEGF	-0.13
endo bFGF KC		40	0.12	0.12	endo bFGF	-1.08
heart Clontech	normal	34.66	3.95	7.90	heart	
heart (T-1) ischemic	29417	30.43	58.48	116.96	heart T-1	14.81
heart (T-14) non-obstructive DCM	29422	30.3	63.76	127.52	heart T-14	16.14
heart (T-3399) DCM	29426	31.14	37.27	74.54	heart T-3399	9.44
adenoid GW99-269	26162	33.15	10.31	20.62	adenoid	
tonsil GW98-280	22582	30.26	65.22	130.44	tonsil	
T cells PC00314	28453	33.29	9.45	18.90	T cells	
PBMNC		40	0	0.00	PBMNC	
monocyte		40	0	0.00	monocyte	
B cells PC00665	28455	32.25	18.35	36.70	B cells	
dendritic cells 28441		30.52	55.34	110.68	dendritic cells	
neutrophils	28440	31.61	27.61	27.61	neutrophils	
eosinophils	28446	33.2	10.01	20.02	eosinophils	
BM unstim		40	0	0.00	BM unstim	
BM stim		40	0	0.00	BM stim	0.00
osteo dif		40	0	0.00	osteo dif	0.00
osteo undif		40	0	0.00	osteo undif	
chondrocytes		29.65	96.25	240.63	chondrocytes	

OA Synovium IP12/01	29462	28.59	190.09	190.09	OA Synovium	
OA Synovium NP10/01	29461	29.06	140.66	281.32	OA Synovium	
OA Synovium NP57/00	28464	28.38	216.61	433.22	OA Synovium	
RA Synovium NP03/01	28466	29.43	111	222.00	RA Synovium	
RA Synovium NP71/00	28467	28.35	220.48	440.96	RA Synovium	
RA Synovium NP45/00	28475	28.7	176.79	353.58	RA Synovium	
OA bone (biobank)	29217	30.6	52.6	52.60	OA bone (biobank)	
OA bone Sample 1	J. Emory	29.64	97.1	194.20	OA bone	
OA bone Sample 2	J. Emory	30.85	44.71	89.42	OA bone	
Cartilage (pool)	Normal	28.07	264.86	529.72	Cartilage (pool)	
Cartilage (pool)	OA	30.47	56.97	113.94	Cartilage (pool)	-4.65
PBL unifected	28441	33.41	8.73	17.46	PBL unifected	
PBL HIV IIIB	28442	32.1	20.17	40.34	PBL HIV IIIB	2.31
MRC5 uninfected (100%)	29158	31.09	38.5	77.00	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	28.24	237.46	474.92	MRC5 HSV strain F	6.17
W12 cells	29179	28.83	162.45	324.90	W12 cells	
Keratinocytes	29180	29.21	127.89	255.78	Keratinocytes	
B-actin control		26.99	528.52			
genomic		25.66	1229.15			
1.00E+05		18.76	100000			
1.00E+05		19.03	100000			
1.00E+04		22.01	10000			
1.00E+04		22.05	10000			
1.00E+03		26.01	1000			
1.00E+03		25.68	1000			
1.00E+02		30.57	100			
1.00E+02		30.32	100			
1.00E+01		32.24	10			
1.00E+01		40	0			
1.00E-00		40	0			
1.00E-00		40	0			
NTC		40	0			

Gene Name sbg120703RNase

Disease tissues	**Fold Change in Disease Population Relative to Normal**
colon tumor	1.59
colon tumor	10.95
colon tumor	-1.29
colon tumor	-2.19
lung tumor	-7.77

lung tumor	3.87
lung tumor	-5.80
lung tumor	1.26
breast tumor	2.45
breast tumor	5.96
breast tumor	6.73
breast tumor	-3.21
brain stage 5 ALZ	-1.26
brain stage 5 ALZ	3.94
brain stage 5 ALZ	1.94
brain stage 5 ALZ	-1.77
lung 24	-40.17
lung 28	-40.17
lung 23	-40.17
asthmatic lung	-3.72
asthmatic lung	4.00
asthmatic lung	4.38
asthmatic lung	3.65
endo VEGF	-0.13
endo bFGF	-1.08
heart T-1	14.81
heart T-14	16.14
heart T-3399	9.44
BM stim	0.00
osteo undif	0.00
Cartilage (pool)	-4.65
PBL HIV IIIB	2.31
MRC5 HSV strain F	6.17

Gene Name sbg98530TS

Moderate overall expression in normal and disease samples. Highest normal expression in whole brain, endometrium, and testis. Moderate expression in normal heart, skeletal muscle, and esophagus. Shows expression in most of the GI tract samples as well as the female reproductive tract samples. Highest disease expression in one of the colon tumor samples, all 3 of the heart samples, and the chondrocytes. Data predominantly shows a muscle-specific pattern of expression. Upregulation in 1 of 4 colon tumors and upregulation in 2 of 4 breast tumors implies an involvement in cancers of the colon and breast. Downregulation in 3 of 3 COPD samples implies a role in chronic obstructive pulmonary disease. Downregulation in HSV implicates involvement in herpes simplex virus as a potential host factor. Moderate to low overall expression in immune cells. High expression in chondrocytes and OA and RA synovium suggests possible involvement in osteoarthritis and rheumatoid arthritis.

Sample sbg98530TS	**Ct (sample 1 and 2)**	**Mean GOI copies (sample 1)**	**Mean GOI copies (sample 2)**	**Average GOI Copies**	**18S rRNA (ng)**	**50 ng/18S rRNA (ng)**	**copies of mRNA detected/50 ng total RNA**
Subcutaneous Adipocytes Zenbio	40, 36.35	0	4.22	2.11	3.06	16.34	34.48
Subcutaneous Adipose Zenbio	35.78, 40	5.89	0	2.95	0.96	52.36	154.19
Adrenal Gland Clontech	40, 40	0	0	0.00	0.61	81.97	0.00

Whole Brain Clontech	26.63, 26.42	1253.02	1414.2	1333.61	7.24	6.91	9210.01
Fetal Brain Clontech	40, 37.33	0	2.38	1.19	0.48	103.95	123.70
Cerebellum Clontech	35.9, 40	5.5	0	2.75	2.17	23.04	63.36
Cervix	33.47, 34.27	22.86	14.26	18.56	2.42	20.66	383.47
Colon	34.49, 34.05	12.58	16.28	14.43	2.71	18.45	266.24
Endometrium	33.28, 32.94	25.41	31.15	28.28	0.73	68.21	1929.06
Esophagus	33.61, 32.9	21.02	31.85	26.44	1.37	36.50	964.78
Heart Clontech	33.32, 33.03	24.91	29.42	27.17	1.32	37.88	1028.98
Hypothalamus	40, 40	0	0	0.00	0.32	155.28	0.00
Ileum	35.89, 33.37	5.53	24.14	14.84	2.58	19.38	287.50
Jejunum	31.55, 31.42	70.2	75.71	72.96	6.60	7.58	552.69
Kidney	40, 35.5	0	6.96	3.48	2.12	23.58	82.08
Liver	34.29, 33.63	14.07	20.78	17.43	1.50	33.33	580.83
Fetal Liver Clontech	32.16, 32.92	49.02	31.52	40.27	10.40	4.81	193.61
Lung	40, 35.78	0		2.95	2.57	19.46	57.30
Mammary Gland Clontech	31.42, 32.08	75.62	51.54	63.58	13.00	3.85	244.54
Myometrium	32.93, 32.03	31.21	52.84	42.03	2.34	21.37	897.97
Omentum	35.21, 40	8.23	0	4.12	3.94	12.69	52.22
Ovary	35.36, 35.51	7.53	6.89	7.21	4.34	11.52	83.06
Pancreas	40, 40	0	0	0.00	0.81	61.80	0.00
Head of Pancreas	40, 37.54	0	2.11	1.06	1.57	31.85	33.60
Parotid Gland	31.67, 31.01	65.33	96.46	80.90	5.48	9.12	738.09
Placenta Clontech	33.13, 32.05	27 88	52.3	40.09	5.26	9.51	381.08
Prostate	35.03, 40	9.13	5.22	7.18	3.00	16.67	119.58
Rectum	40, 35.19	0	8.32	4.16	1.23	40.65	169.11
Salivary Gland Clontech	32.41, 34.06	42.32	16.15	29.24	7.31	6.84	199.97
Skeletal Muscle Clontech	33.93, 33.76	17.41	19.28	18.35	1.26	39.68	727.98
Skin	40, 40	0	0	0.00	1.21	41.32	0.00
Small Intestine Clontech	34.11	11.73	15.7	13.72	0.98	51.07	700.46
Spleen	36.08, 40	4.94	0.37	2.66	4.92	10.16	26.98
Stomach	40, 40	0	0	0.00	2.73	18.32	0.00
Testis Clontech	35.54, 33.26	6.79	25.83	16.31	0.57	87.87	1433.22
Thymus Clontech	33.66, 34.12	20.35	15.62	17.99	9.89	5.06	90.93
Thyroid	40, 35.46	0	7.12	3.56	2.77	18.05	64.26
Trachea Clontech	32.08, 31.84	51.54	59.21	55.38	9.71	5.15	285.14
Urinary Bladder	34.75, 36.99	10.8	2.91	6.86	5.47	9.14	62.66
Uterus	31.79, 32.2	60.97	47.95	54.46	5 34	9.36	509.93
genomic	26.8	1133.17					
b-actin	27.6	706.62					
1.00E+05	19.53	100000					
1.00E+05	19.54	100000					
1.00E+04	22.8	10000					
1.00E+04	23.02	10000					
1 00E+03	26.14	1000					
1.00E+03	26.59	1000					

1.00E+02	31.41	100					
1.00E+02	30.97	100					
1.00E+01	40	0					
1.00E+01	35.24	10					
1.00E-00	40	0					
1.00E-00	40	0					
NTC	40	0					
NTC	40	0					

Sample sbg98530TS	**Reg number (GSK identifier)**	**Ct**	**Mean GOI copies**	**copies of mRNA detected/50 ng total RNA**	**Sample**	**Fold Change in Disease Population**
colon normal GW98-167	21941	26.26	1792.89	3585.78	colon normal	
colon tumor GW98-166	21940	26.2	1856.22	3712.44	colon tumor	1.04
colon normal GW98-178	22080	27.25	986.8	1973.60	colon normal	
colon tumor GW98-177	22060	26.7	1369.12	2738.24	colon tumor	1.39
colon normal GW98-561	23514	27.55	821.35	1642.70	colon normal	
colon tumor GW98-560	23513	24.64	4748.96	9497.92	colon tumor	5.78
colon normal GW98-894	24691	27.27	971.87	1943.74	colon normal	
colon tumor GW98-893	24690	25.35	3093.47	6186 94	colon tumor	3.18
lung normal GW98-3	20742	27.02	1133.68	2267.36	lung normal	
lung tumor GW98-2	20741	27.26	981.94	1963.88	lung tumor	-1.15
lung normal GW97-179	20677	29.14	315.07	630.14	lung normal	
lung tumor GW97-178	20676	28.15	571.76	1143.52	lung tumor	1.81
lung normal GW98-165	21922	27.86	682.2	1364.40	lung normal	
lung tumor GW98-164	21921	27.45	871.19	1742.38	lung tumor	1.28
lung normal GW98-282	22584	28.12	581.74	1163.48	lung normal	
lung tumor GW98-281	22583	29.32	283.71	567.42	lung tumor	-2.05
breast normal GW00-392	28750	27.85	687.38	687.38	breast normal	
breast tumor GW00-391	28746	26.61	1444.19	2888.38	breast tumor	4.20
breast normal GW00-413	28798	28.43	483.03	483.03	breast normal	
breast tumor GW00-412	28797	25.49	2836.66	5673.32	breast tumor	11.75
breast normal GW00-235:238	27592-95	32.26	48.29	48.29	breast normal	
breast tumor GW00-231:234	27588-91	29.07	328.46	328.46	breast tumor	6.80
breast normal GW98-621	23656	26.82	1279.07	2558.14	breast normal	
breast tumor GW98-620	23655	26.8	1289.27	2578.54	breast tumor	1.01
brain normal BB99-542	25507	29.03	337.63	675.26	brain normal	
brain normal BB99-406	25509	29.19	305.6	611.20	brain normal	
brain normal BB99-904	25546	30.44	144.55	289.10	brain normal	
brain stage 5 ALZ BB99-874	25502	28.47	471.8	943.60	brain stage 5 ALZ	1.80
brain stage 5 ALZ BB99-887	25503	27.3	955.52	1911.04	brain stage 5 ALZ	3.64

brain stage 5 ALZ BB99-862	25504	27.42	891.77	1783.54	brain stage 5 ALZ	3.40
brain stage 5 ALZ BB99-927	25542	29.31	285.16	570.32	brain stage 5 ALZ	1.09
CT lung KC	normal	27.96	643.88	1287.76	CT lung	
lung 26 KC	normal	35.82	5.66	5.66	lung 26	
lung 27 KC	normal	40	0	0.00	lung 27	
lung 24 KC	COPD	40	0	0.00	lung 24	-325.52
lung 28 KC	COPD	35.3	7.73	7.73	lung 28	-42.11
lung 23 KC	COPD	36.67	3.39	3.39	lung 23	-96.02
lung 25 KC	normal	35.11	8.67	8.67	lung 25	
asthmatic lung ODO3112	29321	31.01	102.08	102.08	asthmatic lung	-3.19
asthmatic lung ODO3433	29323	29.76	216.81	433.62	asthmatic lung	1.33
asthmatic lung ODO3397	29322	29.83	208.08	416.16	asthmatic lung	1.28
asthmatic lung ODO4928	29325	30.37	150.17	300.34	asthmatic lung	-1 08
endo cells KC	control	37.54	2	2.00	endo cells	
endo VEGF KC		35.77	5.83	5.83	endo VEGF	2.92
endo bFGF KC		40	0	0.00	endo bFGF	-2.00
heart Clontech	normal	26.09	1982.44	3964.88	heart	
heart (T-1) ischemic	29417	24	6956.27	13912.54	heart T-1	3.51
heart (T-14) non-obstructive DCM	29422	24.55	5010.03	10020.06	heart T-14	2.53
heart (T-3399) DCM	29426	24.05	6766.57	13533.14	heart T-3399	3.41
adenoid GW99-269	26162	30.56	134.11	268.22	adenoid	
tonsil GW98-280	22582	27.94	651.01	1302.02	tonsil	
T cells PC00314	28453	29.8	212.45	424.90	T cells	
PBMNC		33.01	30.69	30.69	PBMNC	
monocyte		33.42	23.9	47.80	monocyte	
B cells PC00665	28455	33.52	22.59	45.18	B cells	
dendritic cells 28441		29.07	329.58	659.16	dendritic cells	
neutrophils	28440	30.39	149	149.00	neutrophils	
eosinophils	28446	35.41	7.25	14.50	eosinophils	
BM unstim		34.24	14.65	14.65	BM unstim	
BM stim		36.61	3.51	3.51	BM stim	-4.17
osteo dif		30.55	135.33	135.33	osteo dif	3.02
osteo undif		32.38	44.88	44.88	osteo undif	
chondrocytes		25.35	3089.54	7723.85	chondrocytes	
OA Synovium IP12/01	29462	28.75	398.53	398.53	OA Synovium	
OA Synovium NP10/01	29461	27.04	1119.77	2239.54	OA Synovium	
OA Synovium NP57/00	28464	28.85	375.92	751.84	OA Synovium	
RA Synovium NP03/01	28466	28.14	574.66	1149.32	RA Synovium	
RA Synovium NP71/00	28467	27.58	806.11	1612.22	RA Synovium	
RA Synovium NP45/00	28475	28.04	611.1	1222.20	RA Synovium	
OA bone (biobank)	29217	30.25	161.3	161.30	OA bone (biobank)	
OA bone Sample 1	J. Emory	31.24	89.29	178.58	OA bone	
OA bone Sample 2	J. Emory	30.98	104.34	208.68	OA bone	

Cartilage (pool)	Normal	29.86	204.47	408.94	Cartilage (pool)	
Cartilage (pool)	OA	29.37	275.09	550.18	Cartilage (pool)	1.35
PBL unifected	28441	26.45	1598.39	3196.78	PBL unifected	
PBL HIV IIIB	28442	27.57	814.58	1629.16	PBL HIV IIIB	-1.96
MRC5 uninfected (100%)	29158	25.13	3539.95	7079.90	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	30.49	139.89	279.78	MRC5 HSV strain F	-25.31
W12 cells	29179	26.72	1359.04	2718.08	W12 cells	
Keratinocytes	29180	26.41	1633.77	3267.54	Keratinocytes	
B-actin control		27.87	678.8			
genomic		26.9	1214.71			
1.00E+05		19.86	100000			
1.00E+05		19.82	100000			
1.00E+04		23.15	10000			
1.00E+04		23.21	10000			
1.00E+03		26.62	1000			
1.00E+03		26.79	1000			
1.00E+02		31.2	100			
1.00E+02		32.2	100			
1.00E+01		40	0			
1.00E+01		34.53	10			
1.00E-00		40	0			
1.00E-00		40	0			
NTC		40	0			

Gene Name sbg98530TS

Disease tissues	**Fold Change in Disease Population Relative to Normal**
colon tumor	1.04
colon tumor	1.39
colon tumor	5.78
colon tumor	3.18
lung tumor	-1.15
lung tumor	1.81
lung tumor	1.28
lung tumor	-2.05
breast tumor	4.20
breast tumor	11.75
breast tumor	6.80
breast tumor	1.01
brain stage 5 ALZ	1.80
brain stage 5 ALZ	3.64
brain stage 5 ALZ	3.40
brain stage 5 ALZ	1.09
lung 24	-325.52
lung 28	-42.11
lung 23	-96.02
asthmatic lung	-3.19
asthmatic lung	1.33

asthmatic lung	1.28
asthmatic lung	-1.08
endo VEGF	2.92
endo bFGF	-2.00
heart T-1	3.51
heart T-14	2.53
heart T-3399	3.41
BM stim	-4.17
osteo undif	3.02
Cartilage (pool)	1.35
PBL HIV IIIB	-1.96
MRC5 HSV strain F	-25.31

Gene Name sbg563917RDP

Moderate to low overall expression in normal and disease samples. Highest normal expression in testis liver, trachea, and whole brain. Shows good expression in most of the GI tract samples. Highest disease expression in T cells, B cells, neutrophils, and eosinophils. Upregulation in 1 of 4 breast tumors implies involvement in cancer of the breast. Downregulation in 3 of 3 COPD lungs suggests an involvement in chronic obstructive pulmonary disease. Downregulation in the ischemic heart sample implicates this gene in ischemic heart disease. Downregulation in the VEGF and bFGF-treated endothelial cells suggests a role in angiogenesis. Upregulation in HSV implicates involvement in herpes simplex virus as a potential host factor.

Sample *sbg563917RDP*	**Ct (sample 1 and 2)**	**Mean GOI copies (sample 1)**	**Mean GOI copies (sample 2)**	**Average GOI Copies**	**18S rRNA (ng)**	**50 ng/18S rRNA (ng)**	**copies of mRNA detected/50 ng total RNA**
Subcutaneous Adipocytes Zenbio	35.34, 40	3.66	0	1.83	3.06	16.34	29.90
Subcutaneous Adipose Zenbio	40, 40	0		0.00	0.96	52.36	0.00
Adrenal Gland Clontech	40, 40	0	0	0.00	0.61	81.97	0.00
Whole Brain Clontech	30.09, 30.01	91.85	96.8	94.33	7.24	6.91	651.42
Fetal Brain Clontech	40, 40	0	0	0.00	0.48	103.95	0.00
Cerebellum Clontech	35.19, 40	4.03	0	2.02	2.17	23.04	46.43
Cervix	36.08, 40	2.33	0	1.17	2.42	20.66	24.07
Colon	36.07, 35.1	2.35	4.24	3.30	2.71	18.45	60.79
Endometrium	35.01, 40	4.49	0	2.25	0.73	68.21	153.14
Esophagus	34.94, 40	4.68	0	2.34	1.37	36.50	85.40
Heart Clontech	40, 40	0	0	0.00	1.32	37.88	0.00
Hypothalamus	40, 40	0	0	0.00	0.32	155.28	0.00
Ileum	35.24, 40	3.89	0	1.95	2.58	19.38	37.69
Jejunum	35.37, 33.35	3.6	12.44	8.02	6.60	7.58	60.76
Kidney	40, 34.97	0	4.6	2.30	2.12	23.58	54.25
Liver	33.51, 34.6	11.25	5.78	8.52	1.50	33.33	283.83
Fetal Liver Clontech	33.19, 35.54	13.75	3.25	8.50	10.40	4.81	40.87
Lung	34.32	6.84	2.28	4.56	2.57	19.46	88.72
Mammary Gland Clontech	40, 35.14	0	4.15	2.08	13.00	3.85	7.98

Myometrium	40, 40	0	0.09	0.05	2.34	21.37	0.96
Omentum	36.17, 33.01	2.2	15.32	8.76	3.94	12.69	111.17
Ovary	40, 40	0	0	0.00	4.34	11.52	0.00
Pancreas	40, 40	0	0	0.00	0.81	61.80	0.00
Head of Pancreas	40, 40	0	0	0.00	1.57	31.85	0.00
Parotid Gland	35.43, 39.81	3.46	0.24	1.85	5.48	9.12	16.88
Placenta Clontech	33.7, 35.45	10.02	3.42	6.72	5.26	9.51	63.88
Prostate	40, 40	0	0	0.00	3.00	16.67	0.00
Rectum	40, 40	0	0	0.00	1.23	40.65	0.00
Salivary Gland Clontech	34.89, 40	4.83	0	2.42	7.31	6.84	16.52
Skeletal Muscle Clontech	40, 40	0	0	0.00	1.26	39.68	0.00
Skin	40, 40	0	0	0.00	1.21	41.32	0.00
Small Intestine Clontech	40, 40	0	0	0.00	0.98	51.07	0.00
Spleen	35.01, 33.36	4.48	12.38	8.43	4.92	10.16	85.67
Stomach	33.38, 34.18	12.18	7.48	9.83	2.73	18.32	180.04
Testis Clontech	34.25, 32.86	7.17	16.84	12.01	0.57	87.87	1054.92
Thymus Clontech	32.14, 33.25	26.17	13.24	19.71	9.89	5.06	99.62
Thyroid	40, 40	0	0.09	0.05	2.77	18.05	0.81
Trachea Clontech	31.41, 31	41.04	52.65	46.85	9.71	5.15	241.22
Urinary Bladder	40, 35.05	0	4.38	2.19	5.47	9.14	20.02
Uterus	33.77, 33.41	9.62	12	10.81	5.34	9.36	101.22
genomic	26.54	813.56					
b-actin	27.39	481.34					
1.00E+05	18.71	100000					
1.00E+05	18.92	100000					
1.00E+04	22.44	10000					
1.00E+04	22.11	10000					
1.00E+03	26.05	1000					
1.00E+03	26.11	1000					
1.00E+02	30.4	100					
1.00E+02	30.17	100					
1.00E+01	33.87	10					
1.00E+01	33.26	10					
1.00E-00	40	0					
1.00E-00	40	0					
NTC	40	0					
NTC	40	0					

Sample sbg563917RDP	**Reg number (GSK identifier)**	**Ct**	**Mean GOI copies**	**copies of mRNA detected/50 ng total RNA**	**Sample**	**Fold Change in Disease Population**
colon normal GW98-167	21941	30.39	148.35	296.70	colon normal	

colon tumor GW98-166	21940	30.93	110.14	220.28	colon tumor	-1.35
colon normal GW98-178	22080	32.93	36.71	73.42	colon normal	
colon tumor GW98-177	22060	34.8	13.09	26.18	colon tumor	-2.80
colon normal GW98-561	23514	31.41	84.68	169.36	colon normal	
colon tumor GW98-560	23513	32.09	58.33	116.66	colon tumor	-1.45
colon normal GW98-894	24691	30.02	182.15	364.30	colon normal	
colon tumor GW98-893	24690	31.12	99.26	198.52	colon tumor	-1.84
lung normal GW98-3	20742	28.4	443.99	887.98	lung normal	
lung tumor GW98-2	20741	33.59	25.44	50.88	lung tumor	-17.45
lung normal GW97-179	20677	28.63	391.85	783.70	lung normal	
lung tumor GW97-178	20676	29.16	292.08	584.16	lung tumor	-1.34
lung normal GW98-165	21922	29.13	296.8	593.60	lung normal	
lung tumor GW98-164	21921	30.22	163.43	326.86	lung tumor	-1.82
lung normal GW98-282	22584	31.71	71.72	143.44	lung normal	
lung tumor GW98-281	22583	31.74	70.77	141.54	lung tumor	-1.01
breast normal GW00-392	28750	31.49	81.02	81.02	breast normal	
breast tumor GW00-391	28746	33.58	25.62	51.24	breast tumor	-1.58
breast normal GW00-413	28798	35.07	11.31	11.31	breast normal	
breast tumor GW00-412	28797	31.99	61.52	123.04	breast tumor	10.88
breast normal GW00-235:238	27592-95	35.63	8.3	8.30	breast normal	
breast tumor GW00-231:234	27588-91	34.33	16.97	16.97	breast tumor	2.04
breast normal GW98-621	23656	32.07	58.95	117.90	breast normal	
breast tumor GW98-620	23655	32.71	41.33	82.66	breast tumor	-1.43
brain normal BB99-542	25507	30.16	168.86	337.72	brain normal	
brain normal BB99-406	25509	31.12	99.35	198.70	brain normal	
brain normal BB99-904	25546	31.14	98.44	196.88	brain normal	
brain stage 5 ALZ BB99-874	25502	33.16	32.39	64.78	brain stage 5 ALZ	-3.77
brain stage 5 ALZ BB99-887	25503	29.32	267.28	534.56	brain stage 5 ALZ	2.19
brain stage 5 ALZ BB99-862	25504	30.36	150.72	301.44	brain stage 5 ALZ	1.23
brain stage 5 ALZ BB99-927	25542	30.1	174.01	348.02	brain stage 5 ALZ	1.42
CT lung KC	normal	31.06	102.88	205.76	CT lung	
lung 26 KC	normal	32.15	56.21	56.21	lung 26	
lung 27 KC	normal	35.96	6.92	6.92	lung 27	
lung 24 KC	COPD	40	0	0.00	lung 24	-70.34
lung 28 KC	COPD	36.21	6.05	6.05	lung 28	-11.63
lung 23 KC	COPD	34.83	12.87	12.87	lung 23	-5.47
lung 25 KC	normal	34.89	12.45	12.45	lung 25	
asthmatic lung ODO3112	29321	32.57	44.76	44.76	asthmatic lung	-1.57
asthmatic lung ODO3433	29323	32.4	49.04	98.08	asthmatic lung	1.39
asthmatic lung ODO3397	29322	31.79	68.64	137.28	asthmatic lung	1.95
asthmatic lung ODO4928	29325	31.34	88.11	176.22	asthmatic lung	2.51
endo cells KC	control	35.77	7.68	7.68	endo cells	
endo VEGF KC		40	0	0.00	endo VEGF	-7.68

endo bFGF KC		40	0	0.00	endo bFGF	-7.68
heart Clontech	normal	31.09	100.75	201.50	heart	
heart (T-1) ischemic	29417	34.75	13.46	26.92	heart T-1	-7.49
heart (T-14) non-obstructive DCM	29422	33.69	24.17	48.34	heart T-14	-4.17
heart (T-3399) DCM	29426	33.48	27.16	54.32	heart T-3399	-3.71
adenoid GW99-269	26162	30.49	140.7	281.40	adenoid	
tonsil GW98-280	22582	30.07	177.32	354.64	tonsil	
T cells PC00314	28453	27.79	622.1	1244.20	T cells	
PBMNC		36.19	6.11	6.11	PBMNC	
monocyte		33.24	30.91	61.82	monocyte	
B cells PC00665	28455	26.37	1355.2	2710.40	B cells	
dendritic cells 28441		28.69	378.62	757.24	dendritic cells	
neutrophils	28440	23.28	7420.47	7420.47	neutrophils	
eosinophils	28446	25.33	2408.94	4817.88	eosinophils	
BM unstim		32.24	53.57	53.57	BM unstim	
BM stim		31.92	64.05	64.05	BM stim	1.20
osteo dif		40	0	0.00	osteo dif	0.00
osteo undif		40	0	0.00	osteo undif	
chondrocytes		37.59	2.82	7.05	chondrocytes	
OA Synovium IP12/01	29462	31.77	69.48	69.48	OA Synovium	
OA Synovium NP10/01	29461	31.16	96.93	193.86	OA Synovium	
OA Synovium NP57/00	28464	30.84	115.69	231.38	OA Synovium	
RA Synovium NP03/01	28466	30.96	108.37	216.74	RA Synovium	
RA Synovium NP71/00	28467	29.2	285.91	571.82	RA Synovium	
RA Synovium NP45/00	28475	29.87	198.12	396.24	RA Synovium	
OA bone (biobank)	29217	29.67	220.64	220.64	OA bone (biobank)	
OA bone Sample 1	J. Emory	30.54	136.41	272.82	OA bone	
OA bone Sample 2	J. Emory	29.38	259.07	518.14	OA bone	
Cartilage (pool)	Normal	31.34	87.88	175.76	Cartilage (pool)	
Cartilage (pool)	OA	32.9	37.23	74.46	Cartilage (pool)	-2.36
PBL unifected	28441	30.55	135.85	271.70	PBL unifected	
PBL HIV IIIB	28442	31.02	104.8	209.60	PBL HIV IIIB	-1.30
MRC5 uninfected (100%)	29158	35.11	11.06	22.12	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	29.63	226.14	452.28	MRC5 HSV strain F	20.45
W12 cells	29179	37.87	2.42	4.84	W12 cells	
Keratinocytes	29180	36.14	6.26	12.52	Keratinocytes	
B-actin control		27.14	887.42			
genomic		26.16	1520.17			
1.00E+05		19.22	100000			
1.00E+05		19.2	100000			
1.00E+04		22.49	10000			
1.00E+04		22.62	10000			
1.00E+03		26.23	1000			
1.00E+03		26.05	1000			
1.00E+02		30.26	100			

1.00E+02		31.03	100			
1.00E+01		38.68	10			
1.00E+01		33.47	10			
1.00E-00		40	0			
1.00E-00		40	0			
NTC		40	0			

Gene Name sbg563917RDP

Disease tissues	**Fold Change in Disease Population Relative to Normal**
colon tumor	-1.35
colon tumor	-2.80
colon tumor	-1.45
colon tumor	-1.84
lung tumor	-17 45
lung tumor	-1.34
lung tumor	-1.82
lung tumor	-1.01
breast tumor	-1.58
breast tumor	10.88
breast tumor	2.04
breast tumor	-1.43
brain stage 5 ALZ	-3.77
brain stage 5 ALZ	2.19
brain stage 5 ALZ	1.23
brain stage 5 ALZ	1.42
lung 24	-70.34
lung 28	-11.63
lung 23	-5.47
asthmatic lung	-1.57
asthmatic lung	1.39
asthmatic lung	1.95
asthmatic lung	2.51
endo VEGF	-7.68
endo bFGF	-7.68
heart T-1	-7.49
heart T-14	-4.17
heart T-3399	-3.71
BM stim	1.20
osteo undif	0.00
Cartilage (pool)	-2.36
PBL HIV IIIB	-1.30
MRC5 HSV strain F	20.45

Gene Name sbg618069LRR

Low overall expression in normal and disease samples. Highest normal expression in whole brain, fetal brain, cerebellum, and thymus. Highest disease expression in one of the colon tumor samples, one of the lung tumor samples, and the uninfected PBL cells. Downregulation in 2 of 4 colon tumors suggests a role in cancer of the colon. Upregulation in 1 of 4 lung tumors and upregulation in 2 of 4 breast tumors suggest roles in cancers of the lung and breast. Downregulation in 3 of 3 COPD lung samples implicates a role for this gene in COPD. Upregulation in the stimulated bone marrow. Downregulation in an HIV-infected cell line as well as moderate expression in immune

cells suggests an involvement in HIV. Upregulation in HSV implicates involvement in herpes simplex virus as a potential host factor.

Sample sbg618069LRR	Ct (sample 1 and 2)	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detected/50 ng total RNA
Subcutaneous Adipocytes Zenbio	35.24, 34.33	4.38	7.65	6.02	3.06	16.34	98.28
Subcutaneous Adipose Zenbio	40, 40	0	0.08	0.04	0.96	52.36	2.09
Adrenal Gland Clontech	39.9, 38.74	0.13	0.51	0.32	0.61	81.97	26.23
Whole Brain Clontech	27.02, 26.51	673.36	916.93	795.15	7.24	6.91	5491.33
Fetal Brain Clontech	40, 40	0.13	6.01	3.07	0.48	103.95	319.13
Cerebellum Clontech	32.15, 32.13	28.98	29.44	29.21	2.17	23.04	673.04
Cervix	40, 40	0	0	0.00	2.42	20.66	0.00
Colon	36.53, 39.88	1.98	0.25	1.12	2.71	18.45	20.57
Endometrium	37.98, 40	0.82	0.19	0.51	0.73	68.21	34.45
Esophagus	38.86, 40	0.48	0.15	0.32	1.37	36.50	11.50
Heart Clontech	34.17, 34.72	8.41	6.03	7.22	1.32	37.88	273.48
Hypothalamus	40, 40	0	0.07	0.04	0.32	155.28	5.43
Ileum	40, 40	0.17	0.11	0.14	2.58	19.38	2.71
Jejunum	33.07, 34.34	16.52	7.58	12.05	6.60	7.58	91.29
Kidney	36.05, 40	2.67	0.21	1.44	2.12	23.58	33.96
Liver	38.72, 40	0.52	0.61	0.57	1.50	33.33	18.83
Fetal Liver Clontech	33.28, 36.35	14.52	2.22	8.37	10.40	4.81	40.24
Lung	40, 40	0.13	0.08	0.11	2.57	19.46	2.04
Mammary Gland Clontech	40, 34.19	0	8.33	4.17	13.00	3.85	16.02
Myometrium	40, 40	0.28	0	0.14	2.34	21 37	2.99
Omentum	35.01, 35.36	5.04	4.07	4.56	3.94	12.69	57.80
Ovary	34.24, 40	8.07	0.26	4.17	4.34	11.52	47.98
Pancreas	40, 40	0.11	0.13	0.12	0.81	61.80	7.42
Head of Pancreas	40, 40	0	0	0.00	1.57	31.85	0.00
Parotid Gland	34.01, 34.28	9.31	7.9	8.61	5.48	9.12	78.51
Placenta Clontech	40, 40	0	0.07	0.04	5.26	9.51	0.33
Prostate	40, 39.13	0.15	0.4	0.28	3.00	16.67	4.58
Rectum	40, 39.55	0.21	0.31	0.26	1.23	40.65	10.57
Salivary Gland Clontech	32.35, 33.08	25.74	16.45	21.10	7.31	6.84	144.29
Skeletal Muscle Clontech	34.78, 40	5.81	0.27	3.04	1.26	39.68	120.63
Skin	40, 40	0	0	0.00	1.21	41.32	0.00
Small Intestine Clontech	40, 40	0.16	0	0.08	0.98	51.07	4.09
Spleen	35.59, 40	3.53	0.59	2.06	4.92	10.16	20.93
Stomach	36.73, 40	1.76	0.11	0.94	2.73	18.32	17.12
Testis Clontech	37.91, 40	0.86	0.1	0.48	0.57	87.87	42.18

Thymus Clontech	30.22, 29.94	94.88	112.23	103.56	9.89	5.06	523.53
Thyroid	35.15, 40	4.62	0	2.31	2.77	18.05	41.70
Trachea Clontech	33.49, 34.21	12.75	8.22	10.49	9.71	5.15	53.99
Urinary Bladder	40, 40	0.09	0.08	0.09	5.47	9.14	0.78
Uterus	35.26, 33.03	4.31	16.97	10.64	5.34	9.36	99.63
genomic	26.04	1229.54					
b-actin	27.25	584.19					
1.00E+05	19.09	100000					
1.00E+05	19.04	100000					
1.00E+04	22.35	10000					
1.00E+04	22.35	10000					
1.00E+03	26.07	1000					
1.00E+03	26.26	1000					
1.00E+02	30.64	100					
1.00E+02	30.38	100					
1.00E+01	34.04	10					
1.00E+01	33.52	10					
1.00E-00	40	0					
1.00E-00	40	0					
NTC	40	0					
NTC	40	0					

Sample sbg618069LRR	**Reg number (GSK identifier)**	**Ct**	**Mean GOI copies**	**copies of mRNA detected/50 ng total RNA**	**Sample**	**Fold Change in Disease Population**
colon normal GW98-167	21941	29.52	176.51	353.02	colon normal	
colon tumor GW98-166	21940	33.45	18.5	37.00	colon tumor	-9.54
colon normal GW98-178	22080	31.82	47.14	94.28	colon normal	
colon tumor GW98-177	22060	29.68	160.67	321.34	colon tumor	3.41
colon normal GW98-561	23514	30.33	110.78	221.56	colon normal	
colon tumor GW98-560	23513	33.11	22.39	44.78	colon tumor	-4.95
colon normal GW98-894	24691	28.1	396.95	793.90	colon normal	
colon tumor GW98-893	24690	26.93	779.99	1559.98	colon tumor	1.96
lung normal GW98-3	20742	30.41	105.78	211.56	lung normal	
lung tumor GW98-2	20741	26.28	1128.28	2256.56	lung tumor	10.67
lung normal GW97-179	20677	29.28	201.91	403.82	lung normal	
lung tumor GW97-178	20676	28.35	345.36	690.72	lung tumor	1.71
lung normal GW98-165	21922	28.42	331.95	663.90	lung normal	
lung tumor GW98-164	21921	30.98	76.05	152.10	lung tumor	-4.36
lung normal GW98-282	22584	34.15	12.36	24.72	lung normal	
lung tumor GW98-281	22583	32.08	40.6	81.20	lung tumor	3.28
breast normal GW00-392	28750	29.67	161.68	161.68	breast normal	
breast tumor GW00-391	28746	28.98	239.65	479.30	breast tumor	2.96
breast normal GW00-413	28798	31.78	48.04	48.04	breast normal	

breast tumor GW00-412	28797	29.69	159.55	319.10	breast tumor	6.64
breast normal GW00-235:238	27592-95	34.18	12.14	12.14	breast normal	
breast tumor GW00-231:234	27588-91	29.2	211.28	211.28	breast tumor	17.40
breast normal GW98-621	23656	29.72	157.4	314.80	breast normal	
breast tumor GW98-620	23655	31.12	70.17	140.34	breast tumor	-2.24
brain normal BB99-542	25507	30.81	83.89	167.78	brain normal	
brain normal BB99-406	25509	31.02	74.28	148.56	brain normal	
brain normal BB99-904	25546	31.39	60.08	120.16	brain normal	
brain stage 5 ALZ BB99-874	25502	32.54	31.07	62.14	brain stage 5 ALZ	-2.34
brain stage 5 ALZ BB99-887	25503	30.65	92.1	184.20	brain stage 5 ALZ	1.27
brain stage 5 ALZ BB99-862	25504	31.68	50.92	101.84	brain stage 5 ALZ	-1.43
brain stage 5 ALZ BB99-927	25542	31.39	60.36	120.72	brain stage 5 ALZ	-1.21
CT lung KC	normal	30.47	101.87	203.74	CT lung	
lung 26 KC	normal				lung 26	
lung 27 KC	normal	39.27	0.65	0.65	lung 27	
lung 24 KC	COPD	40	0	0.00	lung 24	-68.13
lung 28 KC	COPD	37.38	1.93	1.93	lung 28	-35.30
lung 23 KC	COPD	34.28	11.47	11.47	lung 23	-5.94
lung 25 KC	normal	40	0	0.00	lung 25	
asthmatic lung ODO3112	29321	33.17	21.73	21.73	asthmatic lung	-3.14
asthmatic lung ODO3433	29323	32.35	34.64	69.28	asthmatic lung	1.02
asthmatic lung ODO3397	29322	30.83	83.1	166.20	asthmatic lung	2.44
asthmatic lung ODO4928	29325	30.94	77.99	155.98	asthmatic lung	2.29
endo cells KC	control	40	0	0.00	endo cells	
endo VEGF KC		40	0	0.00	endo VEGF	0.00
endo bFGF KC		40	0	0.00	endo bFGF	0.00
heart Clontech	normal	30.52	99.45	198.90	heart	
heart (T-1) ischemic	29417	28.78	270.18	540.36	heart T-1	2.72
heart (T-14) non-obstructive DCM	29422	29.62	166.76	333.52	heart T-14	1.68
heart (T-3399) DCM	29426	30.05	129.76	259.52	heart T-3399	1.30
adenoid GW99-269	26162	29.05	230.93	461.86	adenoid	
tonsil GW98-280	22582	29.77	152.22	304.44	tonsil	
T cells PC00314	28453	31.6	53.48	106.96	T cells	
PBMNC		39.8	0.48	0.48	PBMNC	
monocyte		40	0	0.00	monocyte	
B cells PC00665	28455	31.56	54.77	109.54	B cells	
dendritic cells 28441		34.09	12.8	25.60	dendritic cells	
neutrophils	28440	34.03	13.21	13.21	neutrophils	
eosinophils	28446	40	0	0.00	eosinophils	
BM unstim		40	0	0.00	BM unstim	
BM stim		35.71	5.04	5.04	BM stim	5.04
osteo dif		40	0	0.00	osteo dif	0.00
osteo undif		40	0	0.00	osteo undif	

chondrocytes		33.5	17.89	44.73	chondrocytes	
OA Synovium IP12/01	29462	32.24	37.02	37.02	OA Synovium	
OA Synovium NP10/01	29461	27.95	434.95	869.90	OA Synovium	
OA Synovium NP57/00	28464	30.9	79.82	159.64	OA Synovium	
RA Synovium NP03/01	28466	31.79	47.9	95.80	RA Synovium	
RA Synovium NP71/00	28467	33.06	23.05	46.10	RA Synovium	
RA Synovium NP45/00	28475	32.76	27.41	54.82	RA Synovium	
OA bone (biobank)	29217	32.02	42.02	42.02	OA bone (biobank)	
OA bone Sample 1	J. Emory	31.32	62.63	125.26	OA bone	
OA bone Sample 2	J. Emory	33.13	22.24	44.48	OA bone	
Cartilage (pool)	Normal	30.76	86.51	173.02	Cartilage (pool)	
Cartilage (pool)	OA	33.13	22.15	44.30	Cartilage (pool)	-3.91
PBL unifected	28441	26.78	847.01	1694.02	PBL unifected	
PBL HIV IIIB	28442	28.21	374.26	748.52	PBL HIV IIIB	-2.26
MRC5 uninfected (100%)	29158	40	0	0.00	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	31.26	64.96	129.92	MRC5 HSV strain F	129.92
W12 cells	29179	40	0	0.00	W12 cells	
Keratinocytes	29180	39.77	0.49	0.98	Keratinocytes	
B-actin control		27.18	675.17			
genomic		25.96	1358.6			
1.00E+05		18.58	100000			
1.00E+05		18.53	100000			
1.00E+04		22.04	10000			
1.00E+04		22.1	10000			
1.00E+03		25.85	1000			
1.00E+03		26.11	1000			
1.00E+02		34.02	100			
1.00E+02		30.53	100			
1.00E+01		32.98	10			
1.00E+01		40	0			
1.00E-00		40	0			
1.00E-00		38.21	1			
NTC		40	0			

Gene Name sbg618069LRR

Disease tissues	**Fold Change in Disease Population Relative to Normal**
colon tumor	-9.54
colon tumor	3.41
colon tumor	-4.95
colon tumor	1.96
lung tumor	10.67
lung tumor	1.71
lung tumor	-4.36
lung tumor	3.28

breast tumor	2.96
breast tumor	6.64
breast tumor	17.40
breast tumor	-2.24
brain stage 5 ALZ	-2.34
brain stage 5 ALZ	1.27
brain stage 5 ALZ	-1.43
brain stage 5 ALZ	-1.21
lung 24	-68.13
lung 28	-35.30
lung 23	-5.94
asthmatic lung	-3.14
asthmatic lung	1.02
asthmatic lung	2.44
asthmatic lung	2.29
endo VEGF	0.00
endo bFGF	0.00
heart T-1	2.72
heart T-14	1.68
heart T-3399	1.30
BM stim	5.04
osteo dif	0.00
Cartilage (pool)	-3.91
PBL HIV IIIB	-2.26
MRC5 HSV strain F	129.92

Gene Name sbg934114Relaxin

Low overall expression in normal and disease samples. Highest normal expression in testis, liver, and whole brain. Highest disease expression in 3 of the normal lung samples, one of the normal tumor samples, the HSV-infected MRC5 cells, the adenoid, and the T cells. Highest disease expression in 2 of the normal lung samples, one of the lung tumor samples, 1 of the normal breast samples, 1 of the breast tumor samples, and the uninfected PBL samples. Downregulation in 1 of 4 colon tumors and downregulation in 2 of 4 lung tumors imply roles in cancers of the colon and lung. Downregulation in 3 of 3 COPD lung samples and upregulation in 3 of 4 asthmatic lung samples implicates this gene in COPD and asthma. Upregulation in 2 of 3 heart samples proposes roles in non-obstructive and obstructive DCM. Downregulation in the OA cartilage pool and low expression in RA and OA synovium, OA bone, and chondrocytes suggests an involvement in osteoarthritis and rheumatoid arthritis. Downregulation in an HIV-infected primary cell line suggests an involvement in HIV. Upregulation in HSV implicates involvement in herpes simplex virus as a potential host factor.

Sample sbg934114Relaxin	**Ct (sample 1 and 2)**	**Mean GOI copies (sample 1)**	**Mean GOI copies (sample 2)**	**Average GOI Copies**	**18S rRNA (ng)**	**50 ng/18S rRNA (ng)**	**copies of mRNA detected/50 ng total RNA**
Subcutaneous Adipocytes Zenbio	37.4, 40	5.41	0	2.71	3.06	16.34	44.20

Subcutaneous Adipose Zenbio	40, 40	0.73	0	0.37	0.96	52.36	19.11
Adrenal Gland Clontech	40, 40	0.73	0.69	0.71	0.61	81.97	58.20
Whole Brain Clontech	33.52, 34.72	47.76	24.26	36.01	7.24	6.91	248.69
Fetal Brain Clontech	39.51, 40	1.65	0.86	1.26	0.48	103.95	130.46
Cerebellum Clontech	40, 39.84	0.99	1.37	1.18	2.17	23.04	27.19
Cervix	40, 40	1.05	0	0.53	2.42	20.66	10.85
Colon	40, 37.31	0	5.7	2.85	2.71	18.45	52.58
Endometrium	40, 40	0	0	0.00	0.73	68.21	0.00
Esophagus	40, 40	0	0	0.00	1.37	36.50	0.00
Heart Clontech	38.11, 40	3.63	1.31	2.47	1.32	37.88	93.56
Hypothalamus	40, 40	0	1.06	0.53	0.32	155.28	82.30
Ileum	40, 36.79	0	7.62	3.81	2.58	19.38	73.84
Jejunum	35.14, 35.9	19.25	12.54	15.90	6.60	7.58	120.42
Kidney	40, 40	0	0	0.00	2.12	23.58	0.00
Liver	37.25, 35.17	5.88	18.92	12.40	1.50	33.33	413.33
Fetal Liver Clontech	40, 37.38	0.73	5.47	3.10	10.40	4.81	14.90
Lung	37.07, 40	6.52	0	3.26	2.57	19.46	63.42
Mammary Gland Clontech	40, 40	0	0	0.00	13.00	3.85	0.00
Myometrium	37.95, 40	3.98	0	1.99	2.34	21.37	42.52
Omentum	36.24, 37.04	10.39	6.63	8.51	3.94	12.69	107.99
Ovary	35.29, 36.26	17.66	10.28	13.97	4.34	11.52	160.94
Pancreas	39.48, 40	1.69	0	0.85	0.81	61.80	52.22
Head of Pancreas	36.17, 39.82	10.79	1.39	6.09	1.57	31.85	193.95
Parotid Gland	40, 38.66	0	2.67	1.34	5.48	9.12	12.18
Placenta Clontech	40, 36.57	0	8.63	4.32	5.26	9.51	41.02
Prostate	36.91, 40	7.14	0	3.57	3.00	16.67	59.50
Rectum	40, 37.34	0	5.61	2.81	1.23	40.65	114.02
Salivary Gland Clontech	40, 40	0	0	0.00	7.31	6.84	0.00
Skeletal Muscle Clontech	40, 39.45	0	1.71	0.86	1.26	39.68	33.93
Skin	39.2, 40	1.98	0	0 99	1.21	41.32	40.91
Small Intestine Clontech	40, 40	0	0	0.00	0.98	51.07	0.00
Spleen	36, 40	11.84	0	5.92	4.92	10.16	60.16
Stomach	35.48, 39.19	15.9	1.98	8.94	2.73	18.32	163.74
Testis Clontech	40, 36.09	0	11.27	5.64	0.57	87.87	495.17
Thymus Clontech	34.34, 36.66	30.03	8.2	19.12	9.89	5.06	96.64
Thyroid	40, 40	0	0	0.00	2.77	18.05	0.00
Trachea Clontech	40, 37.8	0	4.33	2.17	9.71	5.15	11.15
Urinary Bladder	40, 40	0	0	0.00	5.47	9.14	0.00
Uterus	37.11, 35.16	6.36	18.96	12.66	5.34	9.36	118.54
genomic	27.61	1307.98					
b-actin	27.15	1697.68					
1.00E+05	19.88	100000					
1.00E+05	20.05	100000					
1.00E+04	24.01	10000					

1.00E+04	23.92	10000					
1.00E+03	27.98	1000					
1.00E+03	27.6	1000					
1.00E+02	32.89	100					
1.00E+02	32.2	100					
1.00E+01	36.1	10					
1.00E+01							
1.00E-00							
1.00E-00							
NTC	40	0					
NTC	40	0					

Sample sbg934114Relaxin	**Reg number (GSK identifier)**	**Ct**	**Mean GOI copies**	**copies of mRNA detected/50 ng total RNA**	**Sample**	**Fold Change in Disease Population**
colon normal GW98-167	21941	36.1	22.33	44.66	colon normal	
colon tumor GW98-166	21940	36.47	18.37	36.74	colon tumor	-1.22
colon normal GW98-178	22080	35.7	27.58	55.16	colon normal	
colon tumor GW98-177	22060	38.05	7.98	15.96	colon tumor	-3.46
colon normal GW98-561	23514	33.57	84.85	169.70	colon normal	
colon tumor GW98-560	23513	37.66	9.8	19.60	colon tumor	-8.66
colon normal GW98-894	24691	36.39	19.09	38.18	colon normal	
colon tumor GW98-893	24690	36.43	18.74	37.48	colon tumor	-1.02
lung normal GW98-3	20742	32.48	150.6	301.20	lung normal	
lung tumor GW98-2	20741	36.65	16.64	33.28	lung tumor	-9.05
lung normal GW97-179	20677	33.22	102.07	204.14	lung normal	
lung tumor GW97-178	20676	32.31	164.63	329.26	lung tumor	1.61
lung normal GW98-165	21922	32.08	185.96	371.92	lung normal	
lung tumor GW98-164	21921	35.14	37.09	74.18	lung tumor	-5.01
lung normal GW98-282	22584	36.41	18.93	37.86	lung normal	
lung tumor GW98-281	22583	35.24	35.13	70.26	lung tumor	1.86
breast normal GW00-392	28750	34.04	66.25	66.25	breast normal	
breast tumor GW00-391	28746	37.9	8.61	17.22	breast tumor	-3.85
breast normal GW00-413	28798	36.36	19.44	19.44	breast normal	
breast tumor GW00-412	28797	36.79	15.49	30.98	breast tumor	1.59
breast normal GW00-235:238	27592-95	36.91	14.52	14.52	breast normal	
breast tumor GW00-231:234	27588-91	35.43	31.71	31.71	breast tumor	2.18
breast normal GW98-621	23656	36.26	20.51	41.02	breast normal	
breast tumor GW98-620	23655	35.76	26.68	53.36	breast tumor	1.30
brain normal BB99-542	25507	37.99	8.21	16.42	brain normal	
brain normal BB99-406	25509	40	1.41	2.82	brain normal	
brain normal BB99-904	25546	40	0	0.00	brain normal	
brain stage 5 ALZ BB99-	25502	38.65	5.82	11.64	brain stage 5 ALZ	1.81

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brain stage 5 ALZ BB99-887	25503	37	13.9	27.80	brain stage 5 ALZ	4.33
brain stage 5 ALZ BB99-862	25504	37.4	11.24	22.48	brain stage 5 ALZ	3.51
brain stage 5 ALZ BB99-927	25542	38	8.19	16.38	brain stage 5 ALZ	2.55
CT lung KC	normal	35.32	33.59	67.18	CT lung	
lung 26 KC	normal	37.02	13.72	13.72	lung 26	
lung 27 KC	normal	40	0	0.00	lung 27	
lung 24 KC	COPD	39.97	2.78	2.78	lung 24	-7.81
lung 28 KC	COPD	40	0	0.00	lung 28	-21.71
lung 23 KC	COPD	39.06	4.67	4.67	lung 23	-4.65
lung 25 KC	normal	38.61	5.92	5.92	lung 25	
asthmatic lung ODO3112	29321	36.02	23.31	23.31	asthmatic lung	1.07
asthmatic lung ODO3433	29323	34.12	63.36	126.72	asthmatic lung	5.84
asthmatic lung ODO3397	29322	33.99	68.06	136.12	asthmatic lung	6.27
asthmatic lung ODO4928	29325	33.77	76.08	152.16	asthmatic lung	7.01
endo cells KC	control	40	0	0.00	endo cells	
endo VEGF KC		40	0	0.00	endo VEGF	0.00
endo bFGF KC		38.16	7.54	7.54	endo bFGF	7.54
heart Clontech	normal	40	0	0.00	heart	
heart (T-1) ischemic	29417	40	1.36	2.72	heart T-1	2.72
heart (T-14) non-obstructive DCM	29422	36.31	20.01	40.02	heart T-14	40.02
heart (T-3399) DCM	29426	37.17	12.7	25.40	heart T-3399	25.40
adenoid GW99-269	26162	33.33	96.07	192.14	adenoid	
tonsil GW98-280	22582	34.86	42.85	85.70	tonsil	
T cells PC00314	28453	33.48	88.65	177.30	T cells	
PBMNC		40	0	0.00	PBMNC	
monocyte		40	0	0.00	monocyte	
B cells PC00665	28455	32.44	153.68	307.36	B cells	
dendritic cells 28441		35.78	26.47	52.94	dendritic cells	
neutrophils	28440	36.18	21.43	21.43	neutrophils	
eosinophils	28446	39.2	4.34	8.68	eosinophils	
BM unstim		39.56	3.6	3.60	BM unstim	
BM stim		40	1.34	1.34	BM stim	-2.69
osteo dif		40	0	0.00	osteo dif	0.00
osteo undif		40	0	0.00	osteo undif	
chondrocytes		36.64	16.79	41.98	chondrocytes	
OA Synovium IP12/01	29462	34.75	45.45	45.45	OA Synovium	
OA Synovium NP10/01	29461	36.02	23.28	46.56	OA Synovium	
OA Synovium NP57/00	28464	34.24	59.37	118.74	OA Synovium	
RA Synovium NP03/01	28466	37.88	8.71	17.42	RA Synovium	
RA Synovium NP71/00	28467	36.02	23.22	46.44	RA Synovium	
RA Synovium NP45/00	28475	34.9	41.9	83.80	RA Synovium	
OA bone (biobank)	29217	33.59	83.75	83.75	OA bone (biobank)	
OA bone Sample 1	J. Emory	37.31	11.8	23.60	OA bone	

OA bone Sample 2	J. Emory	37.47	10.81	21.62	OA bone	
Cartilage (pool)	Normal	34.61	49.07	98.14	Cartilage (pool)	
Cartilage (pool)	OA	40	0	0.00	Cartilage (pool)	-98.14
PBL unifected	28441	33.86	72.8	145.60	PBL unifected	
PBL HIV IIIB	28442	37.08	13.28	26.56	PBL HIV IIIB	-5.48
MRC5 uninfected (100%)	29158	39.01	4.81	9.62	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	31.5	252.68	505.36	MRC5 HSV strain F	52.53
W12 cells	29179	39.84	3.1	6.20	W12 cells	
Keratinocytes	29180	39.07	4.64	9.28	Keratinocytes	
B-actin control		27.9	1683.49			
genomic		28.13	1492.71			
1.00E+05		20.5	100000			
1.00E+05		20.61	100000			
1.00E+04		24.56	10000			
1.00E+04		24.17	10000			
1.00E+03		28.14	1000			
1.00E+03		28.32	1000			
1.00E+02		34.26	100			
1.00E+02		32.76	100			
1.00E+01		38.07	10			
1.00E+01		37.53	10			
1.00E-00		40	0			
1.00E-00		40	1			
NTC		38.42	-1			

Gene Name sbg934114Relaxin

Disease tissues	**Fold Change in Disease Population Relative to Normal**
colon tumor	-1.22
colon tumor	-3.46
colon tumor	-8.66
colon tumor	-1.02
lung tumor	-9.05
lung tumor	1.61
lung tumor	-5.01
lung tumor	1.86
breast tumor	-3.85
breast tumor	1.59
breast tumor	2.18
breast tumor	1.30
brain stage 5 ALZ	1.81
brain stage 5 ALZ	4.33
brain stage 5 ALZ	3.51
brain stage 5 ALZ	2.55
lung 24	-7.81
lung 28	-21.71
lung 23	-4.65
asthmatic lung	1.07

asthmatic lung	5.84
asthmatic lung	6.27
asthmatic lung	7.01
endo VEGF	0.00
endo bFGF	7.54
heart T-1	2.72
heart T-14	40.02
heart T-3399	25.40
BM stim	-2.69
osteo dif	0.00
Cartilage (pool)	-98.14
PBL HIV IIIB	-5.48
MRC5 HSV strain F	52.53

Gene Name sbg99174LOX-like

Moderate overall expression in normal and disease samples. Highest normal expression in whole brain, liver, skin, spleen, testis. Shows relatively good expression in the female reproductive samples as well as the GI tract samples. Highest disease expression in one of the normal lung samples, one of the asthmatic lung samples, neutrophils, eosinophils, 2 of the RA synovium samples, and one of the OA bone samples. Downregulation in 1 of 4 lung tumor samples suggests possible implication in lung cancer. Upregulation in 2 of 4 breast tumors implies an involvement in cancers of the breast. Downregulation in 1 of 4 AD brains along with the high expression seen in the brain suggests an involvement in Alzheimer's disease. Downregulation in 2 of 3 COPD lung samples implies an involvement in chronic obstructive pulmonary disease. Upregulation in 1 of 4 asthmatic lung samples implies a role in asthma. Downregulation in OA cartilage and high expression in OA and RA synovium suggests possible involvement in osteoarthritis and rheumatoid arthritis. Corroborating high expression in the T cells provides additional evidence for a role in RA/OA. Moderate expression in other immune cells.

Sample sbg99174LOX-like	**Ct (sample 1 and 2)**	**Mean GOI copies (sample 1)**	**Mean GOI copies (sample 2)**	**Average GOI Copies**	**18S rRNA (ng)**	**50 ng/18S rRNA (ng)**	**copies of mRNA detected/50 ng total RNA**
Subcutaneous Adipocytes Zenbio	39.67, 34.48	0.53	11.91	6.22	3.06	16.34	101.63
Subcutaneous Adipose Zenbio	40, 39.75	0.39	0.51	0.45	0.96	52.36	23.56
Adrenal Gland Clontech	38.61, 37.69	1	1.75	1.38	0.61	81.97	112.70
Whole Brain Clontech	30.59, 31.07	122.95	92.57	107.76	7.24	6.91	744.20
Fetal Brain Clontech	40, 40	0	0.29	0.15	0.48	103.95	15.07
Cerebellum Clontech	40, 40	0.4	0.4	0.40	2.17	23.04	9.22
Cervix	35.77, 40	5.52	0.62	3.07	2.42	20.66	63.43
Colon	40, 39.41	0.34	0.62	0.48	2.71	18.45	8.86
Endometrium	40, 38.65	0	0.98	0.49	0.73	68.21	33.42
Esophagus	40, 40	0.35	0.41	0.38	1.37	36.50	13.87
Heart Clontech	39.33, 40	0.65	0	0.33	1.32	37.88	12.31
Hypothalamus	40, 39.54	0	0.58	0.29	0.32	155.28	45.03
Ileum	35.42, 35.76	6.79	5.55	6.17	2.58	19.38	119.57
Jejunum	34.13, 33.4	14.77	22.9	18.84	6.60	7.58	142.69

Kidney	40, 37.22	0.68	2.32	1.50	2.12	23.58	35.38
Liver	33.5, 33.86	21.47	17.3	19.39	1.50	33.33	646.17
Fetal Liver Clontech	32.78, 33.23	33.08	25.33	29.21	10.40	4.81	140.41
Lung	33.96, 34.44	16.33	12.25	14.29	2.57	19.46	278.02
Mammary Gland Clontech	35.05, 36.02	8.51	4.76	6.64	13.00	3.85	25.52
Myometrium	35.08, 35.49	8.34	6.52	7.43	2.34	21.37	158.76
Omentum	37.6, 35.05	1.83	8.49	5.16	3.94	12.69	65.48
Ovary	35.57, 32.76	6.21	33.46	19.84	4.34	11.52	228.51
Pancreas	40, 40	0	0.42	0.21	0.81	61.80	12.98
Head of Pancreas	40, 38.65	0.56	0.98	0.77	1.57	31.85	24.52
Parotid Gland	35.28, 40	7.4	0.64	4.02	5.48	9.12	36.68
Placenta Clontech	40, 39.17	0.32	0.72	0.52	5.26	9.51	4.94
Prostate	40, 35.34	0	7.15	3.58	3.00	16.67	59.58
Rectum	37.29, 39.02	2.22	0.78	1.50	1.23	40.65	60.98
Salivary Gland Clontech	40, 38.15	0.27	1.32	0.80	7.31	6.84	5.44
Skeletal Muscle Clontech	40, 38.56	0.56	1.03	0.80	1.26	39.68	31.55
Skin	35.1, 34.19	8.22	14.22	11.22	1.21	41.32	463.64
Small Intestine Clontech	40, 40	0	0.85	0.43	0.98	51.07	21.71
Spleen	32.2, 32.08	46.76	50.49	48.63	4.92	10.16	494.16
Stomach	34.28, 34.07	13.5	15.3	14.40	2.73	18.32	263.74
Testis Clontech	34.05, 32.7	15.46	34.82	25.14	0.57	87.87	2209.14
Thymus Clontech	33.85, 32.4	17.44	41.71	29.58	9.89	5.06	149.52
Thyroid	34.22, 34.29	13.93	13.37	13.65	2.77	18.05	246.39
Trachea Clontech	32.51, 32.4	38.89	41.53	40.21	9.71	5.15	207.05
Urinary Bladder	35.47, 40	6.6	0	3.30	5.47	9.14	30.16
Uterus	33.8, 33.6	18.01	20.22	19.12	5.34	9.36	178.98
genomic	26.31	1603.29					
b-actin	27.35	860.96					
1.00E+05	19.71	100000					
1.00E+05	19.88	100000					
1.00E+04	22.98	10000					
1.00E+04	23.01	10000					
1.00E+03	26.44	1000					
1.00E+03	26.54	1000					
1.00E+02	31.28	100					
1.00E+02	31.29	100					
1.00E+01	35.79	10					
1.00E+01	34.36	10					
1.00E-00	38.32	1					
1.00E-00	40	1					
NTC	40	0					
NTC	40	0					

Sample sbg99174LOX-like	**Reg number**	**Ct**	**Mean GOI**	**copies of**	**Sample**	**Fold Change**

	(GSK identifier)		copies	mRNA detected/50 ng total RNA		in Disease Population
colon normal GW98-167	21941	29.81	184.31	368.62	colon normal	
colon tumor GW98-166	21940	29.25	254.48	508.96	colon tumor	1.38
colon normal GW98-178	22080	32.06	50.31	100.62	colon normal	
colon tumor GW98-177	22060	31.77	59.28	118.56	colon tumor	1.18
colon normal GW98-561	23514	33.21	25.83	51.66	colon normal	
colon tumor GW98-560	23513	31.74	60.51	121.02	colon tumor	2.34
colon normal GW98-894	24691	30.17	149.84	299.68	colon normal	
colon tumor GW98-893	24690	29.41	232.23	464.46	colon tumor	1.55
lung normal GW98-3	20742	25.76	1914.72	3829.44	lung normal	
lung tumor GW98-2	20741	30.12	154.63	309.26	lung tumor	-12.38
lung normal GW97-179	20677	29.59	209.5	419.00	lung normal	
lung tumor GW97-178	20676	27.2	835.04	1670.08	lung tumor	3.99
lung normal GW98-165	21922	28.22	462.22	924.44	lung normal	
lung tumor GW98-164	21921	29.27	251.87	503.74	lung tumor	-1.84
lung normal GW98-282	22584	30.18	149.17	298.34	lung normal	
lung tumor GW98-281	22583	28.47	399.41	798.82	lung tumor	2.68
breast normal GW00-392	28750	30.24	143.58	143.58	breast normal	
breast tumor GW00-391	28746	30.16	151.08	302.16	breast tumor	2.10
breast normal GW00-413	28798	31.51	68.87	68.87	breast normal	
breast tumor GW00-412	28797	28.91	310.66	621.32	breast tumor	9.02
breast normal GW00-235:238	27592-95	40	0	0.00	breast normal	
breast tumor GW00-231:234	27588-91	33.55	21.28	21.28	breast tumor	21.28
breast normal GW98-621	23656	31.57	66.56	133.12	breast normal	
breast tumor GW98-620	23655	31.15	84.8	169.60	breast tumor	1.27
brain normal BB99-542	25507	29.55	214.38	428.76	brain normal	
brain normal BB99-406	25509	29.15	270.89	541.78	brain normal	
brain normal BB99-904	25546	30.48	124.98	249.96	brain normal	
brain stage 5 ALZ BB99-874	25502	33.57	20.99	41.98	brain stage 5 ALZ	-9.69
brain stage 5 ALZ BB99-887	25503	29.89	176.42	352.84	brain stage 5 ALZ	-1.15
brain stage 5 ALZ BB99-862	25504	31.65	63.83	127.66	brain stage 5 ALZ	-3.19
brain stage 5 ALZ BB99-927	25542	31.04	90.73	181.46	brain stage 5 ALZ	-2.24
CT lung KC	normal	29.94	170.8	341.60	CT lung	
lung 26 KC	normal	30.63	115.04	115.04	lung 26	
lung 27 KC	normal	32.22	45.83	45.83	lung 27	
lung 24 KC	COPD	34.16	14.91	14.91	lung 24	-9.21
lung 28 KC	COPD	33.51	21.7	21.70	lung 28	-6.33
lung 23 KC	COPD	32.51	38.67	38.67	lung 23	-3.55
lung 25 KC	normal	32.18	46.79	46.79	lung 25	
asthmatic lung ODO3112	29321	31.84	56.95	56.95	asthmatic lung	-2.41

asthmatic lung ODO3433	29323	31.12	86.42	172.84	asthmatic lung	1.26
asthmatic lung ODO3397	29322	27.13	867.31	1734.62	asthmatic lung	12.63
asthmatic lung ODO4928	29325	30.25	142.92	285.84	asthmatic lung	2.08
endo cells KC	control	31.23	81.05	81.05	endo cells	
endo VEGF KC		31.87	56.15	56.15	endo VEGF	-1.44
endo bFGF KC		32.64	35.97	35.97	endo bFGF	-2.25
heart Clontech	normal	35.46	7.06	14.12	heart	
heart (T-1) ischemic	29417	35.73	6.03	12.06	heart T-1	-1.17
heart (T-14) non-obstructive DCM	29422	34.34	13.49	26.98	heart T-14	1.91
heart (T-3399) DCM	29426	33.65	20.01	40.02	heart T-3399	2.83
adenoid GW99-269	26162	31.2	82.69	165.38	adenoid	
tonsil GW98-280	22582	30.8	103.96	207.92	tonsil	
T cells PC00314	28453	28.16	480.4	960.80	T cells	
PBMNC		30.25	143.11	143.11	PBMNC	
monocyte		30.05	160.68	321.36	monocyte	
B cells PC00665	28455	30.75	107.02	214.04	B cells	
dendritic cells 28441		30.32	137.17	274.34	dendritic cells	
neutrophils	28440	26.32	1390.87	1390.87	neutrophils	
eosinophils	28446	25.07	2854.44	5708.88	eosinophils	
BM unstim		30.72	109.05	109.05	BM unstim	
BM stim		28.61	369.2	369.20	BM stim	3.39
osteo dif		40	0	0.00	osteo dif	-0.28
osteo undif		40	0.28	0.28	osteo undif	
chondrocytes		34.3	13.76	34.40	chondrocytes	
OA Synovium IP12/01	29462	27.56	676.63	676.63	OA Synovium	
OA Synovium NP10/01	29461	31.41	73.19	146.38	OA Synovium	
OA Synovium NP57/00	28464	28.02	518.05	1036.10	OA Synovium	
RA Synovium NP03/01	28466	27.03	921.88	1843.76	RA Synovium	
RA Synovium NP71/00	28467	27.04	914.02	1828.04	RA Synovium	
RA Synovium NP45/00	28475	29.06	285.08	570.16	RA Synovium	
OA bone (biobank)	29217	26.78	1065.84	1065.84	OA bone (biobank)	
OA bone Sample 1	J. Emory	30.27	141.07	282.14	OA bone	
OA bone Sample 2	J. Emory	27.04	917.04	1834.08	OA bone	
Cartilage (pool)	Normal	28.23	461.21	922.42	Cartilage (pool)	
Cartilage (pool)	OA	33.16	26.65	53.30	Cartilage (pool)	-17.31
PBL unifected	28441	28.72	346.97	693.94	PBL unifected	
PBL HIV IIIB	28442	28.54	384.02	768.04	PBL HIV IIIB	1.11
MRC5 uninfected (100%)	29158	31.64	64.07	128.14	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	31.53	68.31	136.62	MRC5 HSV strain F	1.07
W12 cells	29179	34.44	12.72	25.44	W12 cells	
Keratinocytes	29180	36.02	5.1	10.20	Keratinocytes	
B-actin control		27.2	835.98			
genomic		26.76	1073.72			
1.00E+05		19.13	100000			
1.00E+05		19.61	100000			

1.00E+04		22.79	10000			
1.00E+04		22.5	10000			
1.00E+03		26.36	1000			
1.00E+03		26.23	1000			
1.00E+02		31.25	100			
1.00E+02		30.82	100			
1.00E+01		35.02	10			
1.00E+01		35.15	10			
1.00E-00		40	0			
1.00E-00		40	0			
NTC		40	0			

Gene Name sbg99174LOX-like

Disease tissues	**Fold Change in Disease Population Relative to Normal**
colon tumor	1.38
colon tumor	1.18
colon tumor	2.34
colon tumor	1.55
lung tumor	-12.38
lung tumor	3.99
lung tumor	-1.84
lung tumor	2.68
breast tumor	2.10
breast tumor	9.02
breast tumor	21.28
breast tumor	1.27
brain stage 5 ALZ	-9.69
brain stage 5 ALZ	-1.15
brain stage 5 ALZ	-3.19
brain stage 5 ALZ	-2.24
lung 24	-9.21
lung 28	-6.33
lung 23	-3.55
asthmatic lung	-2.41
asthmatic lung	1.26
asthmatic lung	12.63
asthmatic lung	2.08
endo VEGF	-1.44
endo bFGF	-2.25
heart T-1	-1.17
heart T-14	1.91
heart T-3399	2.83
BM stim	3.39
osteo dif	-0.28
Cartilage (pool)	-17.31
PBL HIV IIIB	1.11
MRC5 HSV strain F	1.07

Gene Name sbg995002PIGR (Taqman)

Extremely low overall expression in normal and disease samples. Highest normal expression in the colon and the parotid gland. Highest disease expression in the one of the lung tumors and one of the colon tumors. Upregulation in 1 of 4 colon tumors and 1 of 4 lung tumors imply roles in cancers of the colon and lung. Downregulation in 3 of 4 AD brain samples as well as high expression in whole brain suggests an involvement in Alzheimer's disease. Downregulation in 3 of 3 COPD lung samples implicates this gene in COPD. Downregulation in the ischemic and non-obstructive DCM heart samples suggests a role for this gene in cardiovascular disease. Upregulation in the stimulated bone marrow sample. Upregulation in HSV implicates involvement in herpes simplex virus as a potential host factor. High expression in neutrophils and eosinophils.

Sample sbg995002PIGR	**Ct (sample 1 and 2)**	**Mean GOI copies (sample 1)**	**Mean GOI copies (sample 2)**	**Average GOI Copies**	**18S rRNA (ng)**	**50 ng/18S rRNA (ng)**	**copies of mRNA detected/50 ng total RNA**
Subcutaneous Adipocytes Zenbio	40, 40	0	0	0.00	3.06	16.34	0.00
Subcutaneous Adipose Zenbio	40, 40	0	0	0.00	0.96	52.36	0.00
Adrenal Gland Clontech	40, 40	0	0	0.00	0.61	81.97	0.00
Whole Brain Clontech	36.78, 40	11.16	0	5.58	7.24	6.91	38.54
Fetal Brain Clontech	40, 40	0	0	0.00	0.48	103.95	0.00
Cerebellum Clontech	40, 40	0	0	0.00	2.17	23.04	0.00
Cervix	40, 40	0	0	0.00	2.42	20.66	0.00
Colon	37.16, 37.12	8.81	9.05	8.93	2.71	18.45	164.76
Endometrium	40, 40	0	0	0.00	0.73	68.21	0.00
Esophagus	40, 40	0	0	0.00	1.37	36.50	0.00
Heart Clontech	40, 40	0	0	0.00	1.32	37.88	0.00
Hypothalamus	40, 40	0	0	0.00	0.32	155.28	0.00
Ileum	40, 40	0	0	0.00	2.58	19.38	0.00
Jejunum	40, 40	0	0	0.00	6.60	7.58	0.00
Kidney	40, 40	0	0	0.00	2.12	23.58	0.00
Liver	40, 39.16	0	2.58	1.29	1.50	33.33	43.00
Fetal Liver Clontech	40, 40	0	0	0.00	10.40	4.81	0.00
Lung	40, 40	0	0	0.00	2.57	19.46	0.00
Mammary Gland Clontech	40, 39.18	0	2.55	1.28	13.00	3.85	4.90
Myometrium	40, 40	0	0	0.00	2.34	21.37	0.00
Omentum	40, 38.04	0	5.15	2.58	3.94	12.69	32.68
Ovary	39.29, 40	2.37	0	1.19	4.34	11.52	13.65
Pancreas	40, 40	0	0	0.00	0.81	61.80	0.00
Head of Pancreas	40, 40	0	0	0.00	1.57	31.85	0.00
Parotid Gland	36.7, 37.94	11.72	5.46	8.59	5.48	9.12	78.38
Placenta Clontech	40, 40	0	0	0.00	5.26	9.51	0.00
Prostate	40, 40	0	0	0.00	3.00	16.67	0.00
Rectum	40, 40	0	0	0.00	1.23	40.65	0.00
Salivary Gland Clontech	37.23, 39.21	8.45	2.5	5.48	7.31	6.84	37.45
Skeletal Muscle Clontech	40, 40	0	0	0.00	1.26	39.68	0.00

Skin	40, 40	0	0	0.00	1.21	41.32	0.00
Small Intestine Clontech	40, 40	0	0	0.00	0.98	51.07	0.00
Spleen	40, 38.76	1.25	3.3	2.28	4.92	10.16	23.12
Stomach	40, 39.25	1.25	2.43	1.84	2.73	18.32	33.70
Testis Clontech	40, 40	0	0	0.00	0.57	87.87	0.00
Thymus Clontech	37.82, 40	5.88	0	2.94	9.89	5.06	14.86
Thyroid	40, 40	0	0	0.00	2.77	18.05	0.00
Trachea Clontech	40, 40	0	0	0.00	9.71	5.15	0.00
Urinary Bladder	40, 40	0	0	0.00	5.47	9.14	0.00
Uterus	38.34, 40	4.27	0	2.14	5.34	9.36	19.99
genomic	29.66	888.99					
b-actin	30.72	462.87					
1.00E+05	22.2	100000					
1.00E+05	22.14	100000					
1.00E+04	25.72	10000					
1.00E+04	25.66	10000					
1.00E+03	29.16	1000					
1.00E+03	29.07	1000					
1.00E+02	32.37	100					
1.00E+02	34.12	100					
1.00E+01	37.12	10					
1.00E+01	37.11	10					
1.00E-00	40	0					
1.00E-00	40	0					
NTC	40	0					
NTC	38.03	-1					

Sample sbg995002PIGR	**Reg number (GSK identifier)**	**Ct**	**Mean GOI copies**	**copies of mRNA detected/50 ng total RNA**	**Sample**	**Fold Change in Disease Population**
colon normal GW98-167	21941	33.43	149.84	299.68	colon normal	
colon tumor GW98-166	21940	32.49	274.64	549.28	colon tumor	1.83
colon normal GW98-178	22080	40	0	0.00	colon normal	
colon tumor GW98-177	22060	31.11	675.8	1351.60	colon tumor	1351.60
colon normal GW98-561	23514	37.74	9.09	18.18	colon normal	
colon tumor GW98-560	23513	35.81	31.94	63.88	colon tumor	3.51
colon normal GW98-894	24691	33.17	177.11	354.22	colon normal	
colon tumor GW98-893	24690	31.61	488.49	976.98	colon tumor	2.76
lung normal GW98-3	20742	35.48	39.55	79.10	lung normal	
lung tumor GW98-2	20741	28.32	4121.56	8243.12	lung tumor	104.21
lung normal GW97-179	20677	36.47	20.69	41.38	lung normal	
lung tumor GW97-178	20676	37.24	12.59	25.18	lung tumor	-1.64
lung normal GW98-165	21922	37.32	11.96	23.92	lung normal	
lung tumor GW98-164	21921	36.07	26.9	53.80	lung tumor	2.25

lung normal GW98-282	22584	38.49	5.58	11.16	lung normal	
lung tumor GW98-281	22583	37.89	8.24	16.48	lung tumor	1.48
breast normal GW00-392	28750	39.03	3.93	3.93	breast normal	
breast tumor GW00-391	28746	38.01	7.65	15.30	breast tumor	3.89
breast normal GW00-413	28798	40	0	0.00	breast normal	
breast tumor GW00-412	28797	38.67	4.98	9.96	breast tumor	9.96
breast normal GW00-235:238	27592-95	40	0	0.00	breast normal	
breast tumor GW00-231:234	27588-91	40	0	0.00	breast tumor	0.00
breast normal GW98-621	23656	36.12	26.13	52.26	breast normal	
breast tumor GW98-620	23655	40	0	0.00	breast tumor	-52.26
brain normal BB99-542	25507	37.14	13.43	26.86	brain normal	
brain normal BB99-406	25509	40	0	0.00	brain normal	
brain normal BB99-904	25546	40	0	0.00	brain normal	
brain stage 5 ALZ BB99-874	25502	40	0	0.00	brain stage 5 ALZ	-8.95
brain stage 5 ALZ BB99-887	25503	40	0.51	1.02	brain stage 5 ALZ	-8.78
brain stage 5 ALZ BB99-862	25504	40	0.88	1.76	brain stage 5 ALZ	-5.09
brain stage 5 ALZ BB99-927	25542	40	1.9	3.80	brain stage 5 ALZ	-2.36
CT lung KC	normal	36.59	19.23	38.46	CT lung	
lung 26 KC	normal	40	0	0.00	lung 26	
lung 27 KC	normal	40	0	0.00	lung 27	
lung 24 KC	COPD	40	0	0.00	lung 24	-9.62
lung 28 KC	COPD	40	0	0.00	lung 28	-9.62
lung 23 KC	COPD	40	0	0.00	lung 23	-9.62
lung 25 KC	normal	40	0	0.00	lung 25	
asthmatic lung ODO3112	29321	40	0	0.00	asthmatic lung	-9.62
asthmatic lung ODO3433	29323	38.36	6.1	12.20	asthmatic lung	1.27
asthmatic lung ODO3397	29322	37.29	12.16	24.32	asthmatic lung	2.53
asthmatic lung ODO4928	29325	38.01	7.64	15.28	asthmatic lung	1.59
endo cells KC	control	40	0	0.00	endo cells	
endo VEGF KC		40	0	0.00	endo VEGF	0.00
endo bFGF KC		40	0	0.00	endo bFGF	0.00
heart Clontech	normal	37.85	8.49	16.98	heart	
heart (T-1) ischemic	29417	40	0	0.00	heart T-1	-16.98
heart (T-14) non-obstructive DCM	29422	40	0	0.00	heart T-14	-16.98
heart (T-3399) DCM	29426	39.5	2.9	5.80	heart T-3399	-2.93
adenoid GW99-269	26162	40	0	0.00	adenoid	
tonsil GW98-280	22582	36.35	22.46	44.92	tonsil	
T cells PC00314	28453	36.17	25.23	50.46	T cells	
PBMNC		40	0	0.00	PBMNC	
monocyte		40	0.45	0.90	monocyte	
B cells PC00665	28455	40	0.6	1.20	B cells	
dendritic cells 28441		38.07	7.37	14.74	dendritic cells	
neutrophils	28440	32.73	236.09	236.09	neutrophils	

eosinophils	28446	33.68	126.65	253.30	eosinophils	
BM unstim		40	0	0.00	BM unstim	
BM stim		36.52	20.1	20.10	BM stim	20.10
osteo dif		40	0	0.00	osteo dif	0.00
osteo undif		40	0	0.00	osteo undif	
chondrocytes		39.61	2.7	6.75	chondrocytes	
OA Synovium IP12/01	29462	39.91	1.59	1.59	OA Synovium	
OA Synovium NP10/01	29461	38.98	4.07	8.14	OA Synovium	
OA Synovium NP57/00	28464	36.29	23.27	46.54	OA Synovium	
RA Synovium NP03/01	28466	35.81	31.94	63.88	RA Synovium	
RA Synovium NP71/00	28467	34.79	61.79	123.58	RA Synovium	
RA Synovium NP45/00	28475	35.08	51.15	102.30	RA Synovium	
OA bone (biobank)	29217	40	1.12	1.12	OA bone (biobank)	
OA bone Sample 1	J. Emory	36.8	16.77	33.54	OA bone	
OA bone Sample 2	J. Emory	34.72	64.74	129.48	OA bone	
Cartilage (pool)	Normal	37.46	10.93	21.86	Cartilage (pool)	
Cartilage (pool)	OA	40	0	0.00	Cartilage (pool)	-21.86
PBL unifected	28441	35.05	52.27	104.54	PBL unifected	
PBL HIV IIIB	28442	37.31	12.04	24.08	PBL HIV IIIB	-4.34
MRC5 uninfected (100%)	29158	40	0	0.00	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	38.19	6.8	13.60	MRC5 HSV strain F	13.60
W12 cells	29179	40	0	0.00	W12 cells	
Keratinocytes	29180	40	0	0.00	Keratinocytes	
B-actin control	B-actin control	29.77	1604.25			
genomic	genomic	30.5	1001.61			
1.00E+05	1.00E+05	22.95	100000			
1.00E+05	1.00E+05	22.91	100000			
1.00E+04	1.00E+04	26.49	10000			
1.00E+04	1.00E+04	26.66	10000			
1.00E+03	1.00E+03	30.62	1000			
1.00E+03	1.00E+03	30.43	1000			
1.00E+02	1.00E+02	36.12	100			
1.00E+02	1.00E+02	34.73	100			
1.00E+01	1.00E+01	38.58	10			
1.00E+01	1.00E+01	38.82	10			
1.00E-00	1.00E-00	40	0			
1.00E-00	1.00E-00	37.86	1			
NTC	NTC	40	0			

Gene Name sbg995002PIGR

Disease tissues	**Fold Change in Disease Population Relative to Normal**
colon tumor	1.83

colon tumor	1351.60
colon tumor	3.51
colon tumor	2.76
lung tumor	104.21
lung tumor	-1.64
lung tumor	2.25
lung tumor	1.48
breast tumor	3.89
breast tumor	9.96
breast tumor	0.00
breast tumor	-52.26
brain stage 5 ALZ	-8.95
brain stage 5 ALZ	-8.78
brain stage 5 ALZ	-5.09
brain stage 5 ALZ	-2.36
lung 24	-9.62
lung 28	-9.62
lung 23	-9.62
asthmatic lung	-9.62
asthmatic lung	1.27
asthmatic lung	2.53
asthmatic lung	1.59
endo VEGF	0.00
endo bFGF	0.00
heart T-1	-16.98
heart T-14	-16.98
heart T-3399	-2.93
BM stim	20.10
osteo dif	0.00
Cartilage (pool)	-21.86
PBL HIV IIIB	-4.34
MRC5 HSV strain F	13.60

Gene Name sbg1033026C1q

Low to moderate overall expression in normal and disease samples. Highest normal expression in the subcutaneous adipocytes, subcutaneous adipose, whole brain, and heart. Highest disease expression in the 3 heart samples. Downregulation in 1 of 4 lung tumor samples and upregulation in 2 of 4 breast tumor samples indicates a role for this gene in cancers of the lung and breast. Upregulation in 2 of 4 AD brain samples suggests an involvement in Alzheimer's disease. Upregulation in 3 of 3 heart samples implies an involvement in cardiovascular diseases such as non-obstructive and obstructive DCM as well as ischemia. Low expression in all of the immune cells. Low to moderate expression in the OA synovium and bone samples as well as in the RA synovium samples.

Sample sbg1033026C1q	**Ct (sample 1 and 2)**	**Mean GOI copies (sample 1)**	**Mean GOI copies (sample 2)**	**Average GOI Copies**	**18S rRNA (ng)**	**50 ng/18S rRNA (ng)**	**copies of mRNA detected/50 ng total RNA**
Subcutaneous Adipocytes Zenbio	32.32, 31.18	11.99	24.91	18.45	3.06	16.34	301.47
Subcutaneous Adipose Zenbio	34.95, 33.78	2.2	4.69	3.45	0.96	52.36	180.37

Adrenal Gland Clontech	40, 40	0	0	0.00	0.61	81.97	0.00
Whole Brain Clontech	28.5, 28.04	140.11	187.98	164.05	7.24	6.91	1132.91
Fetal Brain Clontech	40, 40	0	0	0.00	0.48	103.95	0.00
Cerebellum Clontech	40, 40	0	0	0.00	2.17	23.04	0.00
Cervix	40, 40	0	0	0.00	2.42	20.66	0.00
Colon	34.82, 38.44	2.39	0.23	1.31	2.71	18.45	24.17
Endometrium	40, 35.09	0	2.01	1.01	0.73	68.21	68.55
Esophagus	40, 40	0	0	0.00	1.37	36.50	0.00
Heart Clontech	32.53, 34.31	10.45	3.32	6.89	1.32	37.88	260.80
Hypothalamus	40, 40	0	0	0.00	0.32	155.28	0.00
Ileum	40, 34.55	0	2.85	1.43	2.58	19.38	27.62
Jejunum	33.04, 34.86	7.51	2.33	4.92	6.60	7.58	37.27
Kidney	40, 40	0	0	0.00	2.12	23.58	0.00
Liver	35.81, 33.92	1.26	4.28	2.77	1.50	33.33	92.33
Fetal Liver Clontech	32.05, 40	14.25	0	7.13	10.40	4.81	34.25
Lung	40, 33.51	0	5.58	2.79	2.57	19.46	54.28
Mammary Gland Clontech	31.05, 30.69	27.02	34.2	30.61	13.00	3.85	117.73
Myometrium	33.29, 35.1	6.42	2	4.21	2.34	21.37	89.96
Omentum	34.44, 40	3.07	0	1.54	3.94	12.69	19.48
Ovary	32.59, 35.04	10.03	2.07	6.05	4.34	11.52	69.70
Pancreas	40, 40	0	0	0.00	0.81	61.80	0.00
Head of Pancreas	40, 40	0	0	0.00	1.57	31.85	0.00
Parotid Gland	34.63, 33.09	2.71	7.29	5.00	5.48	9.12	45.62
Placenta Clontech	32.77, 33.01	8.94	7.7	8.32	5.26	9.51	79.09
Prostate	40, 40	0	0	0.00	3.00	16.67	0.00
Rectum	40, 34.44	0	3.06	1.53	1.23	40.65	62.20
Salivary Gland Clontech	32.96, 40	7.94	0	3.97	7.31	6.84	27.15
Skeletal Muscle Clontech	40, 40	0	0	0.00	1.26	39.68	0.00
Skin	40, 33.46	0.6	5.75	3.18	1.21	41.32	131.20
Small Intestine Clontech	40, 40	0	0	0.00	0.98	51.07	0.00
Spleen	35.65, 35	1.4	2.13	1.77	4.92	10.16	17.94
Stomach	40, 34.73	0	2.54	1.27	2.73	18.32	23.26
Testis Clontech	40, 35.12	0	1.98	0.99	0.57	87.87	86.99
Thymus Clontech	32.44, 31.57	11.11	19.37	15.24	9.89	5.06	77.05
Thyroid	40, 40	0	0	0.00	2.77	18.05	0.00
Trachea Clontech	34.58, 33.56	2.79	5.4	4.10	9.71	5.15	21.09
Urinary Bladder	33.45, 33.34	5.8	6.21	6.01	5.47	9.14	54.89
Uterus	33.19, 32.41	6.82	11.32	9.07	5.34	9.36	84.93
genomic	25.47	981.57					
b-actin	26.87	398.61					
1.00E+05	18.24	100000					
1.00E+05	18.35	100000					
1.00E+04	21.53	10000					
1.00E+04	21.62	10000					

1.00E+03	25.17	1000					
1.00E+03	25.03	1000					
1.00E+02	30.53	100					
1.00E+02	30.49	100					
1.00E+01	30.85	10					
1.00E+01	40	10					
1.00E-00	40	0					
1.00E-00	40	0					
NTC	40	0					
NTC	40	0					

Sample sbg1033026C1q	**Reg number (GSK identifier)**	**Ct**	**Mean GOI copies**	**copies of mRNA detected/50 ng total RNA**	**Sample**	**Fold Change in Disease Population**
colon normal GW98-167	21941	27.03	397.15	794.30	colon normal	
colon tumor GW98-166	21940	29.53	91.39	182.78	colon tumor	-4.35
colon normal GW98-178	22080	30.3	57.81	115.62	colon normal	
colon tumor GW98-177	22060	29.31	103.84	207.68	colon tumor	1.80
colon normal GW98-561	23514	28.79	140.64	281.28	colon normal	
colon tumor GW98-560	23513	30.18	62.18	124.36	colon tumor	-2.26
colon normal GW98-894	24691	28.31	187.28	374.56	colon normal	
colon tumor GW98-893	24690	28.75	143.93	287.86	colon tumor	-1.30
lung normal GW98-3	20742	28.18	201.78	403.56	lung normal	
lung tumor GW98-2	20741	32.35	17.41	34.82	lung tumor	-11.59
lung normal GW97-179	20677	29.94	71.52	143.04	lung normal	
lung tumor GW97-178	20676	28 76	143.36	286.72	lung tumor	2.00
lung normal GW98-165	21922	28.69	149.49	298.98	lung normal	
lung tumor GW98-164	21921	31.28	32.63	65.26	lung tumor	-4.58
lung normal GW98-282	22584	31.42	30.07	60.14	lung normal	
lung tumor GW98-281	22583	30.33	56.83	113.66	lung tumor	1.89
breast normal GW00-392	28750	28.72	146.7	146.70	breast normal	
breast tumor GW00-391	28746	27.02	398.56	797.12	breast tumor	5.43
breast normal GW00-413	28798	30.95	39.63	39.63	breast normal	
breast tumor GW00-412	28797	30.58	49.03	98.06	breast tumor	2.47
breast normal GW00-235:238	27592-95	32.53	15.6	15.60	breast normal	
breast tumor GW00-231:234	27588-91	29.58	88.49	88.49	breast tumor	5.67
breast normal GW98-621	23656	27.5	300.39	600.78	breast normal	
breast tumor GW98-620	23655	29.28	105.43	210.86	breast tumor	-2.85
brain normal BB99-542	25507	30.67	46.59	93.18	brain normal	
brain normal BB99-406	25509	29.54	90.66	181.32	brain normal	
brain normal BB99-904	25546	31.13	35.58	71.16	brain normal	
brain stage 5 ALZ BB99-874	25502	31.4	30.36	60.72	brain stage 5 ALZ	-1.90

brain stage 5 ALZ BB99-887	25503	28.39	177.94	355.88	brain stage 5 ALZ	3.09
brain stage 5 ALZ BB99-862	25504	28.92	130.19	260.38	brain stage 5 ALZ	2.26
brain stage 5 ALZ BB99-927	25542	28.2	198.98	397.96	brain stage 5 ALZ	3.45
CT lung KC	normal	31.24	33.37	66.74	CT lung	
lung 26 KC	normal	33.59	8.37	8.37	lung 26	
lung 27 KC	normal	37.8	0.7	0.70	lung 27	
lung 24 KC	COPD	34.56	4.73	4.73	lung 24	-4.39
lung 28 KC	COPD	35.39	2.91	2.91	lung 28	-7.13
lung 23 KC	COPD	34.74	4.26	4.26	lung 23	-4.87
lung 25 KC	normal	33.85	7.19	7.19	lung 25	
asthmatic lung ODO3112	29321	35.04	3.57	3.57	asthmatic lung	-5.81
asthmatic lung ODO3433	29323	32.44	16.48	32.96	asthmatic lung	1.59
asthmatic lung ODO3397	29322	29.4	98.44	196.88	asthmatic lung	9.49
asthmatic lung ODO4928	29325	31.1	36.23	72.46	asthmatic lung	3.49
endo cells KC	control	40	0	0.00	endo cells	
endo VEGF KC		40	0	0.00	endo VEGF	0.00
endo bFGF KC		35.4	2.89	2.89	endo bFGF	2.89
heart Clontech	normal	29.05	120.78	241.56	heart	
heart (T-1) ischemic	29417	26.23	633.79	1267.58	heart T-1	5.25
heart (T-14) non-obstructive DCM	29422	25.74	847.85	1695.70	heart T-14	7.02
heart (T-3399) DCM	29426	25.03	1289.37	2578.74	heart T-3399	10.68
adenoid GW99-269	26162	35.24	3.17	6.34	adenoid	
tonsil GW98-280	22582	31	38.35	76.70	tonsil	
T cells PC00314	28453	31.75	24.69	49.38	T cells	
PBMNC		40	0	0.00	PBMNC	
monocyte		40	0	0.00	monocyte	
B cells PC00665	28455	31.35	31.31	62.62	B cells	
dendritic cells 28441		32.81	13.25	26.50	dendritic cells	
neutrophils	28440	31.76	24.51	24.51	neutrophils	
eosinophils	28446	33.08	11.29	22.58	eosinophils	
BM unstim		36.9	1.19	1.19	BM unstim	
BM stim		38.86	0.38	0.38	BM stim	-3.13
osteo dif		37.77	0.72	0.72	osteo dif	0.72
osteo undif		40	0	0.00	osteo undif	
chondrocytes		33.14	10.88	27.20	chondrocytes	
OA Synovium IP12/01	29462	30.61	48.28	48.28	OA Synovium	
OA Synovium NP10/01	29461	27.5	300.97	601.94	OA Synovium	
OA Synovium NP57/00	28464	29.28	105.55	211.10	OA Synovium	
RA Synovium NP03/01	28466	30.18	62.3	124.60	RA Synovium	
RA Synovium NP71/00	28467	29.22	109.5	219.00	RA Synovium	
RA Synovium NP45/00	28475	30.06	66.71	133.42	RA Synovium	
OA bone (biobank)	29217	32.6	14.99	14.99	OA bone (biobank)	
OA bone Sample 1	J. Emory	30.48	52.25	104.50	OA bone	
OA bone Sample 2	J. Emory	32.31	17.76	35.52	OA bone	
Cartilage (pool)	Normal	30.45	53.05	106.10	Cartilage (pool)	

Cartilage (pool)	OA	30.81	43.01	86.02	Cartilage (pool)	-1.23
PBL unifected	28441	30.19	61.92	123.84	PBL unifected	
PBL HIV IIIB	28442	31.19	34.35	68.70	PBL HIV IIIB	-1.80
MRC5 uninfected (100%)	29158	30.19	62.02	124.04	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	31.13	35.48	70.96	MRC5 HSV strain F	-1.75
W12 cells	29179	32	21.32	42.64	W12 cells	
Keratinocytes	29180	33.3	9.92	19.84	Keratinocytes	
B-actin control		26.66	492.23			
genomic		24.83	1443.91			
1.00E+05		18.12	100000			
1.00E+05		18.12	100000			
1.00E+04		21.28	10000			
1.00E+04		21.31	10000			
1.00E+03		24.92	1000			
1.00E+03		24.9	1000			
1.00E+02		29.22	100			
1.00E+02		29.26	100			
1.00E+01		33.13	10			
1.00E+01		34.32	10			
1.00E-00		40	0			
1.00E-00		40	0			
NTC		40	0			

Gene Name sbg1033026C1q

Disease tissues	**Fold Change in Disease Population Relative to Normal**
colon tumor	-4.35
colon tumor	1.80
colon tumor	-2.26
colon tumor	-1.30
lung tumor	-11.59
lung tumor	2.00
lung tumor	-4.58
lung tumor	1.89
breast tumor	5.43
breast tumor	2.47
breast tumor	5.67
breast tumor	-2.85
brain stage 5 ALZ	-1.90
brain stage 5 ALZ	3.09
brain stage 5 ALZ	2.26
brain stage 5 ALZ	3.45
lung 24	-4.39
lung 28	-7.13
lung 23	-4.87
asthmatic lung	-5.81
asthmatic lung	1.59
asthmatic lung	9.49

asthmatic lung	3.49
endo VEGF	0.00
endo bFGF	2.89
heart T-1	5.25
heart T-14	7.02
heart T-3399	10.68
BM stim	-3.13
osteo dif	0.72
Cartilage (pool)	-1.23
PBL HIV IIIB	-1.80
MRC5 HSV strain F	-1.75

Gene Name sbg1003675Rnase

FAILED

Gene Name sbg1015258PLM

Low overall expression in normal and disease samples. Highest normal expression in the endometrium, hypothalamus, liver small intestine, and the testis. Highest disease expression in one of the breast normal/tumor pairs, one of the normal brain samples, two of the Alzheimer's disease brain samples, the B cells and the HSV-infected MRC5 cells. Downregulation in 1 of 4 lung tumor samples is sufficient to claim a role in cancer of the lung. Upregulation in 2 of 4 breast tumor samples indicates an involvement in cancer of the breast. Downregulation in 2 of 3 COPD samples and in 1 of 4 asthmatic lung samples implies a role in chronic obstructive pulmonary disease and asthma. Upregulation in the obstructive DCM heart sample suggests a potential role in cardiovascular disease. Downregulation in the stimulated bone marrow sample. Downregulation in the OA cartilage pool implicates this gene in osteoarthritis. Upregulation in the HSV-infected MRC5 cells suggests that this gene may be a host factor in HSV. Low expression in all immune cells except the B cells which show moderate expression.

Sample sbg1015258PLM	**Ct (sample 1 and 2)**	**Mean GOI copies (sample 1)**	**Mean GOI copies (sample 2)**	**Average GOI Copies**	**18S rRNA (ng)**	**50 ng/18S rRNA (ng)**	**copies of mRNA detected/ 50 ng total RNA**
Subcutaneous Adipocytes Zenbio	39.96, 39.32	0.39	0.73	0.56	3.06	16.34	9.15
Subcutaneous Adipose Zenbio	39.61, 37.77	0.62	1.84	1.23	0.96	52.36	64.40
Adrenal Gland Clontech	36.89, 37.65	3.12	1.98	2.55	0.61	81.97	209.02
Whole Brain Clontech	32.77, 33.06	36.18	30.37	33.28	7.24	6.91	229.80
Fetal Brain Clontech	38.01, 37.52	1.6	2.14	1.87	0.48	103.95	194.39
Cerebellum Clontech	38.34, 37.8	1.31	1.81	1.56	2.17	23.04	35.94
Cervix	36.9, 37.17	3.1	2.64	2.87	2.42	20.66	59.30
Colon	35.93, 37.95	5.51	1.66	3.59	2.71	18.45	66.14
Endometrium	34.62, 37.51	12.02	2.15	7.09	0.73	68.21	483.29
Esophagus	35.76, 37.39	6.1	2.31	4.21	1.37	36.50	153.47
Heart Clontech	36.78, 38.53	3.33	1.17	2.25	1.32	37.88	85.23
Hypothalamus	37.12, 36.52	2.71	3.87	3.29	0.32	155.28	510.87
Ileum	36.15, 36.19	4.84	4.72	4.78	2.58	19.38	92.64
Jejunum	34.6, 33.48	12.14	23.65	17.90	6.60	7.58	135.57
Kidney	37.16, 37.9	2.65	1.7	2.18	2.12	23.58	51.30

Liver	34.6, 36.06	12.13	5.11	8.62	1.50	33.33	287.33
Fetal Liver Clontech	34.32, 36.91	14.35	3.07	8.71	10.40	4.81	41.88
Lung	36.94, 35.31	3.02	7.98	5.50	2.57	19.46	107.00
Mammary Gland Clontech	38.03, 36.89	1.58	3.11	2.35	13.00	3.85	9.02
Myometrium	38.44, 38	1.24	1.6	1.42	2.34	21.37	30.34
Omentum	35.41, 35.38	7.51	7.64	7.58	3.94	12.69	96.13
Omentum							
Ovary	34.32, 34.36	14.4	14.07	14.24	4.34	11.52	164.00
Pancreas	36.44, 36.82	4.07	3.25	3.66	0.81	61.80	226.21
Head of Pancreas	37.54, 36.96	2.11	2.98	2.55	1.57	31.85	81.05
Parotid Gland	37.1, 35.46	2.75	7.29	5.02	5.48	9.12	45.80
Placenta Clontech	36.07, 35.36	5.08	7.74	6.41	5.26	9.51	60.93
Prostate	37.4, 37.82	2.3	1.79	2.05	3.00	16.67	34.08
Rectum	36.65, 37.39	3.59	2.32	2.96	1.23	40.65	120.12
Salivary Gland Clontech	38.55, 39.31	1.16	0.74	0.95	7.31	6.84	6.50
Skeletal Muscle Clontech	37.59, 36.87	2.06	3.15	2.61	1.26	39.68	103.37
Skin	38.36, 36.33	1.3	4.34	2.82	1.21	41.32	116.53
Small Intestine Clontech	36.05, 36.76	5.14	3.37	4.26	0.98	51.07	217.31
Spleen	37.62, 35.34	2.02	7.83	4.93	4.92	10.16	50.05
Stomach	35.8, 35.15	5.95	8.76	7.36	2.73	18.32	134.71
Testis Clontech	35.14, 37.08	8.82	2.77	5.80	0.57	87.87	509.23
Thymus Clontech	35.89, 35.06	5.65	9.22	7.44	9.89	5.06	37.59
Thyroid	37.59, 37.2	2.06	2.59	2.33	2.77	18.05	41.97
Trachea Clontech	37.52, 37.95	2.14	1.66	1.90	9.71	5.15	9.78
Urinary Bladder	37.47, 35.44	2.2	7.38	4.79	5.47	9.14	43.78
Uterus	34.17, 34.12	15.66	16.17	15.92	5.34	9.36	149.02
genomic	27.03	1097.52					
b-actin	27.23	974.77					
1.00E+05	19.25	100000					
1.00E+05	19.2	100000					
1.00E+04	22.99	10000					
1.00E+04	22.94	10000					
1.00E+03	27.09	1000					
1.00E+03	27.28	1000					
1.00E+02	31.49	100					
1.00E+02	31.46	100					
1.00E+01	37.86	10					
1.00E+01	35.45	10					
1.00E-00	37.08	1					
1.00E-00	37.4	1					
NTC	36.45	-1					
NTC	36.15	-1					

Sample sbg1015258PLM	**Reg number**	**Ct**	**Mean GOI**	**copies of mRNA**	**Sample**	**Fold Change in**

	(GSK identifier)		copies	detected/ 50 ng total RNA		Disease Population
colon normal GW98-167	21941	35.4	9.91	19.82	colon normal	
colon tumor GW98-166	21940	35.13	11.61	23.22	colon tumor	1.17
colon normal GW98-178	22080	34.84	13.83	27.66	colon normal	
colon tumor GW98-177	22060	35	12.59	25.18	colon tumor	-1.10
colon normal GW98-561	23514	35.48	9.4	18.80	colon normal	
colon tumor GW98-560	23513	36.2	6.14	12.28	colon tumor	-1.53
colon normal GW98-894	24691	34.53	16.62	33.24	colon normal	
colon tumor GW98-893	24690	34.29	19.25	38.50	colon tumor	1.16
lung normal GW98-3	20742	34.53	16.69	33.38	lung normal	
lung tumor GW98-2	20741	37.87	2.25	4.50	lung tumor	-7.42
lung normal GW97-179	20677	34.59	16.02	32.04	lung normal	
lung tumor GW97-178	20676	34.45	17.43	34.86	lung tumor	1.09
lung normal GW98-165	21922	33.89	24.39	48.78	lung normal	
lung tumor GW98-164	21921	35.48	9.43	18.86	lung tumor	-2.59
lung normal GW98-282	22584	36.67	4.62	9.24	lung normal	
lung tumor GW98-281	22583	37.87	2.26	4.52	lung tumor	-2.04
breast normal GW00-392	28750	34.17	20.64	20.64	breast normal	
breast tumor GW00-391	28746	33.54	30.09	60.18	breast tumor	2.92
breast normal GW00-413	28798	39.05	1.11	1.11	breast normal	
breast tumor GW00-412	28797	35.01	12.46	24.92	breast tumor	22.45
breast normal GW00-235:238	27592-95	40	0.55	0.55	breast normal	
breast tumor GW00-231:234	27588-91	35.07	12.02	12.02	breast tumor	21.85
breast normal GW98-621	23656	33	41.58	83.16	breast normal	
breast tumor GW98-620	23655	33.05	40.47	80.94	breast tumor	-1.03
brain normal BB99-542	25507	32.73	48.93	97.86	brain normal	
brain normal BB99-406	25509	33.97	23.34	46.68	brain normal	
brain normal BB99-904	25546	37.88	2.24	4.48	brain normal	
brain stage 5 ALZ BB99-874	25502	35.92	7.25	14.50	brain stage 5 ALZ	-3.43
brain stage 5 ALZ BB99-887	25503	31.57	97.99	195.98	brain stage 5 ALZ	3.95
brain stage 5 ALZ BB99-862	25504	36.08	6.57	13.14	brain stage 5 ALZ	-3.78
brain stage 5 ALZ BB99-927	25542	32.66	50.98	101.96	brain stage 5 ALZ	2.05
CT lung KC	normal	37.37	3.04	6.08	CT lung	
lung 26 KC	normal				lung 26	
lung 27 KC	normal	38.52	1.52	1.52	lung 27	
lung 24 KC	COPD	40	0	0.00	lung 24	-3.07
lung 28 KC	COPD	37.4	2.99	2.99	lung 28	-1.03
lung 23 KC	COPD	39.56	0.82	0.82	lung 23	-3.74
lung 25 KC	normal	38.43	1.61	1.61	lung 25	

asthmatic lung ODO3112	29321	39.45	0.88	0.88	asthmatic lung	-3.49
asthmatic lung ODO3433	29323	36.48	5.19	10.38	asthmatic lung	3.38
asthmatic lung ODO3397	29322	35.56	8.99	17.98	asthmatic lung	5.86
asthmatic lung ODO4928	29325	37.06	3.66	7.32	asthmatic lung	2.38
endo cells KC	control	39.29	0.96	0.96	endo cells	
endo VEGF KC		37.65	2.57	2.57	endo VEGF	2.68
endo bFGF KC		40	0.48	0.48	endo bFGF	-2.00
heart Clontech	normal	40	0.68	1.36	heart	
heart (T-1) ischemic	29417	39.29	0.96	1.92	heart T-1	1.41
heart (T-14) non-obstructive DCM	29422	38.21	1.84	3.68	heart T-14	2.71
heart (T-3399) DCM	29426	35.49	9.35	18.70	heart T-3399	13.75
adenoid GW99-269	26162	39.63	0.78	1.56	adenoid	
tonsil GW98-280	22582	34.5	16.92	33.84	tonsil	
T cells PC00314	28453	34.57	16.25	32.50	T cells	
PBMNC		37.32	3.13	3.13	PBMNC	
monocyte		37.74	2.44	4.88	monocyte	
B cells PC00665	28455	33.32	34.36	68.72	B cells	
dendritic cells 28441		37.29	3.19	6.38	dendritic cells	
neutrophils	28440	36.01	6.85	6.85	neutrophils	
eosinophils	28446	35.38	9.98	19.96	eosinophils	
BM unstim		37.44	2.91	2.91	BM unstim	
BM stim		40	0.53	0.53	BM stim	-5 49
osteo dif		38.15	1.91	1.91	osteo dif	-1.38
osteo undif		37.6	2.64	2.64	osteo undif	
chondrocytes		36.1	6.51	16.28	chondrocytes	
OA Synovium IP12/01	29462	35.58	8.86	8.86	OA Synovium	
OA Synovium NP10/01	29461	35.46	9.54	19.08	OA Synovium	
OA Synovium NP57/00	28464	34.05	22.23	44.46	OA Synovium	
RA Synovium NP03/01	28466	37.92	2.19	4.38	RA Synovium	
RA Synovium NP71/00	28467	35 39	9.92	19.84	RA Synovium	
RA Synovium NP45/00	28475	35.03	12.37	24.74	RA Synovium	
OA bone (biobank)	29217	39.98	0.67	0.67	OA bone (biobank)	
OA bone Sample 1	J. Emory	36.06	6.68	13.36	OA bone	
OA bone Sample 2	J. Emory	39.89	0.67	1.34	OA bone	
Cartilage (pool)	Normal	35.57	8.92	17.84	Cartilage (pool)	
Cartilage (pool)	OA	39.5	0.85	1.70	Cartilage (pool)	-10.49
PBL unifected	28441	36.65	4.67	9.34	PBL unifected	
PBL HIV IIIB	28442	36.94	3.92	7.84	PBL HIV IIIB	-1.19
MRC5 uninfected (100%)	29158	37.54	2.74	5.48	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	33.19	37.18	74.36	MRC5 HSV strain F	13.57
W12 cells	29179	37.23	3.3	6.60	W12 cells	
Keratinocytes	29180	37.18	3.4	6.80	Keratinocytes	

B-actin control		27.26	1296.87			
genomic		27.2	1345.34			
1.00E+05		19.44	100000			
1.00E+05		19.81	100000			
1.00E+04		23.63	10000			
1.00E+04		23.41	10000			
1.00E+03		27.77	1000			
1.00E+03		27.89	1000			
1.00E+02		32.32	100			
1.00E+02		32.3	100			
1.00E+01		36.77	10			
1.00E+01		36.39	10			
1.00E-00		38.06	1			
1.00E-00		37.56	1			
NTC		38.18	-1			

Gene Name sbg1015258PLM

Disease tissues	**Fold Change in Disease Population Relative to Normal**
colon tumor	1.17
colon tumor	-1.10
colon tumor	-1.53
colon tumor	1.16
lung tumor	-7.42
lung tumor	1.09
lung tumor	-2.59
lung tumor	-2.04
breast tumor	2.92
breast tumor	22.45
breast tumor	21.85
breast tumor	-1.03
brain stage 5 ALZ	-3.43
brain stage 5 ALZ	3.95
brain stage 5 ALZ	-3.78
brain stage 5 ALZ	2.05
lung 24	-3.07
lung 28	-1.03
lung 23	-3.74
asthmatic lung	-3.49
asthmatic lung	3.38
asthmatic lung	5.86
asthmatic lung	2.38
endo VEGF	2.68
endo bFGF	-2.00

heart T-1	1.41
heart T-14	2.71
heart T-3399	13.75
BM stim	-5.49
osteo dif	-1.38
Cartilage (pool)	-10.49
PBL HIV IIIB	-1.19
MRC5 HSV strain F	13.57

Gene Name sbg1003328IG (Taqman)
Moderate overall expression. Highest normal expression in whole brain, fetal brain, and cerebellum with slightly lower levels of expression in the colon and mammary gland. Highest disease expression in the colon and lung tumor pairs as well as the normal and Alzheimer's brain. Significant upregulation in 2 of 4 breast tumor samples with slight upregulation in 1 of 4 breast tumor samples implicates this gene in breast cancer. Downregulation in 3 of 3 COPD samples may suggest an involvement in chronic obstructive pulmonary disease. Downregulation in 1 of 4 asthma samples suggests a potential role for this gene in asthma. Downregulation in the HSV-infected MRC5 cells suggests that this gene may play a role in HSV. High expression in 3 of 3 OA synovium samples, 3 of 3 RA synovium samples, 2 of 2 OA bone samples, and corroborating high expression in the T cells and B cells implicates this gene in osteoarthritis and rheumatoid arthritis.

Sample sbg1003328IG	**Ct (sample 1 and 2)**	**Mean GOI copies (sample 1)**	**Mean GOI copies (sample 2)**	**Average GOI Copies**	**18S rRNA (ng)**	**50 ng/18S rRNA (ng)**	**copies of mRNA detected /50 ng total RNA**
Subcutaneous Adipocytes Zenbio	32.35, 32.1	109.15	127.12	118.14	3.06	16.34	1930.31
Subcutaneous Adipose Zenbio	37.92, 40	3.84	0	1.92	0.96	52.36	100.52
Adrenal Gland Clontech	38.07, 35.73	3.5	14.32	8.91	0.61	81.97	730.33
Whole Brain Clontech	22.72, 23.09	35640.5	28576.52	32108.51	7.24	6.91	221743.85
Fetal Brain Clontech	33.39, 34.06	58.43	39.04	48.74	0.48	103.95	5066.01
Cerebellum Clontech	31.32, 31.02	202.49	242.95	222.72	2.17	23.04	5131.80
Cervix	36.36, 35.6	9.78	15.49	12.64	2.42	20.66	261.05
Colon	30.74, 32.11	286.9	125.78	206.34	2.71	18.45	3807.01
Endometrium	34.58, 36.01	28.47	12.11	20.29	0.73	68.21	1384.04
Esophagus	37.54, 36.05	4.82	11.78	8.30	1.37	36.50	302.92
Heart Clontech	36.23, 36.85	10.56	7.3	8.93	1.32	37.88	338.26
Hypothalamus	40, 36.96	0	6.81	3.41	0.32	155.28	528.73
Ileum	34.79, 34.48	25.09	30.4	27.75	2.58	19.38	537.69
Jejunum	30.14, 31.02	412.72	242.47	327.60	6.60	7.58	2481.78
Kidney	33.94, 34.61	41.89	28.12	35.01	2.12	23.58	825.59
Liver	36.11, 35.38	11.41	17.61	14.51	1.50	33.33	483.67
Fetal Liver Clontech	30.24, 30.27	388.12	381.28	384.70	10.40	4.81	1849.52
Lung	35.59, 35.09	15.59	20.98	18.29	2.57	19.46	355.74
Mammary Gland Clontech	29.21, 28.52	718.74	1090.18	904.46	13.00	3.85	3478.69

Myometrium	33.7, 34.11	48.42	37.85	43.14	2.34	21.37	921.69
Omentum	33.83, 33.57	44.75	52.27	48.51	3.94	12.69	615.61
Ovary	32.47, 32.34	101.42	109.96	105.69	4.34	11.52	1217.63
Pancreas	38.16, 40	3.31	0	1.66	0.81	61.80	102.29
Head of Pancreas	40, 36.68	0	8.07	4.04	1.57	31.85	128.50
Parotid Gland	31.68, 31.03	162.92	241.11	202.02	5.48	9.12	1843.20
Placenta Clontech	30.48, 30.82	335.37	274.53	304.95	5.26	9.51	2898.76
Prostate	33.39, 32.15	58.39	122.82	90.61	3.00	16.67	1510.08
Rectum	35.95, 35.32	12.5	18.32	15.41	1.23	40.65	626.42
Salivary Gland Clontech	31.25, 30.65	211.88	303.2	257.54	7.31	6.84	1761.56
Skeletal Muscle Clontech	36.61, 37.62	8.44	4.6	6.52	1.26	39.68	258.73
Skin	36.37, 36.08	9.71	11.56	10.64	1.21	41.32	439.46
Small Intestine Clontech	36.74, 34.51	7.79	29.79	18.79	0.98	51.07	959.65
Spleen	34.78, 35.63	25.25	15.18	20.22	4.92	10.16	205.44
Stomach	40, 35.13	0.88	20.56	10.72	2.73	18.32	196.34
Testis Clontech	35.01, 39.68	22.07	1.33	11.70	0.57	87.87	1028.12
Thymus Clontech	29.15, 29.2	749.23	724.61	736.92	9.89	5.06	3725.58
Thyroid	32.02, 32.14	133.23	123.77	128.50	2.77	18.05	2319.49
Trachea Clontech	31.28, 30.17	207.67	405.04	306.36	9.71	5.15	1577.52
Urinary Bladder	33.07, 32.91	70.6	78.07	74.34	5.47	9.14	679.48
Uterus	33.01, 33.15	73.56	67.48	70.52	5.34	9.36	660.30
genomic	29.15	746.77					
b-actin	30.2	397.52					
1.00E+05	21.06	100000					
1.00E+05	20.94	100000					
1.00E+04	25.06	10000					
1.00E+04	24.54	10000					
1.00E+03	28.32	1000					
1.00E+03	28.77	1000					
1.00E+02	33	100					
1.00E+02	32.74	100					
1.00E+01	35.9	10					
1.00E+01	40	0					
1.00E-00	40	0					
1.00E-00	40	0					
NTC	40	0					
NTC	40	0					

Sample sbg1003328IG	**Reg number (GSK identifier)**	**Ct**	**Mean GOI copies**	**copies of mRNA detected/ 50 ng total RNA**	**Sample**	**Fold Change in Disease Population**
colon normal GW98-167	21941	24.26	15509.01	31018.02	colon normal	

colon tumor GW98-166	21940	24.5	13727.44	27454.88	colon tumor	-1.13
colon normal GW98-178	22080	28.01	2276.97	4553.94	colon normal	
colon tumor GW98-177	22060	27.11	3618.2	7236.40	colon tumor	1.59
colon normal GW98-561	23514	24.47	13993.67	27987.34	colon normal	
colon tumor GW98-560	23513	25.32	9040.47	18080.94	colon tumor	-1.55
colon normal GW98-894	24691	24.17	16251.61	32503.22	colon normal	
colon tumor GW98-893	24690	25.15	9872.46	19744.92	colon tumor	-1.65
lung normal GW98-3	20742	24.4	14498.52	28997.04	lung normal	
lung tumor GW98-2	20741	24.66	12640.32	25280.64	lung tumor	-1.15
lung normal GW97-179	20677	24.12	16680.84	33361.68	lung normal	
lung tumor GW97-178	20676	24.69	12468.91	24937.82	lung tumor	-1.34
lung normal GW98-165	21922	25.09	10168.18	20336.36	lung normal	
lung tumor GW98-164	21921	25.49	8296.37	16592.74	lung tumor	-1.23
lung normal GW98-282	22584	26.85	4131.52	8263.04	lung normal	
lung tumor GW98-281	22583	26.59	4702	9404.00	lung tumor	1.14
breast normal GW00-392	28750	25.9	6719.98	6719.98	breast normal	
breast tumor GW00-391	28746	25.04	10402.11	20804.22	breast tumor	3.10
breast normal GW00-413	28798	32.51	226.94	226.94	breast normal	
breast tumor GW00-412	28797	26.37	5261.73	10523.46	breast tumor	46.37
breast normal GW00-235:238	27592-95	34.58	78.63	78.63	breast normal	
breast tumor GW00-231:234	27588-91	28.45	1812.86	1812.86	breast tumor	23.06
breast normal GW98-621	23656	25.26	9289.36	18578.72	breast normal	
breast tumor GW98-620	23655	25.66	7579.13	15158.26	breast tumor	-1.23
brain normal BB99-542	25507	22.52	37845.47	75690.94	brain normal	
brain normal BB99-406	25509	23.07	28574.8	57149.60	brain normal	
brain normal BB99-904	25546	23.85	19214.49	38428.98	brain normal	
brain stage 5 ALZ BB99-874	25502	25.98	6442.51	12885.02	brain stage 5 ALZ	-4.43
brain stage 5 ALZ BB99-887	25503	23.19	26936.06	53872.12	brain stage 5 ALZ	-1.06
brain stage 5 ALZ BB99-862	25504	23.42	23948.83	47897.66	brain stage 5 ALZ	-1.19
brain stage 5 ALZ BB99-927	25542	24.15	16419.33	32838.66	brain stage 5 ALZ	-1.74
CT lung KC	normal	25.63	7714.35	15428.70	CT lung	
lung 26 KC	normal	32.34	247.99	247.99	lung 26	
lung 27 KC	normal	33.71	122.77	122.77	lung 27	
lung 24 KC	COPD	32.47	231.47	231.47	lung 24	-17.21
lung 28 KC	COPD	32.63	213.14	213.14	lung 28	-18.70
lung 23 KC	COPD	31.2	444.95	444.95	lung 23	-8.96
lung 25 KC	normal	33.46	139.4	139.40	lung 25	
asthmatic lung ODO3112	29321	31.6	360.95	360.95	asthmatic lung	-11.04
asthmatic lung ODO3433	29323	28.66	1634.71	3269.42	asthmatic lung	-1.22
asthmatic lung	29322	26.36	5294.26	10588.52	asthmatic lung	2.66

ODO3397						
asthmatic lung ODO4928	29325	28.23	2033.93	4067.86	asthmatic lung	1.02
endo cells KC	control	30.68	580.47	580.47	endo cells	
endo VEGF KC		31.08	471.26	471.26	endo VEGF	-1.23
endo bFGF KC		32.25	259.04	259.04	endo bFGF	-2.24
heart Clontech	normal	27.28	3312.82	6625.64	heart	
heart (T-1) ischemic	29417	27.48	2979.22	5958.44	heart T-1	-1.11
heart (T-14) non-obstructive DCM	29422	27.74	2613.8	5227.60	heart T-14	-1.27
heart (T-3399) DCM	29426	26.66	4541.38	9082.76	heart T-3399	1.37
adenoid GW99-269	26162	27.83	2493.31	4986.62	adenoid	
tonsil GW98-280	22582	25.68	7506.04	15012.08	tonsil	
T cells PC00314	28453	27.18	3487.61	6975.22	T cells	
PBMNC		32.6	216.73	216.73	PBMNC	
monocyte		32.27	256.89	513.78	monocyte	
B cells PC00665	28455	27.83	2492.12	4984.24	B cells	
dendritic cells 28441		26.67	4528.97	9057.94	dendritic cells	
neutrophils	28440	28.4	1862.35	1862.35	neutrophils	
eosinophils	28446	31.69	344.59	689.18	eosinophils	
BM unstim		32.04	289.03	289.03	BM unstim	
BM stim		30.59	607.18	607.18	BM stim	2.10
osteo dif		28.43	1831.57	1831.57	osteo dif	3.42
osteo undif		30.83	536	536.00	osteo undif	
chondrocytes		26.74	4368.46	10921.15	chondrocytes	
OA Synovium IP12/01	29462	27.91	2391.03	2391.03	OA Synovium	
OA Synovium NP10/01	29461	27.4	3109.93	6219.86	OA Synovium	
OA Synovium NP57/00	28464	27.05	3729.47	7458.94	OA Synovium	
RA Synovium NP03/01	28466	25.53	8116.96	16233.92	RA Synovium	
RA Synovium NP71/00	28467	26.06	6167.42	12334.84	RA Synovium	
RA Synovium NP45/00	28475	25.35	8888.66	17777.32	RA Synovium	
OA bone (biobank)	29217	30.23	729.87	729.87	OA bone (biobank)	
OA bone Sample 1	J. Emory	27.65	2743.38	5486.76	OA bone	
OA bone Sample 2	J. Emory	28.02	2258.96	4517.92	OA bone	
Cartilage (pool)	Normal	25.82	7006.64	14013.28	Cartilage (pool)	
Cartilage (pool)	OA	27.22	3408.61	6817.22	Cartilage (pool)	-2.06
PBL unifected	28441	24.24	15680.49	31360.98	PBL unifected	
PBL HIV IIIB	28442	25.43	8521.98	17043.96	PBL HIV IIIB	-1.84
MRC5 uninfected (100%)	29158	25.58	7922.19	15844.38	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	32.02	291.12	582.24	MRC5 HSV strain F	-27.21
W12 cells	29179	26.03	6269.24	12538.48	W12 cells	
Keratinocytes	29180	25.43	8538.15	17076.30	Keratinocytes	
B-actin control		29.74	938.61			
genomic		28.79	1522.16			
1.00E+05		20.84	100000			
1.00E+05		21.4	100000			

1.00E+04		24.5	10000			
1.00E+04		25.2	10000			
1.00E+03		28.45	1000			
1.00E+03		29.25	1000			
1.00E+02		35.34	100			
1.00E+02		33.61	100			
1.00E+01		38.95	10			
1.00E+01		40	0			
1.00E-00		40	0			
1.00E-00		40	0			
NTC		40	0			

Gene Name sbg1003328IG

Disease tissues	**Fold Change in Disease Population Relative to Normal**
colon tumor	-1.13
colon tumor	1.59
colon tumor	-1.55
colon tumor	-1.65
lung tumor	-1.15
lung tumor	-1.34
lung tumor	-1.23
lung tumor	1.14
breast tumor	3.10
breast tumor	46.37
breast tumor	23.06
breast tumor	-1.23
brain stage 5 ALZ	-4.43
brain stage 5 ALZ	-1.06
brain stage 5 ALZ	-1.19
brain stage 5 ALZ	-1.74
lung 24	-17.21
lung 28	-18.70
lung 23	-8.96
asthmatic lung	-11.04
asthmatic lung	-1.22
asthmatic lung	2.66
asthmatic lung	1.02
endo VEGF	-1.23
endo bFGF	-2.24
heart T-1	-1.11
heart T-14	-1.27
heart T-3399	1.37
BM stim	2.10
osteo dif	3.42

Cartilage (pool)	-2.06
PBL HIV IIIB	-1.84
MRC5 HSV strain F	-27.21

Gene Name sbg1020829SGLT

Low overall expression in normal and disease samples. Highest normal expression in the whole brain, kidney, and thymus. Highest disease expression in the adenoid, tonsil, T cells, B cells, and eosinophils. Highly immune cell specific. Downregulation in 1 of 4 lung tumor samples and upregulation in 1 of 4 breast tumor samples indicates involvement in cancers of the lung and breast. Upregulation in 3 of 4 AD brain samples suggests an involvement in Alzheimer's disease. Downregulation in 3 of 3 COPD samples implies a role in chronic obstructive pulmonary disease. Downregulation in the stimulated bone marrow sample. Upregulation in the differentiated osteoblast sample. Upregulation in the HSV-infected MRC5 cells suggests that this gene may be a host factor in HSV. Moderate to high expression in the OA and RA samples indicates a potential role in osteoarthritis and rheumatoid arthritis.

Sample sbg1020829SGLT	**Ct (sample 1 and 2)**	**Mean GOI copies (sample 1)**	**Mean GOI copies (sample 2)**	**Average GOI Copies**	**18S rRNA (ng)**	**50 ng/18S rRNA (ng)**	**copies of mRNA detected/50 ng total RNA**
Subcutaneous Adipocytes Zenbio	37.07, 40	7.33	0	3.67	3.06	16.34	59.89
Subcutaneous Adipose Zenbio	40, 40	0	0	0.00	0.96	52.36	0.00
Adrenal Gland Clontech	40, 40	0	0	0.00	0.61	81.97	0.00
Whole Brain Clontech	32.13, 32.38	138.5	119.48	128.99	7.24	6.91	890.81
Fetal Brain Clontech	40, 40	0	0	0.00	0.48	103.95	0.00
Cerebellum Clontech	40, 40	0	0	0.00	2.17	23.04	0.00
Cervix	36.13, 40	12.82	0	6.41	2.42	20.66	132.44
Colon	36.93, 36.84	7.97	8.41	8.19	2.71	18.45	151.11
Endometrium	37.45, 37.41	5.84	5.98	5.91	0.73	68.21	403.14
Esophagus	40, 40	0	0	0.00	1.37	36.50	0.00
Heart Clontech	40, 40	0	0	0.00	1.32	37.88	0.00
Hypothalamus	40, 40	0	0	0.00	0.32	155.28	0.00
Ileum	36.53, 35.17	10.09	22.67	16.38	2.58	19.38	317.44
Jejunum	40, 35.73	0	16.2	8.10	6.60	7.58	61.36
Kidney	31.93, 31.01	155.27	269.39	212.33	2.12	23.58	5007.78
Liver	36.1, 35.88	13.05	14.82	13.94	1.50	33.33	464.50
Fetal Liver Clontech	35.06, 34.36	24.26	36.78	30.52	10.40	4.81	146.73
Lung	37.24, 40	6.63	0	3.32	2.57	19.46	64.49
Mammary Gland Clontech	34.25, 34.21	39.27	40.17	39.72	13.00	3.85	152.77
Myometrium	38.48, 35.31	3.16	20.87	12.02	2.34	21.37	256.73
Omentum	40, 38.91	0	2.45	1.23	3.94	12.69	15.55
Ovary	37.87, 37.06	4.56	7.37	5.97	4.34	11.52	68.72
Pancreas	40, 40	0	0	0.00	0.81	61.80	0.00
Head of Pancreas	40, 40	0	0	0.00	1.57	31.85	0.00

Parotid Gland	36.06, 37.07	13.32	7.31	10.32	5.48	9.12	94.11
Placenta Clontech	35.98, 38.73	13.96	2.72	8.34	5.26	9.51	79.28
Prostate	40, 40	0	0	0.00	3.00	16.67	0.00
Rectum	40, 40	0	0	0.00	1.23	40.65	0.00
Salivary Gland Clontech	37.05, 37.06	7.4	7.36	7.38	7.31	6.84	50.48
Skeletal Muscle Clontech	40, 40	0	0	0.00	1.26	39.68	0.00
Skin	40, 40	0	0	0.00	1.21	41.32	0.00
Small Intestine Clontech	40, 40	0	0	0.00	0.98	51.07	0.00
Spleen	35.62, 35.72	17.34	16.35	16.85	4.92	10.16	171.19
Stomach	40, 40	0	1.61	0.81	2.73	18.32	14.74
Testis Clontech	40, 40	0	0	0.00	0.57	87.87	0.00
Thymus Clontech	31.3, 31.09	226.24	257.15	241.70	9.89	5.06	1221.92
Thyroid	40, 40	0	0	0.00	2.77	18.05	0.00
Trachea Clontech	36.6, 36.64	9.68	9.44	9.56	9.71	5.15	49.23
Urinary Bladder	40, 40	0	0	0.00	5.47	9.14	0.00
Uterus	34.64, 36.65	31.06	9.41	20.24	5.34	9.36	189.47
genomic	29.07	853.08					
b-actin	27.08	2793.5					
1.00E+05	20.85	100000					
1.00E+05	21.11	100000					
1.00E+04	24.81	10000					
1.00E+04	24.95	10000					
1.00E+03	28.39	1000					
1.00E+03	28.9	1000					
1.00E+02	34.1	100					
1.00E+02	32.86	100					
1.00E+01	35.52	10					
1.00E+01	40	0					
1.00E-00	40	0					
1.00E-00	40	0					
NTC	40	0					
NTC	40	0					

Sample sbg1020829SGLT	**Reg number (GSK identifier)**	**Ct**	**Mean GOI copies**	**copies of mRNA detected/ 50 ng total RNA**	**Sample**	**Fold Change in Disease Population**
colon normal GW98-167	21941	31.06	206.55	413.10	colon normal	
colon tumor GW98-166	21940	31.18	193.59	387.18	colon tumor	-1.07
colon normal GW98-178	22080	30.74	244.37	488.74	colon normal	
colon tumor GW98-177	22060	30.37	299.28	598.56	colon tumor	1.22
colon normal GW98-561	23514	29.31	527.04	1054.08	colon normal	
colon tumor GW98-560	23513	31.86	134.48	268.96	colon tumor	-3.92

colon normal GW98-894	24691	31.84	135.33	270.66	colon normal	
colon tumor GW98-893	24690	31.9	131.57	263.14	colon tumor	-1.03
lung normal GW98-3	20742	28.81	689.14	1378.28	lung normal	
lung tumor GW98-2	20741	31.91	130.71	261.42	lung tumor	-5.27
lung normal GW97-179	20677	30.04	356.26	712.52	lung normal	
lung tumor GW97-178	20676	29.05	605.73	1211.46	lung tumor	1.70
lung normal GW98-165	21922	28.42	852.41	1704.82	lung normal	
lung tumor GW98-164	21921	30.51	277.13	554.26	lung tumor	-3.08
lung normal GW98-282	22584	31.23	188.34	376.68	lung normal	
lung tumor GW98-281	22583	30.46	285	570.00	lung tumor	1.51
breast normal GW00-392	28750	31.14	197.15	197.15	breast normal	
breast tumor GW00-391	28746	32.15	114.65	229.30	breast tumor	1.16
breast normal GW00-413	28798	34.87	26.64	26.64	breast normal	
breast tumor GW00-412	28797	31.83	136.42	272.84	breast tumor	10.24
breast normal GW00-235:238	27592-95	36.34	12.09	12.09	breast normal	
breast tumor GW00-231:234	27588-91	33.48	56.11	56.11	breast tumor	4.64
breast normal GW98-621	23656	32.39	100.78	201.56	breast normal	
breast tumor GW98-620	23655	31.4	171.82	343.64	breast tumor	1.70
brain normal BB99-542	25507	34.49	32.75	65.50	brain normal	
brain normal BB99-406	25509	34.01	42.2	84.40	brain normal	
brain normal BB99-904	25546	36.17	13.3	26.60	brain normal	
brain stage 5 ALZ BB99-874	25502	31.16	195.23	390.46	brain stage 5 ALZ	6.64
brain stage 5 ALZ BB99-887	25503	31.56	157.33	314.66	brain stage 5 ALZ	5.35
brain stage 5 ALZ BB99-862	25504	32.62	89.2	178.40	brain stage 5 ALZ	3.03
brain stage 5 ALZ BB99-927	25542	33.26	63.43	126.86	brain stage 5 ALZ	2.16
CT lung KC	normal	30.82	234.88	469.76	CT lung	
lung 26 KC	normal	30.21	325.42	325.42	lung 26	
lung 27 KC	normal	36.89	9	9.00	lung 27	
lung 24 KC	COPD	36.17	13.24	13.24	lung 24	-15.84
lung 28 KC	COPD	38.38	4.06	4.06	lung 28	-51.66
lung 23 KC	COPD	35.53	18.67	18.67	lung 23	-11.23
lung 25 KC	normal	34.37	34.83	34.83	lung 25	
asthmatic lung ODO3112	29321	33.65	51.41	51.41	asthmatic lung	-4.08
asthmatic lung ODO3433	29323	30.62	260.95	521.90	asthmatic lung	2.49
asthmatic lung ODO3397	29322	31.31	180.14	360.28	asthmatic lung	1.72
asthmatic lung ODO4928	29325	31.14	197.09	394.18	asthmatic lung	1.88
endo cells KC	control	32.56	92.23	92.23	endo cells	
endo VEGF KC		33.29	62.39	62.39	endo VEGF	-1.48
endo bFGF KC		32.55	92.65	92.65	endo bFGF	1.00
heart Clontech	normal	33.17	66.25	132.50	heart	
heart (T-1) ischemic	29417	33.07	70.16	140.32	heart T-1	1.06
heart (T-14) non-obstructive DCM	29422	34.64	30.13	60.26	heart T-14	-2.20
heart (T-3399) DCM	29426	32.53	93.63	187.26	heart T-3399	1.41

adenoid GW99-269	26162	28.92	650.55	1301.10	adenoid	
tonsil GW98-280	22582	27.11	1719.42	3438.84	tonsil	
T cells PC00314	28453	28.05	1037.04	2074.08	T cells	
PBMNC		36.57	10.71	10.71	PBMNC	
monocyte		33.22	64.68	129.36	monocyte	
B cells PC00665	28455	27.07	1757.79	3515.58	B cells	
dendritic cells 28441		33.77	48.05	96.10	dendritic cells	
neutrophils	28440	30.71	248.56	248.56	neutrophils	
eosinophils	28446	27.3	1549.7	3099.40	eosinophils	
BM unstim		30.06	352.26	352.26	BM unstim	
BM stim		34.14	39.39	39.39	BM stim	-8.94
osteo dif		36.29	12.42	12.42	osteo dif	12.42
osteo undif		40	0	0.00	osteo undif	
chondrocytes		32.11	117.39	293.48	chondrocytes	
OA Synovium IP12/01	29462	30.17	331.7	331.70	OA Synovium	
OA Synovium NP10/01	29461	32.05	120.98	241.96	OA Synovium	
OA Synovium NP57/00	28464	30.13	339.03	678.06	OA Synovium	
RA Synovium NP03/01	28466	31.28	182.96	365.92	RA Synovium	
RA Synovium NP71/00	28467	29.81	402.34	804.68	RA Synovium	
RA Synovium NP45/00	28475	30.22	324.14	648.28	RA Synovium	
OA bone (biobank)	29217	28.45	837.78	837.78	OA bone (biobank)	
OA bone Sample 1	J. Emory	30.21	325.03	650.06	OA bone	
OA bone Sample 2	J. Emory	29.8	406	812.00	OA bone	
Cartilage (pool)	Normal	31.09	203.28	406.56	Cartilage (pool)	
Cartilage (pool)	OA	32.18	112.77	225.54	Cartilage (pool)	-1.80
PBL unfected	28441	29.17	567.22	1134.44	PBL unifected	
PBL HIV IIIB	28442	30.73	246.69	493.38	PBL HIV IIIB	-2.30
MRC5 uninfected (100%)	29158	35.54	18.61	37.22	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	30.54	272.3	544.60	MRC5 HSV strain F	14.63
W12 cells	29179	32.28	107.25	214.50	W12 cells	
Keratinocytes	29180	34.27	36.84	73.68	Keratinocytes	
B-actin control		27.03	1793.92			
genomic		27.77	1204.8			
1.00E+05		19.84	100000			
1.00E+05		19.86	100000			
1.00E+04		23.46	10000			
1.00E+04		23.8	10000			
1.00E+03		27.45	1000			
1.00E+03		27.94	1000			
1.00E+02		33.86	100			
1.00E+02		31.41	100			
1.00E+01		40	0			
1.00E+01		36.88	10			
1.00E-00		40	0			
1.00E-00		40	0			
NTC		40	0			

Gene Name sbg1020829SGLT

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	-1.07
colon tumor	1.22
colon tumor	-3.92
colon tumor	-1.03
lung tumor	-5.27
lung tumor	1.70
lung tumor	-3.08
lung tumor	1.51
breast tumor	1.16
breast tumor	10.24
breast tumor	4.64
breast tumor	1.70
brain stage 5 ALZ	6.64
brain stage 5 ALZ	5.35
brain stage 5 ALZ	3.03
brain stage 5 ALZ	2.16
lung 24	-15.84
lung 28	-51.66
lung 23	-11.23
asthmatic lung	-4.08
asthmatic lung	2.49
asthmatic lung	1.72
asthmatic lung	1.88
endo VEGF	-1.48
endo bFGF	1.00
heart T-1	1.06
heart T-14	-2.20
heart T-3399	1.41
BM stim	-8.94
osteo dif	12.42
Cartilage (pool)	-1.80
PBL HIV IIIB	-2.30
MRC5 HSV strain F	14.63

Gene Name sbg1005450UDPGT

Low to moderate overall expression. Highest normal expression in endometrium, esophagus, and spleen with lower levels of expression in cerebellum, hypothalamus, rectum, and uterus. Highest disease expression in one of the OA synovium samples. Downregulation in 1 of 4 colon tumor samples is sufficient to make a disease claim in cancer of the colon. Upregulation in 1 of 4 lung tumor samples indicates a potential role for this gene in cancer of the lung. Downregulation in 2 of 4 AD brain samples suggests an involvement in Alzheimer's disease. Downregulation in 3 of 3 COPD lung samples and 4 of 4 asthmatic lung samples suggests involvement in chronic obstructive

pulmonary disease and asthma. Upregulation in the HSV-infected MRC5 cells suggests that this gene may be a host factor in HSV. Moderate expression in the B cells and the dendritic cells.

Sample sbg1005450UDPGT	Ct (sample 1 and 2)	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detected/50 ng total RNA
Subcutaneous Adipocytes Zenbio	40, 40	0.15	0.17	0.16	3.06	16.34	2.61
Subcutaneous Adipose Zenbio	40, 40	0	0	0.00	0.96	52.36	0.00
Adrenal Gland Clontech	40, 40	0	0.14	0.07	0.61	81.97	5.74
Whole Brain Clontech	33.74, 40	12.07	0	6.04	7.24	6.91	41.68
Fetal Brain Clontech	40, 40	0	0	0.00	0.48	103.95	0.00
Cerebellum Clontech	32.07, 33.2	32.85	16.64	24.75	2.17	23.04	570.16
Cervix	40, 40	0	0	0.00	2.42	20.66	0.00
Colon	40, 35.16	0	5.12	2.56	2.71	18.45	47.23
Endometrium	32.73, 31.85	22.19	37.5	29.85	0.73	68.21	2035.81
Esophagus	32.67, 29.39	22.91	165.34	94.13	1.37	36.50	3435.22
Heart Clontech	37.12, 35.03	1.58	5.55	3.57	1.32	37.88	135.04
Hypothalamus	34.08, 40	9.84	0	4.92	0.32	155.28	763.98
Ileum	34.35	8.33		8.33	2.58	19.38	161.43
Jejunum	40, 40	0	0	0.00	6.60	7.58	0.00
Kidney	38.89, 40	0.54	0	0.27	2.12	23.58	6.37
Liver	36.32, 40	2.55	0	1.28	1.50	33.33	42.50
Fetal Liver Clontech	36.96	1.74		1.74	10.40	4.81	8.37
Lung	40, 40	0	0	0.00	2.57	19.46	0.00
Mammary Gland Clontech	40, 40	0	0	0.00	13.00	3.85	0.00
Myometrium	40, 38.22	0	0.82	0.41	2.34	21.37	8.76
Omentum	36.17, 40	2.8	0	1.40	3.94	12.69	17.77
Ovary	40, 40	0	0	0.00	4.34	11.52	0.00
Pancreas	40, 40	0	0	0.00	0.81	61.80	0.00
Head of Pancreas	40, 38.35	0	0.75	0.38	1.57	31.85	11.94
Parotid Gland	40, 40	0	0	0.00	5.48	9.12	0.00
Placenta Clontech	39.06, 35.49	0.49	4.22	2.36	5.26	9.51	22.39
Prostate	38.81, 40	0.57	0	0.29	3.00	16.67	4.75
Rectum	35.22, 33.25	4.94	16.2	10.57	1.23	40.65	429.67
Salivary Gland Clontech	32.56, 34.56	24.55	7.36	15.96	7.31	6.84	109.13
Skeletal Muscle Clontech	40, 40	0	0	0.00	1.26	39.68	0.00
Skin	34.26, 40	8.8	0	4.40	1.21	41.32	181.82
Small Intestine Clontech	40	0	6.23	3.12	0.98	51.07	159.09
Spleen	40, 27.36	0	560.92	280.46	4.92	10.16	2850.20
Stomach	33.49, 39.12	13.98	0.47	7.23	2.73	18.32	132.33

Testis Clontech	40, 40	0	0	0.00	0.57	87.87	0.00
Thymus Clontech	40, 35.33	0	4.64	2.32	9.89	5.06	11.73
Thyroid	37.18, 35.52	1.53	4.13	2.83	2.77	18.05	51.08
Trachea Clontech	40, 40	0	0	0.00	9.71	5.15	0.00
Urinary Bladder	40, 40	0	0.16	0.08	5.47	9.14	0.73
Uterus	30.11	106.94	0	53.47	5.34	9.36	500.66
genomic	35.81	3.47					
b-actin	26.86	757.01					
1.00E+05	18.99	100000					
1.00E+05	19.13	100000					
1.00E+04	22.43	10000					
1.00E+04	22.31	10000					
1.00E+03	25.74	1000					
1.00E+03	25.99	1000					
1.00E+02	31.47	100					
1.00E+02	29.82	100					
1.00E+01	40	0					
1.00E+01	40	0					
1.00E-00	40	0					
1.00E-00	40	0					
NTC	26.02	-1					
NTC	40	0					

Sample sbg1005450UDPGT	**Reg number (GSK identifier)**	**Ct**	**Mean GOI copies**	**copies of mRNA detected/50 ng total RNA**	**Sample**	**Fold Change in Disease Population**
colon normal GW98-167	21941	40	0.17	0.34	colon normal	
colon tumor GW98-166	21940	39.88	0.29	0.58	colon tumor	1.71
colon normal GW98-178	22080	40	0	0.00	colon normal	
colon tumor GW98-177	22060	40	0	0.00	colon tumor	0.00
colon normal GW98-561	23514	40	0	0.00	colon normal	
colon tumor GW98-560	23513	40	0	0.00	colon tumor	0.00
colon normal GW98-894	24691	33.84	10.47	20.94	colon normal	
colon tumor GW98-893	24690	40	0	0.00	colon tumor	-20.94
lung normal GW98-3	20742	40	0	0.00	lung normal	
lung tumor GW98-2	20741	40	0	0.00	lung tumor	0.00
lung normal GW97-179	20677	31.67	37.94	75.88	lung normal	
lung tumor GW97-178	20676	33.08	16.47	32.94	lung tumor	-2.30
lung normal GW98-165	21922	40	0	0.00	lung normal	
lung tumor GW98-164	21921	40	0	0.00	lung tumor	0.00
lung normal GW98-282	22584	40	0	0.00	lung normal	
lung tumor GW98-281	22583	35.03	5.16	10.32	lung tumor	10.32
breast normal GW00-392	28750	32.64	21.38	21.38	breast normal	

breast tumor GW00-391	28746	31.67	37.98	75.96	breast tumor	3.55
breast normal GW00-413	28798	32.54	22.63	22.63	breast normal	
breast tumor GW00-412	28797	29.23	161.71	323.42	breast tumor	14.29
breast normal GW00-235:238	27592-95	37.05	1.55	1.55	breast normal	
breast tumor GW00-231:234	27588-91	35.03	5.17	5.17	breast tumor	3.34
breast normal GW98-621	23656	34.12	8.87	17.74	breast normal	
breast tumor GW98-620	23655	40	0	0.00	breast tumor	-17.74
brain normal BB99-542	25507	34.28	8.05	16.10	brain normal	
brain normal BB99-406	25509	40	0	0.00	brain normal	
brain normal BB99-904	25546	40	0	0.00	brain normal	
brain stage 5 ALZ BB99-874	25502	38.8	0.55	1.10	brain stage 5 ALZ	-4.88
brain stage 5 ALZ BB99-887	25503	40	0	0.00	brain stage 5 ALZ	-5.37
brain stage 5 ALZ BB99-862	25504	36.16	2.64	5.28	brain stage 5 ALZ	-1.02
brain stage 5 ALZ BB99-927	25542	40	0	0.00	brain stage 5 ALZ	-5.37
CT lung KC	normal	36.61	2.02	4.04	CT lung	
lung 26 KC	normal				lung 26	
lung 27 KC	normal	40	0	0.00	lung 27	
lung 24 KC	COPD	40	0	0.00	lung 24	-1.35
lung 28 KC	COPD	40	0	0.00	lung 28	-1.35
lung 23 KC	COPD	40	0	0.00	lung 23	-1.35
lung 25 KC	normal	40	0	0.00	lung 25	
asthmatic lung ODO3112	29321	38.19	0.79	0.79	asthmatic lung	-1.70
asthmatic lung ODO3433	29323	36.09	2.76	5.52	asthmatic lung	4.10
asthmatic lung ODO3397	29322	40	0	0.00	asthmatic lung	-1 35
asthmatic lung ODO4928	29325	40	0	0.00	asthmatic lung	-1.35
endo cells KC	control	40	0	0.00	endo cells	
endo VEGF KC		40	0	0.00	endo VEGF	0.00
endo bFGF KC		40	0	0.00	endo bFGF	0.00
heart Clontech	normal	40	0	0.00	heart	
heart (T-1) ischemic	29417	38.36	0.71	1.42	heart T-1	1.42
heart (T-14) non-obstructive DCM	29422	40	0	0.00	heart T-14	0.00
heart (T-3399) DCM	29426	40	0	0.00	heart T-3399	0.00
adenoid GW99-269	26162	38.96	0.5	1.00	adenoid	
tonsil GW98-280	22582	35.44	4.04	8.08	tonsil	
T cells PC00314	28453	38.83	0.54	1.08	T cells	
PBMNC		40	0	0.00	PBMNC	
monocyte		35.1	4.94	9.88	monocyte	
B cells PC00665	28455	33.32	14.31	28.62	B cells	
dendritic cells 28441		32.53	22.85	45.70	dendritic cells	
neutrophils	28440	34.43	7.39	7.39	neutrophils	
eosinophils	28446	40	0	0.00	eosinophils	
BM unstim		40	0	0.00	BM unstim	
BM stim		34.12	8.87	8.87	BM stim	8.87

osteo dif		40	0	0.00	osteo dif	0.00
osteo undif		40	0	0.00	osteo undif	
chondrocytes		34.51	7.05	17.63	chondrocytes	
OA Synovium IP12/01	29462	40	0	0.00	OA Synovium	
OA Synovium NP10/01	29461	27.21	538.51	1077.02	OA Synovium	
OA Synovium NP57/00	28464	33.5	12.85	25.70	OA Synovium	
RA Synovium NP03/01	28466	39.09	0.46	0.92	RA Synovium	
RA Synovium NP71/00	28467	40	0	0.00	RA Synovium	
RA Synovium NP45/00	28475	40	0	0.00	RA Synovium	
OA bone (biobank)	29217	40	0	0.00	OA bone (biobank)	
OA bone Sample 1	J. Emory	35.23	4.59	9.18	OA bone	
OA bone Sample 2	J. Emory	37.1	1.51	3.02	OA bone	
Cartilage (pool)	Normal	35.45	4.01	8.02	Cartilage (pool)	
Cartilage (pool)	OA	40	0	0.00	Cartilage (pool)	-8.02
PBL unifected	28441	40	0	0.00	PBL unifected	
PBL HIV IIIB	28442	40	0	0.00	PBL HIV IIIB	0.00
MRC5 uninfected (100%)	29158	40	0.17	0.34	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	30.15	93.76	187.52	MRC5 HSV strain F	551.53
W12 cells	29179	40	0	0.00	W12 cells	
Keratinocytes	29180	35.72	3.44	6.88	Keratinocytes	
B-actin control		26.57	788.4			
genomic		25.69	1326.94			
1.00E+05		18.72	100000			
1.00E+05		18.74	100000			
1.00E+04		22.11	10000			
1.00E+04		22.15	10000			
1.00E+03		25.57	1000			
1.00E+03		25.54	1000			
1.00E+02		31.37	100			
1.00E+02		29.65	100			
1.00E+01		40	0			
1.00E+01		40	0			
1.00E-00		40	0			
1.00E-00		40	0			
NTC		40	0			

Gene Name sbg1005450UDPGT

Disease tissues	**Fold Change in Disease Population Relative to Normal**
colon tumor	1.71
colon tumor	0.00
colon tumor	0.00
colon tumor	-20.94

lung tumor	0.00
lung tumor	-2.30
lung tumor	0.00
lung tumor	10.32
breast tumor	3.55
breast tumor	14.29
breast tumor	3.34
breast tumor	-17.74
brain stage 5 ALZ	-4.88
brain stage 5 ALZ	-5.37
brain stage 5 ALZ	-1.02
brain stage 5 ALZ	-5.37
lung 24	-1.35
lung 28	-1.35
lung 23	-1.35
asthmatic lung	-1.70
asthmatic lung	4.10
asthmatic lung	-1.35
asthmatic lung	-1.35
endo VEGF	0.00
endo bFGF	0.00
heart T-1	1.42
heart T-14	0.00
heart T-3399	0.00
BM stim	8.87
osteo undif	0.00
Cartilage (pool)	-8.02
PBL HIV IIIB	0.00
MRC5 HSV strain F	551.53

Gene Name sbg1002620Tia

Moderate overall expression. Highest normal expression in the whole brain, endometrium, myometrium, placenta, and rectum. Highest disease expression in the one of the colon normal/tumor pairs, the normal lung samples, one of the asthmatic lung samples, the neutrophils, the eosinophils, and one of the RA synovium samples. Expressed at high levels in all of the samples representative of the GI tract indicating a potential role for this gene in IBS, IBD, and Crohn's disease. Downregulation in 1 of 3 COPD lung samples suggests involvement in chronic obstructive pulmonary disease. Upregulation in 1 of 4 asthmatic lung samples implies a role in asthma. High expression in the OA synovium and bone samples as well as in the RA synovium samples. Also high expression in the chondrocytes. Variable expression in the immune cells with highest expression in the neutrophils and eosinophils and lowest expression in the dendritic cells. Corroborating high expression in B and T cells as well as OA samples implicates this gene in osteoarthritis and rheumatoid arthritis.

Sample sbg1002620TIa	**Ct (sample 1 and 2)**	**Mean GOI copies (sample 1)**	**Mean GOI copies (sample 2)**	**Average GOI Copies**	**18S rRNA (ng)**	**50 ng/18 S rRNA (ng)**	**copies of mRNA detected/ 50 ng total RNA**

Subcutaneous Adipocytes Zenbio	35.04, 34.4	201.66	274.43	238.05	3.06	16.34	3889.62
Subcutaneous Adipose Zenbio	38.03, 38.45	48.67	39.85	44.26	0.96	52.36	2317.28
Adrenal Gland Clontech	38.71, 38.14	35.25	46.23	40.74	0.61	81.97	3339.34
Whole Brain Clontech	29.27, 29.32	3152.23	3071.49	3111.86	7.24	6.91	21490.75
Fetal Brain Clontech	40, 37.57	0	60.7	30.35	0.48	103.95	3154.89
Cerebellum Clontech	39.37, 39.14	25.78	28.75	27.27	2.17	23.04	628.23
Cervix	34.05, 34.32	323.57	285.02	304.30	2.42	20.66	6287.09
Colon	32.64, 32.98	633.12	537.54	585.33	2.71	18.45	10799.45
Endometrium	34.44, 33.84	269.09	357.16	313.13	0.73	68.21	21359.14
Esophagus	35.48, 35.21	163.52	186.15	174.84	1.37	36.50	6380.84
Heart Clontech	38.67, 39.08	35.94	29.52	32.73	1.32	37.88	1239.77
Hypothalamus	40, 40	0	0	0.00	0.32	155.28	0.00
Ileum	33.07, 32.9	516.19	559.94	538.07	2.58	19.38	10427.62
Jejunum	30.58, 30.66	1688.39	1625.61	1657.00	6.60	7.58	12553.03
Kidney	34.9, 33.68	216.07	385.19	300.63	2.12	23.58	7090.33
Liver	37.17, 36.49	73.4	101.31	87.36	1.50	33.33	2911.83
Fetal Liver Clontech	33.99, 34.79	332.15	227.82	279.99	10.40	4.81	1346.08
Lung	34.67, 34.06	240.47	321.54	281.01	2.57	19.46	5467.02
Mammary Gland Clontech	29.3, 29.19	3098.36	3272.39	3185.38	13.00	3.85	12251.44
Myometrium	32.45, 31.79	692.54	946.75	819.65	2.34	21.37	17513.78
Omentum	32.88, 33.43	563.23	434.44	498.84	3.94	12.69	6330.39
Ovary	33.02, 32.92	528.43	553.26	540.85	4.34	11.52	6230.93
Pancreas	37.31, 39.81	68.49	20.84	44.67	0.81	61.80	2760.51
Head of Pancreas	38.5, 39.16	38.99	28.45	33.72	1.57	31.85	1073.89
Parotid Gland	34.48, 34.22	263.15	298.49	280.82	5.48	9.12	2562.23
Placenta Clontech	31.16, 30.91	1280.82	1442.99	1361.91	5.26	9.51	12945.87
Prostate	33.5, 33.11	420.13	506.76	463.45	3.00	16.67	7724.08
Rectum	34.48, 33.88	263.61	350.22	306.92	1.23	40.65	12476.22
Salivary Gland Clontech	34.48, 34.32	263.4	284.18	273.79	7.31	6.84	1872.71
Skeletal Muscle Clontech	40, 39.37	0	25.73	12.87	1.26	39.68	510.52
Skin	35.52, 35.13	160.58	193.62	177.10	1.21	41.32	7318.18
Small Intestine Clontech	36.79, 36.59	87.74	96.5	92.12	0.98	51.07	4704.80
Spleen	34.45, 34.51	267.45	260	263.73	4.92	10.16	2680.13
Stomach	35.16, 33.89	191.03	348.48	269.76	2.73	18.32	4940.57
Testis Clontech	38.19, 37.07	45.22	76.91	61.07	0.57	87.87	5365.99
Thymus Clontech	33.74, 33.57	374.59	406.79	390.69	9.89	5.06	1975.18
Thyroid	34.18, 33.46	304.38	427.57	365.98	2.77	18.05	6606.05
Trachea Clontech	32.67, 31.27	623.94	1213.65	918.80	9.71	5.15	4731.18
Urinary Bladder	32.07, 31.34	830.04	1176.15	1003.10	5.47	9.14	9169.06
Uterus	31.75, 31.37	968.5	1157.09	1062.80	5.34	9.36	9951.26
genomic	31.33	1181.44					
b-actin	28.56	4411.32					
1.00E+05	22.12	100000					

1.00E+05	22.12	100000					
1.00E+04	26.72	10000					
1.00E+04	26.91	10000					
1.00E+03	31.28	1000					
1.00E+03	31.5	1000					
1.00E+02	36.35	100					
1.00E+02	37.09	100					
1.00E+01	40	10					
1.00E+01	40	10					
1.00E-00	40	1					
1.00E-00	40	0					
NTC	40	0					
NTC	40	0					

Sample sbg1002620TIa	**Reg number (GSK identifier)**	**Ct**	**Mean GOI copies**	**copies of mRNA detected/ 50 ng total RNA**	**Sample**	**Fold Change in Disease Population**
colon normal GW98-167	21941	24.54	22693.01	45386.02	colon normal	
colon tumor GW98-166	21940	24.18	26862.61	53725.22	colon tumor	1.18
colon normal GW98-178	22080	27.08	6895.34	13790.68	colon normal	
colon tumor GW98-177	22060	28.41	3692.19	7384.38	colon tumor	-1.87
colon normal GW98-561	23514	26.58	8698.68	17397.36	colon normal	
colon tumor GW98-560	23513	27.85	4799.22	9598.44	colon tumor	-1.81
colon normal GW98-894	24691	25.9	11972.57	23945.14	colon normal	
colon tumor GW98-893	24690	28.04	4396.4	8792.80	colon tumor	-2.72
lung normal GW98-3	20742	24.25	26016.9	52033.80	lung normal	
lung tumor GW98-2	20741	27.64	5300.37	10600.74	lung tumor	-4.91
lung normal GW97-179	20677	25.1	17476.66	34953.32	lung normal	
lung tumor GW97-178	20676	25.53	14274.54	28549.08	lung tumor	-1.22
lung normal GW98-165	21922	24.62	21917.37	43834.74	lung normal	
lung tumor GW98-164	21921	25.64	13526.49	27052.98	lung tumor	-1.62
lung normal GW98-282	22584	27.08	6884.03	13768.06	lung normal	
lung tumor GW98-281	22583	25.37	15385.8	30771.60	lung tumor	2.23
breast normal GW00-392	28750	26.07	11065.25	11065.25	breast normal	
breast tumor GW00-391	28746	26.87	7611.48	15222.96	breast tumor	1.38
breast normal GW00-413	28798	28.65	3294.68	3294.68	breast normal	
breast tumor GW00-412	28797	28.52	3496.94	6993.88	breast tumor	2.12
breast normal GW00-235:238	27592-95	29.47	2243.69	2243.69	breast normal	
breast tumor GW00-231:234	27588-91	25.83	12385.23	12385.23	breast tumor	5.52
breast normal GW98-621	23656	26.05	11188.07	22376.14	breast normal	
breast tumor GW98-620	23655	26.03	11303.95	22607.90	breast tumor	1.01

brain normal BB99-542	25507	27.68	5198.79	10397.58	brain normal	
brain normal BB99-406	25509	29.81	1909.01	3818.02	brain normal	
brain normal BB99-904	25546	31.84	735.25	1470.50	brain normal	
brain stage 5 ALZ BB99-874	25502	28.43	3650.66	7301.32	brain stage 5 ALZ	1.40
brain stage 5 ALZ BB99-887	25503	29.01	2785.56	5571.12	brain stage 5 ALZ	1.07
brain stage 5 ALZ BB99-862	25504	29.65	2059.62	4119.24	brain stage 5 ALZ	-1.27
brain stage 5 ALZ BB99-927	25542	30.01	1742.3	3484.60	brain stage 5 ALZ	-1.50
CT lung KC	normal	25.49	14553.17	29106.34	CT lung	
lung 26 KC	normal	31.8	749.93	749.93	lung 26	
lung 27 KC	normal	33.35	362.66	362.66	lung 27	
lung 24 KC	COPD	30.67	1275.68	1275.68	lung 24	-6.03
lung 28 KC	COPD	29.25	2490.39	2490.39	lung 28	-3.09
lung 23 KC	COPD	30.11	1661.24	1661.24	lung 23	-4.63
lung 25 KC	normal	32.45	553.75	553.75	lung 25	
asthmatic lung ODO3112	29321	27.3	6215.19	6215.19	asthmatic lung	-1.24
asthmatic lung ODO3433	29323	26.66	8407.3	16814.60	asthmatic lung	2.19
asthmatic lung ODO3397	29322	24.06	28466.73	56933.46	asthmatic lung	7.40
asthmatic lung ODO4928	29325	26.22	10313.71	20627.42	asthmatic lung	2.68
endo cells KC	control	40	0	0.00	endo cells	
endo VEGF KC		40	0	0.00	endo VEGF	0.00
endo bFGF KC		40	0	0.00	endo bFGF	0.00
heart Clontech	normal	27.58	5449.78	10899.56	heart	
heart (T-1) ischemic	29417	28.42	3670.86	7341.72	heart T-1	-1.48
heart (T-14) non-obstructive DCM	29422	27.18	6570.11	13140.22	heart T-14	1.21
heart (T-3399) DCM	29426	26.23	10277.2	20554.40	heart T-3399	1.89
adenoid GW99-269	26162	31.98	688.86	1377.72	adenoid	
tonsil GW98-280	22582	29.31	2421.67	4843.34	tonsil	
T cells PC00314	28453	29.53	2178.21	4356.42	T cells	
PBMNC		33.23	383.88	383.88	PBMNC	
monocyte		31.07	1057.9	2115.80	monocyte	
B cells PC00665	28455	35.97	106.01	212.02	B cells	
dendritic cells 28441		33.56	328.62	657.24	dendritic cells	
neutrophils	28440	22.32	64510.36	64510.36	neutrophils	
eosinophils	28446	24.18	26910.17	53820.34	eosinophils	
BM unstim		30.35	1480.07	1480.07	BM unstim	
BM stim		31.71	782.56	782.56	BM stim	-1.89
osteo dif		31.42	895.71	895.71	osteo dif	2.03
osteo undif		32.93	440.66	440.66	osteo undif	
chondrocytes		28.98	2820.8	7052.00	chondrocytes	
OA Synovium IP12/01	29462	25.37	15383.84	15383.84	OA Synovium	
OA Synovium NP10/01	29461	27.12	6763.44	13526.88	OA Synovium	

OA Synovium NP57/00	28464	26.48	9130.81	18261.62	OA Synovium	
RA Synovium NP03/01	28466	27.78	4967.23	9934.46	RA Synovium	
RA Synovium NP71/00	28467	24.72	20923.66	41847.32	RA Synovium	
RA Synovium NP45/00	28475	26.15	10658.82	21317.64	RA Synovium	
OA bone (biobank)	29217	28.68	3248.19	3248.19	OA bone (biobank)	
OA bone Sample 1	J. Emory	27.19	6545.82	13091.64	OA bone	
OA bone Sample 2	J. Emory	27.24	6384.92	12769.84	OA bone	
Cartilage (pool)	Normal	26.28	10016.65	20033.30	Cartilage (pool)	
Cartilage (pool)	OA	26.67	8342.92	16685.84	Cartilage (pool)	-1.20
PBL unifected	28441	31.05	1069.84	2139.68	PBL unifected	
PBL HIV IIIB	28442	31.7	788.06	1576.12	PBL HIV IIIB	-1.36
MRC5 uninfected (100%)	29158	26.37	9631.13	19262.26	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	28.38	3747.38	7494.76	MRC5 HSV strain F	-2.57
W12 cells	29179	35.15	155.25	310.50	W12 cells	
Keratinocytes	29180	34.93	172.87	345.74	Keratinocytes	
B-actin control		28.06	4342.74			
genomic		30.54	1356.79			
1.00E+05		21.39	100000			
1.00E+05		21.64	100000			
1.00E+04		26.21	10000			
1.00E+04		26.24	10000			
1.00E+03		30.9	1000			
1.00E+03		30.97	1000			
1.00E+02		36.34	100			
1.00E+02		36.22	100			
1.00E+01		40	10			
1.00E+01		40	0			
1.00E-00		40	0			
1.00E-00		40	0			
NTC		40	0			

Gene Name sbg1002620TIa

Disease tissues	**Fold Change in Disease Population Relative to Normal**
colon tumor	1.18
colon tumor	-1.87
colon tumor	-1.81
colon tumor	-2.72
lung tumor	-4.91
lung tumor	-1.22
lung tumor	-1.62
lung tumor	2.23
breast tumor	1.38

breast tumor	2.12
breast tumor	5.52
breast tumor	1.01
brain stage 5 ALZ	1.40
brain stage 5 ALZ	1.07
brain stage 5 ALZ	-1.27
brain stage 5 ALZ	-1.50
lung 24	-6.03
lung 28	-3.09
lung 23	-4.63
asthmatic lung	-1.24
asthmatic lung	2.19
asthmatic lung	7.40
asthmatic lung	2.68
endo VEGF	0.00
endo bFGF	0.00
heart T-1	-1.48
heart T-14	1.21
heart T-3399	1.89
BM stim	-1.89
osteo dif	2.03
Cartilage (pool)	-1.20
PBL HIV IIIB	-1.36
MRC5 HSV strain F	-2.57

Gene Name sbg1002620TIb

Moderate to high overall expression. Highest normal expression in whole brain, endometrium, jejunum, placenta, thymus, and urinary bladder. Highest disease expression in one of the colon normal/tumor pairs, one of the normal lung samples, one of the asthmatic lung samples, the neutrophils, and the eosinophils. Strong expression in all of the GI tract samples implicates this gene in IBS, IBD, and Crohn's disease. Downregulation in 1 of 4 lung tumor samples is sufficient to make a disease claim in cancer of the lung. Downregulation in 3 of 3 COPD lung samples suggests involvement in chronic obstructive pulmonary disease. Upregulation in 1 of 4 asthmatic lung samples implies a role in asthma. Upregulation in 2 of 3 heart samples suggests this gene may play a role in non-obstructive and obstructive dilated cardiac myopathy. High expression in the RA and OA synovium samples as well as high expression in the chondrocytes and T cells implicates this gene in osteoarthritis and rheumatoid arthritis.

Sample sbg1002620TIb	**Ct (sample 1 and 2)**	**Mean GOI copies (sample 1)**	**Mean GOI copies (sample 2)**	**Average GOI Copies**	**18S rRNA (ng)**	**50 ng/18S rRNA (ng)**	**copies of mRNA detected /50 ng total RNA**
Subcutaneous Adipocytes Zenbio	31.35, 31.44	58.54	55.11	56.83	3.06	16.34	928.51
Subcutaneous Adipose Zenbio	35.12, 34.21	5	9.05	7.03	0.96	52.36	367.80
Adrenal Gland Clontech	40, 34.29	0	8.61	4.31	0.61	81.97	352.87
Whole Brain Clontech	26.02, 26.06	1897.9	1849.19	1873.55	7.24	6.91	12938.85

Fetal Brain Clontech	40, 36.43	0	2.13	1.07	0.48	103.95	110.71
Cerebellum Clontech	40, 36.05	0	2.74	1.37	2.17	23.04	31.57
Cervix	32.23, 33.04	33.11	19.47	26.29	2.42	20.66	543.18
Colon	30.44, 30.45	105.93	105.29	105.61	2.71	18.45	1948.52
Endometrium	30.86, 30.56	80.75	97.92	89.34	0.73	68.21	6093.79
Esophagus	33.03, 32.34	19.62	30.66	25.14	1.37	36.50	917.52
Heart Clontech	40, 35.05	0	5.26	2.63	1.32	37.88	99.62
Hypothalamus	40, 36.17	0	2.53	1.27	0.32	155.28	196.43
Ileum	31.25, 30.31	62.52	115.58	89.05	2.58	19.38	1725.78
Jejunum	27.75, 27.93	612.01	543.46	577.74	6.60	7.58	4376.78
Kidney	32.59, 31.86	26.03	42.14	34.09	2.12	23.58	803.89
Liver	34.66, 34.5	6.77	7.52	7.15	1.50	33.33	238.17
Fetal Liver Clontech	29.08, 28.58	256.83	356.67	306.75	10.40	4.81	1474.76
Lung	30.74, 30.68	87.44	90.91	89.18	2.57	19.46	1734.92
Mammary Gland Clontech	27.49, 26.81	725.02	1132.42	928.72	13.00	3.85	3572.00
Myometrium	31.2, 30.29	64.54	117.26	90.90	2.34	21.37	1942.31
Omentum	31.19, 30.12	65.05	130.86	97.96	3.94	12.69	1243.08
Ovary	30.24, 30.54	120.95	99.3	110.13	4.34	11.52	1268.72
Pancreas	36.01, 36.55	2.81	1.97	2.39	0.81	61.80	147.71
Head of Pancreas	33.95, 35.73	10.72	3.36	7.04	1.57	31.85	224.20
Parotid Gland	32.16, 33.16	34.51	18.05	26.28	5.48	9.12	239.78
Placenta Clontech	28.42, 28.02	395.01	512.77	453.89	5.26	9.51	4314.54
Prostate	30.61, 31.28	95.23	61.5	78.37	3.00	16.67	1306.08
Rectum	30.5, 30.93	101.73	76.9	89.32	1.23	40.65	3630.69
Salivary Gland Clontech	31.17, 31.07	65.95	70.23	68.09	7.31	6.84	465.73
Skeletal Muscle Clontech	40, 40	0	0	0.00	1.26	39.68	0.00
Skin	34.37, 33.12	8.18	18.53	13.36	1.21	41.32	551.86
Small Intestine Clontech	36.71, 34.96	1.78	5.55	3.67	0.98	51.07	187.18
Spleen	30.54, 31.29	99.47	60.88	80.18	4.92	10.16	814.79
Stomach	32.4, 31.53	29.49	52	40.75	2.73	18.32	746.25
Testis Clontech	34.4, 35.19	8.03	4.79	6.41	0.57	87.87	563.27
Thymus Clontech	27.18, 27.12	888.84	924.29	906.57	9.89	5.06	4583.24
Thyroid	32.17, 30.89	34.36	79.27	56.82	2.77	18.05	1025.54
Trachea Clontech	30.01, 29.25	140.31	230.28	185.30	9.71	5.15	954.15
Urinary Bladder	28.33, 27.87	420.47	565.71	493.09	5.47	9.14	4507.22
Uterus	29.09, 28.81	255.27	308	281.64	5.34	9.36	2637.03
genomic	27.16	900.78					
b-actin	27.4	769.87					
1.00E+05	19.87	100000					
1.00E+05	19.95	100000					
1.00E+04	23.4	10000					
1.00E+04	23.39	10000					
1.00E+03	26.94	1000					
1.00E+03	26.95	1000					
1.00E+02	31.02	100					

1.00E+02	30.96	100					
1.00E+01	33.46	10					
1.00E+01	40	0					
1.00E-00	40	0					
1.00E-00	40	0					
NTC	40	0					
NTC	40	0					

Sample sbg1002620TIb	**Reg number (GSK identifier)**	**Ct**	**Mean GOI copies**	**copies of mRNA detected /50 ng total RNA**	**Sample**	**Fold Change in Disease Population**
colon normal GW98-167	21941	22.85	18631.2	37262.40	colon normal	
colon tumor GW98-166	21940	22.51	23090.96	46181.92	colon tumor	1.24
colon normal GW98-178	22080	25.49	3620.45	7240.90	colon normal	
colon tumor GW98-177	22060	26.88	1527.3	3054.60	colon tumor	-2.37
colon normal GW98-561	23514	25.37	3901.36	7802.72	colon normal	
colon tumor GW98-560	23513	26.08	2512.21	5024.42	colon tumor	-1.55
colon normal GW98-894	24691	23.78	10441.49	20882.98	colon normal	
colon tumor GW98-893	24690	25.54	3515.48	7030.96	colon tumor	-2.97
lung normal GW98-3	20742	22.6	21810.56	43621.12	lung normal	
lung tumor GW98-2	20741	26.19	2349.32	4698.64	lung tumor	-9.28
lung normal GW97-179	20677	23.38	13423.28	26846.56	lung normal	
lung tumor GW97-178	20676	24.51	6653.03	13306.06	lung tumor	-2.02
lung normal GW98-165	21922	23.68	11120.91	22241.82	lung normal	
lung tumor GW98-164	21921	24.37	7242.32	14484.64	lung tumor	-1.54
lung normal GW98-282	22584	25.05	4745.83	9491.66	lung normal	
lung tumor GW98-281	22583	23.57	11943.28	23886.56	lung tumor	2.52
breast normal GW00-392	28750	24.84	5415.88	5415.88	breast normal	
breast tumor GW00-391	28746	24.98	4973.9	9947.80	breast tumor	1.84
breast normal GW00-413	28798	24.69	5954.77	5954.77	breast normal	
breast tumor GW00-412	28797	26.38	2081.99	4163.98	breast tumor	-1.43
breast normal GW00-235:238	27592-95	25.04	4792.18	4792.18	breast normal	
breast tumor GW00-231:234	27588-91	23.63	11520.86	11520.86	breast tumor	2.40
breast normal GW98-621	23656	23.22	14836.24	29672.48	breast normal	
breast tumor GW98-620	23655	24.24	7879	15758.00	breast tumor	-1.88
brain normal BB99-542	25507	25.16	4447.15	8894.30	brain normal	
brain normal BB99-406	25509	27.05	1377.71	2755.42	brain normal	
brain normal BB99-904	25546	29.35	330.53	661.06	brain normal	
brain stage 5 ALZ BB99-874	25502	27.64	956.16	1912.32	brain stage 5 ALZ	-2.15
brain stage 5 ALZ	25503	27.02	1400.04	2800.08	brain stage 5	-1.47

BB99-887					ALZ	
brain stage 5 ALZ BB99-862	25504	27.4	1105.21	2210.42	brain stage 5 ALZ	-1.86
brain stage 5 ALZ BB99-927	25542	27.1	1336.02	2672.04	brain stage 5 ALZ	-1.54
CT lung KC	normal	23.52	12295.29	24590.58	CT lung	
lung 26 KC	normal	31.42	91.19	91.19	lung 26	
lung 27 KC	normal	32.34	51.71	51.71	lung 27	
lung 24 KC	COPD	31.27	100.29	100.29	lung 24	-61.80
lung 28 KC	COPD	28.64	511.37	511.37	lung 28	-12.12
lung 23 KC	COPD	30.52	159.17	159.17	lung 23	-38.94
lung 25 KC	normal	32.15	57.91	57.91	lung 25	
asthmatic lung ODO3112	29321	23.19	15086.65	15086.65	asthmatic lung	2.43
asthmatic lung ODO3433	29323	24.76	5706.9	11413.80	asthmatic lung	1.84
asthmatic lung ODO3397	29322	21.71	37760.01	75520.02	asthmatic lung	12.18
asthmatic lung ODO4928	29325	24.16	8255.16	16510.32	asthmatic lung	2.66
endo cells KC	control	37.31	2.36	2.36	endo cells	
endo VEGF KC		40	0	0.00	endo VEGF	-2.36
endo bFGF KC		35.67	6.54	6.54	endo bFGF	2.77
heart Clontech	normal	26.32	2170.24	4340.48	heart	
heart (T-1) ischemic	29417	25.87	2863.04	5726.08	heart T-1	1.32
heart (T-14) non-obstructive DCM	29422	24.62	6200.03	12400.06	heart T-14	2.86
heart (T-3399) DCM	29426	24.06	8775.18	17550.36	heart T-3399	4.04
adenoid GW99-269	26162	29.2	362.88	725.76	adenoid	
tonsil GW98-280	22582	27.24	1222.33	2444.66	tonsil	
T cells PC00314	28453	28.09	723.06	1446.12	T cells	
PBMNC		30.67	145.75	145.75	PBMNC	
monocyte		28.42	587.16	1174.32	monocyte	
B cells PC00665	28455	34.17	16.57	33.14	B cells	
dendritic cells 28441		31.78	72.95	145.90	dendritic cells	
neutrophils	28440	21.46	44297.23	44297.23	neutrophils	
eosinophils	28446	22.79	19332.21	38664.42	eosinophils	
BM unstim		29.22	358.53	358.53	BM unstim	
BM stim		31.27	100.39	100.39	BM stim	-3.57
osteo dif		30.14	202.25	202.25	osteo dif	4.97
osteo undif		32.72	40.67	40.67	osteo undif	
chondrocytes		27.3	1178.3	2945.75	chondrocytes	
OA Synovium IP12/01	29462	23.33	13860.23	13860.23	OA Synovium	
OA Synovium NP10/01	29461	25.3	4080.49	8160.98	OA Synovium	
OA Synovium NP57/00	28464	25.23	4253.8	8507.60	OA Synovium	
RA Synovium NP03/01	28466	25.46	3686.62	7373.24	RA Synovium	
RA Synovium NP71/00	28467	23.31	14036.44	28072.88	RA Synovium	
RA Synovium NP45/00	28475	24.28	7658.52	15317.04	RA Synovium	
OA bone (biobank)	29217	26.48	1958.1	1958.10	OA bone (biobank)	

OA bone Sample 1	J. Emory	25.28	4131.76	8263.52	OA bone	
OA bone Sample 2	J. Emory	25.23	4242.9	8485.80	OA bone	
Cartilage (pool)	Normal	24.05	8829.67	17659.34	Cartilage (pool)	
Cartilage (pool)	OA	24.28	7685.44	15370.88	Cartilage (pool)	-1.15
PBL unifected	28441	29.33	334.71	669.42	PBL unifected	
PBL HIV IIIB	28442	29.59	283.96	567.92	PBL HIV IIIB	-1.18
MRC5 uninfected (100%)	29158	23.92	9595.12	19190.24	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	25.2	4341.36	8682.72	MRC5 HSV strain F	-2.21
W12 cells	29179	30.43	168.9	337.80	W12 cells	
Keratinocytes	29180	29.66	272.9	545.80	Keratinocytes	
B-actin control		27.64	956.41			
genomic		27.35	1143.39			
1.00E+05		20.14	100000			
1.00E+05		20.26	100000			
1.00E+04		23.6	10000			
1.00E+04		24.02	10000			
1.00E+03		27.49	1000			
1.00E+03		27.5	1000			
1.00E+02		31.66	100			
1.00E+02		31.01	100			
1.00E+01		40	0			
1.00E+01		40	0			
1.00E-00		40	0			
1.00E-00		40	0			
NTC		40	0			

Gene Name sbg1002620TIb

Disease tissues	**Fold Change in Disease Population Relative to Normal**
colon tumor	1.24
colon tumor	-2.37
colon tumor	-1.55
colon tumor	-2.97
lung tumor	-9.28
lung tumor	-2.02
lung tumor	-1.54
lung tumor	2.52
breast tumor	1.84
breast tumor	-1.43
breast tumor	2.40
breast tumor	-1.88
brain stage 5 ALZ	-2.15
brain stage 5 ALZ	-1.47
brain stage 5 ALZ	-1.86
brain stage 5 ALZ	-1.54
lung 24	-61.80
lung 28	-12.12

lung 23	-38.94
asthmatic lung	2.43
asthmatic lung	1.84
asthmatic lung	12.18
asthmatic lung	2.66
endo VEGF	-2.36
endo bFGF	2.77
heart T-1	1.32
heart T-14	2.86
heart T-3399	4.04
BM stim	-3.57
osteo dif	4.97
Cartilage (pool)	-1.15
PBL HIV IIIB	-1.18
MRC5 HSV strain F	-2.21

Gene Name sbg102200MCTa

Moderate to low overall expression. Highest normal expression in the subcutaneous adipose tissue, whole brain, fetal brain, cerebellum, and fetal liver. Highest disease expression in 2 of 4 lung tumor samples, one of the normal lung samples, one of the normal breast samples, and the CT lung sample. Downregulation in 1 of 4 breast cancer samples implicates this gene in cancer of the breast. Downregulation in 3 of 3 COPD lung samples suggests involvement in chronic obstructive pulmonary disease. Moderate expression in the OA and RA synovium as well as the PBLs, adenoid, tonsil, T cells, B cells, and the chondrocytes indicates involvement in osteoarthritis and rheumatoid arthritis.

Sample sbg102200MCTa	**Ct (sample 1 and 2)**	**Mean GOI copies (sample 1)**	**Mean GOI copies (sample 2)**	**Average GOI Copies**	**18S rRNA (ng)**	**50 ng/18S rRNA (ng)**	**copies of mRNA detected/50 ng total RNA**
Subcutaneous Adipocytes Zenbio	36.01, 34.76	3.83	8.04	5.94	3.06	16.34	96.98
Subcutaneous Adipose Zenbio	34.85, 33.96	7.63	12.94	10.29	0.96	52.36	538.48
Adrenal Gland Clontech	40, 40	0	0	0.00	0.61	81.97	0.00
Whole Brain Clontech	26.05, 26.18	1434.25	1331.2	1382.73	7.24	6.91	9549.21
Fetal Brain Clontech	40, 34.46	0	9.63	4.82	0.48	103.95	500.52
Cerebellum Clontech	31.7, 32.73	49.65	26.9	38.28	2.17	23.04	881.91
Cervix	40, 40	0	0	0.00	2.42	20.66	0.00
Colon	38.55, 38.57	0.84	0.83	0.84	2.71	18.45	15.41
Endometrium	40, 40	0	0	0.00	0.73	68.21	0.00
Esophagus	35.23, 40	6.09	0	3.05	1.37	36.50	111.13
Heart Clontech	40, 40	0	0	0.00	1.32	37.88	0.00
Hypothalamus	39.8, 40	0.4	0	0.20	0.32	155.28	31.06
Ileum	34.16, 40	11.53	0	5.77	2.58	19.38	111.72
Jejunum	32.82, 33.18	25.46	20.6	23.03	6.60	7.58	174.47
Kidney	34.23, 34.1	11.02	11.9	11.46	2.12	23.58	270.28
Liver	35.35, 37.28	5.65	1.79	3.72	1.50	33.33	124.00
Fetal Liver Clontech	29.45, 28.98	189.89	250.96	220.43	10.40	4.81	1059.74

Lung	34.99, 33.43	7.04	17.81	12.43	2.57	19.46	241.73
Mammary Gland Clontech	31.76, 31.05	48.02	73.18	60.60	13.00	3.85	233.08
Myometrium	34.46, 35.22	9.64	6.12	7.88	2.34	21.37	168.38
Omentum	37.94, 34.13	1.21	11.71	6.46	3.94	12.69	81.98
Ovary	34.03, 33.43	12.44	17.77	15.11	4.34	11.52	174.02
Pancreas	40, 40	0	0	0.00	0.81	61.80	0.00
Head of Pancreas	40, 40	0	0	0.00	1.57	31.85	0.00
Parotid Gland	32.56, 31.81	29.88	46.65	38.27	5.48	9.12	349.13
Placenta Clontech	40, 40	0	0	0.00	5.26	9.51	0.00
Prostate	40, 36.21	0	3.39	1.70	3.00	16.67	28.25
Rectum	40, 39.37	0	0.52	0.26	1.23	40.65	10.57
Salivary Gland Clontech	30.6, 31.77	95.89	47.76	71.83	7.31	6.84	491.28
Skeletal Muscle Clontech	40, 40	0	0	0.00	1.26	39.68	0.00
Skin	34.47, 35.32	9.58	5.75	7.67	1.21	41.32	316.74
Small Intestine Clontech	40, 40	0	0	0.00	0.98	51.07	0.00
Spleen	34.1, 36.49	11.93	2.87	7.40	4.92	10.16	75.20
Stomach	35.17, 36.07	6.3	3.68	4.99	2.73	18.32	91.39
Testis Clontech	37.98, 40	1.19	0	0.60	0.57	87.87	52.28
Thymus Clontech	31.28, 30.4	63.69	108.05	85.87	9.89	5.06	434.13
Thyroid	33.08, 32.96	21.88	23.47	22.68	2.77	18.05	409.30
Trachea Clontech	32.54, 31.34	30.14	61.71	45.93	9.71	5.15	236.48
Urinary Bladder	33.91, 40	13.32	0	6.66	5.47	9.14	60.88
Uterus	33.71, 32.43	15.04	32.13	23.59	5.34	9.36	220.83
genomic	26.3	1237.42					
b-actin	27.49	610.72					
1.00E+05	19.18	100000					
1.00E+05	19.45	100000					
1.00E+04	22.6	10000					
1.00E+04	22.53	10000					
1.00E+03	26.17	1000					
1.00E+03	26.19	1000					
1.00E+02	30.61	100					
1.00E+02	30.53	100					
1.00E+01	40	0					
1.00E+01	34.91	10					
1.00E-00	40	0					
1.00E-00	40	0					
NTC	40	0					
NTC	40	0					

Sample sbg102200MCTa	**Reg number (GSK identifier**	**Ct**	**Mean GOI copies**	**copies of mRNA detecte**	**Sample**	**Fold Change in Disease Populatio**

	)			d/50 ng total RNA		n
colon normal GW98-167	21941	28.58	519.72	1039.44	colon normal	
colon tumor GW98-166	21940	30.18	202.86	405.72	colon tumor	-2.56
colon normal GW98-178	22080	31.39	100.15	200.30	colon normal	
colon tumor GW98-177	22060	29.62	282.42	564.84	colon tumor	2.82
colon normal GW98-561	23514	30.36	183.13	366.26	colon normal	
colon tumor GW98-560	23513	30.45	173.87	347.74	colon tumor	-1.05
colon normal GW98-894	24691	30.23	196.98	393.96	colon normal	
colon tumor GW98-893	24690	30.35	183.76	367.52	colon tumor	-1.07
lung normal GW98-3	20742	26.68	1575.72	3151.44	lung normal	
lung tumor GW98-2	20741	28.8	456.47	912.94	lung tumor	-3.45
lung normal GW97-179	20677	27.94	754.47	1508.94	lung normal	
lung tumor GW97-178	20676	26.27	2002.28	4004.56	lung tumor	2.65
lung normal GW98-165	21922	26.87	1411.09	2822.18	lung normal	
lung tumor GW98-164	21921	29.38	325.51	651.02	lung tumor	-4.34
lung normal GW98-282	22584	30	225.32	450.64	lung normal	
lung tumor GW98-281	22583	28.64	502.02	1004.04	lung tumor	2.23
breast normal GW00-392	28750	28.32	602.59	602.59	breast normal	
breast tumor GW00-391	28746	28.05	709.37	1418.74	breast tumor	2.35
breast normal GW00-413	28798	29.56	292.43	292.43	breast normal	
breast tumor GW00-412	28797	30.05	218.89	437.78	breast tumor	1.50
breast normal GW00-235:238	27592-95	30.96	128.91	128.91	breast normal	
breast tumor GW00-231:234	27588-91	30.57	161.3	161.30	breast tumor	1.25
breast normal GW98-621	23656	27.04	1275.81	2551.62	breast normal	
breast tumor GW98-620	23655	31.35	102.26	204.52	breast tumor	-12.48
brain normal BB99-542	25507	28.44	564.32	1128.64	brain normal	
brain normal BB99-406	25509	29.01	402.37	804.74	brain normal	
brain normal BB99-904	25546	29.67	274.03	548.06	brain normal	
brain stage 5 ALZ BB99-874	25502	29.6	284.82	569.64	brain stage 5 ALZ	-1.45
brain stage 5 ALZ BB99-887	25503	27.92	765.16	1530.32	brain stage 5 ALZ	1.85
brain stage 5 ALZ BB99-862	25504	28.74	472.27	944.54	brain stage 5 ALZ	1.14
brain stage 5 ALZ BB99-927	25542	29.3	340.25	680.50	brain stage 5 ALZ	-1.22
CT lung KC	normal	26.69	1569.87	3139.74	CT lung	
lung 26 KC	normal	31.07	120.9	120.90	lung 26	
lung 27 KC	normal	31.17	113.69	113.69	lung 27	
lung 24 KC	COPD	31.8	78.78	78.78	lung 24	-10.98
lung 28 KC	COPD	32.79	44.02	44.02	lung 28	-19.65
lung 23 KC	COPD	31.35	102.33	102.33	lung 23	-8.45
lung 25 KC	normal	31.66	85.57	85.57	lung 25	
asthmatic lung ODO3112	29321	28.76	467.45	467.45	asthmatic lung	-1.85
asthmatic lung ODO3433	29323	27.73	851.21	1702.42	asthmatic lung	1.97
asthmatic lung ODO3397	29322	27.81	812.68	1625.36	asthmatic lung	1.88

asthmatic lung ODO4928	29325	29.42	317.12	634.24	asthmatic lung	-1.36
endo cells KC	control	33.06	37.57	37.57	endo cells	
endo VEGF KC		33.9	22.97	22.97	endo VEGF	-1.64
endo bFGF KC		33.13	36.03	36.03	endo bFGF	-1.04
heart Clontech	normal	31.1	118.18	236.36	heart	
heart (T-1) ischemic	29417	31.16	114.67	229.34	heart T-1	-1.03
heart (T-14) non-obstructive DCM	29422	30.52	166.47	332.94	heart T-14	1.41
heart (T-3399) DCM	29426	30.14	208.3	416.60	heart T-3399	1.76
adenoid GW99-269	26162	29.07	388.9	777.80	adenoid	
tonsil GW98-280	22582	28.29	614.82	1229.64	tonsil	
T cells PC00314	28453	29.78	256.1	512.20	T cells	
PBMNC		33.73	25.44	25.44	PBMNC	
monocyte		33.52	28.71	57.42	monocyte	
B cells PC00665	28455	28.66	495.36	990.72	B cells	
dendritic cells 28441		30.81	140.17	280.34	dendritic cells	
neutrophils	28440	30.17	204.92	204.92	neutrophils	
eosinophils	28446	34.19	19.39	38.78	eosinophils	
BM unstim		35.9	7.11	7.11	BM unstim	
BM stim		35.77	7.7	7.70	BM stim	1.08
osteo dif		34.98	12.18	12.18	osteo dif	2.55
osteo undif		36.59	4.77	4.77	osteo undif	
chondrocytes		32.91	41.03	102.58	chondrocytes	
OA Synovium IP12/01	29462	29.16	370.33	370.33	OA Synovium	
OA Synovium NP10/01	29461	30 69	151.13	302.26	OA Synovium	
OA Synovium NP57/00	28464	29.51	301.55	603.10	OA Synovium	
RA Synovium NP03/01	28466	30.36	183.35	366.70	RA Synovium	
RA Synovium NP71/00	28467	29.27	346.61	693.22	RA Synovium	
RA Synovium NP45/00	28475	29.13	376.88	753.76	RA Synovium	
OA bone (biobank)	29217	30.47	171.6	171.60	OA bone (biobank)	
OA bone Sample 1	J. Emory	30.05	219.19	438.38	OA bone	
OA bone Sample 2	J. Emory	31.13	116.62	233.24	OA bone	
Cartilage (pool)	Normal	30.65	154.56	309.12	Cartilage (pool)	
Cartilage (pool)	OA	32.01	69.39	138.78	Cartilage (pool)	-2.23
PBL unifected	28441	27.91	769.91	1539.82	PBL unifected	
PBL HIV IIIB	28442	28.14	672.12	1344.24	PBL HIV IIIB	-1.15
MRC5 uninfected (100%)	29158	31.66	85.38	170.76	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	30.08	214.88	429.76	MRC5 HSV strain F	2.52
W12 cells	29179	33.33	32.15	64.30	W12 cells	
Keratinocytes	29180	30.64	155.16	310.32	Keratinocytes	
B-actin control		27.55	946.64			
genomic		26.82	1451.22			
1.00E+05		19.71	100000			
1.00E+05		19.95	100000			
1.00E+04		23.43	10000			
1.00E+04		23.38	10000			

1.00E+03		26.88	1000			
1.00E+03		26.8	1000			
1.00E+02		31.99	100			
1.00E+02		32.15	100			
1.00E+01		34.99	10			
1.00E+01		40	0			
1.00E-00		40	0			
1.00E-00		40	0			
NTC		40	0			

Gene Name sbg102200MCTa

Disease tissues	**Fold Change in Disease Population Relative to Normal**
colon tumor	-2.56
colon tumor	2.82
colon tumor	-1.05
colon tumor	-1.07
lung tumor	-3.45
lung tumor	2.65
lung tumor	-4.34
lung tumor	2.23
breast tumor	2.35
breast tumor	1.50
breast tumor	1.25
breast tumor	-12.48
brain stage 5 ALZ	-1.45
brain stage 5 ALZ	1.85
brain stage 5 ALZ	1.14
brain stage 5 ALZ	-1.22
lung 24	-10.98
lung 28	-19.65
lung 23	-8.45
asthmatic lung	-1.85
asthmatic lung	1.97
asthmatic lung	1.88
asthmatic lung	-1.36
endo VEGF	-1.64
endo bFGF	-1.04
heart T-1	-1.03
heart T-14	1.41
heart T-3399	1.76
BM stim	1.08
osteo dif	2.55
Cartilage (pool)	-2.23
PBL HIV IIIB	-1.15
MRC5 HSV strain F	2.52

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Gene Name sbg102200MCTb

High to moderate overall expression. Highest normal expression in the whole brain, liver, fetal liver, and thymus. Highest disease expression in one of the colon normal/tumor pairs, one of the lung normal/tumor pairs, one of the asthmatic lung samples, the dendritic cells, and the uninfected and HIV-infected PBL cells. Upregulation in 2 of 4 breast tumor samples is sufficient to make a disease claim in cancer of the breast. Upregulation in 1 of 4 AD brain samples indicates a potential role in Alzheimer's disease. Downregulation in 3 of 3 COPD lung samples suggests involvement in chronic obstructive pulmonary disease. Upregulation in 1 of 4 asthmatic lung samples indicates a potential role for this gene in lung cancer. High expression in all of the immune cells. Also high to moderate expression in the OA and RA synovium samples, the OA bone samples, and in the chondrocytes suggests an involvement in osteoarthritis and rheumatoid arthritis.

Sample sbg102200MCTb	**Ct (sample 1 and 2)**	**Mean GOI copies (sample 1)**	**Mean GOI copies (sample 2)**	**Average GOI Copies**	**18S rRNA (ng)**	**50 ng/18S rRNA (ng)**	**copies of mRNA detected/50 ng total RNA**
Subcutaneous Adipocytes Zenbio	35.66, 34.05	3.76	10.2	6.98	3.06	16.34	114.05
Subcutaneous Adipose Zenbio	40, 36	0.17	3.07	1.62	0.96	52.36	84.82
Adrenal Gland Clontech	40, 40	0	0	0.00	0.61	81.97	0.00
Whole Brain Clontech	26.32, 26.41	1192.66	1124.69	1158.68	7.24	6.91	8001.90
Fetal Brain Clontech	40, 35.84	0	3.38	1.69	0.48	103.95	175.68
Cerebellum Clontech	34.51, 34.28	7.68	8.8	8.24	2.17	23.04	189.86
Cervix	40, 34.34	3.17	8.5	5.84	2.42	20.66	120.56
Colon	33.67, 35.6	12.86	3.91	8.39	2.71	18.45	154.70
Endometrium	35.32, 34.43	4.66	8.05	6.36	0.73	68.21	433.49
Esophagus	34.27, 35.14	8.86	5.19	7.03	1.37	36.50	256.39
Heart Clontech	40, 35.05	0	5.5	2.75	1.32	37.88	104.17
Hypothalamus	40, 40	0	0	0.00	0.32	155.28	0.00
Ileum	35.29, 33.68	4.74	12.8	8.77	2.58	19.38	169.96
Jejunum	31.23, 30.98	57.65	67.22	62.44	6.60	7.58	472.99
Kidney	34.67, 34.21	6.95	9.2	8.08	2.12	23.58	190.45
Liver	30.76, 30.65	77.12	82.56	79.84	1.50	33.33	2661.33
Fetal Liver Clontech	26.8, 27.1	885.14	734.31	809.73	10.40	4.81	3892.91
Lung	40, 40	0	0.17	0.09	2.57	19.46	1.65
Mammary Gland Clontech	31.28, 31.37	56.1	52.95	54.53	13.00	3.85	209.71
Myometrium	34.16, 36.28	9.48	2.57	6.03	2.34	21.37	128.74
Omentum	34.18, 33.42	9.38	15	12.19	3.94	12.69	154.70
Ovary	34.21, 34.18	9.24	9.39	9.32	4.34	11.52	107.32
Pancreas	40, 40	0	0.14	0.07	0.81	61.80	4.33
Head of Pancreas	40, 35.02	0	5.59	2.80	1.57	31.85	89.01
Parotid Gland	31.23, 31.9	57.68	38.33	48.01	5.48	9.12	438.00
Placenta Clontech	31.77, 33.13	41.33	17.94	29.64	5.26	9.51	281.70
Prostate	39.72, 35.03	0.31	5.56	2.94	3.00	16.67	48.92
Rectum	35.36, 34.34	4.53	8.5	6.52	1.23	40.65	264.84
Salivary Gland Clontech	30.52, 30.54	89.5	88.43	88.97	7.31	6.84	608.52

Skeletal Muscle Clontech	40, 40	0	0	0.00	1.26	39.68	0.00
Skin	40, 40	0	0	0.00	1.21	41.32	0.00
Small Intestine Clontech	40, 39.27	0	0.41	0.21	0.98	51.07	10.47
Spleen	34.21, 33.54	9.2	13.91	11.56	4.92	10.16	117.43
Stomach	35.05, 33.62	5.51	13.22	9.37	2.73	18.32	171.52
Testis Clontech	40, 40	0	0	0.00	0.57	87.87	0.00
Thymus Clontech	28.56, 28.44	299.45	322.02	310.74	9.89	5.06	1570.96
Thyroid	31.65, 32.3	44.76	29.81	37.29	2.77	18.05	673.01
Trachea Clontech	32.3, 31.9	29.9	38.28	34.09	9.71	5.15	175.54
Urinary Bladder	34.34, 35.02	8.49	5.59	7.04	5.47	9.14	64.35
Uterus	33.07, 34.56	18.62	7.45	13.04	5.34	9.36	122.05
genomic	25.84	1597.08					
b-actin	27.32	643.56					
1.00E+05	19.22	100000					
1.00E+05	19.33	100000					
1.00E+04	22.48	10000					
1.00E+04	22.95	10000					
1.00E+03	26.19	1000					
1.00E+03	26.37	1000					
1.00E+02	31.23	100					
1.00E+02	30.48	100					
1.00E+01	32.76	10					
1.00E+01	35.02	10					
1.00E-00	40	0					
1.00E-00	40	0					
NTC	40	0					
NTC	40	0					

Sample sbg102200MCTb	**Reg number (GSK identifier)**	**Ct**	**Mean GOI copies**	**copies of mRNA detected /50 ng total RNA**	**Sample**	**Fold Change in Disease Population**
colon normal GW98-167	21941	26.48	1723.59	3447.18	colon normal	
colon tumor GW98-166	21940	26.06	2195.04	4390.08	colon tumor	1.27
colon normal GW98-178	22080	29.03	389.88	779.76	colon normal	
colon tumor GW98-177	22060	27.39	1015.65	2031.30	colon tumor	2.61
colon normal GW98-561	23514	26.74	1478.76	2957.52	colon normal	
colon tumor GW98-560	23513	26.37	1831.8	3663.60	colon tumor	1.24
colon normal GW98-894	24691	25.58	2918.02	5836.04	colon normal	
colon tumor GW98-893	24690	25	4089.75	8179.50	colon tumor	1.40
lung normal GW98-3	20742	24.59	5183.31	10366.62	lung normal	
lung tumor GW98-2	20741	24.94	4232.23	8464.46	lung tumor	-1.22
lung normal GW97-179	20677	25.73	2672.73	5345.46	lung normal	
lung tumor GW97-178	20676	25.36	3307.37	6614.74	lung tumor	1.24
lung normal GW98-165	21922	26.13	2109.28	4218.56	lung normal	

lung tumor GW98-164	21921	25.54	2973.82	5947.64	lung tumor	1.41
lung normal GW98-282	22584	27.08	1212.64	2425.28	lung normal	
lung tumor GW98-281	22583	27.45	979.82	1959.64	lung tumor	-1.24
breast normal GW00-392	28750	26.68	1536.57	1536.57	breast normal	
breast tumor GW00-391	28746	26.58	1626.58	3253.16	breast tumor	2.12
breast normal GW00-413	28798	31.71	81.9	81.90	breast normal	
breast tumor GW00-412	28797	26.57	1632	3264.00	breast tumor	39.85
breast normal GW00-235:238	27592-95	32.52	51.1	51.10	breast normal	
breast tumor GW00-231:234	27588-91	29.67	268.7	268.70	breast tumor	5.26
breast normal GW98-621	23656	26.48	1727.44	3454.88	breast normal	
breast tumor GW98-620	23655	25.65	2793.6	5587.20	breast tumor	1.62
brain normal BB99-542	25507	28.62	494	988.00	brain normal	
brain normal BB99-406	25509	29.45	304.68	609.36	brain normal	
brain normal BB99-904	25546	30.08	211.25	422.50	brain normal	
brain stage 5 ALZ BB99-874	25502	28.75	458.64	917.28	brain stage 5 ALZ	1.36
brain stage 5 ALZ BB99-887	25503	26.86	1383.71	2767.42	brain stage 5 ALZ	4.11
brain stage 5 ALZ BB99-862	25504	28.02	702.59	1405.18	brain stage 5 ALZ	2.09
brain stage 5 ALZ BB99-927	25542	29.57	284.31	568.62	brain stage 5 ALZ	-1.18
CT lung KC	normal	26.58	1624.29	3248.58	CT lung	
lung 26 KC	normal	34.19	19.27	19.27	lung 26	
lung 27 KC	normal	32.45	53.23	53.23	lung 27	
lung 24 KC	COPD	33	38.6	38.60	lung 24	-21.75
lung 28 KC	COPD	32.24	59.95	59.95	lung 28	-14.01
lung 23 KC	COPD	32.87	41.63	41.63	lung 23	-20.17
lung 25 KC	normal	33.04	37.52	37.52	lung 25	
asthmatic lung ODO3112	29321	30.13	205.46	205.46	asthmatic lung	-4.09
asthmatic lung ODO3433	29323	27.82	788.82	1577.64	asthmatic lung	1.88
asthmatic lung ODO3397	29322	25.17	3695.43	7390.86	asthmatic lung	8.80
asthmatic lung ODO4928	29325	27.6	894.3	1788.60	asthmatic lung	2.13
endo cells KC	control	28.2	633.43	633.43	endo cells	
endo VEGF KC		28.86	429.51	429 51	endo VEGF	-1.47
endo bFGF KC		28.97	403.08	403.08	endo bFGF	-1.57
heart Clontech	normal	28.83	437.62	875.24	heart	
heart (T-1) ischemic	29417	28.42	557.54	1115.08	heart T-1	1.27
heart (T-14) non-obstructive DCM	29422	27.72	835.11	1670.22	heart T-14	1.91
heart (T-3399) DCM	29426	28.63	493.01	986.02	heart T-3399	1.13
adenoid GW99-269	26162	27	1269.75	2539.50	adenoid	
tonsil GW98-280	22582	26.33	1876.29	3752.58	tonsil	
T cells PC00314	28453	29.15	363.35	726.70	T cells	
PBMNC		33.05	37.41	37.41	PBMNC	
monocyte		31.49	92.84	185.68	monocyte	
B cells PC00665	28455	26.5	1700.87	3401.74	B cells	
dendritic cells 28441		24.2	6511.17	13022.34	dendritic cells	

neutrophils	28440	27.01	1262.74	1262.74	neutrophils	
eosinophils	28446	29.23	347.08	694.16	eosinophils	
BM unstim		30.85	135.01	135.01	BM unstim	
BM stim		28.68	478.5	478.50	BM stim	3.54
osteo dif		31.03	121.2	121.20	osteo dif	3.93
osteo undif		33.38	30.85	30.85	osteo undif	
chondrocytes		26.63	1579.73	3949.33	chondrocytes	
OA Synovium IP12/01	29462	29.11	371.98	371.98	OA Synovium	
OA Synovium NP10/01	29461	29.45	304.55	609.10	OA Synovium	
OA Synovium NP57/00	28464	27.83	784.87	1569.74	OA Synovium	
RA Synovium NP03/01	28466	27.31	1063.77	2127.54	RA Synovium	
RA Synovium NP71/00	28467	27.08	1217.21	2434.42	RA Synovium	
RA Synovium NP45/00	28475	26.6	1606.41	3212.82	RA Synovium	
OA bone (biobank)	29217	28.65	485.63	485.63	OA bone (biobank)	
OA bone Sample 1	J. Emory	28.78	451.74	903.48	OA bone	
OA bone Sample 2	J. Emory	28.27	607.15	1214.30	OA bone	
Cartilage (pool)	Normal	29.42	310.76	621.52	Cartilage (pool)	
Cartilage (pool)	OA	30.09	209.7	419.40	Cartilage (pool)	-1.48
PBL unifected	28441	23.85	7997.03	15994.06	PBL unifected	
PBL HIV IIIB	28442	24.85	4447.34	8894.68	PBL HIV IIIB	-1.80
MRC5 uninfected (100%)	29158	27.02	1258.46	2516.92	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	29.6	278.84	557.68	MRC5 HSV strain F	-4.51
W12 cells	29179	27.21	1122.77	2245.54	W12 cells	
Keratinocytes	29180	25.64	2815.12	5630.24	Keratinocytes	
B-actin control		27.78	807.72			
genomic		27.04	1246.22			
1.00E+05		19.69	100000			
1.00E+05		20.01	100000			
1.00E+04		23.15	10000			
1.00E+04		23.2	10000			
1.00E+03		27.02	1000			
1.00E+03		26.76	1000			
1.00E+02		31.45	100			
1.00E+02		32.39	100			
1.00E+01		35.72	10			
1.00E+01		34.74	10			
1.00E-00		40	0			
1.00E-00		40	0			
NTC		40	0			

Gene Name sbg102200MCTb

Disease tissues	**Fold Change in Disease Population Relative to Normal**
colon tumor	1.27
colon tumor	2.61
colon tumor	1.24

colon tumor	1.40
lung tumor	-1.22
lung tumor	1.24
lung tumor	1.41
lung tumor	-1.24
breast tumor	2.12
breast tumor	39.85
breast tumor	5.26
breast tumor	1.62
brain stage 5 ALZ	1.36
brain stage 5 ALZ	4.11
brain stage 5 ALZ	2.09
brain stage 5 ALZ	-1.18
lung 24	-21.75
lung 28	-14.01
lung 23	-20.17
asthmatic lung	-4.09
asthmatic lung	1.88
asthmatic lung	8.80
asthmatic lung	2.13
endo VEGF	-1.47
endo bFGF	-1.57
heart T-1	1.27
heart T-14	1.91
heart T-3399	1.13
BM stim	3.54
osteo dif	3.93
Cartilage (pool)	-1.48
PBL HIV IIIB	-1.80
MRC5 HSV strain F	-4.51

Gene Name sbg1020380LYG

Failed

Gene Name sbg1007026SGLT

Good to moderate overall expression. The highest normal expression is seen in the whole brain, cerebellum, hypothalamus, jejunum, fetal liver, rectum, and uterus. This gene shows system specific expression in samples representing the central nervous system, the female reproductive organs, and the GI tract. The expression seen in the disease samples confirms that seen in the normal samples with the highest levels of expression seen in the normal and Alzheimer's brain samples. Upregulation in 1 of 4 colon tumor samples and 2 of 4 breast tumor samples as well as downregulation in 1 of 4 lung tumors poses a potential role for this gene in cancers of the colon and breast. Downregulation in 2 of 4 Alzheimer's brain samples implies involvement in Alzheimer's disease. Downregulation in 3 of 3 COPD samples and upregulation in 2 of 4 asthmatic lung samples suggests a potential role for this gene in chronic obstructive pulmonary disorder. Upregulation in the VEGF-treated endothelial cell line implicates a possible role for this gene in angiogenesis. Downregulated in the stimulated bone marrow sample. High expression in the RA and OA synovium samples, the OA bone samples, and the chondrocytes with corroborating high expression in the T cells, B cells, neutrophils, and eosinophils implicates this gene in osteoarthritis and rheumatoid arthritis.

Sample sbg1007026SGLT	Ct (sample 1 and 2)	Mean GOI	Mean GOI	Average GOI	18S rRNA	50 ng/18	copies of mRNA

		copies (sample 1)	copies (sample 2)	Copies	(ng)	S rRNA (ng)	detected/ 50 ng total RNA
Subcutaneous Adipocytes Zenbio	40, 40	0	0	0.00	3.06	16.34	0.00
Subcutaneous Adipose Zenbio	40, 40	0	0.1	0.05	0.96	52.36	2.62
Adrenal Gland Clontech	40, 38.76	0	0.31	0.16	0.61	81.97	12.70
Whole Brain Clontech	23.01, 22.63	3438.45	4301.69	3870.07	7.24	6.91	26727.00
Fetal Brain Clontech	35.91, 39.16	1.66	0.24	0.95	0.48	103.95	98.75
Cerebellum Clontech	34.55, 32.7	3.71	11.08	7.40	2.17	23.04	170.39
Cervix	34.21, 34.61	4.54	3.58	4.06	2.42	20.66	83.88
Colon	33.44, 33.7	7.16	6.14	6.65	2.71	18.45	122.69
Endometrium	34.88, 40	3.05	0.1	1.58	0.73	68.21	107.44
Esophagus	40, 40	0	0.1	0.05	1.37	36.50	1.82
Heart Clontech	39.63, 39.53	0.18	0.19	0.19	1.32	37.88	7.01
Hypothalamus	40, 35.34	0	2.33	1.17	0.32	155.28	180.90
Ileum	40, 40	0	0	0.00	2.58	19.38	0.00
Jejunum	30.1, 30.34	51.59	44.92	48.26	6.60	7.58	365.57
Kidney	33.49, 40	6.96	0	3.48	2.12	23.58	82.08
Liver	40, 33.7	0	6.15	3.08	1.50	33.33	102.50
Fetal Liver Clontech	29.58, 29.41	70.26	77.58	73.92	10.40	4.81	355.38
Lung	35.61, 37.83	1.98	0.53	1.26	2.57	19.46	24 42
Mammary Gland Clontech	33.05, 34.04	9.02	5.03	7.03	13.00	3.85	27.02
Myometrium	33.63, 34.13	6.38	4.77	5.58	2.34	21.37	119.12
Omentum	40, 40	0	0	0.00	3.94	12.69	0.00
Ovary	35.38, 37.6	2.27	0.61	1.44	4.34	11.52	16.59
Pancreas	40, 37.1	0	0.82	0.41	0.81	61.80	25.34
Head of Pancreas	35.45, 36.72	2.18	1.03	1.61	1.57	31.85	51.11
Parotid Gland	36.88, 40	0.94	0	0.47	5.48	9.12	4.29
Placenta Clontech	33.84, 38.46	5.66	0.37	3.02	5.26	9.51	28.66
Prostate	38.76, 37.12	0.31	0.81	0.56	3.00	16.67	9.33
Rectum	36.18, 33.82	1.42	5.7	3.56	1.23	40.65	144.72
Salivary Gland Clontech	38.36, 39.93	0.39	0.12	0.26	7.31	6.84	1.74
Skeletal Muscle Clontech	35.69, 36.23	1.9	1.38	1.64	1.26	39.68	65.08
Skin	39.51, 40	0.2	0.09	0.15	1.21	41.32	5.99
Small Intestine Clontech	40, 36.04	0.1	1.53	0.82	0.98	51.07	41.62
Spleen	33.51, 38.51	6.87	0.36	3.62	4.92	10.16	36.74
Stomach	34.14, 34.19	4.73	4.59	4.66	2.73	18.32	85.35
Testis Clontech	35.81, 40	1.76	0.11	0.94	0.57	87.87	82.16
Thymus Clontech	33.26, 32.49	7.96	12.55	10.26	9.89	5.06	51.85
Thyroid	40, 39.9	0.08	0.16	0.12	2.77	18.05	2.17
Trachea Clontech	34.25, 33.8	4.42	5.77	5.10	9.71	5.15	26.24
Urinary Bladder	39.95, 36.54	0.1	1.14	0.62	5.47	9.14	5.67
Uterus	33, 31.23	9.3	26.52	17.91	5.34	9.36	167.70
genomic	24.72	1251.19					

b-actin	25.89	625.04					
1.00E+05	17.54	100000					
1.00E+05	17.65	100000					
1.00E+04	21.03	10000					
1.00E+04	20.92	10000					
1.00E+03	24.87	1000					
1.00E+03	24.96	1000					
1.00E+02	29.1	100					
1.00E+02	29.04	100					
1.00E+01	32.05	10					
1.00E+01	33.51	10					
1.00E-00	36.41	1					
1.00E-00	37.41	1					
NTC	40	0					
NTC	40	-1					

Sample sbg1007026SGLT	**Reg number (GSK identifier)**	**Ct**	**Mean GOI copies**	**copies of mRNA detected/ 50 ng total RNA**	**Sample**	**Fold Change in Disease Population**
colon normal GW98-167	21941	29.22	127.1	254.20	colon normal	
colon tumor GW98-166	21940	31.07	44.11	88.22	colon tumor	-2.88
colon normal GW98-178	22080	38.41	0.65	1.30	colon normal	
colon tumor GW98-177	22060	31.17	41.5	83.00	colon tumor	63.85
colon normal GW98-561	23514	31.21	40.69	81.38	colon normal	
colon tumor GW98-560	23513	33.06	14.04	28.08	colon tumor	-2.90
colon normal GW98-894	24691	29.63	100.41	200.82	colon normal	
colon tumor GW98-893	24690	32.22	22.7	45.40	colon tumor	-4.42
lung normal GW98-3	20742	29.8	91.46	182.92	lung normal	
lung tumor GW98-2	20741	34.26	7.02	14.04	lung tumor	-13.03
lung normal GW97-179	20677	29.59	103.13	206.26	lung normal	
lung tumor GW97-178	20676	29.84	89.09	178.18	lung tumor	-1.16
lung normal GW98-165	21922	29.6	102.46	204.92	lung normal	
lung tumor GW98-164	21921	30.8	51.53	103.06	lung tumor	-1.99
lung normal GW98-282	22584	32.53	18.97	37.94	lung normal	
lung tumor GW98-281	22583	32.29	21.8	43.60	lung tumor	1.15
breast normal GW00-392	28750	28.77	164.85	164.85	breast normal	
breast tumor GW00-391	28746	30.64	56.21	112.42	breast tumor	-1.47
breast normal GW00-413	28798	34.49	6.17	6.17	breast normal	
breast tumor GW00-412	28797	30.37	65.97	131.94	breast tumor	21.38
breast normal GW00-235:238	27592-95	32.87	15.66	15.66	breast normal	
breast tumor GW00-231:234	27588-91	29.8	91.07	91.07	breast tumor	5.82
breast normal GW98-621	23656	28.95	149.19	298.38	breast normal	
breast tumor GW98-620	23655	29.62	101.25	202.50	breast tumor	-1.47
brain normal BB99-542	25507	24.5	1917.28	3834.56	brain normal	

brain normal BB99-406	25509	21.35	11736.92	23473.84	brain normal	
brain normal BB99-904	25546	25.25	1248.68	2497.36	brain normal	
brain stage 5 ALZ BB99-874	25502	27.29	386.81	773.62	brain stage 5 ALZ	-12.84
brain stage 5 ALZ BB99-887	25503	23.61	3196.37	6392.74	brain stage 5 ALZ	-1.55
brain stage 5 ALZ BB99-862	25504	25.56	1045.09	2090.18	brain stage 5 ALZ	-4.75
brain stage 5 ALZ BB99-927	25542	24.45	1976.24	3952.48	brain stage 5 ALZ	-2.51
CT lung	normal	31.07	44.03	88.06	CT lung Nml	
lung 26	normal	24.93	1496.87		lung 26 Nml	
lung 27	normal	34.06	7.92	7.92	lung 27 Nml	
lung 24	COPD	34.58	5.87	5.87	lung 24 COPD	-5.45
lung 28	COPD	40	0	0.00	lung 28 COPD	-31.99
lung 23	COPD	40	0	0.00	lung 23 COPD	-31.99
lung 25	normal	40	0	0.00	lung 25 Nml	
asthmatic lung ODO3112	29321	33.19	13.04	13.04	asthmatic lung	-2.45
asthmatic lung ODO3433	29323	30.61	57.38	114.76	asthmatic lung	3.59
asthmatic lung ODO3397	29322	29.2	129.16	258.32	asthmatic lung	8.07
asthmatic lung ODO4928	29325	30.32	67.67	135.34	asthmatic lung	4.23
endo cells	control	35.09	4.37	4.37	endo cells	
endo VEGF		32.22	22.7	22.70	endo VEGF	5.19
endo bFGF		33.23	12.7	12.70	endo bFGF	2.91
heart Clontech	normal	33.53	10.71	21.42	heart	
heart (T-1) ischemic	29417	33.43	11.37	22.74	heart (T-1) ischemic	1.06
heart (T-14) non-obstructive DCM	29422	34.45	6.32	12.64	heart (T-14) non-obstructive DCM	-1.69
heart (T-3399) DCM	29426	31.98	26.02	52.04	heart (T-3399) DCM	2.43
adenoid GW99-269	26162	29.56	104.93	209.86	adenoid	
tonsil GW98-280	22582	29	144.55	289.10	tonsil	
T cells PC00314	28453	32.03	25.34	50.68	T cells	
PBMNC		37.71	0.97	0.97	PBMNC	
monocyte		37.49	1.1	2.20	monocyte	
B cells PC00665	28455	27.18	410.49	820.98	B cells	
dendritic cells	28441	33.7	9.73	19.46	dendritic cells	
neutrophils	28440	32.48	19.6	19.60	neutrophils	
eosinophils	28446	32.44	20.08	40.16	eosinophils	
BM unstim		33.8	9.17	9.17	BM unstim	
BM stim	treated	38.89	0.49	0.49	BM stim	-18.71
osteo dif	treated	37.26	1.26	1.26	osteo dif	1.26
osteo undif		40	0	0.00	osteo undif	
chondrocytes		32.07	24.82	62.05	chondrocytes	
OA Synovium IP12/01	29462	30.31	68.26	68.26	OA Synovium	
OA Synovium NP10/01	29461	30.74	53.26	106.52	OA Synovium	
OA Synovium NP57/00	28464	31.3	38.48	76.96	OA Synovium	
RA Synovium NP03/01	28466	31.08	43.89	87.78	RA Synovium	
RA Synovium NP71/00	28467	31.35	37.58	75.16	RA Synovium	

RA Synovium NP45/00	28475	30.74	53.21	106.42	RA Synovium	
OA bone (biobank)	29217	30.47	61.99	61.99	OA bone (biobank)	
OA bone Sample 1	J. Emory	29.92	85.09	170.18	OA bone	
OA bone Sample 2	J. Emory	30.91	48.27	96.54	OA bone	
Cartilage (pool)	Normal	31.34	37.68	75.36	Nml Cartilage (pool)	
Cartilage (pool)	OA	31.72	30.35	60.70	OA Cartilage (pool)	-1.24
PBL unifected	28441	30.8	51.54	103.08	PBL unifected	
PBL HIV IIIB	28442	32.03	25.38	50.76	PBL HIV IIIB	-2.03
MRC5 uninfected (100%)	29158	32.29	21.85	43.70	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	31.21	40.73	81.46	MRC5 HSV strain F	1.86
W12 cells	29179	33.12	13.52	27.04	W12 cells	
Keratinocytes	29180	32.35	21.06	42.12	Keratinocytes	
B-actin control		25.63	1002.01			
genomic		25.19	1290.48			
1.00E+05		17.86	100000			
1.00E+05		17.85	100000			
1.00E+04		21.44	10000			
1.00E+04		21.51	10000			
1.00E+03		25.33	1000			
1.00E+03		25.26	1000			
1.00E+02		29.62	100			
1.00E+02		30.55	100			
1.00E+01		32.93	10			
1.00E+01		33.46	10			
1.00E-00		38.18	1			
1.00E-00		40	0			
NTC		38.28	-1			
*lung 26 Normal has been omitted due to multiple amplification failures from that sample						

Gene Name sbg1007026SGLT

Disease tissues	**Fold Change in Disease Population Relative to Normal**
colon tumor	-2.88
colon tumor	63.85
colon tumor	-2.90
colon tumor	-4.42
lung tumor	-13.03
lung tumor	-1.16
lung tumor	-1.99
lung tumor	1.15
breast tumor	-1.47
breast tumor	21.38

breast tumor	5.82
breast tumor	-1.47
brain stage 5 ALZ	-12.84
brain stage 5 ALZ	-1.55
brain stage 5 ALZ	-4.75
brain stage 5 ALZ	-2.51
lung 24	-5.45
lung 28	-31.99
lung 23	-31.99
asthmatic lung	-2.45
asthmatic lung	3.59
asthmatic lung	8.07
asthmatic lung	4.23
endo VEGF	5.19
endo bFGF	2.91
heart T-1	1.06
heart T-14	-1.69
heart T-3399	2.43
BM stim	-18.71
osteo dif	1.26
Cartilage (pool)	-1.24
PBL HIV IIIB	-2.03
MRC5 HSV strain F	1.86

Gene Name sbg1012732GLUT

High to moderate overall expression. This gene is expressed fairly ubiquitously in all normal samples analyzed with highest levels of expression seen in the whole brain, fetal brain cerebellum, kidney, fetal liver, and the placenta. This gene is also expressed fairly ubiquitously in the disease samples. Downregulation in 3 of 3 COPD samples suggests a potential role for this gene in chronic obstructive pulmonary disorder. Upregulation in 3 of 3 disease heart samples implies an involvement in cardiovascular diseases such as non-obstructive and obstructive DCM and ischemia. Downregulation in the HSV-infected MRC5 cells suggests that this gene may play a role in HSV. Upregulated in the differentiated osteoblasts. High expression in the RA and OA synovium samples, the OA bone samples, and the chondrocytes with corroborating high expression in the T cells, B cells, dendritic cells, neutrophils, and eosinophils implicates this gene in osteoarthritis and rheumatoid arthritis.

Sample sbg1012732GLUT	**Ct (sample 1 and 2)**	**Mean GOI copies (sample 1)**	**Mean GOI copies (sample 2)**	**Average GOI Copies**	**18S rRNA (ng)**	**50 ng/18S rRNA (ng)**	**copies of mRNA detected/ 50 ng total RNA**
Subcutaneous Adipocytes Zenbio	30.84, 30.49	46.76	57.63	52.20	3.06	16.34	852.86
Subcutaneous Adipose Zenbio	34.89, 35.19	4.31	3.62	3.97	0.96	52.36	207.59
Adrenal Gland Clontech	33.79, 32.74	8.27	15.31	11.79	0.61	81.97	966.39
Whole Brain Clontech	22.02, 21.91	8374.61	8944.05	8659.33	7.24	6.91	59802.00
Fetal Brain Clontech	32.03, 32.85	23.23	14.34	18.79	0.48	103.95	1952.70
Cerebellum Clontech	28.2, 28.26	221.12	213.07	217.10	2.17	23.04	5002.19
Cervix	32.91, 34.54	13.81	5.31	9.56	2.42	20.66	197.52
Colon	30.88, 32.48	45.58	17.87	31.73	2.71	18.45	585.33
Endometrium	36.13, 32.5	2.08	17.6	9.84	0.73	68.21	671.21

Esophagus	32.19, 33.5	21.15	9.77	15.46	1.37	36.50	564.23
Heart Clontech	31.93, 31.73	24.67	27.76	26.22	1.32	37.88	992.99
Hypothalamus	40, 32.77	0	15.04	7.52	0.32	155.28	1167.70
Ileum	30.94, 30.52	44.17	56.37	50.27	2.58	19.38	974.22
Jejunum	30.04, 29.34	75.03	113.25	94.14	6.60	7.58	713.18
Kidney	29.72, 29.18	90.58	124.19	107.39	2.12	23.58	2532.67
Liver	34.81, 32.2	4.52	21.05	12.79	1.50	33.33	426.17
Fetal Liver Clontech	26.6, 26.85	567.46	488.36	527.91	10.40	4.81	2538.03
Lung	31.61, 30.52	29.69	56.54	43.12	2.57	19.46	838.81
Mammary Gland Clontech	28.06, 27.59	239.58	316.2	277.89	13.00	3.85	1068.81
Myometrium	30.44, 29.88	59.31	82.52	70.92	2.34	21.37	1515.28
Omentum	31.7, 30.82	28.2	47.35	37.78	3.94	12.69	479.38
Ovary	30.92, 31.56	44.74	30.55	37.65	4.34	11.52	433.70
Pancreas	33.08, 32.66	12.54	16.03	14.29	0.81	61.80	882.88
Head of Pancreas	33.98, 34.1	7.36	6.89	7.13	1.57	31.85	226.91
Parotid Gland	29.5, 30.55	102.86	55.41	79.14	5.48	9.12	722.03
Placenta Clontech	25.63, 25.87	1002.18	869.55	935.87	5.26	9.51	8896.06
Prostate	30.23, 31.17	67.04	38.48	52.76	3.00	16.67	879.33
Rectum	31.29, 31.15	35.89	38.94	37.42	1.23	40.65	1520.93
Salivary Gland Clontech	28.82, 28.83	153.9	152.53	153.22	7.31	6.84	1047.98
Skeletal Muscle Clontech	33.23, 32.66	11.48	16.02	13.75	1.26	39.68	545.63
Skin	32.62, 32.57	16.46	16.96	16 71	1.21	41.32	690.50
Small Intestine Clontech	34.63, 32.82	5.03	14.62	9.83	0.98	51.07	501.79
Spleen	31.45, 32.71	32.66	15.56	24.11	4.92	10.16	245.02
Stomach	32.38, 32.43	18.93	18.41	18.67	2.73	18.32	341.94
Testis Clontech	32.32, 32.27	19.58	20.17	19.88	0.57	87.87	1746.49
Thymus Clontech	27.24, 26.75	388.32	518.55	453.44	9.89	5.06	2292.39
Thyroid	30.48, 29.44	57 86	106.5	82.18	2.77	18.05	1483.39
Trachea Clontech	29.96, 30.29	78.48	64.81	71.65	9.71	5.15	368.92
Urinary Bladder	30.59, 30.1	54.25	72.45	63.35	5.47	9.14	579.07
Uterus	30.62, 29.73	53.18	89.72	71.45	5.34	9.36	669.01
genomic	25.15	1330.24					
b-actin	26.01	800.58					
1.00E+05	18.01	100000					
1.00E+05	18.19	100000					
1.00E+04	21.35	10000					
1.00E+04	21.3	10000					
1.00E+03	25.59	1000					
1.00E+03	25.51	1000					
1.00E+02	29.95	100					
1.00E+02	29.37	100					
1.00E+01	34.05	10					
1.00E+01	33.22	10					
1.00E-00	37.19	1					
1.00E-00	40	0					
NTC	40	0					

NTC	40	0					

Sample sbg1012732GLUT	Reg number (GSK identifier)	Ct	Mean GOI copies	copies of mRNA detected/ 50 ng total RNA	Sample	Fold Change in Disease Population
colon normal GW98-167	21941	25.38	1695.47	3390.94	colon normal	
colon tumor GW98-166	21940	25.51	1576.91	3153.82	colon tumor	-1.08
colon normal GW98-178	22080	26.8	765.5	1531.00	colon normal	
colon tumor GW98-177	22060	25.86	1297.34	2594.68	colon tumor	1.69
colon normal GW98-561	23514	26.12	1120.64	2241.28	colon normal	
colon tumor GW98-560	23513	26.12	1121.89	2243.78	colon tumor	1.00
colon normal GW98-894	24691	24.85	2283.56	4567.12	colon normal	
colon tumor GW98-893	24690	24.37	2989.5	5979.00	colon tumor	1.31
lung normal GW98-3	20742	24.37	2984.11	5968.22	lung normal	
lung tumor GW98-2	20741	25.38	1691.06	3382.12	lung tumor	-1.76
lung normal GW97-179	20677	25.07	2020.52	4041.04	lung normal	
lung tumor GW97-178	20676	24.61	2607.03	5214.06	lung tumor	1.29
lung normal GW98-165	21922	24.92	2195.85	4391.70	lung normal	
lung tumor GW98-164	21921	25.36	1712.62	3425.24	lung tumor	-1.28
lung normal GW98-282	22584	26.24	1049.97	2099.94	lung normal	
lung tumor GW98-281	22583	25.94	1241.8	2483.60	lung tumor	1.18
breast normal GW00-392	28750	25.26	1813.7	1813.70	breast normal	
breast tumor GW00-391	28746	24.87	2259.54	4519.08	breast tumor	2.49
breast normal GW00-413	28798	25.4	1672.46	1672.46	breast normal	
breast tumor GW00-412	28797	25.21	1864.18	3728.36	breast tumor	2.23
breast normal GW00-235:238	27592-95	25.68	1435.2	1435.20	breast normal	
breast tumor GW00-231:234	27588-91	24.08	3510.78	3510.78	breast tumor	2.45
breast normal GW98-621	23656	24.16	3363.26	6726.52	breast normal	
breast tumor GW98-620	23655	24.19	3300.23	6600.46	breast tumor	-1.02
brain normal BB99-542	25507	22.64	7880.57	15761.14	brain normal	
brain normal BB99-406	25509	23.32	5357.05	10714.10	brain normal	
brain normal BB99-904	25546	23.66	4436.27	8872.54	brain normal	
brain stage 5 ALZ BB99-874	25502	24.7	2474.23	4948.46	brain stage 5 ALZ	-2.38
brain stage 5 ALZ BB99-887	25503	23.22	5674.88	11349.76	brain stage 5 ALZ	-1.04
brain stage 5 ALZ BB99-862	25504	23.5	4868.6	9737.20	brain stage 5 ALZ	-1.21
brain stage 5 ALZ BB99-927	25542	23.17	5843.2	11686.40	brain stage 5 ALZ	-1.01
CT lung	normal	25.61	1486.99	2973.98	CT lung Nml	
lung 26	normal	26.55	879.91		lung 26 Nml	
lung 27	normal	29.44	174.3	174.30	lung 27 Nml	

lung 24	COPD	29.99	128.5	128.50	lung 24 COPD	-8.67
lung 28	COPD	29.56	163.34	163.34	lung 28 COPD	-6.82
lung 23	COPD	29.59	160.67	160.67	lung 23 COPD	-6.94
lung 25	normal	29.24	194.83	194.83	lung 25 Nml	
asthmatic lung ODO3112	29321	27.22	604.38	604.38	asthmatic lung	-1.84
asthmatic lung ODO3433	29323	26.46	923.43	1846.86	asthmatic lung	1.66
asthmatic lung ODO3397	29322	26.16	1094.36	2188.72	asthmatic lung	1.96
asthmatic lung ODO4928	29325	25.51	1576.72	3153.44	asthmatic lung	2.83
endo cells	control	29.09	211.78	211.78	endo cells	
endo VEGF		30.07	122.67	122.67	endo VEGF	-1.73
endo bFGF		29.93	132.63	132.63	endo bFGF	-1.60
heart Clontech	normal	27.35	561.26	1122.52	heart	
heart (T-1) ischemic	29417	23.82	4053.65	8107.30	heart (T-1) ischemic	7.22
heart (T-14) non-obstructive DCM	29422	23.96	3746.25	7492.50	heart (T-14) non-obstructive DCM	6.67
heart (T-3399) DCM	29426	23.35	5282.35	10564.70	heart (T-3399) DCM	9.41
adenoid GW99-269	26162	25.71	1405.41	2810.82	adenoid	
tonsil GW98-280	22582	23.97	3725.77	7451.54	tonsil	
T cells PC00314	28453	25.03	2062.68	4125.36	T cells	
PBMNC		30.16	116.69	116.69	PBMNC	
monocyte		30.15	117.05	234.10	monocyte	
B cells PC00665	28455	23.22	5673.63	11347.26	B cells	
dendritic cells	28441	25.74	1385.65	2771.30	dendritic cells	
neutrophils	28440	27.14	631.86	631.86	neutrophils	
eosinophils	28446	28.27	335.66	671.32	eosinophils	
BM unstim		30.08	122.25	122.25	BM unstim	
BM stim	treated	29.57	162.71	162.71	BM stim	1.33
osteo dif	treated	29.07	214.84	214.84	osteo dif	2.91
osteo undif		30.98	73.85	73.85	osteo undif	
chondrocytes		25.41	1667.28	4168.20	chondrocytes	
OA Synovium IP12/01	29462	24.65	2554.39	2554.39	OA Synovium	
OA Synovium NP10/01	29461	25.72	1399	2798.00	OA Synovium	
OA Synovium NP57/00	28464	25.24	1828.2	3656.40	OA Synovium	
RA Synovium NP03/01	28466	25.69	1422.61	2845.22	RA Synovium	
RA Synovium NP71/00	28467	25.25	1818.15	3636.30	RA Synovium	
RA Synovium NP45/00	28475	25.22	1857.13	3714.26	RA Synovium	
OA bone (biobank)	29217	26.19	1074.74	1074.74	OA bone (biobank)	
OA bone Sample 1	J. Emory	26.71	805.65	1611.30	OA bone	
OA bone Sample 2	J. Emory	26.96	700.88	1401.76	OA bone	
Cartilage (pool)	Normal	26.38	968.45	1936.90	Nml Cartilage (pool)	
Cartilage (pool)	OA	28.07	376.23	752.46	OA Cartilage (pool)	-2.57
PBL unifected	28441	25.09	1997.75	3995.50	PBL unifected	
PBL HIV IIIB	28442	25.36	1710.81	3421.62	PBL HIV IIIB	-1.17
MRC5 uninfected (100%)	29158	25.28	1788.71	3577.42	MRC5 uninfected (100%)	

MRC5 HSV strain F	29178	30.17	116.17	232.34	MRC5 HSV strain F	-15.40
W12 cells	29179	27.6	489.01	978.02	W12 cells	
Keratinocytes	29180	26.4	959.61	1919.22	Keratinocytes	
B-actin control		25.62	1482.86			
genomic		25.42	1657.68			
1.00E+05		18.49	100000			
1.00E+05		18.49	100000			
1.00E+04		21.94	10000			
1.00E+04		21.98	10000			
1.00E+03		25.34	1000			
1.00E+03		25.39	1000			
1.00E+02		30.59	100			
1.00E+02		30.9	100			
1.00E+01		32.51	10			
1.00E+01		39.12	10			
1.00E-00		39.07	1			
1.00E-00		36.71	1			
NTC		39.63	-1			
*lung 26 Normal has been omitted due to multiple amplification failures from that sample						

Gene Name sbg1012732GLUT

Disease tissues	**Fold Change in Disease Population Relative to Normal**
colon tumor	-1.08
colon tumor	1.69
colon tumor	1.00
colon tumor	1.31
lung tumor	-1.76
lung tumor	1.29
lung tumor	-1.28
lung tumor	1.18
breast tumor	2.49
breast tumor	2.23
breast tumor	2.45
breast tumor	-1.02
brain stage 5 ALZ	-2.38
brain stage 5 ALZ	-1.04
brain stage 5 ALZ	-1.21
brain stage 5 ALZ	-1.01
lung 24	-8.67
lung 28	-6.82
lung 23	-6.94
asthmatic lung	-1.84
asthmatic lung	1.66
asthmatic lung	1.96
asthmatic lung	2.83
endo VEGF	-1.73

endo bFGF	-1.60
heart T-1	7.22
heart T-14	6.67
heart T-3399	9.41
BM stim	1.33
osteo dif	2.91
Cartilage (pool)	-2.57
PBL HIV IIIB	-1.17
MRC5 HSV strain F	-15.40

Gene Name sbg1012732GLUTb

The same as sbg1012732GLUT.

Gene Name sbg1018172CSP

Moderate to low overall expression. Highest normal expression is seen in the whole brain, kidney, thyroid, and uterus. This gene is expressed in all of the samples representing the female reproductive system. Highest disease expression is seen in many of the normal/tumor lung samples and the asthmatic lung samples. Downregulation in 2 of 4 lung tumor samples and upregulation in 2 of 4 breast tumor samples suggests an involvement in cancers of the lung and breast. Downregulation in 3 of 3 COPD samples suggests a potential role for this gene in chronic obstructive pulmonary disorder. Upregulation in 2 of 4 asthmatic lung samples implies an involvement in asthma. Upregulation in 1 of 3 disease heart samples implies an involvement in cardiovascular disease such as obstructive DCM Downregulation in the OA cartilage pool with corroborating low expression in the immune cells (T and B cells in particular) implicates this gene in osteoarthritis and rheumatoid arthritis. Upregulation in the HSV-infected MRC5 cells suggests that this gene may be a host factor in HSV.

Sample sbg1018172CSP	**Ct (sample 1 and 2)**	**Mean GOI copies (sample 1)**	**Mean GOI copies (sample 2)**	**Average GOI Copies**	**18S rRNA (ng)**	**50 ng/18S rRNA (ng)**	**copies of mRNA detected/50 ng total RNA**
Subcutaneous Adipocytes Zenbio	35.54, 34.87	7.65	11.21	9.43	3.06	16.34	154.08
Subcutaneous Adipose Zenbio	40, 40	0.4	0	0.20	0.96	52.36	10.47
Adrenal Gland Clontech	40, 40	0	0	0.00	0.61	81.97	0.00
Whole Brain Clontech	25.71, 25.78	1950.98	1867.58	1909.28	7.24	6.91	13185.64
Fetal Brain Clontech	40, 40	0	0	0.00	0.48	103.95	0.00
Cerebellum Clontech	36.32, 35.16	4.95	9.48	7.22	2.17	23.04	166.24
Cervix	36.76, 36.16	3.85	5.42	4.64	2.42	20.66	95.76
Colon	36.52, 36.41	4.41	4.7	4.56	2.71	18.45	84.04
Endometrium	36.4, 35.92	4.73	6.19	5.46	0.73	68.21	372.44
Esophagus	40, 40	0	0	0.00	1.37	36.50	0.00
Heart Clontech	40, 40	0	0	0.00	1.32	37.88	0.00
Hypothalamus	40, 40	0	0	0.00	0.32	155.28	0.00
Ileum	40, 40	0	0	0.00	2.58	19.38	0.00
Jejunum	36.53, 33.22	4.38	28.28	16.33	6.60	7.58	123.71

Kidney	32.81, 32.45	35.74	43.67	39.71	2.12	23.58	936.44
Liver	35.92, 36.2	6.19	5.29	5.74	1.50	33.33	191.33
Fetal Liver Clontech	31.57, 30.46	71.69	134.34	103.02	10.40	4.81	495.26
Lung	33.35, 36.86	26.32	3.65	14.99	2.57	19.46	291.54
Mammary Gland Clontech	32.99, 32.17	32.23	51.27	41.75	13.00	3.85	160.58
Myometrium	34.99, 40	10.44	0	5.22	2.34	21.37	111.54
Omentum	35.61, 40	7.37	0	3.69	3.94	12.69	46.76
Ovary	35.83, 35.54	6.53	7.67	7.10	4.34	11.52	81.80
Pancreas	35.86, 40	6.39	0	3.20	0.81	61.80	197.47
Head of Pancreas	40, 40	0	0	0.00	1.57	31.85	0.00
Parotid Gland	34.26, 34.03	15.73	17.96	16.85	5.48	9.12	153.70
Placenta Clontech	32.64, 33.16	39.34	29.26	34.30	5.26	9.51	326.05
Prostate	35.71, 40	6.95	0	3.48	3.00	16.67	57.92
Rectum	33.84, 34.42	19.99	14.41	17.20	1.23	40.65	699.19
Salivary Gland Clontech	40, 40	0	0	0.00	7.31	6.84	0.00
Skeletal Muscle Clontech	34.2, 40	16.33	0	8.17	1.26	39.68	324.01
Skin	35.02, 40	10.31	0.48	5.40	1.21	41.32	222.93
Small Intestine Clontech	40, 40	0	0	0.29	0.98	51.07	14.81
Spleen	40, 35.31	0	8.71	4.36	4.92	10.16	44.26
Stomach	40, 35.4	0	8.3	4.15	2.73	18.32	76.01
Testis Clontech	40, 37.31	0	2.82	1.41	0.57	87.87	123.90
Thymus Clontech	30.9, 31.1	104.45	93.52	98.99	9.89	5.06	500.43
Thyroid	31.62, 31.57	69.89	71.93	70.91	2.77	18.05	1279.96
Trachea Clontech	34.19, 34.08	16.41	17.49	16 95	9.71	5.15	87.28
Urinary Bladder	40, 34.4	0	14.55	7.28	5.47	9.14	66.50
Uterus	30.63, 30.6	122.13	123.57	122.85	5.34	9.36	1150.28
genomic	26.58	1190.6					
b-actin	27.38	758.43					
1.00E+05	19.07	100000					
1.00E+05	19.35	100000					
1.00E+04	22.57	10000					
1.00E+04	22.59	10000					
1.00E+03	26.24	1000					
1.00E+03	26.31	1000					
1.00E+02	30.18	100					
1.00E+02	31.64	100					
1.00E+01	35.9	10					
1.00E+01	40	0					
1.00E-00	40	0					
1.00E-00	40	0					
NTC	40	0					
NTC	40	0					

Sample sbg1018172CSP	**Reg number**	**Ct**	**Mean GOI**	**copies of mRNA**	**Sample**	**Fold Change**

	(GSK identifier)		copies	detected/ 50 ng total RNA		in Disease Population
colon normal GW98-167	21941	27.29	1064.89	2129.78	colon normal	
colon tumor GW98-166	21940	26.18	2023.11	4046.22	colon tumor	1.90
colon normal GW98-178	22080	30.45	168.68	337.36	colon normal	
colon tumor GW98-177	22060	29.33	324.49	648.98	colon tumor	1.92
colon normal GW98-561	23514	30.36	177.62	355.24	colon normal	
colon tumor GW98-560	23513	32.27	58.7	117.40	colon tumor	-3.03
colon normal GW98-894	24691	30.71	145.57	291.14	colon normal	
colon tumor GW98-893	24690	32.3	57.43	114.86	colon tumor	-2.53
lung normal GW98-3	20742	24.82	4478.67	8957.34	lung normal	
lung tumor GW98-2	20741	33.61	26.86	53.72	lung tumor	-166.74
lung normal GW97-179	20677	26.31	1874.25	3748.50	lung normal	
lung tumor GW97-178	20676	24.52	5311.72	10623.44	lung tumor	2.83
lung normal GW98-165	21922	24.99	4042.28	8084.56	lung normal	
lung tumor GW98-164	21921	27.19	1127.26	2254.52	lung tumor	-3.59
lung normal GW98-282	22584	25.51	2990.53	5981.06	lung normal	
lung tumor GW98-281	22583	26.67	1522.51	3045.02	lung tumor	-1.96
breast normal GW00-392	28750	32.25	59.17	59.17	breast normal	
breast tumor GW00-391	28746	30.48	165.82	331.64	breast tumor	5.60
breast normal GW00-413	28798	34.58	15.31	15.31	breast normal	
breast tumor GW00-412	28797	30.05	213.4	426.80	breast tumor	27.88
breast normal GW00-235:238	27592-95	34.41	16.85	16.85	breast normal	
breast tumor GW00-231:234	27588-91	33.52	28.31	28.31	breast tumor	1.68
breast normal GW98-621	23656	28.22	618.19	1236.38	breast normal	
breast tumor GW98-620	23655	32.02	67.94	135.88	breast tumor	-9.10
brain normal BB99-542	25507	29.11	367.88	735.76	brain normal	
brain normal BB99-406	25509	28.05	682.39	1364.78	brain normal	
brain normal BB99-904	25546	29.06	379.07	758.14	brain normal	
brain stage 5 ALZ BB99-874	25502	30.06	211.81	423.62	brain stage 5 ALZ	-2.25
brain stage 5 ALZ BB99-887	25503	26.97	1280.13	2560.26	brain stage 5 ALZ	2.69
brain stage 5 ALZ BB99-862	25504	29.85	239.03	478.06	brain stage 5 ALZ	-1.99
brain stage 5 ALZ BB99-927	25542	28.13	652.56	1305.12	brain stage 5 ALZ	1.37
CT lung	normal	26.97	1280.81	2561.62	CT lung Nml	
lung 26	normal	32.21	60.75		lung 26 Nml	
lung 27	normal	34	21.39	21.39	lung 27 Nml	
lung 24	COPD	32.11	64.11	64.11	lung 24 COPD	-13.87
lung 28	COPD	33.01	38.18	38.18	lung 28 COPD	-23.29
lung 23	COPD	32.84	42.15	42.15	lung 23 COPD	-21.10
lung 25	normal	31.63	84.78	84.78	lung 25 Nml	
asthmatic lung ODO3112	29321	29.4	310.75	310.75	asthmatic lung	-2.86
asthmatic lung ODO3433	29323	27.02	1242.79	2485.58	asthmatic lung	2.80

asthmatic lung ODO3397	29322	25.97	2289.74	4579.48	asthmatic lung	5.15
asthmatic lung ODO4928	29325	26.84	1380.5	2761.00	asthmatic lung	3.10
endo cells	control	40	0	0.00	endo cells	
endo VEGF		40	0	0.00	endo VEGF	0.00
endo bFGF		40	1.01	1.01	endo bFGF	1.01
heart Clontech	normal	33.02	37.93	75.86	heart	
heart (T-1) ischemic	29417	34.34	17.51	35.02	heart (T-1) ischemic	-2.17
heart (T-14) non-obstructive DCM	29422	34.85	13.07	26.14	heart (T-14) non-obstructive DCM	-2.90
heart (T-3399) DCM	29426	29.74	254.69	509.38	heart (T-3399) DCM	6.71
adenoid GW99-269	26162	35.07	11.5	23.00	adenoid	
tonsil GW98-280	22582	40	0	0.00	tonsil	
T cells PC00314	28453	36.12	6.22	12.44	T cells	
PBMNC		40	0	0.00	PBMNC	
monocyte		40	0	0.00	monocyte	
B cells PC00665	28455	40	0	0.00	B cells	
dendritic cells	28441	40	0	0.00	dendritic cells	
neutrophils	28440	35.43	9.3	9.30	neutrophils	
eosinophils	28446	40	1.32	2.64	eosinophils	
BM unstim		40	0	0.00	BM unstim	
BM stim	treated	40	0	0.00	BM stim	0.00
osteo dif	treated	40	0	0.00	osteo dif	0.00
osteo undif		40	0	0.00	osteo undif	
chondrocytes		33.23	33.49	83.73	chondrocytes	
OA Synovium IP12/01	29462	34.9	12.68	12.68	OA Synovium	
OA Synovium NP10/01	29461	28.55	510.63	1021.26	OA Synovium	
OA Synovium NP57/00	28464	34	21.41	42.82	OA Synovium	
RA Synovium NP03/01	28466	40	0	0.00	RA Synovium	
RA Synovium NP71/00	28467	36.2	5.96	11.92	RA Synovium	
RA Synovium NP45/00	28475	36.38	5.34	10.68	RA Synovium	
OA bone (biobank)	29217	35.58	8.52	8.52	OA bone (biobank)	
OA bone Sample 1	J. Emory	33.54	27.91	55.82	OA bone	
OA bone Sample 2	J. Emory	34.92	12.54	25.08	OA bone	
Cartilage (pool)	Normal	33.88	22.98	45.96	Nml Cartilage (pool)	
Cartilage (pool)	OA	40	0	0.00	OA Cartilage (pool)	-45.96
PBL unifected	28441	30.74	142.65	285.30	PBL unifected	
PBL HIV IIIB	28442	32.47	52.13	104.26	PBL HIV IIIB	-2.74
MRC5 uninfected (100%)	29158	40	0	0.00	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	30.06	211.88	423.76	MRC5 HSV strain F	423.76
W12 cells	29179	39.65	0.8	1.60	W12 cells	
Keratinocytes	29180	33.76	24.58	49.16	Keratinocytes	
B-actin control		27.17	1140.82			
genomic		26.81	1405.46			

1.00E+05		19.68	100000			
1.00E+05		19.63	100000			
1.00E+04		23.15	10000			
1.00E+04		23.27	10000			
1.00E+03		27.1	1000			
1.00E+03		27.33	1000			
1.00E+02		31.34	100			
1.00E+02		32.04	100			
1.00E+01		35.09	10			
1.00E+01		40	10			
1.00E-00		40	0			
1.00E-00		40	0			
NTC		40	0			
*lung 26 Normal has been omitted due to multiple amplification failures from that sample						

Gene Name sbg1018172CSP

Disease tissues	**Fold Change in Disease Population Relative to Normal**
colon tumor	1.90
colon tumor	1.92
colon tumor	-3.03
colon tumor	-2.53
lung tumor	-166.74
lung tumor	2.83
lung tumor	-3.59
lung tumor	-1.96
breast tumor	5.60
breast tumor	27.88
breast tumor	1.68
breast tumor	-9.10
brain stage 5 ALZ	-2.25
brain stage 5 ALZ	2.69
brain stage 5 ALZ	-1.99
brain stage 5 ALZ	1.37
lung 24	-13.87
lung 28	-23.29
lung 23	-21.10
asthmatic lung	-2.86
asthmatic lung	2.80
asthmatic lung	5.15
asthmatic lung	3.10
endo VEGF	0.00
endo bFGF	1.01
heart T-1	-2.17
heart T-14	-2.90
heart T-3399	6.71
BM stim	0.00
osteo dif	0.00
Cartilage (pool)	-45.96

PBL HIV IIIB	-2.74
MRC5 HSV strain F	423.76

Gene Name sbg1004570ERGIC

Moderate to low overall expression. This gene is expressed fairly ubiquitously in all normal samples analyzed with highest levels of expression seen in the whole brain, hypothalamus, pancreas, and head of pancreas. This pattern of expression suggests that this gene may be involved in diabetes or other metabolic diseases. Highest disease expression is seen in the colon, breast, and lung normal/tumor pairs as well as the Alzheimer's brain samples and the T cells, B cells, dendritic cells, and eosinophils. Upregulation in 2 of 4 breast tumor samples suggests a role for this gene in breast cancer. Upregulation in 2 of 4 Alzheimer's brain samples implies an involvement in Alzheimer's disease. Downregulation in 3 of 3 COPD samples and 4 of 4 asthmatic lung samples suggests a potential role for this gene in chronic obstructive pulmonary disorder and asthma. Upregulated in the stimulated bone marrow sample.

Sample sbg1004570ERGIC	**Ct (sample 1 and 2)**	**Mean GOI copies (sample 1)**	**Mean GOI copies (sample 2)**	**Average GOI Copies**	**18S rRNA (ng)**	**50 ng/18S rRNA (ng)**	**copies of mRNA detected/50 ng total RNA**
Subcutaneous Adipocytes Zenbio	40, 40	0	0	0.00	3.06	16.34	0.00
Subcutaneous Adipose Zenbio	39.46, 35.22	0.08	1.37	0.73	0.96	52.36	37.96
Adrenal Gland Clontech	36.91, 36.21	0.43	0.7	0.57	0.61	81.97	46.31
Whole Brain Clontech	26.46, 30.31	547.02	39.49	293.26	7.24	6.91	2025.24
Fetal Brain Clontech	36.04, 36.66	0.78	0.51	0.65	0.48	103.95	67.05
Cerebellum Clontech	35.46, 34.63	1.16	2.06	1.61	2.17	23.04	37.10
Cervix	35.63, 36.28	1.04	0.67	0.86	2.42	20.66	17.67
Colon	35.38, 34.57	1.23	2.13	1.68	2.71	18.45	31.00
Endometrium	40, 35.24	0.06	1.35	0.71	0.73	68.21	48.09
Esophagus	35.02, 36.31	1.57	0.65	1.11	1.37	36.50	40.51
Heart Clontech	37.16, 35.48	0.36	1.15	0.76	1.32	37.88	28.60
Hypothalamus	35.15, 36.01	1.44	0.8	1.12	0.32	155.28	173.91
Ileum	35.04, 35.5	1.55	1.13	1.34	2.58	19.38	25.97
Jejunum	35.14, 34.88	1.45	1.73	1.59	6.60	7.58	12.05
Kidney	35.81, 37.16	0.91	0.36	0.64	2.12	23.58	14.98
Liver	36.19, 34.39	0.71	2.42	1.57	1.50	33.33	52.17
Fetal Liver Clontech	32.94, 33.1	6.51	5.85	6.18	10.40	4.81	29.71
Lung	34.54, 35.16	2.18	1.43	1.81	2.57	19.46	35.12
Mammary Gland Clontech	34.45, 34.76	2.33	1.88	2.11	13.00	3.85	8.10
Myometrium	34.08, 34.61	2.98	2.09	2.54	2.34	21.37	54.17
Omentum	35.22, 36.18	1.37	0.71	1.04	3.94	12.69	13.20
Ovary	34.52, 34.83	2.21	1.78	2.00	4.34	11.52	22.98
Pancreas	34.45, 33.99	2.32	3.18	2.75	0.81	61.80	169.96
Head of Pancreas	33.24, 33.63	5.32	4.06	4.69	1.57	31.85	149.36
Parotid Gland	33.22, 33.08	5.38	5.9	5.64	5.48	9.12	51.46
Placenta Clontech	36.02, 35.39	0.79	1.22	1.01	5.26	9.51	9.55

Prostate	35.98, 35.07	0.81	1.51	1.16	3.00	16.67	19.33
Rectum	36.71, 37.13	0.49	0.37	0.43	1.23	40.65	17.48
Salivary Gland Clontech	33.51, 34.22	4.41	2.71	3.56	7.31	6.84	24.35
Skeletal Muscle Clontech	35.53, 34.52	1.11	2.21	1.66	1.26	39.68	65.87
Skin	36.02, 36.07	0.79	0.77	0.78	1.21	41.32	32.23
Small Intestine Clontech	35.02, 37.21	1.57	0.35	0.96	0.98	51.07	49.03
Spleen	35.64, 35.27	1.03	1.33	1.18	4.92	10.16	11.99
Stomach	35.08, 35.41	1.51	1.2	1.36	2.73	18.32	24.82
Testis Clontech	35.48, 38.1	1.15	0.19	0.67	0.57	87.87	58.88
Thymus Clontech	32.15, 31.72	11.16	14.98	13.07	9.89	5.06	66.08
Thyroid	35.61, 35.09	1.05	1.49	1.27	2.77	18.05	22.92
Trachea Clontech	35.04, 34.75	1.55	1.89	1.72	9.71	5.15	8.86
Urinary Bladder	36.11, 36.24	0.74	0.68	0.71	5.47	9.14	6.49
Uterus	35.59, 35.68	1.06	1	1.03	5.34	9.36	9.64
genomic	24.29	2416.83					
b-actin	26.09	706.6					
1.00E+05	20.09	100000					
1.00E+05	19.53	100000					
1.00E+04	21.72	10000					
1.00E+04	21.68	10000					
1.00E+03	24.13	1000					
1.00E+03	24.18	1000					
1.00E+02	29.13	100					
1.00E+02	30.16	100					
1.00E+01	31.7	10					
1.00E+01	33.16	10					
1.00E-00	36.93	1					
1.00E-00	34.75	1					
NTC	36	-1					
NTC	35.85	-1					

Sample sbg1004570ERGIC	**Reg number (GSK identifier)**	**Ct**	**Mean GOI copies**	**copies of mRNA detected/50 ng total RNA**	**Sample**	**Fold Change in Disease Population**
colon normal GW98-167	21941	30.51	38.25	76.50	colon normal	
colon tumor GW98-166	21940	31.28	23.13	46.26	colon tumor	-1.65
colon normal GW98-178	22080	31.79	16.57	33.14	colon normal	
colon tumor GW98-177	22060	31.3	22.86	45.72	colon tumor	1.38
colon normal GW98-561	23514	30.71	33.5	67.00	colon normal	
colon tumor GW98-560	23513	31.18	24.73	49.46	colon tumor	-1.35
colon normal GW98-894	24691	30.16	48.2	96.40	colon normal	
colon tumor GW98-893	24690	29.96	55	110.00	colon tumor	1.14
lung normal GW98-3	20742	30.1	50.19	100.38	lung normal	
lung tumor GW98-2	20741	32.86	8.15	16.30	lung tumor	-6.16

lung normal GW97-179	20677	31.65	18.14	36.28	lung normal	
lung tumor GW97-178	20676	31.05	26.89	53.78	lung tumor	1.48
lung normal GW98-165	21922	30.44	40.16	80.32	lung normal	
lung tumor GW98-164	21921	30.72	33.36	66.72	lung tumor	-1.20
lung normal GW98-282	22584	31.83	16.13	32.26	lung normal	
lung tumor GW98-281	22583	32.09	13.61	27.22	lung tumor	-1.19
breast normal GW00-392	28750	32.76	8.73	8.73	breast normal	
breast tumor GW00-391	28746	30.68	34.38	68.76	breast tumor	7.88
breast normal GW00-413	28798	37.11	0.5	0.50	breast normal	
breast tumor GW00-412	28797	30.8	31.72	63.44	breast tumor	126.88
breast normal GW00-235:238	27592-95	38.8	0.17	0.17	breast normal	
breast tumor GW00-231:234	27588-91	37.36	0.43	0.43	breast tumor	2.53
breast normal GW98-621	23656	31.67	17.86	35.72	breast normal	
breast tumor GW98-620	23655	32.59	9.8	19.60	breast tumor	-1.82
brain normal BB99-542	25507	33.66	4.83	9.66	brain normal	
brain normal BB99-406	25509	33.24	6.37	12.74	brain normal	
brain normal BB99-904	25546	33.2	6.54	13.08	brain normal	
brain stage 5 ALZ BB99-874	25502	33.1	6.97	13.94	brain stage 5 ALZ	1.18
brain stage 5 ALZ BB99-887	25503	30.93	29.17	58.34	brain stage 5 ALZ	4.93
brain stage 5 ALZ BB99-862	25504	31.44	20.73	41.46	brain stage 5 ALZ	3.51
brain stage 5 ALZ BB99-927	25542	32.93	7.83	15.66	brain stage 5 ALZ	1.32
CT lung	normal	32.62	9.6	19.20	CT lung Nml	
lung 26	normal				lung 26 Nml	
lung 27	normal	40	0	0.00	lung 27 Nml	
lung 24	COPD	39.15	0.13	0.13	lung 24 COPD	-49.46
lung 28	COPD	40	0.08	0.08	lung 28 COPD	-80.38
lung 23	COPD	38.59	0.19	0.19	lung 23 COPD	-33.84
lung 25	normal	40	0.09	0.09	lung 25 Nml	
asthmatic lung ODO3112	29321	40	0	0.00	asthmatic lung	-6.43
asthmatic lung ODO3433	29323	38.47	0.2	0.40	asthmatic lung	-16.08
asthmatic lung ODO3397	29322	38.01	0.28	0.56	asthmatic lung	-11.48
asthmatic lung ODO4928	29325	38.13	0.26	0.52	asthmatic lung	-12.37
endo cells	control	36.24	0.89	0.89	endo cells	
endo VEGF		39.8	0.09	0.09	endo VEGF	-9.89
endo bFGF		37.19	0.47	0.47	endo bFGF	-1.89
heart Clontech	normal	35.52	1.43	2.86	heart	
heart (T-1) ischemic	29417	33.79	4.43	8.86	heart (T-1) ischemic	3.10
heart (T-14) non-obstructive DCM	29422	34.81	2.27	4.54	heart (T-14) non-obstructive DCM	1.59
heart (T-3399) DCM	29426	34.11	3.59	7.18	heart (T-3399) DCM	2.51
adenoid GW99-269	26162	34.97	2.05	4.10	adenoid	
tonsil GW98-280	22582	33.05	7.23	14.46	tonsil	

T cells PC00314	28453	31.09	26.2	52.40	T cells	
PBMNC		38.01	0.28	0.28	PBMNC	
monocyte		36.29	0.86	1.72	monocyte	
B cells PC00665	28455	32.13	13.23	26.46	B cells	
dendritic cells	28441	31.94	14.96	29.92	dendritic cells	
neutrophils	28440	34.08	3.66	3.66	neutrophils	
eosinophils	28446	32.23	12.37	24.74	eosinophils	
BM unstim		39.73	0.09	0.09	BM unstim	
BM stim	treated	37.03	0.53	0.53	BM stim	5.89
osteo dif	treated	36.8	0.61	0.61	osteo dif	0.61
osteo undif		40	0	0.00	osteo undif	
chondrocytes		31.85	15.9	39.75	chondrocytes	
OA Synovium IP12/01	29462	38.61	0.19	0.19	OA Synovium	
OA Synovium NP10/01	29461	33.11	6.96	13.92	OA Synovium	
OA Synovium NP57/00	28464	33.81	4.39	8.78	OA Synovium	
RA Synovium NP03/01	28466	33.11	6.96	13.92	RA Synovium	
RA Synovium NP71/00	28467	32.03	14.14	28.28	RA Synovium	
RA Synovium NP45/00	28475	32.47	10.55	21.10	RA Synovium	
OA bone (biobank)	29217	35.25	1.7	1.70	OA bone (biobank)	
OA bone Sample 1	J. Emory	34.54	2.72	5.44	OA bone	
OA bone Sample 2	J. Emory	36.28	0.87	1.74	OA bone	
Cartilage (pool)	Normal	35.24	1.71	3.42	Nml Cartilage (pool)	
Cartilage (pool)	OA	34.45	2.87	5.74	OA Cartilage (pool)	1.68
PBL unifected	28441	32.53	10.19	20.38	PBL unifected	
PBL HIV IIIB	28442	31.77	16.79	33.58	PBL HIV IIIB	1.65
MRC5 uninfected (100%)	29158	33.12	6.87	13.74	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	33.76	4.54	9.08	MRC5 HSV strain F	-1.51
W12 cells	29179	33.1	6.96	13.92	W12 cells	
Keratinocytes	29180	32.67	9.29	18.58	Keratinocytes	
B-actin control		26.03	726.55			
genomic		24.63	1825.58			
1.00E+05		19.96	100000			
1.00E+05		19.27	100000			
1.00E+04		21.83	10000			
1.00E+04		21.45	10000			
1.00E+03		23.86	1000			
1.00E+03		23.84	1000			
1.00E+02		28.42	100			
1.00E+02		29.35	100			
1.00E+01		33.3	10			
1.00E+01		35.09	10			
1.00E-00		35.16	1			
1.00E-00		36.05	1			
NTC		38.24	-1			
*lung 26 Normal has						

been omitted due to multiple amplification failures from that sample						

Gene Name sbg1004570ERGIC

Disease tissues	**Fold Change in Disease Population Relative to Normal**
colon tumor	-1.65
colon tumor	1.38
colon tumor	-1.35
colon tumor	1.14
lung tumor	-6.16
lung tumor	1.48
lung tumor	-1.20
lung tumor	-1.19
breast tumor	7.88
breast tumor	126.88
breast tumor	2.53
breast tumor	-1.82
brain stage 5 ALZ	1.18
brain stage 5 ALZ	4.93
brain stage 5 ALZ	3.51
brain stage 5 ALZ	1.32
lung 24	-49.46
lung 28	-80.38
lung 23	-33.84
asthmatic lung	-6.43
asthmatic lung	-16.08
asthmatic lung	-11.48
asthmatic lung	-12.37
endo VEGF	-9.89
endo bFGF	-1.89
heart T-1	3.10
heart T-14	1.59
heart T-3399	2.51
BM stim	5.89
osteo dif	0.61
Cartilage (pool)	1.68
PBL HIV IIIB	1.65
MRC5 HSV strain F	-1.51

Gene Name sbg1016995IGBrecpt

Moderate to low overall expression. Highest normal expression is seen in the whole brain in lung with slightly lower levels of expression in the endometrium, ileum, rectum, and skin. High level of expression in the skin may suggest a possible role for this gene in psoriasis and Lupus. The patterns of expression in the samples on the disease plate indicate that this gene is highly specific to the adenoid and tonsil. Downregulation in 2 of 4 lung tumor samples and upregulation in 2 of 4 breast tumor samples suggests an involvement in cancers of the lung and breast. Downregulation in 3 of 3 COPD samples suggests a potential role for this gene in chronic obstructive pulmonary disorder. Upregulated in the stimulated bone marrow sample. Downregulated in the differentiated osteoblast. Upregulated in the HIV-infected PBL cells suggests that this gene may be a host factor in HIV.

Sample	**Ct (sample**	**Mean**	**Mean**	**Average**	**18S**	**50**	**copies of**

sbg1016995IGBrecpt	1 and 2)	GOI copies (sample 1)	GOI copies (sample 2)	GOI Copies	rRNA (ng)	ng/18S rRNA (ng)	mRNA detected/ 50 ng total RNA
Subcutaneous Adipocytes Zenbio	40, 40	0.61	0.61	0.61	3.06	16.34	9.97
Subcutaneous Adipose Zenbio	40, 40	0.59	0.56	0.58	0.96	52.36	30.10
Adrenal Gland Clontech	39.89, 39.79	0.54	0.57	0.56	0.61	81.97	45.49
Whole Brain Clontech	30.69, 30.76	108.67	104.35	106.51	7.24	6.91	735.57
Fetal Brain Clontech	39.41, 40	0.71	0.62	0.67	0.48	103.95	69.13
Cerebellum Clontech	39.33, 37.82	0.74	1.78	1.26	2.17	23.04	29.03
Cervix	36.12, 36.58	4.73	3.62	4.18	2.42	20.66	86.26
Colon	35.23, 38.35	7.9	1.31	4.61	2.71	18.45	84.96
Endometrium	35.51, 40	6.73	0	3.37	0.73	68.21	229.54
Esophagus	37.22, 38.18	2.5	1.45	1.98	1.37	36.50	72.08
Heart Clontech	40, 40	0	0	0.00	1.32	37.88	0.00
Hypothalamus	40, 40	0	0	0.00	0.32	155.28	0.00
Ileum	34.65, 34.11	11.04	15.09	13.07	2.58	19.38	253.20
Jejunum	34.84, 34.04	9.91	15.72	12.82	6.60	7.58	97.08
Kidney	38.2, 39.11	1.43	0.84	1.14	2.12	23.58	26.77
Liver	34 47, 38.59	12.26	1.14	6.70	1.50	33.33	223.33
Fetal Liver Clontech	33.51, 33.07	21.26	27.43	24.35	10.40	4.81	117.04
Lung	27.32, 37.11	755.31	2.68	379.00	2.57	19.46	7373.44
Mammary Gland Clontech	36.31, 36.4	4.24	4.03	4.14	13.00	3.85	15.90
Myometrium	40, 38.7	0.7	1.07	0.89	2.34	21.37	18.91
Omentum	35.44, 36.14	6.98	4.68	5.83	3.94	12.69	73.98
Ovary	38.76, 35.49	1.03	6.82	3.93	4.34	11.52	45.22
Pancreas	40, 38.56	0.48	1.16	0.82	0.81	61.80	50.68
Head of Pancreas	40, 40	0	0	0.00	1.57	31.85	0.00
Parotid Gland	36.8, 35.45	3.2	6.98	5.09	5.48	9.12	46.44
Placenta Clontech	35.63, 35.11	6.27	8.47	7.37	5.26	9.51	70.06
Prostate	37.4, 37.5	2.26	2.14	2.20	3.00	16.67	36.67
Rectum	35.45, 35.25	6.94	7.81	7.38	1.23	40.65	299.80
Salivary Gland Clontech	37.3, 37.06	2.4	2.75	2.58	7.31	6.84	17.61
Skeletal Muscle Clontech	40, 39.34	0	0.74	0.37	1.26	39.68	14.68
Skin	38.84, 34.56	0.98	11.63	6.31	1.21	41.32	260.54
Small Intestine Clontech	40, 40	0	0.63	0.32	0.98	51.07	16.09
Spleen	34.37, 34.89	13	9.6	11.30	4.92	10.16	114.84
Stomach	39.73, 35.52	0.59	6.67	3.63	2.73	18.32	66.48
Testis Clontech	38.91, 40	0.94	0	0.47	0.57	87.87	41.30
Thymus Clontech	31.96, 32.96	52.16	29.2	40.68	9.89	5.06	205.66
Thyroid	35.53, 40	6.66	0	3.33	2.77	18.05	60.11
Trachea Clontech	37.99, 37.69	1.61	1.91	1.76	9.71	5.15	9.06

Urinary Bladder	39.69, 39.02	0.6	0.89	0.75	5.47	9.14	6.81
Uterus	34.41, 33.56	12.67	20.75	16.71	5.34	9.36	156.46
genomic	26.31	1359.1					
b-actin	27.2	812.88					
1.00E+05	19.24	100000					
1.00E+05	19.38	100000					
1.00E+04	22.67	10000					
1.00E+04	22.67	10000					
1.00E+03	26.31	1000					
1.00E+03	26.28	1000					
1.00E+02	30.17	100					
1.00E+02	31.02	100					
1.00E+01	36.17	10					
1.00E+01	34.46	10					
1.00E-00	40	0					
1.00E-00	40	1					
NTC	40	-1					
NTC	40	-1					

Sample sbg1016995IGBrecpt	**Reg number (GSK identifier)**	**Ct**	**Mean GOI copies**	**copies of mRNA detected/50 ng total RNA**	**Sample**	**Fold Change in Disease Population**
colon normal GW98-167	21941	29.45	174.86	349.72	colon normal	
colon tumor GW98-166	21940	32.1	33.44	66.88	colon tumor	-5.23
colon normal GW98-178	22080	31.77	41.07	82.14	colon normal	
colon tumor GW98-177	22060	32.66	23.5	47.00	colon tumor	-1.75
colon normal GW98-561	23514	29.15	211.24	422.48	colon normal	
colon tumor GW98-560	23513	31.25	56.95	113.90	colon tumor	-3.71
colon normal GW98-894	24691	30.68	81.3	162.60	colon normal	
colon tumor GW98-893	24690	31.33	54.12	108.24	colon tumor	-1.50
lung normal GW98-3	20742	31.86	38.92	77.84	lung normal	
lung tumor GW98-2	20741	34.55	7.25	14.50	lung tumor	-5.37
lung normal GW97-179	20677	28.38	342.07	684.14	lung normal	
lung tumor GW97-178	20676	32.1	33.52	67.04	lung tumor	-10.20
lung normal GW98-165	21922	32.2	31.46	62.92	lung normal	
lung tumor GW98-164	21921	30.5	90.8	181.60	lung tumor	2.89
lung normal GW98-282	22584	29.82	138.8	277.60	lung normal	
lung tumor GW98-281	22583	32.72	22.64	45.28	lung tumor	-6.13
breast normal GW00-392	28750	31.5	48.65	48.65	breast normal	
breast tumor GW00-391	28746	31.9	37.84	75.68	breast tumor	1.56
breast normal GW00-413	28798	34.37	8.07	8.07	breast normal	
breast tumor GW00-412	28797	29.97	126.73	253.46	breast tumor	31.41
breast normal GW00-	27592-95	35.08	5.2	5.20	breast normal	

235:238						
breast tumor GW00-231:234	27588-91	32.3	29.54	29.54	breast tumor	5.68
breast normal GW98-621	23656	31.11	61.96	123.92	breast normal	
breast tumor GW98-620	23655	31.27	56.22	112.44	breast tumor	-1.10
brain normal BB99-542	25507	33.3	15.82	31.64	brain normal	
brain normal BB99-406	25509	33.02	18.83	37.66	brain normal	
brain normal BB99-904	25546	33.93	10.62	21.24	brain normal	
brain stage 5 ALZ BB99-874	25502	32.36	28.38	56.76	brain stage 5 ALZ	1.88
brain stage 5 ALZ BB99-887	25503	31.79	40.66	81.32	brain stage 5 ALZ	2.69
brain stage 5 ALZ BB99-862	25504	32.04	34.76	69.52	brain stage 5 ALZ	2.30
brain stage 5 ALZ BB99-927	25542	31.79	40.51	81.02	brain stage 5 ALZ	2.68
CT lung	normal	33.32	15.63	31.26	CT lung Nml	
lung 26	normal	29.8	140.4		lung 26 Nml	
lung 27	normal	38.71	0.54	0.54	lung 27 Nml	
lung 24	COPD	39.31	0.37	0.37	lung 24 COPD	-29.00
lung 28	COPD	37.09	1.48	1.48	lung 28 COPD	-7.25
lung 23	COPD	38.02	0.83	0.83	lung 23 COPD	-12.93
lung 25	normal	39.22	0.39	0.39	lung 25 Nml	
asthmatic lung ODO3112	29321	37.96	0.86	0.86	asthmatic lung	-12.48
asthmatic lung ODO3433	29323	31.15	60.54	121.08	asthmatic lung	11.28
asthmatic lung ODO3397	29322	33.74	12.01	24.02	asthmatic lung	2.24
asthmatic lung ODO4928	29325	31.59	46.09	92.18	asthmatic lung	8.59
endo cells	control	36.98	1.58	1.58	endo cells	
endo VEGF		39.28	0.38	0.38	endo VEGF	-4.16
endo bFGF		37.3	1.3	1.30	endo bFGF	-1.22
heart Clontech	normal	35.73	3.45	6.90	heart	
heart (T-1) ischemic	29417	34.7	6.58	13.16	heart (T-1) ischemic	1.91
heart (T-14) non-obstructive DCM	29422	37.5	1.15	2.30	heart (T-14) non-obstructive DCM	-3.00
heart (T-3399) DCM	29426	35.15	4.96	9.92	heart (T-3399) DCM	1.44
adenoid GW99-269	26162	25.98	1528.07	3056.14	adenoid	
tonsil GW98-280	22582	24.6	3626.43	7252.86	tonsil	
T cells PC00314	28453	34.49	7.5	15.00	T cells	
PBMNC		37.58	1.09	1.09	PBMNC	
monocyte		37.4	1.22	2.44	monocyte	
B cells PC00665	28455	31.68	43.59	87.18	B cells	
dendritic cells	28441	35.05	5.28	10.56	dendritic cells	
neutrophils	28440	35.68	3.57	3.57	neutrophils	
eosinophils	28446	35.07	5.23	10.46	eosinophils	
BM unstim		38.19	0.75	0.75	BM unstim	
BM stim	treated	34.27	8.61	8.61	BM stim	11.48
osteo dif	treated	40	0.09	0.09	osteo dif	-5.78
osteo undif		40	0.52	0.52	osteo undif	

chondrocytes		32.86	20.79	51.98	chondrocytes	
OA Synovium IP12/01	29462	31.85	38.99	38.99	OA Synovium	
OA Synovium NP10/01	29461	34.76	6.33	12.66	OA Synovium	
OA Synovium NP57/00	28464	31.39	51.96	103.92	OA Synovium	
RA Synovium NP03/01	28466	31.1	62.3	124.60	RA Synovium	
RA Synovium NP71/00	28467	31.95	36.76	73.52	RA Synovium	
RA Synovium NP45/00	28475	32.43	27.14	54.28	RA Synovium	
OA bone (biobank)	29217	35.84	3.22	3.22	OA bone (biobank)	
OA bone Sample 1	J. Emory	35.43	4.18	8.36	OA bone	
OA bone Sample 2	J. Emory	34.86	5.95	11.90	OA bone	
Cartilage (pool)	Normal	34.79	6.21	12.42	Nml Cartilage (pool)	
Cartilage (pool)	OA	36.55	2.07	4.14	OA Cartilage (pool)	-3.00
PBL unifected	28441	30.02	122.76	245.52	PBL unifected	
PBL HIV IIIB	28442	28.17	388.59	777.18	PBL HIV IIIB	3.17
MRC5 uninfected (100%)	29158	34.6	7.01	14.02	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	33.27	16.13	32.26	MRC5 HSV strain F	2.30
W12 cells	29179	34.43	7.8	15.60	W12 cells	
Keratinocytes	29180	35.04	5.31	10.62	Keratinocytes	
B-actin control		27	808.77			
genomic		26.18	1353.11			
1.00E+05		19.37	100000			
1.00E+05		19.59	100000			
1.00E+04		22.75	10000			
1.00E+04		22.8	10000			
1.00E+03		26.43	1000			
1.00E+03		26.17	1000			
1.00E+02		30.09	100			
1.00E+02		30.21	100			
1.00E+01		35.27	10			
1.00E+01		35.55	10			
1.00E-00		39.31	1			
1.00E-00		34.53	1			
NTC		40	-1			
*lung 26 Normal has been omitted due to multiple amplification failures from that sample						

Gene Name sbg1016995IGBrecpt

Disease tissues	**Fold Change in Disease Population Relative to Normal**
colon tumor	-5.23
colon tumor	-1.75
colon tumor	-3.71
colon tumor	-1.50

lung tumor	-5.37
lung tumor	-10.20
lung tumor	2.89
lung tumor	-6.13
breast tumor	1.56
breast tumor	31.41
breast tumor	5.68
breast tumor	-1.10
brain stage 5 ALZ	1.88
brain stage 5 ALZ	2.69
brain stage 5 ALZ	2.30
brain stage 5 ALZ	2.68
lung 24	-29.00
lung 28	-7.25
lung 23	-12.93
asthmatic lung	-12.48
asthmatic lung	11.28
asthmatic lung	2.24
asthmatic lung	8.59
endo VEGF	-4.16
endo bFGF	-1.22
heart T-1	1.91
heart T-14	-3.00
heart T-3399	1.44
BM stim	11.48
osteo dif	-5.78
Cartilage (pool)	-3.00
PBL HIV IIIB	3.17
MRC5 HSV strain F	2.30

Gene Name sbg1151bSREC

Highest overall expression in normal and disease samples. Fairly ubiquitously expressed but highest normal expression in adipocytes, adipose, whole brain, fetal brain, and endometrium. Highest disease expression in one of the colon tumor samples, one of the normal lung samples, chondrocytes, and the uninfected MRC5. There are no significant changes in brains from patients with Alzheimer's disease. Downregulation in 1 of 4 lung tumors suggests possible implication in lung cancer. Upregulation in 1 of 4 breast tumor samples is sufficient to claim a role in cancer of the breast. Upregulation in 1 of 4 asthma lungs implies a role in asthma. Downregulation in HSV implicates involvement in herpes simplex virus as a potential host factor. High expression in immune cells. High expression in cartilage and bone samples from patients with OA as well as high expression in chondrocytes possible involvement in osteoarthritis and rheumatoid arthritis. Additionally, the corroborating expression in immune cells (particularly B and T cells) provides additional evidence for a role in RA/OA.

Sample sbg1151bSREC	**Ct (sample 1 and 2)**	**Mean GOI copies (sample 1)**	**Mean GOI copies (sample 2)**	**Average GOI Copies**	**18S rRNA (ng)**	**50 ng/18S rRNA (ng)**	**copies of mRNA detected /50 ng total RNA**
Subcutaneous Adipocytes Zenbio	28.31, 28.35	477.04	466.02	471.53	3.06	16.34	7704.74
Subcutaneous Adipose Zenbio	30.79, 30.22	122.3	166.95	144.63	0.96	52.36	7571.99
Adrenal Gland Clontech	33.96, 33.47	21.39	27.97	24.68	0.61	81.97	2022.95
Whole Brain Clontech	24.07, 23.98	4889.28	5123.8	5006.54	7.24	6.91	34575.55

Fetal Brain Clontech	31.1, 32.29	103.16	53.55	78.36	0.48	103.95	8145.01
Cerebellum Clontech	31.03, 31.99	107.02	63.18	85.10	2.17	23.04	1960.83
Cervix	31.22, 30.06	96.6	182.64	139.62	2.42	20.66	2884.71
Colon	30.68, 30.53	129.52	140.99	135.26	2.71	18.45	2495.48
Endometrium	30.59, 30.44	136.06	147.8	141.93	0.73	68.21	9681.45
Esophagus	33.11, 32.17	34.08	57.32	45.70	1.37	36.50	1667.88
Heart Clontech	33.19, 32.41	32.68	50.11	41.40	1.32	37.88	1567.99
Hypothalamus	34.34, 40	17.4	0	8.70	0.32	155.28	1350.93
Ileum	31.29, 30.13	92.84	174.99	133.92	2.58	19.38	2595.25
Jejunum	29.7, 29.48	221.9	251.05	236.48	6.60	7.58	1791.48
Kidney	31.03, 30.17	107.15	171.45	139.30	2.12	23.58	3285.38
Liver	32.89, 33.16	38.61	33.17	35.89	1.50	33.33	1196.33
Fetal Liver Clontech	28.05, 28.15	550.64	518.95	534.80	10.40	4.81	2571.13
Lung	29.39, 28.63	263.85	398.99	331.42	2.57	19.46	6447.86
Mammary Gland Clontech	27.56, 27.39	717.67	789.94	753.81	13.00	3.85	2899.25
Myometrium	29.08, 28.93	312.86	339.46	326.16	2.34	21.37	6969.23
Omentum	30.72, 29.32	126.7	273.04	199.87	3.94	12.69	2536.42
Ovary	28.89, 28.68	346.91	388.02	367.47	4.34	11.52	4233.47
Pancreas	35.24, 35.75	10.59	8.02	9.31	0.81	61.80	575.09
Head of Pancreas	35.25, 33.21	10.57	32.34	21.46	1.57	31.85	683.28
Parotid Gland	28.46, 27.84	438.62	615.36	526.99	5.48	9.12	4808.30
Placenta Clontech	28.67, 28.66	391.9	393.15	392.53	5.26	9.51	3731.23
Prostate	30.55, 31.46	139.05	84.64	111.85	3.00	16.67	1864.08
Rectum	31.28, 31.43	93.33	85.92	89.63	1.23	40.65	3643.29
Salivary Gland Clontech	31.13, 30.57	101.46	138.16	119.81	7.31	6.84	819.49
Skeletal Muscle Clontech	34.05, 35.24	20.38	10.59	15.49	1.26	39.68	614.48
Skin	31.53, 31.2	81.49	97.36	89.43	1.21	41.32	3695.25
Small Intestine Clontech	34.81, 33.82	13.41	23.18	18.30	0.98	51.07	934.37
Spleen	31.01, 30.44	108.41	147.9	128.16	4.92	10.16	1302.39
Stomach	32.01, 31.1	62.6	102.97	82.79	2.73	18.32	1516.21
Testis Clontech	31.74, 32.29	72.49	53.45	62.97	0.57	87.87	5533.39
Thymus Clontech	28.84, 28.53	356.64	421.44	389.04	9.89	5.06	1966.84
Thyroid	30.12, 30.04	176.76	184.5	180.63	2.77	18.05	3260.47
Trachea Clontech	28.48, 28.38	434.3	459.42	446.86	9.71	5.15	2301.03
Urinary Bladder	29.63, 29.55	230.25	241.15	235.70	5.47	9.14	2154.48
Uterus	28.69, 28.37	387.47	461.07	424.27	5.34	9.36	3972.57
genomic	26.24	1487.44					
b-actin	27.28	839.2					
1.00E+05	18.96	100000					
1.00E+05	19.34	100000					
1.00E+04	22.64	10000					
1.00E+04	22.84	10000					
1.00E+03	26.22	1000					
1.00E+03	26.04	1000					
1.00E+02	31.04	100					

1.00E+02	30.1	100					
1.00E+01	33.33	10					
1.00E+01	39.08	10					
1.00E-00	40	0					
1.00E-00	40	1					
NTC	40	0					
NTC	40	0					

Sample sbg1151bSREC	**Reg number (GSK identifier)**	**Ct**	**Mean GOI copies**	**copies of mRNA detected /50 ng total RNA**	**Sample**	**Fold Change in Disease Population**
colon normal GW98-167	21941	24.55	5357.25	10714.50	colon normal	
colon tumor GW98-166	21940	22.61	19769.94	39539.88	colon tumor	3.69
colon normal GW98-178	22080	26.71	1252.3	2504.60	colon normal	
colon tumor GW98-177	22060	26.13	1854.49	3708.98	colon tumor	1.48
colon normal GW98-561	23514	26.82	1165.06	2330.12	colon normal	
colon tumor GW98-560	23513	25.75	2390.26	4780.52	colon tumor	2.05
colon normal GW98-894	24691	26.06	1948.57	3897.14	colon normal	
colon tumor GW98-893	24690	26.59	1362.55	2725.10	colon tumor	-1.43
lung normal GW98-3	20742	22.77	17753	35506.00	lung normal	
lung tumor GW98-2	20741	26.17	1803.8	3607.60	lung tumor	-9.84
lung normal GW97-179	20677	25.24	3370.88	6741.76	lung normal	
lung tumor GW97-178	20676	24.14	7057.92	14115.84	lung tumor	2.09
lung normal GW98-165	21922	23.87	8442.49	16884.98	lung normal	
lung tumor GW98-164	21921	24.08	7339.83	14679.66	lung tumor	-1.15
lung normal GW98-282	22584	25.51	2804.42	5608.84	lung normal	
lung tumor GW98-281	22583	24.2	6787.31	13574.62	lung tumor	2.42
breast normal GW00-392	28750	25.7	2480.5	2480.50	breast normal	
breast tumor GW00-391	28746	25.77	2364.2	4728.40	breast tumor	1.91
breast normal GW00-413	28798	26.06	1948.1	1948.10	breast normal	
breast tumor GW00-412	28797	27.21	894.11	1788.22	breast tumor	-1.09
breast normal GW00-235:238	27592-95	26.64	1317.83	1317.83	breast normal	
breast tumor GW00-231:234	27588-91	23.91	8225.11	8225.11	breast tumor	6.24
breast normal GW98-621	23656	24.46	5693.73	11387.46	breast normal	
breast tumor GW98-620	23655	23.91	8218.73	16437.46	breast tumor	1.44
brain normal BB99-542	25507	26.39	1553.13	3106.26	brain normal	
brain normal BB99-406	25509	26.63	1325.63	2651.26	brain normal	
brain normal BB99-904	25546	27.05	1001.6	2003.20	brain normal	
brain stage 5 ALZ BB99-874	25502	26.97	1052.15	2104.30	brain stage 5 ALZ	-1.23
brain stage 5 ALZ BB99-887	25503	25.28	3289.99	6579.98	brain stage 5 ALZ	2.54
brain stage 5 ALZ BB99-862	25504	26.24	1725.06	3450.12	brain stage 5 ALZ	1.33
brain stage 5 ALZ BB99-	25542	26.12	1864.26	3728.52	brain stage 5 ALZ	1.44

927						
CT lung KC	normal	24.74	4711.99	9423.98	CT lung	
lung 26 KC	normal	27.78	611.36	611.36	lung 26	
lung 27 KC	normal	28.27	439.19	439.19	lung 27	
lung 24 KC	COPD	26.92	1091.11	1091.11	lung 24	-2.56
lung 28 KC	COPD	26.93	1085.65	1085.65	lung 28	-2.57
lung 23 KC	COPD	27.19	909.68	909.68	lung 23	-3.07
lung 25 KC	normal	27.62	678.79	678.79	lung 25	
asthmatic lung ODO3112	29321	25.33	3173.52	3173.52	asthmatic lung	1.14
asthmatic lung ODO3433	29323	25.36	3106.89	6213.78	asthmatic lung	2.23
asthmatic lung ODO3397	29322	23.81	8809.42	17618.84	asthmatic lung	6.32
asthmatic lung ODO4928	29325	24.76	4649.98	9299.96	asthmatic lung	3.34
endo cells KC	control	26	2021.13	2021.13	endo cells	
endo VEGF KC		25.78	2343.21	2343.21	endo VEGF	1.16
endo bFGF KC		26.7	1264.03	1264.03	endo bFGF	-1.60
heart Clontech	normal	26.62	1330.64	2661.28	heart	
heart (T-1) ischemic	29417	27.07	984.33	1968.66	heart T-1	-1.35
heart (T-14) non-obstructive DCM	29422	26.11	1877.75	3755.50	heart T-14	1.41
heart (T-3399) DCM	29426	26.34	1608.79	3217.58	heart T-3399	1.21
adenoid GW99-269	26162	27.64	670.25	1340.50	adenoid	
tonsil GW98-280	22582	27.61	684.15	1368.30	tonsil	
T cells PC00314	28453	25.95	2098.64	4197.28	T cells	
PBMNC		31.16	63.19	63.19	PBMNC	
monocyte		31.32	56.63	113.26	monocyte	
B cells PC00665	28455	26.34	1609.52	3219.04	B cells	
dendritic cells 28441		28.25	444.68	889.36	dendritic cells	
neutrophils	28440	26.11	1874.13	1874.13	neutrophils	
eosinophils	28446	26.39	1553.82	3107.64	eosinophils	
BM unstim		31.45	51.76	51.76	BM unstim	
BM stim		31.28	58.37	58.37	BM stim	1.13
osteo dif		24.62	5118.74	5118.74	osteo dif	1.70
osteo undif		25.41	3015.6	3015.60	osteo undif	
chondrocytes		22.12	27351.89	68379.73	chondrocytes	
OA Synovium IP12/01	29462	24.5	5551.61	5551.61	OA Synovium	
OA Synovium NP10/01	29461	25.1	3711.29	7422.58	OA Synovium	
OA Synovium NP57/00	28464	24.5	5537.1	11074.20	OA Synovium	
RA Synovium NP03/01	28466	26.45	1492.95	2985.90	RA Synovium	
RA Synovium NP71/00	28467	24.44	5783.96	11567.92	RA Synovium	
RA Synovium NP45/00	28475	25.94	2112.54	4225.08	RA Synovium	
OA bone (biobank)	29217	26.16	1811.72	1811.72	OA bone (biobank)	
OA bone Sample 1	J. Emory	24.54	5399.31	10798.62	OA bone	
OA bone Sample 2	J. Emory	26.07	1931.94	3863.88	OA bone	
Cartilage (pool)	Normal	25.09	3730.42	7460.84	Cartilage (pool)	
Cartilage (pool)	OA	25.79	2328.66	4657.32	Cartilage (pool)	-1.60
PBL unifected	28441	26.95	1068.16	2136.32	PBL unifected	
PBL HIV IIIB	28442	28.41	401.86	803.72	PBL HIV IIIB	-2.66

MRC5 uninfected (100%)	29158	22.28	24694.87	49389.74	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	29.07	256.64	513.28	MRC5 HSV strain F	-96.22
W12 cells	29179	28.37	410.68	821.36	W12 cells	
Keratinocytes	29180	29.12	249.25	498.50	Keratinocytes	
B-actin control		27.53	721.15			
genomic		26.92	1091.74			
1.00E+05		19.96	100000			
1.00E+05		20.19	100000			
1.00E+04		23.43	10000			
1.00E+04		23.34	10000			
1.00E+03		26.64	1000			
1.00E+03		26.8	1000			
1.00E+02		31.34	100			
1.00E+02		31.48	100			
1.00E+01		34.9	10			
1.00E+01		34.19	10			
1.00E-00		40	0			
1.00E-00		35.53	1			
NTC		40	0			

Gene Name sbg1151bSREC

Disease tissues	**Fold Change in Disease Population Relative to Normal**
colon tumor	3.69
colon tumor	1.48
colon tumor	2.05
colon tumor	-1.43
lung tumor	-9.84
lung tumor	2.09
lung tumor	-1.15
lung tumor	2.42
breast tumor	1.91
breast tumor	-1.09
breast tumor	6.24
breast tumor	1.44
brain stage 5 ALZ	-1.23
brain stage 5 ALZ	2.54
brain stage 5 ALZ	1.33
brain stage 5 ALZ	1.44
lung 24	-2.56
lung 28	-2.57
lung 23	-3.07
asthmatic lung	1.14
asthmatic lung	2.23
asthmatic lung	6.32
asthmatic lung	3.34
endo VEGF	1.16
endo bFGF	-1.60
heart T-1	-1.35

heart T-14	1.41
heart T-3399	1.21
BM stim	1.13
osteo dif	1.70
Cartilage (pool)	-1.60
PBL HIV IIIB	-2.66
MRC5 HSV strain F	-96.22

Gene Name sbg1399854ANK

Low overall expression. Highest normal expression is seen in the whole brain, fetal brain, and liver. Good levels of expression are seen in all of the samples representing the female reproductive system. Highest disease expression is seen in the normal and Alzheimer's brain samples as well as in the dendritic cells. Upregulation in 2 of 4 colon tumor samples and in 2 of 4 breast tumor samples as well as downregulation in 2 of 4 lung tumor samples implicates this gene in cancers of the colon, breast, and lung. Downregulation in 3 of 3 COPD samples and in 2 of 4 asthmatic lung samples suggests a potential role for this gene in chronic obstructive pulmonary disorder and asthma. Downregulation in the OA cartilage sample as well as corroborating low expression in the normal chondrocytes and many of the immune cells suggests involvement in osteoarthritis. Upregulation in the HSV-infected MRC5 cells suggests that this gene may be a host factor in HSV.

Sample sbg1399854ANK	**Ct (sample 1 and 2)**	**Mean GOI copies (sample 1)**	**Mean GOI copies (sample 2)**	**Average GOI Copies**	**18S rRNA (ng)**	**50 ng/18S rRNA (ng)**	**copies of mRNA detected/50 ng total RNA**
Subcutaneous Adipocytes Zenbio	40, 40	0	0	0.00	3.06	16.34	0.00
Subcutaneous Adipose Zenbio	40, 40	1.83	1.77	1.80	0.96	52.36	94.24
Adrenal Gland Clontech	40, 40	1.75	0	0.88	0.61	81.97	71.72
Whole Brain Clontech	28.57, 28.35	944.29	1058.09	1001.19	7.24	6.91	6914.30
Fetal Brain Clontech	36.57, 34.65	14.38	39.28	26.83	0.48	103.95	2788.98
Cerebellum Clontech	37.21, 36.71	10.3	13.37	11.84	2.17	23.04	272.70
Cervix	36.3, 40	16.52	0	8.26	2.42	20.66	170.66
Colon	36.17, 35.71	17.73	22.5	20.12	2.71	18.45	371.13
Endometrium	40, 36.1	0	18.41	9.21	0.73	68.21	627.90
Esophagus	40, 40	0	1.58	0.79	1.37	36.50	28.83
Heart Clontech	40, 40	0	0	0.00	1.32	37.88	0.00
Hypothalamus	40, 40	0	0	0.00	0.32	155.28	0.00
Ileum	40, 40	0	0	0.00	2.58	19.38	0.00
Jejunum	34.07, 34.37	53.18	45.33	49.26	6.60	7.58	373.14
Kidney	37.55, 40	8.58	0	4.29	2.12	23.58	101.18
Liver	36.53, 35.62	14.69	23.59	19.14	1.50	33.33	638.00
Fetal Liver Clontech	34.56, 34.61	41.04	40.04	40.54	10.40	4.81	194.90
Lung	40, 40	0	0	0.00	2.57	19.46	0.00
Mammary Gland Clontech	39.07, 39.45	3.89	3.18	3.54	13.00	3.85	13.60
Myometrium	39.5, 35.37	3.1	26.93	15.02	2.34	21.37	320.83
Omentum	40, 36.18	0	17.61	8.81	3.94	12.69	111.74
Ovary	35.87, 34.34	20.75	46.22	33.49	4.34	11.52	385.77

Pancreas	40, 40	0	0	0.00	0.81	61.80	0.00
Head of Pancreas	40, 39.79	0	2.66	1.33	1.57	31.85	42.36
Parotid Gland	35.2, 38.6	29.46	4.97	17.22	5.48	9.12	157.07
Placenta Clontech	40, 38.14	0	6.32	3.16	5.26	9.51	30.04
Prostate	40, 40	0	0	0.00	3.00	16.67	0.00
Rectum	40, 39.2	0	3.63	1.82	1.23	40.65	73.78
Salivary Gland Clontech	40, 39.19	2.19	3.64	2.92	7.31	6.84	19.94
Skeletal Muscle Clontech	40, 39.37	0	3.32	1.66	1.26	39.68	65.87
Skin	40, 40	0	2.09	1.05	1.21	41.32	43.18
Small Intestine Clontech	40, 40	1.44	0	0.72	0.98	51.07	36.77
Spleen	35.36, 40	27.05	1.84	14.45	4.92	10.16	146.80
Stomach	40, 37.03	1.93	11.29	6.61	2.73	18.32	121.06
Testis Clontech	40, 37.99	0	6.82	3.41	0.57	87.87	299.65
Thymus Clontech	38.47, 35.55	5.32	24.52	14.92	9.89	5.06	75.43
Thyroid	40, 40	0	2.15	1.08	2.77	18.05	19.40
Trachea Clontech	35.37, 36.67	26.97	13.66	20.32	9.71	5.15	104.61
Urinary Bladder	39.07, 40	3.89	1.42	2.66	5.47	9.14	24.27
Uterus	36.01, 33.41	19.29	75.06	47.18	5.34	9.36	441.71
genomic	29.57	558.84					
b-actin	27.57	1592.66					
1.00E+05	19.91	100000					
1.00E+05	20.08	100000					
1.00E+04	23.79	10000					
1.00E+04	24.06	10000					
1.00E+03	27.72	1000					
1.00E+03	28.29	1000					
1.00E+02	31.95	100					
1.00E+02	33.62	100					
1.00E+01	39.75	10					
1.00E+01	35.41	10					
1.00E-00	40	0					
1.00E-00	40	0					
NTC	40	-1					
NTC	40	-1					

Sample sbg1399854ANK	**Reg number (GSK identifier)**	**Ct**	**Mean GOI copies**	**copies of mRNA detected/50 ng total RNA**	**Sample**	**Fold Change in Disease Population**
colon normal GW98-167	21941	35.32	22.34	44.68	colon normal	
colon tumor GW98-166	21940	34.14	47.5	95.00	colon tumor	2.13
colon normal GW98-178	22080	36.16	13.07	26.14	colon normal	
colon tumor GW98-177	22060	35.58	18.93	37.86	colon tumor	1.45

colon normal GW98-561	23514	36.58	10.03	20.06	colon normal	
colon tumor GW98-560	23513	32.61	126.48	252.96	colon tumor	12.61
colon normal GW98-894	24691	35.61	18.62	37.24	colon normal	
colon tumor GW98-893	24690	33.24	84.75	169.50	colon tumor	4.55
lung normal GW98-3	20742	34.77	31.8	63.60	lung normal	
lung tumor GW98-2	20741	33.63	66.03	132.06	lung tumor	2.08
lung normal GW97-179	20677	34.76	32.04	64.08	lung normal	
lung tumor GW97-178	20676	34.44	39.23	78.46	lung tumor	1.22
lung normal GW98-165	21922	35.18	24.44	48.88	lung normal	
lung tumor GW98-164	21921	37.99	4.06	8.12	lung tumor	-6.02
lung normal GW98-282	22584	33.64	65.37	130.74	lung normal	
lung tumor GW98-281	22583	37.3	6.34	12.68	lung tumor	-10.31
breast normal GW00-392	28750	36.29	12.08	12.08	breast normal	
breast tumor GW00-391	28746	36.14	13.29	26.58	breast tumor	2.20
breast normal GW00-413	28798	37.08	7.29	7.29	breast normal	
breast tumor GW00-412	28797	33.26	83.58	167.16	breast tumor	22.93
breast normal GW00-235:238	27592-95	38.93	2.24	2.24	breast normal	
breast tumor GW00-231:234	27588-91	36.57	10.08	10.08	breast tumor	4.50
breast normal GW98-621	23656	34.9	29.32	58.64	breast normal	
breast tumor GW98-620	23655	36.11	13.51	27.02	breast tumor	-2.17
brain normal BB99-542	25507	29.6	866.9	1733.80	brain normal	
brain normal BB99-406	25509	31.93	194.87	389.74	brain normal	
brain normal BB99-904	25546	30.38	526.58	1053.16	brain normal	
brain stage 5 ALZ BB99-874	25502	32.7	119.57	239.14	brain stage 5 ALZ	-4.43
brain stage 5 ALZ BB99-887	25503	30.08	634.97	1269.94	brain stage 5 ALZ	1.20
brain stage 5 ALZ BB99-862	25504	29.7	809.22	1618.44	brain stage 5 ALZ	1.53
brain stage 5 ALZ BB99-927	25542	29.93	700.82	1401.64	brain stage 5 ALZ	1.32
CT lung	normal	35.1	25.82	51.64	CT lung Nml	
lung 26	normal	36.74	9.07		lung 26 Nml	
lung 27	normal	40	0	0.00	lung 27 Nml	
lung 24	COPD	40	2.5	2.50	lung 24 COPD	-7.11
lung 28	COPD	40	0	0.00	lung 28 COPD	-17.77
lung 23	COPD	40	0	0.00	lung 23 COPD	-17.77
lung 25	normal	39.39	1.67	1.67	lung 25 Nml	
asthmatic lung ODO3112	29321	40	0	0.00	asthmatic lung	-17.77
asthmatic lung ODO3433	29323	37	7.68	15.36	asthmatic lung	-1.16
asthmatic lung ODO3397	29322	36.08	13.8	27.60	asthmatic lung	1.55
asthmatic lung ODO4928	29325	40	0	0.00	asthmatic lung	-17.77
endo cells	control	40	0	0.00	endo cells	
endo VEGF		40	0	0.00	endo VEGF	0.00
endo bFGF		35.68	17.77	17.77	endo bFGF	17.77
heart Clontech	normal	35.03	26.95	53.90	heart	
heart (T-1) ischemic	29417	36.36	11.53	23.06	heart (T-1) ischemic	-2.34

heart (T-14) non-obstructive DCM	29422	34.57	36.11	72.22	heart (T-14) non-obstructive DCM	1.34
heart (T-3399) DCM	29426	36.25	12.37	24.74	heart (T-3399) DCM	-2.18
adenoid GW99-269	26162	38.51	2.92	5.84	adenoid	
tonsil GW98-280	22582	35.05	26.54	53.08	tonsil	
T cells PC00314	28453	35.5	19.98	39.96	T cells	
PBMNC		40	0	0.00	PBMNC	
monocyte		40	0	0.00	monocyte	
B cells PC00665	28455	33.78	59.82	119.64	B cells	
dendritic cells	28441	29.33	1026.14	2052.28	dendritic cells	
neutrophils	28440	31.3	292.56	292.56	neutrophils	
eosinophils	28446	35.97	14.79	29.58	eosinophils	
BM unstim		35.56	19.16	19.16	BM unstim	
BM stim	treated	34.79	31.48	31.48	BM stim	1.64
osteo dif	treated	40	2.59	2.59	osteo dif	2.59
osteo undif		40	0	0.00	osteo undif	
chondrocytes		37.11	7.15	17.88	chondrocytes	
OA Synovium IP12/01	29462	35.95	14.93	14.93	OA Synovium	
OA Synovium NP10/01	29461	35.74	17.17	34.34	OA Synovium	
OA Synovium NP57/00	28464	39.09	2.02	4.04	OA Synovium	
RA Synovium NP03/01	28466	38.03	3.97	7.94	RA Synovium	
RA Synovium NP71/00	28467	35.08	26.03	52.06	RA Synovium	
RA Synovium NP45/00	28475	37.11	7.13	14.26	RA Synovium	
OA bone (biobank)	29217	33.76	60.54	60.54	OA bone (biobank)	
OA bone Sample 1	J. Emory	33.35	78.68	157.36	OA bone	
OA bone Sample 2	J. Emory	34.15	47.2	94.40	OA bone	
Cartilage (pool)	Normal	35.05	26.63	53.26	Nml Cartilage (pool)	
Cartilage (pool)	OA	37.42	5.87	11.74	OA Cartilage (pool)	-4.54
PBL unifected	28441	33.95	53.63	107.26	PBL unifected	
PBL HIV IIIB	28442	33.3	81.2	162.40	PBL HIV IIIB	1.51
MRC5 uninfected (100%)	29158	39.41	1.64	3.28	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	35.73	17.22	34.44	MRC5 HSV strain F	10.50
W12 cells	29179	35.08	26.08	52.16	W12 cells	
Keratinocytes	29180	36.69	9.33	18.66	Keratinocytes	
B-actin control		28.13	2213.67			
genomic		29.03	1240.79			
1.00E+05		22.03	100000			
1.00E+05		22.36	100000			
1.00E+04		25.68	10000			
1.00E+04		25.78	10000			
1.00E+03		29.01	1000			
1.00E+03		28.67	1000			
1.00E+02		33.46	100			
1.00E+02		40	100			

1.00E+01		38.75	10			
1.00E+01		40	10			
1.00E-00		40	0			
1.00E-00		38.6	1			
NTC		40	0			
*lung 26 Normal has been omitted due to multiple amplification failures from that sample						

Gene Name sbg1399854ANK

Disease tissues	**Fold Change in Disease Population Relative to Normal**
colon tumor	2.13
colon tumor	1.45
colon tumor	12.61
colon tumor	4.55
lung tumor	2.08
lung tumor	1.22
lung tumor	-6.02
lung tumor	-10.31
breast tumor	2.20
breast tumor	22.93
breast tumor	4.50
breast tumor	-2.17
brain stage 5 ALZ	-4.43
brain stage 5 ALZ	1.20
brain stage 5 ALZ	1.53
brain stage 5 ALZ	1.32
lung 24	-7.11
lung 28	-17.77
lung 23	-17.77
asthmatic lung	-17.77
asthmatic lung	-1.16
asthmatic lung	1.55
asthmatic lung	-17.77
endo VEGF	0.00
endo bFGF	17.77
heart T-1	-2.34
heart T-14	1.34
heart T-3399	-2.18
BM stim	1.64
osteo dif	2.59
Cartilage (pool)	-4.54
PBL HIV IIIB	1.51
MRC5 HSV strain F	10.50

Table V. Additional diseases based on mRNA expression in specific tissues

Tissue Expression	Additional Diseases
Brain	Neurological and psychiatric diseases, including Alzheimers, parasupranuclear palsey, Huntington's disease, myotonic dystrophy, anorexia, depression, schizophrenia, headache, amnesias, anxiety disorders, sleep disorders, multiple sclerosis
Heart	Cardiovascular diseases, including congestive heart failure, dilated cardiomyopathy, cardiac arrhythmias, Hodgson's Disease, myocardial infarction, cardiac arrhythmias
Lung	Respiratory diseases, including asthma, Chronic Obstructive Pulmonary Disease, cystic fibrosis, acute bronchitis, adult respiratory distress syndrome
Liver	Dyslipidemia, hypercholesterolemia, hypertriglyceridemia, cirrhosis, hepatic encephalopathy, fatty hepatocirrhosis, viral and nonviral hepatitis, Type II Diabetes Mellitis, impaired glucose tolerance
Kidney	Renal diseases, including acute and chronic renal failure, acute tubular necrosis, cystinuria, Fanconi's Syndrome, glomerulonephritis, renal cell carcinoma, renovascular hypertension
Skeletal muscle	Eulenburg's Disease, hypoglycemia, obesity, tendinitis, periodic paralyses, malignant hyperthermia, paramyotonia congenita, myotonia congenita
Intestine	Gastrointestinal diseases, including Myotonia congenita, Ileus, Intestinal Obstruction, Tropical Sprue, Pseudomembranous Enterocolitis
Spleen/lymph	Lymphangiectasia, hypersplenism, angiomas, ankylosing spondylitis, Hodgkin's Disease, macroglobulinemia, malignant lymphomas, rheumatoid arthritis
Placenta	Choriocarcinoma, hydatidiform mole, placenta previa
Testis	Testicular cancer, male reproductive diseases, including low testosterone and male infertility
Pancreas	Diabetic ketoacidosis, Type 1 & 2 diabetes, obesity, impaired glucose tolerance

What is claimed is:

1. An isolated polypeptide selected from the group consisting of:
(a) an isolated polypeptide encoded by a polynucleotide comprising a sequence set forth in Table I;
(b) an isolated polypeptide comprising a polypeptide sequence set forth in Table I; and
(c) a polypeptide sequence of a gene set forth in Table I.

2. An isolated polynucleotide selected from the group consisting of:
(a) an isolated polynucleotide comprising a polynucleotide sequence set forth in Table I;
(b) an isolated polynucleotide of a gene set forth in Table I;
(c) an isolated polynucleotide comprising a polynucleotide sequence encoding a polypeptide set forth in Table I;
(d) an isolated polynucleotide encoding a polypeptide set forth in Table I;
(e) a polynucleotide which is an RNA equivalent of the polynucleotide of (a) to (d);
or a polynucleotide sequence complementary to said isolated polynucleotide.

3. An expression vector comprising a polynucleotide capable of producing a polypeptide of claim 1 when said expression vector is present in a compatible host cell.

4. A process for producing a recombinant host cell which comprises the step of introducing an expression vector comprising a polynucleotide capable of producing a polypeptide of claim 1 into a cell such that the host cell, under appropriate culture conditions, produces said polypeptide.

5. A recombinant host cell produced by the process of claim 4.

6. A membrane of a recombinant host cell of claim 5 expressing said polypeptide.

7. A process for producing a polypeptide which comprises culturing a host cell of claim 5 under conditions sufficient for the production of said polypeptide and recovering said polypeptide from the culture.