



- (51) **International Patent Classification:**
C12Q 1/68 (2006.01)
- (21) **International Application Number:**
PCT/US2015/040557
- (22) **International Filing Date:**
15 July 2015 (15.07.2015)
- (25) **Filing Language:** English
- (26) **Publication Language:** English
- (30) **Priority Data:**
62/025,872 17 July 2014 (17.07.2014) US
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- (81) **Designated States** (unless otherwise indicated, for every kind of national protection available): AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY,

BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, JP, KE, KG, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

- (84) **Designated States** (unless otherwise indicated, for every kind of regional protection available): ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

Published:

- with international search report (Art. 21(3))
- before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments (Rule 48.2(h))

(54) **Title:** TERT FUSIONS

(57) **Abstract:** The invention provides TERT gene fusions, TERT fusion proteins, and fragments of those genes and polypeptides. The invention further provides methods of diagnosing diseases or disorders associated with TERT fusions, such as conditions mediated by aberrant TERT expression or activity, or overexpression of TERT.



TERT FUSIONS

CLAIM OF PRIORITY

[0001] This application claims the benefit of U.S. Provisional Application No. 62/025,872, filed July 17, 2014, which is incorporated here by reference in its entirety to provide continuity of disclosure.

[0002] This invention relates to TERT (telomerase reverse transcriptase) gene fusions and TERT fusion proteins. The invention further relates to methods of diagnosing diseases or disorders associated with TERT fusions, such as conditions mediated by TERT activity, or conditions associated with aberrant TERT expression or activity, or overexpression of TERT.

[0003] Many forms of cancer are caused by genetic lesions that give rise to tumor initiation and growth. Genetic lesions may include chromosomal aberrations, such as translocations, inversions, deletions, copy number changes, gene expression level changes, and somatic and germline mutations. Indeed, the presence of such genomic aberrations is a hallmark feature of many cancers, including, for example, B cell cancer, lung cancer, breast cancer, ovarian cancer, pancreatic cancer, and colon cancer. In some models, cancer represents the phenotypic end-point of multiple genetic lesions that endow cells with a full range of biological properties required for tumorigenesis.

[0004] Recent efforts by The Cancer Genome Atlas (TCGA), the International Cancer Genome Consortium (ICGC), and dozens of other large-scale profiling efforts have generated an enormous amount of new sequencing data for dozens of cancer types – this includes whole-genome DNA, whole-exome DNA, and full-transcriptome RNA sequencing. These efforts have led to the identification of new driver genes and fusion genes within multiple cancer types. Fusions, particularly fusions involving kinases, are of particular interest, as such fusions have been shown to be oncogenic, and have been successfully targeted by new therapeutics. For example, anaplastic lymphoma kinase (ALK), one of the receptor tyrosine kinases, is known to become oncogenic when fused with various genes. See, e.g., M. Soda et al, “Identification of the transforming EML4-ALK fusion gene in non-small-cell lung cancer,” *Nature* 444:561-566 (2007).

[0005] A need exists for identifying novel genetic lesions associated with cancer. For example, the presence of fusions involving a gene in samples collected from more than one source can indicate that the gene is an oncogenic driver. The identification of such fusions can

be an effective approach to diagnosis of cancers and development of compounds, compositions, methods, and assays for evaluating and treating cancer patients.

[0006] In one aspect, the invention provides methods for detecting the presence of a TERT fusion in a biological sample. The methods include the steps of: (a) obtaining a biological sample from a mammal; and (b) contacting the sample with a reagent that detects a TERT fusion, to determine whether a TERT fusion is present in the biological sample. In some embodiments, the sample can be from, e.g., a cancer patient, such as, e.g., a patient having sarcoma. In some embodiments, the fusion can be, e.g., a TRIO:TERT fusion. In some embodiments, the TRIO:TERT fusion has all or a part of the nucleotide and/or amino acid sequence (such as, e.g., the fusion junction) set forth in SEQ ID NO:1 and SEQ ID NO:2, respectively.

[0007] In another aspect, the invention provides methods of diagnosing a patient having a disease or disorder associated with aberrant TERT expression or activity, or overexpression of TERT; the methods include: (a) obtaining a biological sample from the patient; and (b) contacting the sample with a reagent that detects a TERT fusion to determine whether a TERT fusion is present in the biological sample, whereby the detection of the TERT fusion indicates the presence of a disorder associated with aberrant TERT expression or activity, or overexpression of TERT.

BRIEF DESCRIPTION OF THE FIGURES

[0008] FIG. 1A, 1B, and 1C depict the nucleotide sequence of a TRIO:TERT gene fusion (SEQ ID NO:1) comprising a portion of the TRIO gene (NM_007118) up to and including exon 33 and a portion of the TERT gene (NM_198253) starting at exon 2. The underlined codons at nucleotides 4957-4959 and 4960-4962 encode the last amino acid of TRIO and the first amino acid of TERT, respectively. The slash after nucleotide 4959 indicates the breakpoint (fusion junction) where translocation and in-frame fusion has occurred.

[0009] FIG. 2 depicts the amino acid sequence of a TRIO:TERT fusion protein (SEQ ID NO:2). The slash between amino acids 1653 and 1654 indicates the breakpoint or fusion junction between the TRIO and TERT proteins. Amino acids 1653 and 1654 correspond to nucleotides 4957-4959 and 4960-4962 in SEQ ID NO:1, respectively.

[0010] FIG. 3 is a graph showing TERT DNA copy number versus the mRNA expression in sarcoma samples.

EXEMPLARY EMBODIMENTS OF THE INVENTION

[0011] The invention is based, at least in part, on the discovery of novel recombination or translocation events in cancer patients that result in at least a fragment of a TERT gene linked to a non-homologous promoter via a recombination or translocation event that may result in aberrant expression (e.g., in a location where TERT is not typically expressed) or overexpression of the reverse transcriptase (RT) domain of the TERT gene and thus, an increase in RT activity. Thus, a new patient population is identified, which is characterized by the presence of a TERT fusion, e.g., a TERT gene fusion or fusion protein. This new patient population suffers from or is susceptible to disorders mediated by aberrant TERT expression or activity, or overexpression of TERT, such as, e.g., a cancer. In another aspect of the invention, a new subtype of cancer is identified, which is characterized by the presence of the TERT fusions described herein. In some embodiments, the new patient population suffers from or is susceptible to a sarcoma characterized by the presence of a TERT fusion. New methods of diagnosing the patient population and the TERT fusion cancer subtype are also provided.

[0012] The term “TERT fusion” is used generically herein, and includes any fusion molecule (e.g., gene, gene product (e.g., cDNA, mRNA, or protein), and variants thereof) that includes a fragment of TERT, particularly the coding region for the RT domain of TERT, and a fragment of a second, non-homologous gene. In some embodiments, the coding sequence for the RT domain of TERT is under control of the promoter of the non-homologous gene. A TERT fusion protein generally includes the RT domain of TERT. In some embodiments, the TERT fusion is a TRIO:TERT fusion.

TERT Gene Fusions and Fusion proteins

[0013] TERT is a catalytic subunit of the enzyme telomerase, which, together with the telomerase RNA component (TERC), comprises the most important unit of the telomerase complex. Telomerases are part of a distinct subgroup of RNA-dependent polymerases. Telomerase lengthens chromosomes' telomeres, thereby allowing senescent cells that would otherwise become postmitotic and undergo apoptosis to exceed the Hayflick limit and become potentially immortal, as is often the case with cancerous cells. TERT is responsible for catalyzing the addition of nucleotides in a TTAGGG sequence to the ends of a chromosome's telomeres. This addition of repetitive DNA sequences prevents degradation of the chromosomal ends following multiple rounds of replication. Telomerase expression plays a role in cellular senescence, as it is normally repressed in postnatal somatic cells, resulting in progressive shortening of telomeres. Telomere deficiency is often linked to aging, cancers, and

the conditions dyskeratosis congenita (DKC) and Cri du chat. Meanwhile, overexpression of TERT is often associated with cancers and tumor formation. Telomerase activity is a hallmark of many cancers, and two other genetic mechanisms of TERT reactivation have been described previously; both somatic mutations in the promoter of the TERT gene and DNA copy number gains of TERT were shown to activate its transcription. See Huang, F. W. et al. "Highly recurrent TERT promoter mutations in human melanoma," *Science* 339: 957–959 (2013); see also Zhang, A. et al. "Frequent amplification of the telomerase reverse transcriptase gene in human tumors," *Cancer Res.* 60: 6230–6235 (2000).

[0014] The invention provides novel TERT fusions that are associated with different types of disorders. These findings provide a reasonable expectation that TERT fusions represent an alternative mechanism for telomerase reactivation in cancers. For example, the TERT fusions disclosed herein can be associated with certain cancers, such as, e.g., sarcoma. In some embodiments, the sarcoma associated with a TERT fusion is liposarcoma. In some embodiments, the TERT fusions disclosed herein can be associated with other disorders mediated by aberrant TERT expression or activity, or overexpression of TERT.

[0015] TERT gene fusions are generated by a fusion between at least a part of the TERT gene and a part of another gene as a result of a translocation (including inversion) within a chromosome or between chromosomes. As a result of a translocation, the TERT gene may be placed under the transcriptional control of the partner gene promoter, e.g., TRIO, resulting in aberrant TERT expression or activity, or overexpression of TERT. The overexpression can lead to certain cancers. As used herein, the 5'-region is upstream of, and the 3'-region is downstream of, a fusion junction or breakpoint in one of the component genes. TERT and the gene or protein that it is fused to are referred to as "fusion partners." Alternatively, they may be identified as a "TERT gene fusion" or a "TERT fusion protein," which are collectively termed "TERT fusions." The TERT fusions disclosed herein possess a RT activity. The phrase "having a RT activity" as used in this application means having an activity as an enzyme catalyzing the generation of complementary DNA (cDNA) from an RNA template, such as, e.g., having a telomerase RT activity, which means having an activity as an enzyme, when together with the telomerase RNA component (TERC), catalyzing the addition of nucleotides (e.g., a TTAGGG sequence) to the ends of a chromosome's telomeres.

[0016] In some exemplary embodiments, the fusion partner is all or a portion of the DNA or amino acid sequence for TRIO (trio Rho guanine nucleotide exchange factor). In certain embodiments of the invention, a fusion includes an in-frame fusion of all or a portion of the

TRIO gene (e.g., a fragment of the TRIO gene comprising a TRIO promotor or a functional fragment thereof, and one or more exons encoding TRIO or a fragment thereof) and an portion of the TERT gene (e.g., one or more exons encoding the RT domain or a functional fragment thereof). Such a fusion can be referred to as a TRIO:TERT fusion. In one embodiment, the TRIO:TERT fusion comprises sufficient TERT sequence to drive expression of a fusion protein that has a RT activity. In some embodiments, the TRIO:TERT fusion drives expression of a fusion protein that has elevated TERT activity as compared with wild type TERT in the same tissue or cell. In some embodiments, the TRIO:TERT fusion drives expression of a fusion protein that confers a tissue or cell elevated RT activity as compared with a wild type tissue or cell without such a fusion. In some embodiments, the TRIO:TERT fusion comprises the non-catalytic portion of TRIO kinase, which resulted in the upregulation of the transcription of TERT.

[0017] In some embodiments, the invention provides a TRIO:TERT gene fusion comprising all or a portion of the nucleotide sequence depicted in FIG. 1A-1C (SEQ ID NO:1) that includes the fusion junction. SEQ ID NO:1 comprises TRIO (NM_007118) up to exon 33 fused to TERT (NM_198253), beginning at exon 2. In some embodiments, the TRIO:TERT gene fusion comprises a nucleotide sequence that is at least 85%, at least 90%, at least 95%, at least 97%, at least 98%, or at least 99% identical to all or part of SEQ ID NO:1 or its complement. Reference to “all or a portion” or “all or part” of a TRIO:TERT gene fusion, means that the nucleotide sequence comprises the entire TRIO:TERT gene fusion nucleotide sequence or a fragment of that sequence that comprises the fusion junction breakpoint point between TRIO and TERT. The fragment may comprise 7, 8, 9, 10, 12, 14, 16, 18, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 150, 175, 200, 250, 300, or more nucleotides spanning the fusion junction. An exemplary TRIO:TERT gene fusion junction is identified by a slash (“/”) in FIG. 1B. Unless specified, a reference to all or part of SEQ ID NO:1 encompasses either the coding strand or the complementary strand, or both.

[0018] The nucleic acid sequences of TERT gene fusions may be used as probes, primers, or bait to identify nucleotides from a biological sample that include, flank, or hybridize to TERT fusions, such as TRIO:TERT (e.g., all or part of SEQ ID NO: 1), at, e.g., the fusion junctions. In certain embodiments, the probe, primer, and/or bait molecule is an oligonucleotide that allows capture, detection, or isolation of a TERT gene fusion in a biological sample. In certain embodiments, the probes or primers derived from the nucleic acid sequences of TERT gene fusions (e.g., from the fusion junctions) may be used, for example, for polymerase chain

reaction (PCR) amplification. The oligonucleotide can comprise a nucleotide sequence substantially complementary to a fragment of the TERT gene fusion nucleic acid molecules described herein. The sequence identity between the nucleic acid fragment, e.g., the oligonucleotide and the target TERT gene fusion sequence, need not be exact, so long as the sequences are sufficiently complementary to allow the capture, detection, and/or isolation of the target sequence. In one embodiment, the nucleic acid fragment is a probe or primer that includes an oligonucleotide between about 5 and 25, e.g., between 10 and 20, or 10 and 15 nucleotides in length that includes the fusion junction of a TERT fusion, such as, e.g., TRIO:TERT (e.g., all or part of SEQ ID NO: 1). In other embodiments, the nucleic acid fragment is a bait that includes an oligonucleotide between about 100 to 300 nucleotides, 130 and 230 nucleotides, or 150 and 200 nucleotides in length that includes the fusion junction of a TERT gene fusion, such as, e.g., TRIO:TERT (e.g., all or part of SEQ ID NO: 1).

[0019] In certain embodiments, the nucleic acid fragments hybridize to a nucleotide sequence that includes a breakpoint or fusion junction, e.g., a breakpoint or fusion junction as identified by a slash ("/") in FIG. 1B. For example, the nucleic acid fragment can hybridize to a nucleotide sequence that includes the fusion junction between the TRIO transcript and the TERT transcript (e.g., nucleotides 4957-4962 of SEQ ID NO:1), e.g., a nucleotide sequence that includes all or a portion of SEQ ID NO:1. In exemplary embodiments, the nucleic acid fragments include or hybridize to a nucleotide sequence within exons 1-33 of a TRIO gene and exons 2-16 of a TERT gene (e.g., a portion of SEQ ID NO:1 comprising nucleotides 4957-4962, 4955-4964, 4950-4969, 4935-4984, or 4910-5009).

[0020] In other embodiments, the nucleic acid fragment includes a bait that comprises a nucleotide sequence that hybridizes to a TERT gene fusion nucleic acid molecule described herein, and thereby allows the detection, capture, and/or isolation of the nucleic acid molecule. In one embodiment, a bait is suitable for solution phase hybridization. In other embodiments, a bait includes a binding entity or detection entity, e.g., an affinity tag or fluorescent label, that allows detection, capture, and/or separation, e.g., by binding to a binding entity, of a hybrid formed by a bait and a nucleic acid hybridized to the bait.

[0021] In exemplary embodiments, the nucleic acid fragments used as bait hybridize to a nucleotide sequence that includes a fusion junction between the TRIO transcript and the TERT transcript, e.g., a nucleotide sequence within SEQ ID NO:1 comprising nucleotides 4957-4962 (such as, e.g., a sequence comprising nucleotides 4955-4964, 4950-4969, 4935-4984, or 4910-5009 of SEQ ID NO:1).

[0022] The nucleic acid fragments can be detectably labeled with, e.g., a radiolabel, a fluorescent label, a bioluminescent label, a chemiluminescent label, an enzyme label, a binding pair label (e.g., biotin/streptavidin), an antigen label, or can include an affinity tag or identifier (e.g., an adaptor, a barcode, or other sequence identifier). Labeled or unlabeled nucleic acids and/or nucleic acid fragments may be used in reagents for detecting, capturing, or isolating TERT gene fusions, , such as, e.g., TRIO:TERT (for example, all or part of SEQ ID NO: 1).

[0023] Another aspect of the invention provides TERT fusion proteins (such as, e.g., a purified or isolated TRIO:TERT fusion protein), biologically active or antigenic fragments thereof, and use of those polypeptides for detecting the biological activity (such as tumorigenic activity) of a TERT fusion protein. Exemplary embodiments of the TERT fusion protein is a TRIO:TERT fusion protein that comprises all or part of the amino acid sequence set forth in SEQ ID NO:2 that includes the fusion junction. In some embodiments, the TRIO:TERT gene fusion encodes a protein having a sequence that is at least 85%, at least 90%, at least 95%, at least 97%, at least 98%, or at least 99% identical to all or part of the sequence depicted in FIG. 2 (SEQ ID NO:2). Reference to “all or a portion” or “all or part” of a TERT fusion protein, means an amino acid sequence that comprises the entire TERT fusion protein amino acid sequence or a fragment of that sequence that comprises the fusion junction breakpoint point between TERT and its fusion partner, e.g., TRIO. The fragment may comprise 8, 10, 12, 14, 15, 16, 18, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 75, or more amino acids spanning the fusion junction. An example of a specific TRIO:TERT fusion protein junction is identified by a slash (“/”) in FIG. 2.

[0024] In other embodiments, the TERT fusion protein of the invention can include a fragment of a TRIO protein and a fragment of a TERT protein. In one embodiment, the TERT fusion protein is a TRIO:TERT fusion protein having the amino acid sequence of SEQ ID NO:2 or a fragment thereof that includes the fusion junction, such as, e.g., amino acids 1649-1658, 1644-1663, or 1629-1678 of SEQ ID NO:2. In some embodiments, the TERT fusion protein is a TRIO:TERT fusion protein comprising an amino acid sequence that is at least 85%, at least 90%, at least 95%, at least 97%, at least 98%, or at least 99% identical to SEQ ID NO:2 or a fragment thereof (e.g., amino acids 1649-1658, 1644-1663, or 1629-1678 of SEQ ID NO:2).

[0025] In certain embodiments, the TERT fusion protein includes a functional RT domain. In some embodiments, the TERT fusion protein results in elevated TERT activity (e.g., elevated activity in a cancer cell) as compared with wild type TERT activity (e.g., in a cancer cell, a non-cancer cell adjacent to the cancer cell, or a non-cancer cell from a control sample, such as

a cancer free subject). In one exemplary embodiment, the TERT fusion protein is a TRIO:TERT fusion and includes a TERT RT domain or a functional fragment thereof.

[0026] In another embodiment, the TERT fusion protein or fragment is a peptide, e.g., an immunogenic peptide or protein, that contains a fusion junction with a heterologous protein as described herein. Such immunogenic peptides or proteins can be used for vaccine preparation for use in the treatment or prevention of cancers caused by or exacerbated by TERT gene fusions and TERT fusion proteins. In other embodiments, such immunogenic peptides or proteins can be used to raise antibodies specific to the fusion protein. In some embodiments, the TERT fusion protein is present in combination with or is further conjugated to one or more adjuvant(s) or immunogen(s), e.g., a protein capable of enhancing an immune response to the TERT fusion protein (e.g., a hapten, a toxoid, etc.). In some embodiments, the TERT fusion protein is a TRIO:TERT fusion protein. In some embodiments, the TERT fusion protein comprises the fusion junction of SEQ ID NO:2.

[0027] Thus, another aspect of the invention provides an antibody that binds to a TERT fusion protein (such as, e.g., a TRIO:TERT fusion protein) or a fragment thereof. In certain embodiments, the antibody recognizes a TERT fusion protein but does not recognize wild type TERT or the wild type fusion partner (such as, e.g., TRIO). In some embodiments, the antibody binds to an epitope comprising the junction between TERT and the fusion partner (e.g., the junction of TRIO:TERT). In one embodiment, the antibody binds to a TRIO:TERT fusion protein having the amino acid sequence of SEQ ID NO:2 or a fragment thereof, such as, e.g., amino acids 1649-1658, 1644-1663, or 1629-1678 of SEQ ID NO:2.

[0028] In certain embodiments, the antibodies of the invention inhibit and/or neutralize the biological activity of the TERT fusion protein, and more specifically, in some embodiments, the kinase activity of the TERT fusion protein. In other embodiments, the antibodies may be used to detect a TERT fusion protein or to diagnose a patient suffering from a disease or disorder associated with the expression of a TERT fusion protein

Detection and Diagnostic Methods

[0029] In another aspect, the invention provides a method of detecting the presence of a TERT gene fusion or fusion protein, such as, e.g., a TRIO:TERT fusion as described herein. The presence of a TERT gene fusion indicates that the mammal providing the biological sample suffers from or is at risk of developing a disorder mediated by aberrant TERT expression or activity, or overexpression of TERT, such as, e.g., a cancer. The presence of a TERT gene fusion may also indicate that the disorder is treatable with a TERT fusion inhibitor. In some

embodiments the cancer is associated with aberrant TERT expression or activity, or overexpression of TERT. In some embodiments, the cancer is sarcoma. In some embodiments, the cancer is liposarcoma. In some embodiments, the TERT fusion present in the sample is TRIO:TERT and the cancer to be treated is sarcoma, e.g., liposarcoma.

[0030] In one embodiment, the TERT fusion detected is a nucleic acid molecule or a polypeptide. The method includes detecting whether a TERT fusion nucleic acid molecule or polypeptide is present in a cell (e.g., a circulating cell or a cancer cell), a tissue (e.g., a tumor), or a sample, e.g., a tumor sample, from a subject. In one embodiment, the sample is a nucleic acid sample. In one embodiment, the nucleic acid sample comprises DNA, e.g., genomic DNA or cDNA, or RNA, e.g., mRNA. In other embodiments, the sample is a protein sample.

[0031] The sample can be chosen from one or more sample types, such as, for example, tissue, e.g., cancerous tissue (e.g., a tissue biopsy), whole blood, serum, plasma, buccal scrape, sputum, saliva, cerebrospinal fluid, urine, stool, circulating tumor cells, circulating nucleic acids, or bone marrow.

I. Methods for Detecting Gene Fusions

[0032] In certain embodiments, the sample is acquired from a subject having or at risk of having a cancer (e.g., a patient), or alternatively, the method further includes acquiring a sample from the subject. In some embodiments, the TERT fusion is detected in a nucleic acid molecule by one or more methods chosen from: e.g., nucleic acid hybridization assay (e.g. in situ hybridization, comparative genomic hybridization, microarray, Southern blot, northern blot), amplification-based assays (e.g., PCR, PCR-RFLP assay, or real-time PCR), sequencing and genotyping (e.g. sequence-specific primers, high-performance liquid chromatography, or mass-spectrometric genotyping), and screening analysis (including metaphase cytogenetic analysis by karyotype methods).

(1) Hybridization methods

[0033] In some embodiments, the reagent hybridizes to a TERT gene fusion, such as, e.g., nucleotides 4957-4962, 4955-4964, 4950-4969, 4935-4984, or 4910-5009 of SEQ ID NO:1. In one embodiment, the method includes: contacting a nucleic acid sample, e.g., a genomic DNA sample (e.g., a chromosomal sample or a fractionated, enriched or otherwise pre-treated sample) or a gene product (e.g., mRNA, or cDNA), obtained from the subject, with a nucleic acid fragment, e.g., a probe or primer as described herein (e.g., an exon-specific or a breakpoint-specific probe or primer), under conditions suitable for hybridization, and

determining the presence or absence of the TERT gene fusion, such as, e.g. a TRIO:TERT gene fusion. In an alternate embodiment, the method includes the steps of obtaining a sample; exposing the sample to a nucleic acid probe which hybridizes to an mRNA or cDNA encoding a TERT fusion protein that comprises amino acids 1649-1658, 1644-1663, or 1629-1678 of SEQ ID NO:2

[0034] Hybridization, as described throughout the specification, may be carried out under stringent conditions, e.g., medium or high stringency. See, e.g., J. Sambrook, E.F. Fritsch, and T. Maniatis, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press; 2nd edition (1989); T. Brown, *Hybridization Analysis of DNA Blots. Current Protocols in Molecular Biology* at 21:2.10.1–2.10.16 (2001). High stringency conditions for hybridization refer to conditions under which two nucleic acids must possess a high degree of base pair homology to each other in order to hybridize. Examples of highly stringent conditions for hybridization include hybridization in 4×sodium chloride/sodium citrate (SSC), at 65 or 70° C., or hybridization in 4×SSC plus 50% formamide at about 42 or 50° C., followed by at least one, at least two, or at least three washes in 1×SSC, at 65 or 70° C. Another example of highly stringent conditions includes hybridization in 2×SSC; 10×Denhardt solution (Fikoll 400+PEG+BSA; ratio 1:1:1); 0.1% SDS; 5 mM EDTA; 50 mM Na₂HPO₄; 250 µg/ml of herring sperm DNA; 50 µg/ml of tRNA; or 0.25 M of sodium phosphate buffer, pH 7.2; 1 mM EDTA 7% SDS at 60°C; followed by washing 2×SSC, 0.1% SDS at 60° C.

[0035] In some embodiments, the nucleic acid fragments can be detectably labeled with, e.g., a radiolabel, a fluorescent label, a bioluminescent label, a chemiluminescent label, an enzyme label, a binding pair label (e.g., biotin/streptavidin), an antigen-label, or can include an affinity tag or identifier (e.g., an adaptor, barcode or other sequence identifier). Labeled or unlabeled nucleic acids and/or nucleic acid fragments may be used in reagents for detecting, capturing, or isolating TERT gene fusions. Labeled or unlabeled nucleic acids and/or nucleic acid fragments may be used in reagents for detecting, capturing, and/or isolating TERT gene fusions, such as, e.g., TRIO:TERT (e.g., all or part of SEQ ID NO: 1). In some embodiments, the labeled nucleic acid fragments can be detected using, e.g., autoradiography, microscopy (e.g., brightfield, fluorescence, or electron microscopy), enzyme-linked immunosorbent assay (ELISA), or immunohistochemistry.

[0036] In some embodiments, the method of determining the presence of a TERT gene fusion (such as, e.g., TRIO:TERT, as disclosed herein) in a mammal comprises the steps of obtaining a biological sample of the mammal (such as, e.g., from a human cancer); exposing the sample

to a nucleic acid probe which hybridizes to a DNA which comprises a TERT gene fusion; wherein hybridization of the probe to the DNA in the sample indicates the presence of a TERT gene fusion in the mammal. In some embodiments, the human cancer is sarcoma. In some embodiments, the human cancer is liposarcoma.

[0037] In some embodiments, the method comprises performing chromosome in situ hybridization with chromosomal DNA from a biological sample to detect the presence of a TERT gene fusion (such as, e.g., TRIO:TERT, as disclosed herein). In some embodiments, the chromosome in situ hybridization comprises the steps of: providing a chromosome (e.g., interphase or metaphase chromosome) preparation (e.g., by attaching the chromosomes to a substrate (e.g., glass)); denaturing the chromosomal DNA (e.g., by exposure to formamide) to separate the double strands of the polynucleotides from each other; exposing the nucleic acid probe to the chromosomes under conditions to allow hybridization of the probe to the target DNA; removing unhybridized or non-specifically hybridized probes by washing; and detecting the hybridization of the probe with the target DNA. In some embodiments, the chromosome in situ hybridization is fluorescence in situ hybridization (FISH). In some embodiments, the probe is labeled directly by a fluorescent label, or indirectly by incorporation of a nucleotide containing a tag or reporter molecule (e.g., biotin, digoxigenin, or hapten) which after hybridization to the target DNA is then bound by fluorescently labeled affinity molecule (e.g., an antibody or streptavidin). In some embodiments, the hybridization of the probe with the target DNA in FISH can be visualized using a fluorescence microscope.

[0038] In other embodiments, the method comprises performing Southern blot with DNA polynucleotides from a biological sample to detect the presence of a TERT gene fusion (such as, e.g., TRIO:TERT, as disclosed herein). In some embodiments, the Southern blot comprises the steps of: optionally fragmenting the polynucleotides into smaller sizes by restriction endonucleases; separating the polynucleotides by gel electrophoresis; denaturing the polynucleotides (e.g., by heat or alkali treatment) to separate the double strands of the polynucleotides from each other; transferring the polynucleotides from the gel to a membrane (e.g., a nylon or nitrocellulose membrane); immobilizing the polynucleotides to the membrane (e.g., by UV light or heat); exposing the nucleic acid probe to the polynucleotides under conditions to allow hybridization of the probe to the target DNA; removing unhybridized or non-specifically hybridized probes by washing; and detecting the hybridization of the probe with the target DNA.

(2) Amplification-based assays

[0039] In certain embodiments, the method of determining the presence of a TERT gene fusion, comprises (a) performing a PCR amplification reaction with polynucleotides from a biological sample, wherein the amplification reaction utilizes a pair of primers which will amplify at least a fragment of the TERT gene fusion, wherein the fragment comprises the fusion junction, wherein the first primer is in sense orientation and the second primer is in antisense orientation; and (b) detecting an amplification product, wherein the presence of the amplification product is indicative of the presence of a TERT fusion polynucleotide in the sample. In specific exemplary embodiments, the TERT gene fusion is TRIO:TERT, such as, e.g., the gene fusion of SEQ ID NO: 1 or a fragment thereof comprising nucleotides 4957-4962, 4955-4964, 4950-4969, 4935-4984, or 4910-5009 of SEQ ID NO:1

[0040] In some embodiments, step (a) of performing a PCR amplification reaction comprises: (i) providing a reaction mixture comprising the polynucleotides (e.g., DNA or cDNA) from the biological sample, the pair of primers which will amplify at least a fragment of the TERT gene fusion wherein the first primer is complementary to a sequence on the first strand of the polynucleotides and the second primer is complementary to a sequence on the second strand of the polynucleotides, a DNA polymerase, and a plurality of free nucleotides comprising adenine, thymine, cytosine, and guanine (dNTPs); (ii) heating the reaction mixture to a first predetermined temperature for a first predetermined time to separate the double strands of the polynucleotides from each other; (iii) cooling the reaction mixture to a second predetermined temperature for a second predetermined time under conditions to allow the first and second primers to hybridize with their complementary sequences on the first and second strands of the polynucleotides, and to allow the DNA polymerase to extend the primers; and (iv) repeating steps (ii) and (iii) for a predetermined number of cycles (e.g., 10, 15, 20, 25, 30, 35, 40, 45, or 50 cycles).

[0041] In some embodiments, the polynucleotides from the biological sample comprise RNA, and the method further comprises performing a RT-PCR amplification reaction with the RNA to synthesize cDNA as the template for subsequent or simultaneous PCR reactions. In some embodiments, the RT-PCR amplification reaction comprises providing a reaction mixture comprising the RNA, a primer which will amplify the RNA (e.g., a sequence-specific primer, a random primer, or oligo(dT)s), a reverse transcriptase, and dNTPs, and heating the reaction mixture to a third predetermined temperature for a third predetermined time under conditions to allow the reverse transcriptase to extend the primer.

(3) Sequencing and Genotyping

[0042] Another method for determining the presence of a TERT gene fusion molecule (such as, e.g., TRIO:TERT, as disclosed herein) includes: sequencing a portion of the nucleic acid molecule (e.g., sequencing the portion of the nucleic acid molecule that comprises the fusion junction of a TERT gene fusion), thereby determining that the TERT gene fusion is present in the nucleic acid molecule. Optionally, the sequence acquired is compared to a reference sequence, or a wild type reference sequence. In one embodiment, the sequence is determined by a next generation sequencing method. In some embodiments, the sequencing is automated and/or high-throughput sequencing. The method can further include acquiring, e.g., directly or indirectly acquiring, a sample, e.g., a tumor or cancer sample, from a patient.

[0043] In some embodiments, the sequencing comprises chain terminator sequencing (Sanger sequencing), comprising: providing a reaction mixture comprising a nucleic acid molecule from a biological sample, a primer complementary to a region of the template nucleic acid molecule, a DNA polymerase, a plurality of free nucleotides comprising adenine, thymine, cytosine, and guanine (dNTPs), and at least one chain terminating nucleotide (e.g., at least one di-deoxynucleotide (ddNTPs) chosen from ddATP, ddTTP, ddCTP, and ddGTP), wherein the at least one chain terminating nucleotide is present in a low concentration so that chain termination occurs randomly at any one of the positions containing the corresponding base on the DNA strand; annealing the primer to a single strand of the nucleic acid molecule; extending the primer to allow incorporation of the chain terminating nucleotide by the DNA polymerase to produce a series of DNA fragments that are terminated at positions where that particular nucleotide is used; separating the polynucleotides by electrophoresis (e.g., gel or capillary electrophoresis); and determining the nucleotide order of the template nucleic acid molecule based on the positions of chain termination on the DNA fragments. In some embodiments, the sequencing is carried out with four separate base-specific reactions, wherein the primer or the chain terminating nucleotide in each reaction is labeled with a separate fluorescent label. In other embodiments, the sequencing is carried out in a single reaction, wherein the four chain terminating nucleotides mixed in the single reaction are each labeled with a separate fluorescent label.

[0044] In some embodiments, the sequencing comprises pyrosequencing (sequencing by synthesis), comprising: (i) providing a reaction mixture comprising a nucleic acid molecule from a biological sample, a primer complementary to a region of the template nucleic acid molecule, a DNA polymerase, a first enzyme capable of converting pyrophosphate into ATP,

and a second enzyme capable using ATP to generates a detectable signal (e.g., a chemiluminescent signal, such as light) in an amount that is proportional to the amount of ATP; (ii) annealing the primer to a single strand of the nucleic acid molecule; (iii) adding one of the four free nucleotides (dNTPs) to allow incorporation of the correct, complementary dNTP onto the template by the DNA polymerase and release of pyrophosphate stoichiometrically; (iv) converting the released pyrophosphate to ATP by the first enzyme; (v) generating a detectable signal by the second enzyme using the ATP; (vi) detecting the generated signal and analyzing the amount of signal generated in a pyrogram; (vii) removing the unincorporated nucleotides; and (viii) repeating steps (iii) to (vii). The method allows sequencing of a single strand of DNA, one base pair at a time, and detecting which base was actually added at each step. The solutions of each type of nucleotides are sequentially added and removed from the reaction. Light is produced only when the nucleotide solution complements the first unpaired base of the template. The order of solutions which produce detectable signals allows the determination of the sequence of the template.

[0045] In some embodiments, the method of determining the presence of a TERT fusion (such as, e.g., TRIO:TERT, as disclosed herein) comprises analyzing a nucleic acid sample (e.g., DNA, cDNA, or RNA, or an amplification product thereof) by HPLC. The method may comprise: passing a pressurized liquid solution containing the sample through a column filled with a sorbent, wherein the nucleic acid or protein components in the sample interact differently with the sorbent, causing different flow rates for the different components; separating the components as they flow out the column at different flow rates. In some embodiments, the HPLC is chosen from, e.g., reverse-phase HPLC, size exclusion HPLC, ion-exchange HPLC, and bioaffinity HPLC.

[0046] In some embodiments, the method of determining the presence of a TERT fusion (such as, e.g., TRIO:TERT, as disclosed herein) comprises analyzing a nucleic acid sample (e.g., DNA, cDNA, or RNA, or an amplification product thereof) by mass spectrometry. The method may comprise: ionizing the components in the sample (e.g., by chemical or electron ionization); accelerating and subjecting the ionized components to an electric or magnetic field; separating the ionized components based on their mass-to-charge ratios; and detecting the separated components by a detector capable of detecting charged particles (e.g., by an electron multiplier).

II. Methods for detecting Fusion Proteins

[0047] Another aspect of the invention provides a method of detecting the presence of a TERT fusion protein (such as, e.g., TRIO:TERT, as disclosed herein), in a mammal. The method comprises the steps of obtaining a biological sample of a mammal (such as, e.g., from a human cancer), and exposing that sample to at least one reagent that detects a TERT fusion protein (e.g., an antibody that recognizes the TERT fusion but does not recognize the wild type TERT or the wild type fusion partner) to determine whether a TERT fusion protein is present in the biological sample. The detection of a TERT fusion protein indicates the presence of a mutant TERT in the mammal (such as, e.g., in the human cancer). In some embodiments, the TERT fusion protein comprises an amino acid sequence having at least 85%, 90%, 95%, 97%, 98%, or 99% identity with an amino acid sequence of all or part of SEQ ID NO 2 that includes the fusion junction. In some embodiments, the cancer is sarcoma. In some embodiments, the cancer is liposarcoma.

[0048] In some embodiments, the reagent that detects a TERT fusion protein can be detectably labeled with, e.g., a radiolabel, a fluorescent label, a bioluminescent label, a chemiluminescent label, an enzyme label, a binding pair label (e.g., biotin/streptavidin), an antigen label, or can include an affinity tag or identifier (e.g., an adaptor, barcode or other sequence identifier). In some embodiments, the labeled reagent can be detected using, e.g., autoradiography, microscopy (e.g., brightfield, fluorescence, or electron microscopy), ELISA, or immunohistochemistry. In some embodiments, the TERT fusion protein can be detected in a biological sample by one or more methods chosen from: such as, e.g., antibody-based detection (western blot, ELISA, immunohistochemistry), size-based detection methods (e.g., HPLC, or mass spectrometry), or protein sequencing.

(1) Antibody-based detection

[0049] In some embodiments, the method comprises performing a western blot with polypeptides from a biological sample to detect the presence of a TERT fusion protein (such as, e.g., TRIO:TERT, as disclosed herein). In some embodiments, the western blot comprises the steps of: separating the polypeptides by gel electrophoresis; transferring the polypeptides from the gel to a membrane (e.g., a nitrocellulose or polyvinylidene difluoride (PVDF) membrane); blocking the membrane to prevent nonspecific binding by incubating the membrane in a dilute solution of protein (e.g., 3-5% bovine serum albumin (BSA) or non-fat dry milk in Tris-Buffered Saline (TBS) or I-Block, with a minute percentage (e.g., 0.1%) of detergent, such as, e.g., Tween 20 or Triton X-100); exposing the polypeptides to at least one reagent that detects a

TERT fusion protein (e.g., an antibody that recognizes the TERT fusion but does not recognize the wild type TERT or the wild type fusion partner); removing unbound or non-specifically bound reagent by washing; and detecting the binding of the reagent with the target protein. In some embodiments, the method comprises two-step detection: exposing the polypeptides to a primary antibody that specifically binds to a TERT fusion protein; removing unbound or non-specifically bound primary antibody by washing; exposing the polypeptides to a secondary antibody that recognizes the primary antibody; removing unbound or non-specifically bound secondary antibody by washing; and detecting the binding of the secondary antibody. In some embodiments, the reagent that detects a TERT fusion protein (e.g., the fusion specific antibody, or the secondary antibody) is directly labeled for detection. In other embodiments, the reagent is linked to an enzyme, and the method further comprises adding a substrate of the enzyme to the membrane; and developing the membrane by detecting a detectable signal produced by the reaction between the enzyme and the substrate. For example, the reagent may be linked with horseradish peroxidase to cleave a chemiluminescent agent as a substrate, producing luminescence in proportion to the amount of the target protein for detection.

[0050] In some embodiments, the method comprises performing ELISA with polypeptides from a biological sample to detect the presence of a TERT fusion protein (such as, e.g., TRIO:TERT, as disclosed herein). In some embodiments, the ELISA is chosen from, e.g., direct ELISA, indirect ELISA, sandwich ELISA, and competitive ELISA.

[0051] In one embodiment, the direct ELISA comprises the steps of: attaching polypeptides from a biological sample to a surface; blocking the surface to prevent nonspecific binding by incubating the surface in a dilute solution of protein; exposing the polypeptides to an antibody that specifically binds to a TERT fusion protein (e.g., an antibody that recognizes the TERT fusion (such as, e.g., TRIO:TERT, as disclosed herein) but does not recognize the wild type TERT or the wild type fusion partner); removing unbound or non-specifically bound antibody by washing; and detecting the binding of the antibody with the target protein. In some embodiments, the antibody is directly labeled for detection. In other embodiments, the antibody is linked to an enzyme, and the method further comprises adding a substrate of the enzyme; and detecting a detectable signal produced by the reaction between the enzyme and the substrate.

[0052] In another embodiment, the indirect ELISA comprises the steps of: attaching polypeptides from a biological sample to a surface; blocking the surface to prevent nonspecific binding by incubating the surface in a dilute solution of protein; exposing the polypeptides to a

primary antibody that specifically binds to a TERT fusion protein (such as, e.g., TRIO:TERT, as disclosed herein); removing unbound or non-specifically bound primary antibody by washing; exposing the polypeptides to a secondary antibody that recognizes the primary antibody; removing unbound or non-specifically bound secondary antibody by washing; and detecting the binding of the secondary antibody. In some embodiments, the secondary antibody is directly labeled for detection. In other embodiments, the secondary antibody is linked to an enzyme, and the method further comprises adding a substrate of the enzyme; and detecting a detectable signal produced by the reaction between the enzyme and the substrate.

[0053] In some embodiments, the method comprises performing immunohistochemistry with polypeptides from a biological sample to detect the presence of a TERT fusion protein (such as, e.g., TRIO:TERT, as disclosed herein). In some embodiments, the immunohistochemistry comprises the steps of: fixing a cell or a tissue section (e.g., by paraformaldehyde or formalin treatment); permeabilizing the cell or tissue section to allow target accessibility; blocking the cell or tissue section to prevent nonspecific binding; exposing the cell or tissue section to at least one reagent that detects a TERT fusion protein (e.g., an antibody that recognizes the TERT fusion but does not recognize the wild type TERT or the wild type fusion partner); removing unbound or non-specifically bound reagent by washing; and detecting the binding of the reagent with the target protein. In some embodiments, the reagent is directly labeled for detection. In other embodiments, the reagent is linked to an enzyme, and the method further comprises adding a substrate of the enzyme; and detecting a detectable signal produced by the reaction between the enzyme and the substrate. In some embodiments, the immunohistochemistry may comprise the two-step detection as in the indirect ELISA.

(2) Size-based detection methods

[0054] In some embodiments, the method of determining the presence of a TERT fusion (such as, e.g., TRIO:TERT, as disclosed herein) comprises analyzing a protein sample by HPLC. The method may comprise: passing a pressurized liquid solution containing the sample through a column filled with a sorbent, wherein the nucleic acid or protein components in the sample interact differently with the sorbent, causing different flow rates for the different components; separating the components as they flow out the column at different flow rates. In some embodiments, the HPLC is chosen from, e.g., reverse-phase HPLC, size exclusion HPLC, ion-exchange HPLC, and bioaffinity HPLC.

[0055] In some embodiments, the method of determining the presence of a TERT fusion (such as, e.g., TRIO:TERT, as disclosed herein) comprises analyzing a protein sample by mass

spectrometry. The method may comprise: ionizing the components in the sample (e.g., by chemical or electron ionization); accelerating and subjecting the ionized components to an electric or magnetic field; separating the ionized components based on their mass-to-charge ratios; and detecting the separated components by a detector capable of detecting charged particles (e.g., by an electron multiplier).

[0056] Detection of a TERT gene fusion or a TERT fusion protein in a patient can lead to assignment of the patient to the newly identified patient population that bears the TERT fusion. Because this patient population can suffer from or be susceptible to a disorder associated with an aberrant TERT expression or activity, or overexpression of TERT, detection of the TERT fusion can also lead to diagnosis of such disorder. Thus, a further aspect of the invention provides a method of stratifying a patient population (e.g., assigning a patient to a group or class) and/or diagnosing a patient, comprising: obtaining a biological sample from the patient, contacting the sample with at least one reagent that detects a TERT gene fusion or a TERT fusion protein to determine whether a TERT fusion is present in the biological sample. The detection of a TERT fusion indicates that the patient belongs to the newly identified patient population that bears the TERT fusion, and/or the presence of a disorder associated with aberrant TERT expression or activity, or overexpression of TERT, such as, e.g., a cancer. The detection of a TERT fusion also identifies a new subtype of cancer, which is characterized by the presence of the TERT fusion. In some embodiments, the cancer is sarcoma. In some embodiments, the cancer is liposarcoma. In certain embodiments, the TERT fusion is TRIO:TERT. In some embodiments, the TRIO:TERT fusion comprises all or part of the nucleotide and/or amino acid sequence (such as, e.g., the fusion junction) set forth in SEQ ID NO:1 and SEQ ID NO:2, respectively.

Methods for Validating TERT Fusions

[0057] TERT gene fusions (such as, e.g., a TRIO:TERT gene fusion) may be evaluated to ensure that the breakpoints are in-frame and can produce a protein product containing the full RT domain, i.e., that the breakpoint occurs such that complete triplet codons are intact, and that the RNA sequence will produce a viable protein. The TERT gene fusion can be transfected into cells to confirm that the protein is functionally active with respect to RT activity and oncogenic activity. cDNA encoding the TERT fusion protein can be produced by standard solid-phase DNA synthesis. Alternatively the TERT fusion cDNA can be produced by RT-PCR using tumor mRNA extracted from samples containing the gene fusion. The DNA

amplified can be subcloned into an appropriate vector and characterized by DNA sequence analysis or in vitro/in vivo expression analyses.

[0058] Expression vectors containing the TERT gene fusion (such as, e.g., a TRIO:TERT gene fusion) can be introduced into host cells to thereby produce a TERT fusion protein (such as, e.g., a TRIO:TERT fusion protein). The TERT fusion protein expression vector can be a yeast expression vector, a vector for expression in insect cells, e.g., a baculovirus expression vector, or a vector suitable for expression in mammalian cells. Vector DNA can be introduced into host cells via conventional transformation or transfection techniques. As used herein, the terms “transformation” and “transfection” are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (e.g., DNA) into a host cell.

[0059] Cells harboring the expression vector carrying the recombinant TERT gene fusion can then be tested for production of the unique fusion protein via standard western blotting using either an antibody probe that detects the gene product itself or that recognizes a tag peptide (e.g., FLAG tag) that can be added to the gene product via the expression vector (using standard, commercially available reagents). Western blotting can be used to confirm the ectopic expression of the encoded TERT fusion protein by comparing the samples from cells transfected with the vector containing the TERT gene fusion cDNA to cells transfected with the empty expression vector. The functional activity can be assessed by measuring the level of RT activity, e.g., telomere length. Comparison of the level of RT activity between the wild type (normal) form of TERT and the TERT fusion protein can indicate if the TERT fusion protein has elevated activity that could drive oncogenic activity. Whether the TERT gene fusion is oncogenic can be assessed by measuring capacity of the expressed TERT fusion protein to transform cells, that is, to enable cells to grow and proliferate under conditions which are not permissive for growth of normal cells. For example, one method of measuring the transforming activity of the fusion is by assessing if expression of the gene product can allow BaF3 cells to grow in the absence of the growth factor IL3, which is required for the survival and growth of BaF3 cells. Another assay for measuring transforming activity is a soft agar growth assay. This is another standard method which tests the capacity of an introduced gene product to confer the ability to grow in a soft agar matrix, or anchorage-independent conditions. These methods and others can be used to test the oncogenic activity of a TERT gene fusion (such as, e.g., a TRIO:TERT gene fusion) and provide a level of validation of a TERT fusion protein (such as, e.g., a TRIO:TERT fusion protein) as a potential target for treating patients that harbor these fusions.

[0060] A change in an activity of a cell can be detected in a cell in culture, e.g., a cell expressing a fusion (e.g., a mammalian cell, a tumor cell or cell line, a recombinant cell). The transfected cell can show a change in response to the expressed fusion, e.g., increased proliferation, changes in morphology, increased tumorigenicity, and/or an acquired transformed phenotype.

[0061] All publications and patents mentioned herein are hereby incorporated by reference in their entirety as if each individual publication or patent was specifically and individually indicated to be incorporated by reference. To the extent publications and patents or patent applications incorporated by reference contradict the disclosure contained in the specification, the specification will supersede any contradictory material. Unless otherwise required by context, singular terms shall include the plural and plural terms shall include the singular. The use of “or” means “and/or” unless stated otherwise. The use of the term “including,” as well as other forms, such as “includes” and “included,” is not limiting. All ranges given in the application encompass the endpoints unless stated otherwise.

[0062] Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

We claim:

1. A method for detecting the presence of a TERT fusion in a biological sample, comprising the steps of:

- (a) obtaining a biological sample from a mammal; and
- (b) contacting the sample with a reagent that detects a TERT fusion to determine whether a TERT fusion is present in the biological sample,

wherein the detection of the TERT fusion indicates the presence of a TERT fusion in the biological sample.

2. A method of diagnosing a patient, the method comprising:

- (a) obtaining a biological sample from a patient; and
- (b) contacting the sample with a reagent that detects a TERT fusion to determine whether a TERT fusion is present in the biological sample,

whereby the detection of the TERT fusion indicates the presence of or susceptibility to a disorder associated with aberrant TERT expression or activity, or overexpression of TERT.

3. The method of any one of claims 1-2, wherein the method of detecting a TERT fusion in the biological sample comprises one or more assays selected from: in situ hybridization, comparative genomic hybridization, microarray, Southern blot, northern blot, PCR, PCR-RFLP assay, real-time PCR, sequence-specific primers, high-performance liquid chromatography, or mass-spectrometric genotyping, and metaphase cytogenetic analysis by karyotype methods.

4. The method of any one of claims 1-3, wherein the method comprises:

- (a) performing a PCR amplification reaction with polynucleotides from the biological sample,

wherein the amplification reaction utilizes a pair of primers which will amplify at least a fragment of a TERT fusion comprising a fusion junction, and

wherein the first primer is in sense orientation and the second primer is in antisense orientation; and

- (b) detecting an amplification product, wherein the presence of the amplification product is indicative of the presence of a TERT fusion polynucleotide in the sample.

5. The method of claim 4, wherein the step of performing a PCR amplification reaction comprises:

(i) providing a reaction mixture comprising polynucleotides from the biological sample, the pair of primers which will amplify at least a fragment of a TERT gene fusion comprising a fusion junction, wherein the first primer is complementary to a sequence on the first strand of the polynucleotides and the second primer is complementary to a sequence on the second strand of the polynucleotides, a DNA polymerase, and a plurality of free nucleotides comprising adenine, thymine, cytosine, and guanine (dNTPs);

(ii) heating the reaction mixture to a first predetermined temperature for a first predetermined time to separate the double strands of the polynucleotides from each other;

(iii) cooling the reaction mixture to a second predetermined temperature for a second predetermined time under conditions to allow the first and second primers to hybridize with their complementary sequences on the first and second strands of the polynucleotides, and to allow the DNA polymerase to extend the primers; and

(iv) repeating steps (ii) and (iii) for a predetermined number of cycles.

6. The method of any one of claims 1-5, where in the method employs a probe or primer that is detectably labeled with a radiolabel, a fluorescent label, a bioluminescent label, a chemiluminescent label, an enzyme label, a binding pair label, an antigen-label, a reporter molecule, an affinity tag, an adaptor, a barcode, or a sequence identifier.

7. The method of claim 6, wherein the labeled probe or primer is detected using autoradiography, microscopy, brightfield microscopy, fluorescence microscopy, electron microscopy, enzyme-linked immunosorbent assay (ELISA), or immunohistochemistry.

8. The method of any one of claims 1-7, wherein the biological sample is selected from tissue, whole blood, serum, plasma, buccal scrape, sputum, saliva, cerebrospinal fluid, urine, stool, circulating tumor cells, circulating nucleic acids, or bone marrow.

9. The method of any one of claims 1-8, wherein the biological sample is from a human cancer.

10. The method of claim 9, wherein the human cancer is sarcoma.

11. The method of claim 9, wherein the human cancer is liposarcoma.

12. The method of any of claims 1-11, wherein the TERT gene fusion is a TRIO:TERT gene fusion.

13. The method of claim 12, wherein the TRIO:TERT gene fusion comprises all or part of the nucleotide sequence set forth in SEQ ID NO:1 comprising the fusion junction.

14. The method of any of claims 1-13, wherein the reagent is a probe or primer that hybridizes to the fusion junction of a TERT fusion.

15. The method of any of claims 1-14, wherein the reagent hybridizes to nucleotides 4957-4962, 4955-4964, 4950-4969, 4935-4984, or 4910-5009 of SEQ ID NO:1.

16. The method of any of claims 1-15, wherein the reagent detects an mRNA or cDNA encoding a TERT fusion protein.

17. The method of claim 1 or 2, wherein the reagent detects a TERT fusion protein but does not detect wild type TERT or wild type fusion partner.

18. The method of any one of claims 1, 2, and 17, where in the reagent is detectably labeled with a radiolabel, a fluorescent label, a bioluminescent label, a chemiluminescent label, an enzyme label, a binding pair label, an antigen-label, a reporter molecule, an affinity tag, an adaptor, barcode, or a sequence identifier.

19. The method of claim 18, wherein the labeled reagent is detected using one or more of autoradiography, microscopy, brightfield microscopy, fluorescence microscopy, electron microscopy, enzyme-linked immunosorbent assay (ELISA), direct ELISA, indirect ELISA, sandwich ELISA, competitive ELISA, immunohistochemistry, western blot, HPLC, and mass spectrometry.

20. The method of any one of claims 1, 2, and 17-19, wherein the reagent comprises an antibody specific to a TERT fusion protein.

21. The method of any one of claims 17-20, wherein the TERT fusion protein is a TRIO:TERT fusion protein.

22. The method of claim 21, wherein the TRIO:TERT fusion protein comprises all or part of the amino acid sequence set forth in SEQ ID NO:2 comprising the fusion junction.

23. The method of any of claims 1, 2, and 17-22, wherein the reagent reacts with amino acids 1649-1658, 1644-1663, or 1629-1678 of SEQ ID NO:2.

24. The method of any of claims 17-23, wherein the biological sample is from a human cancer.

25. The method of claim 24, wherein the human cancer is sarcoma.

26. The method of claim 24, wherein the human cancer is liposarcoma.

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FIG. 1A

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ATGAGCGGCA GCAGCGGCGG AGCCGCCGCC CCCGCCGCGT CCTCCGGCCC CGCCGCGGCG 60
GCCAGCGCGG CTGGCTCGGG CTGCGGGGGC GGTGCCGGCG AGGGGGCAGA GGAGGCGGCC 120
AAGGACCTGG CCGACATCGC GGCCTTCTTC CGATCCGGGT TTCGAAAAAA CGATGAAATG 180
AAAGCTATGG ATGTTTACC AATTTTGAAG GAAAAAGTTG CATACCTTTC AGGTGGGAGA 240
GATAAACGTG GAGGTCCCAT TTAAACGTTT CCGGCCCGCA GCAATCATGA CAGAATACGA 300
CAGGAGGATC TCAGGAGACT CATTTCCTAT CTAGCCTGTA TTCCCAGCGA GGAGGTCTGC 360
AAGCGTGGCT TCACGGTGAT CGTGGACATG CGTGGGTCCA AGTGGGACTC CATCAAGCCC 420
CTTCTGAAGA TCCTGCAGGA GTCCTTCCCC TGCTGCATCC ATGTGGCCCT GATCATCAAG 480
CCAGACAAC TCTGGCAGAA ACAGAGGACT AATTTTGGCA GTTCTAAATT TGAATTTGAG 540
ACAAATATGG TCTCTTTAGA AGGCCTTACC AAAGTAGTTG ATCCTTCTCA GCTAACTCCT 600
GAGTTTGATG GCTGCCTGGA ATACAACCAC GAAGAATGGA TTGAAATCAG AGTTGCTTTT 660
GAAGACTACA TTAGCAATGC CACCCACATG CTGTCTCGGC TGGAGGAACT TCAGGACATC 720
CTAGCTAAGA AGGAGCTGCC TCAGGATTTA GAGGGGGCTC GGAATATGAT CGAGGAACAT 780
TCTCAGCTGA AGAAGAAGGT GATTAAGGCC CCCATCGAGG ACCTGGATTT GGAGGGACAG 840
AAGCTGCTTC AGAGGATACA GAGCAGTGAA AGCTTTCCCA AAAAGAACTC AGGCTCAGGC 900
AATGCGGACC TGCAGAACCT CTTGCCCAAG GTGTCCACCA TGCTGGACCG GCTGCACTCG 960
ACACGGCAGC ATCTGCACCA GATGTGGCAT GTGAGGAAGC TGAAGCTGGA CCACTGCTTC 1020
CAGCTGAGGC TGTTTGAACA GGATGCTGAG AAGATGTTTG ACTGGATCAC ACACAACAAA 1080
GGCCTGTTTC TAAACAGCTA CACAGAGATT GGGACCAGCC ACCCTCATGC CATGGAGCTT 1140
CAGACGCAGC ACAATCACTT TGCCATGAAC TGTATGAACG TGTATGTAAA TATAAACCGC 1200
ATCATGTCGG TGGCCAATCG TCTGGTGGAG TCTGGCCACT ATGCCTCGCA GCAGATCAGG 1260
CAGATCGCGA GTCAGCTGGA GCAGGAGTGG AAGGCGTTTG CGGCAGCCCT GGATGAGCGG 1320
AGCACCTTGC TGGACATGTC CTCCATTTTC CACCAGAAGG CCGAAAAGTA TATGAGCAAC 1380
GTGGATTTCAT GGTGTAAAGC TTGCGGTGAG GTAGACCTTC CCTCAGAGCT GCAGGACCTA 1440
GAAGATGCCA TTCATCACCA CCAGGGAATA TATGAACATA TCACTCTTGC TTATTTCTGAG 1500
GTCAGCCAAG ATGGGAAGTC GTCCTTGAC AAGCTCCAGC GGCCCTTGAC TCCCGGCAGC 1560
TCCGATTCCC TGACAGCCTC TGCCAACTAC TCCAAGGCCG TGCACCATGT CCTGGATGTC 1620
ATCCACGAGG TGCTGCACCA CCAGCGGCAG CTGGAGAACA TCTGGCAACA CCGCAAGGTC 1680
CGGCTGCATC AGAGGCTGCA GCTGTGTGTT TTCCAGCAGG ACGTTCAGCA GGTGCTAGAC 1740
TGGATCGAGA ACCACGGAGA AGCATTTCTG AGCAACATA CAGGTGTGGG GAAATCTCTT 1800
CATCGGGCCA GAGCATTGCA GAAACGTCAT GAAGATTTTG AAGAAGTGGC ACAGAACACA 1860
TACACCAATG CGGATAAATT ACTGGAAGCA GCAGAACAGC TGGCTCAGAC TGGGGAATGT 1920
GACCCCGAAG AGATTTATCA GGCTGCCCAT CAGCTGGAAG ACCGGATTCA AGATTTCTGTT 1980
CGGCGTGTTG AGCAGCGAAA GATCCTACTG GACATGTCAG TGTCTTTTCA CACCCATGTG 2040
AAAGAGCTGT GGACGTGGCT GGAGGAGCTG CAGAAGGAGC TGCTGGACGA CGTGTATGCC 2100
GAGTCGGTGG AGGCCGTGCA GGACCTCATC AAGCGCTTTG GCCAGCAGCA GCAGACCACC 2160
CTGCAGGTGA CTGTCAACGT GATCAAGGAA GGGGAGGACC TCATCCAGCA GCTCAGGGAC 2220
TCTGCCATCT CCAGTAACAA GACCCCCCAC AACAGCTCCA TCAACCACAT TGAGACGGTG 2280
CTGCAGCAGC TGGACGAGGC GCAGTCGAG ATGGAGGAGC TCTTCCAGGA GCGCAAGATC 2340
AAGCTGGAGC TCTTCTGCA GCTGCGCATC TTCGAGAGGG ACGCCATCGA CATTTCTCA 2400
GACCTCGAGT CTTGGAATGA TGAGCTTTCT CAGCAAATGA ATGACTTCGA CACAGAAGAT 2460
CTCACGATTG CAGAGCAGCG CCTCCAGCAC CATGCAGACA AAGCCTTGAC CATGAACAAC 2520
TTGACTTTTG ACGTCATCCA CCAAGGGCAA GATCTTCTGC AGTATGTCAA TGAGGTCCAG 2580
GCCTCTGGTG TGGAGCTGCT GTGTGATAGA GATGTAGACA TGGCAACTCG GGTCCAGGAC 2640
CTGCTGGAGT TTCTTCATGA AAAACAGCAG GAATTGGATT TAGCCGCGA GCAGCATCGG 2700
AAACACCTGG AGCAGTGCGT GCAGCTGCGC CACCTGCAGG CAGAAGTGAA ACAGGTGCTG 2760
GGTTGGATCC GCAACGGAGA GTCCATGTTA AATGCCGGAC TTATCACAGC CAGCTCGTTA 2820
CAAGAGGCAG AGCAGCTCCA GCGAGAGCAC GAGCAGTTCC AGCATGCCAT TGAGAAAAACA 2880
CATCAGAGCG CGCTGCAGGT GCAGCAGAAG GCAGAAGCCA TGCTACAGGC CAACCACTAC 2940
GACATGGACA TGATCCGGGA CTGCGCCGAG AAGGTGGCGT CTCCTGGCA ACAGCTCATG 3000
CTCAAGATGG AAGATCGCCT CAAGCTCGTC AACGCCTCTG TCGCTTTCTA CAAAACCTCA 3060

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FIG. 1B

GAGCAGGTCT	GCAGCGTCCT	CGAGAGCCTG	GAACAGGAGT	ACAAGAGAGA	AGAAGACTGG	3120
TGTGGCGGGG	CGGATAAGCT	GGGCCCCAAC	TCTGAGACGG	ACCACGTGAC	GGCCATGATC	3180
AGCAAGCACC	TGGAGCAGAA	GGAGGCATTC	CTGAAGGCTT	GCACCCTTGC	TCGGAGGAAT	3240
GCAGACGTCT	TCCTGAAATA	CCTGCACAGG	AACAGCGTGA	ACATGCCAGG	AATGGTGAAC	3300
CACATCAAAG	CTCCTGAACA	GCAAGTGAAA	AATATCTTGA	ATGAACTCTT	CCAACGGGAG	3360
AACAGGGTAT	TGCATTACTG	GACCATGAGG	AAGAGACGGC	TGGACCAGTG	TCAGCAGTAC	3420
GTGGTCTTTG	AGAGGAGTGC	CAAGCAGGCT	TTGGAATGGA	TCCATGACAA	TGGCGAGTTC	3480
TACCTTTCCA	CACACACCTC	CACGGGCTCC	AGTATACAGC	ACACCCAGGA	GCTCCTGAAA	3540
GAGCACGAGG	AGTTCCAGAT	AACTGCAAAAG	CAAACCAAAG	AGAGAGTGAA	GCTATTGATA	3600
CAGCTGGCTG	ATGGCTTTTG	TGAAAAAGGG	CATGCCCCATG	CGGCAGAGAT	AAAAAAATGT	3660
GTTACTGCTG	TGGATAAGAG	GTACAGAGAT	TTCTCTCTGC	GGATGGAGAA	GTACAGGACC	3720
TCTTTGGAAA	AAGCCCTGGG	GATTTCTTCA	GATTCCAACA	AATCGAGTAA	AGTCTCCAG	3780
CTAGATATCA	TTCCAGCCAG	TATCCCTGGC	TCAGAGGTGA	AACTTCGAGA	TGCTGCTCAT	3840
GAACTTAATG	AAGAGAAGCG	GAAATCTGCC	CGCAGGAAAG	AGTTCATAAT	GGCTGAGCTC	3900
ATTCAAACCTG	AAAAGGCCTTA	TGTAAGAGAC	CTCCGGGAAT	GTATGGATAC	GTACCTGTGG	3960
GAAATGACCA	GTGGCGTGGA	AGAGATTCCA	CCTGGCATTG	TAAACAAAGA	ACTCATCATC	4020
TTCCGAAACA	TGCAAGAAAT	CTACGAATTT	CATAATAACA	TATTCCTAAA	GGAGCTGGAA	4080
AAATATGAAC	AGTTGCCAGA	GGATGTTGGA	CATTGTTTTG	TTACTTGGGC	AGACAAGTTT	4140
CAGATGTATG	TCACATATTG	CAAAAATAAG	CCTGATTCTA	CTCAGCTGAT	ATTGGAACAT	4200
GCAGGGTCCT	ATTTTGAACG	GATACAGCAG	CGACATGGAT	TAGCCAATTC	CATTTCTTCC	4260
TACCTTATTA	AACCACTTCA	GCGAATAACG	AAGTATCAGC	TCCTTTTAAA	AGAGCTGCTG	4320
ACGTGCTGTG	AGGAAGGAAA	GGGAGAGATT	AAAGATGGCC	TGGAGGTGAT	GCTCAGCGTG	4380
CCGAAGCGAG	CCAATGATGC	CATGCACCTC	AGCATGCTGG	AAGGGTTTGA	TGAAAACATT	4440
GAGTCTCAGG	GAGAACTCAT	CCTACAGGAA	TCCTTCCAAG	TGTGGGACCC	AAAAACCTTA	4500
ATTCGAAAGG	GTCGAGAACG	GCATCTCTTC	CTTTTTGAAA	TGTCCTTAGT	ATTTAGTAAA	4560
GAAGTGAAAG	ATTCCAGTGG	GAGAAGCAAG	TACCTTTATA	AAAGCAAATT	GTTTACCTCA	4620
GAGTTGGGTG	TCACAGAACA	TGTTGAAGGA	GACCCTTGCA	AATTTGCACT	GTGGGTGGGG	4680
AGAACACCAA	CTTCAGATAA	TAAATTGTC	CTTAAGGCTT	CCAGCATAGA	GAACAAGCAG	4740
GACTGGATAA	AGCATATCCG	CGAAGTCATC	CAGGAGCGGA	CGATCCACCT	GAAGGGAGCC	4800
CTGAAGGAGC	CCATTACAT	CCCTAAGACC	GCTCCCGCCA	CAAGACAGAA	GGGAAGGAGG	4860
GATGGAGAGG	ATCTGGACAG	CCAAGGAGAC	GGCAGCAGCC	AGCCTGATAC	GATTTCCATC	4920
GCCTCACGGA	CGTCTCAGAA	CACGCTGGAC	AGCGATAAG/G	TGTCCTGCCT	GAAGGAGCTG	4980
GTGGCCCCGAG	TGCTGCAGAG	GCTGTGCGAG	CGCGGCGCGA	AGAACGTGCT	GGCCTTCGGC	5040
TTGCGCTGCT	TGCTGCGGGC	CCGCGGGGGC	CCCCCGAGG	CCTTCACCAC	CAGCGTGCGC	5100
AGCTACCTGC	CCAACACGGT	GACCGACGCA	CTGCGGGGGA	GCGGGGCGTG	GGGGCTGCTG	5160
CTGCGCCGCG	TGGGCGACGA	CGTGCTGGTT	CACCTGCTGG	CACGCTGCGC	GCTCTTTGTG	5220
CTGGTGGCTC	CCAGCTGCGC	CTACCAGGTG	TGCGGGCCGC	CGCTGTACCA	GCTCGGCGCT	5280
GCCACTCAGG	CCCGGCCCCC	GCCACACGCT	AGTGGACCCC	GAAGGCGTCT	GGGATGCGAA	5340
CGGGCCTTGA	ACCATAGCGT	CAGGGAGGCC	GGGGTCCCCC	TGGGCCCTGCC	AGCCCCGGGT	5400
GCGAGGAGGC	GCGGGGGCAG	TGCCAGCCGA	AGTCTGCCGT	TGCCCAAGAG	GCCCAGGCGT	5460
GGCGCTGCCC	CTGAGCCGGA	GCGGACGCCC	GTTGGGCAGG	GGTCCTGGGC	CCACCCGGGC	5520
AGGACGCGTG	GACCGAGTGA	CCGTGGTTTC	TGTGTGGTGT	CACCTGCCAG	ACCCGCCGAA	5580
GAAGCCACCT	CTTTGGAGGG	TGCGCTCTCT	GGCAGCGGCC	ACTCCACCC	ATCCGTGGGC	5640
GCCACACACC	ACGCGGGCCC	CCCATCCACA	TCGCGGCCAC	CACGTCCCTG	GGACACGCCT	5700
TGTCCCCCGG	TGTACGCCGA	GACCAAGCAC	TTCTCTACT	CCTCAGGCGA	CAAGGAGCAG	5760
CTGCGGCCCT	CCTTCTACT	CAGCTCTCTG	AGGCCAGCC	TGACTGGCGC	TCGGAGGCTC	5820
GTGGAGACCA	TCTTTCTGGG	TTCCAGGCCC	TGGATGCCAG	GGACTCCCCG	CAGGTTGCCC	5880
CGCCTGCCCC	AGCGCTACTG	GCAAAATGCGG	CCCCTGTTTT	TGGAGCTGCT	TGGGAACCAC	5940
GCGCAGTGCC	CCTACGGGGT	GCTCCTCAAG	ACGCACTGCC	CGCTGCGAGC	TGCGGTCACC	6000
CCAGCAGCCG	GTGTCTGTGC	CCGGGAGAAG	CCCCAGGGCT	CTGTGGCGGC	CCCCGAGGAG	6060
GAGGACACAG	ACCCCCGTGC	CCTGGTGCAG	CTGCTCCGCC	AGCACAGCAG	CCCCTGGCAG	6120

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FIG. 1C

GTGTACGGCT	TCGTGCGGGC	CTGCCTGCGC	CGGCTGGTGC	CCCCAGGCC	CTGGGGCTCC	6180
AGGCACAACG	AACGCCGCTT	CCTCAGGAAC	ACCAAGAAGT	TCATCTCCCT	GGGGAAGCAT	6240
GCCAAGCTCT	CGCTGCAGGA	GCTGACGTGG	AAGATGAGCG	TGCGGGACTG	CGCTTGGCTG	6300
CGCAGGAGCC	CAGGGGTGG	CTGTGTTCGG	GCCGCAGAGC	ACCGTCTGCG	TGAGGAGATC	6360
CTGGCCAAGT	TCCTGCACTG	GCTGATGAGT	GTGTACGTGC	TCGAGCTGCT	CAGGTCTTTC	6420
TTTTATGTCA	CGGAGACCAC	GTTTCAAAAAG	AACAGGCTCT	TTTTCTACCG	GAAGAGTGTC	6480
TGGAGCAAGT	TGCAAAGCAT	TGGAATCAGA	CAGCACTTGA	AGAGGGTGCA	GCTGCGGGAG	6540
CTGTGCGAAG	CAGAGGTCAG	GCAGCATCGG	GAAGCCAGGC	CCGCCCTGCT	GACGTCCAGA	6600
CTCCGCTTCA	TCCCCAAGCC	TGACGGGCTG	CGGCCGATTG	TGAACATGGA	CTACGTCGTG	6660
GGAGCCAGAA	CGTTCCGCAG	AGAAAAGAGG	GCCGAGCGTC	TCACCTCGAG	GGTGAAGGCA	6720
CTGTTACGCG	TGCTCAACTA	CGAGCGGGCG	CGGCGCCCCG	GCCTCCTGGG	CGCCTCTGTG	6780
CTGGGCCTGG	ACGATATCCA	CAGGGCCTGG	CGCACCTTCG	TGCTGCGTGT	GCGGGCCCAG	6840
GACCCGCCGC	CTGAGCTGTA	CTTTGTCAAG	GTGGATGTGA	CGGGCGCGTA	CGACACCATC	6900
CCCCAGGACA	GGCTCACGGA	GGTCATCGCC	AGCATCATCA	AACCCAGAA	CACGTACTGC	6960
GTGCGTCGGT	ATGCCGTGGT	CCAGAAGGCC	GCCCATGGGC	ACGTCCGCAA	GGCCTTCAAG	7020
AGCCACGTCT	CTACCTTGAC	AGACCTCCAG	CCGTACATGC	GACAGTTCGT	GGCTCACCTG	7080
CAGGAGACCA	GCCCCGTGAG	GGATGCCGTC	GTCATCGAGC	AGAGCTCCTC	CCTGAATGAG	7140
GCCAGCAGTG	GCCTCTTCGA	CGTCTTCCTA	CGCTTCATGT	GCCACCACGC	CGTGCGCATC	7200
AGGGGCAAGT	CCTACGTCCA	GTGCCAGGGG	ATCCCGCAGG	GCTCCATCCT	CTCCACGCTG	7260
CTCTGCAGCC	TGTGCTACGG	CGACATGGAG	AACAAGCTGT	TTGCGGGGAT	TGCGCGGGAC	7320
GGGCTGCTCC	TGCGTTTGGT	GGATGATTTT	TTGTTGGTGA	CACCTCACCT	CACCCACGCG	7380
AAAACCTTCC	TCAGGACCC	GGTCCGAGGT	GTCCCTGAGT	ATGGCTGCGT	GGTGAACCTG	7440
CGGAAGACAG	TGGTGAACCT	CCCTGTAGAA	GACGAGGCC	TGGGTGGCAC	GGCTTTTGTT	7500
CAGATGCCGG	CCCACGGCCT	ATTCCCCTGG	TGCGGCCCTGC	TGCTGGATAC	CCGGACCCTG	7560
GAGGTGCAGA	GCGACTACTC	CAGCTATGCC	CGGACCTCCA	TCAGAGCCAG	TCTCACCTTC	7620
AACCGCGGCT	TCAAGGCTGG	GAGGAACATG	CGTCGCAAAAC	TCTTTGGGGT	CTTGCGGGCTG	7680
AAGTGTCACA	GCCTGTTTCT	GGATTTGCAG	GTGAACAGCC	TCCAGACGGT	GTGCACCAAC	7740
ATCTACAAGA	TCCTCTTGCT	GCAGGCGTAC	AGGTTTTCACG	CATGTGTGCT	GCAGCTCCCA	7800
TTTCATCAGC	AAGTTTGGAA	GAACCCACAC	TTTTTCCTGC	GCGTCATCTC	TGACACGGCC	7860
TCCCTCTGCT	ACTCCATCCT	GAAAGCCAAG	AACGCAGGGA	TGTCGCTGGG	GGCCAAGGGC	7920
GCCGCCGGCC	CTCTGCCCTC	CGAGGCCGTG	CAGTGGCTGT	GCCACCAAGC	ATTCTCTGCTC	7980
AAGCTGACTC	GACACCGTGT	CACCTACGTG	CCACTCCTGG	GGTCACTCAG	GACAGCCCAG	8040
ACGCAGCTGA	GTCGGAAGCT	CCCGGGGACG	ACGCTGACTG	CCCTGGAGGC	CGCAGCCAAC	8100
CCGGCACTGC	CCTCAGACTT	CAAGACCATC	CTGGACTGA			8139

(SEQ ID NO:1)

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FIG. 2

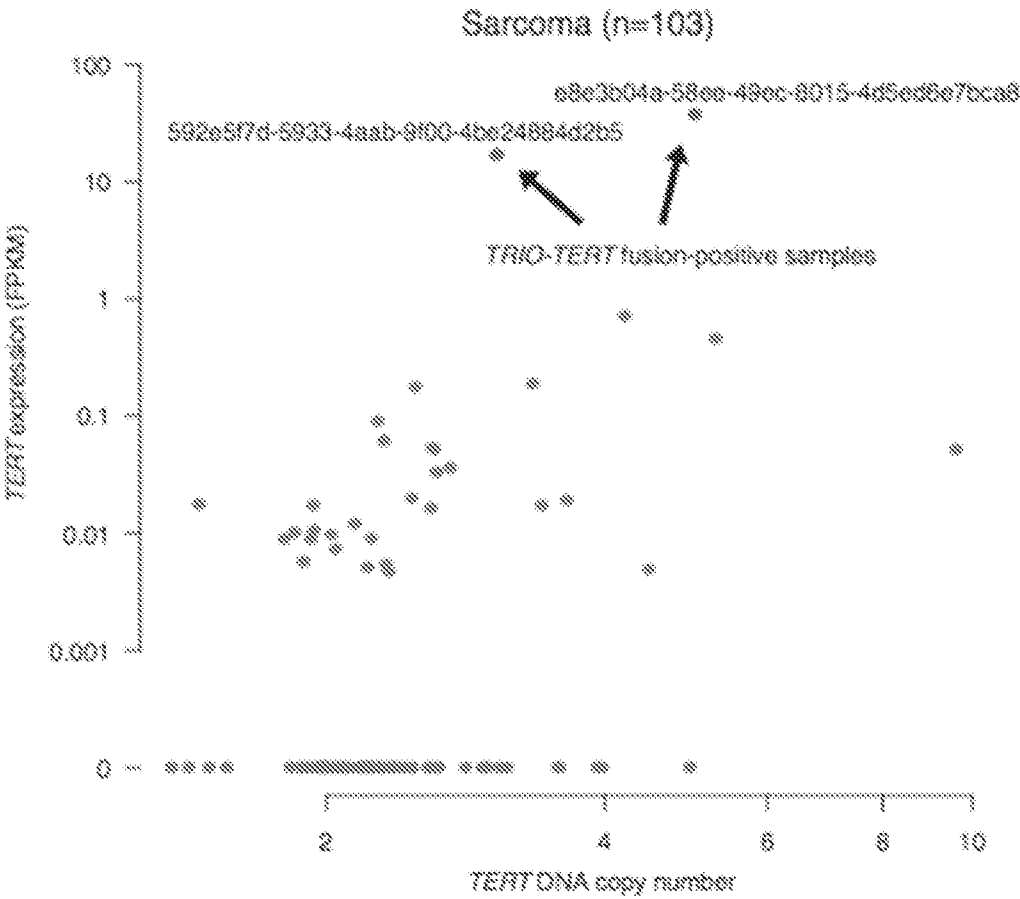
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MSGSSGGAAA PAASSGPAAA ASAAGSGCGG GAGEGAEAAA KDLADIAAFF RSGFRKNDEM 60
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KRGFTVIVDM RGSKWDSIKP LLKILQESFP CCIHVALIHK PDNFWQKQRT NFGSSKFEFE 180
TNMVSLEGLT KVVDPSQLTP EFDGCLEYNH EEWIEIRVAF EDYISNATHM LSRLEELQDI 240
LAKKELPQDL EGARNMIEEH SQLKKKVIKA PIEDLDLEGQ KLLQRIQSSE SFPKKNSSGSG 300
NADLQNLPLK VSTMLDRLHS TRQHLHQMWL VRKLKLDQCF QLRLEQDAE KMFDWITHNK 360
GLFLNSYTEI GTSHPHAMEL QTQHNHFAMN CMNVYVNINR IMSVANRLVE SGHYASQQIR 420
QIASQLEQEW KAFAAALDER STLLDMSSIF HQKAEKYSN VDSWCKACGE VDLPSELQDL 480
EDAIHHHQGI YEHITLAYSE VSQDGKSLLD KLQRPLTPGS SDSLTASANY SKAVHHVLDV 540
IHEVLHHQRO LENIWQHRKV RLHQRLQLCV FQQDVQQVLD WIENHGEAFL SKHTGVGKSL 600
HRRARALQKRH EDFEEVAQNT YTNADKLLEA AEQLAQTGEC DPEEIYQAAH QLEDRIQDFV 660
RRVEQRKILL DMSVSFHTHV KELWTWLEEL QKELLDDVYA ESVEAVQDLI KRFGQQQQT 720
LQVTVNVIKE GEDLIQQLRD SAISSNKTPH NSSINHIEIV LQQLDEAQSQ MEELFQERKI 780
KLELFLQLRI FERDAIDIIS DLESWNDELS QQMNDFTED LTIAEQRLQH HADKALTMNN 840
LTFDVIHQGQ DLLQYVNEVQ ASGVLLCDR DVDMATRVQD LLEFLHEKQQ ELDLAAEQHR 900
KHLEQCVQLR HLQAEVKQVL GWIRNGESML NAGLITASSL QEAEQLQREH EQFQHAIEKT 960
HQSALQVQOK AEAMLQANHY DMDMIRDCAE KVASHWQQLM LKMEDRLKLV NASVAFYKTS 1020
EQVCSVLES L EQEYKREEDW CGGADKLGN SETDHVTPMI SKHLEQKEAF LKACTLARRN 1080
ADVFLKYLHR NSVNMPGMVT HIKAPEQQVK NILNELFORE NRVLHYWTMR KRRLDQCCQY 1140
VVFERSAKQA LEWIHDNGEF YLSTHTSTGS SIQHTQELLK EHEEFQITAK QTKERVKLLI 1200
QLADGFCEKG HAHAAEIKKC VTAVDKRYRD FSLRMEKYRT SLEKALGISS DSNKSSKSLQ 1260
LDIIPASIP SEVKLRDAH ELNEEKRKSA RRKEFIMAEI IQTEKAYVRD LRECMDTYLW 1320
EMTSGVEEIP PGIVNKEIIE FGNMQEIEYF HNNIFLKELE KYEQLPEDVG HCFVTWADKF 1380
QMYVTYCKNK PDSTQLILEH AGSYFDEIQO RHGLANSISS YLIKPVQRIT KYQLLLKELL 1440
TCCEEGKGEI KDGLEVMLSV PKRANDAMHL SMLEGFDENI ESQGELILOE SFQVNDPKTL 1500
IRKGRERHLE LFEMSLVFSK EVKDSSGRSK YLYKSKLFTS ELGVTEHVEG DPCKFALWVG 1560
RTPTSNDKIV LKASSIENKQ DWIKHIREVI QERTIHLKGA LKEPIHIPKT APATROKGR 1620
DGEDLDSQGD GSSQPDITSI ASRTSQNTLD SDK/VSCLEL VARVLQRLCE RGAKNVLAFG 1680
FALLDGARGG PPEAFTTSVR SYLPNTVTDA LRGSGAWGLL LRRVGDDVLV HLLARCALEV 1740
LVAPSCAYQV CGPPYQLGA ATQARPPPHA SGPRRLGCE RAWNHSVREA GVPLGLPAPG 1800
ARRRGGSASR SLPLPKRPRR GAPEPERPTP VGQGSWAHPG RTRGPSDRGF CVVSPARPAE 1860
EATSLEGALS GTRHSHPSVG RQHHAGPPST SRPPRPWDTP CPPVYAETKH FLYSSGDKEQ 1920
LRPSFLLSSL RPSLTGARRL VETIFLGSRP WMPGTPRRLP RLPQRYWQMR PLFLELLGNH 1980
AQCPYGVLLK THCPRAAVT PAAGVCAREK PQGSVAAPPE EDTDPRRLVQ LLRQHSSPWQ 2040
VYGFVRACLR RLVPGLWGS RHNERREFLN TKKFISLGKH AKLSLQELTW KMSVRDCAWL 2100
RRSPGVGCVP AAHRLREEI LAKFLHWLMS VYVVELLSRF FYVTETTFQK NRLFYRKS 2160
WSKLQSIGIR QHLKRVQLRE LSEAEVRQHR EARPALLTSR LRFIPKPDGL RPIVNMDYVV 2220
GARTFRREKR AERLTSRVKA LFSVLNYERA RRPGLLGASV LGLDDIHRW RTFVLRVRAQ 2280
DPPPELYFVK VDVGTAYDTI PQDRLTEVIA SIIKPQNTYC VRRYAVVQKA AHGHVRKAFK 2340
SHVSTLTDLQ PYMRQFVAHL QETSPLRDAV VIEQSSSLNE ASSGLFDVFL RFMCHHAVRI 2400
RGKSYVQCQG IPQGSILSTL LCSLCYGDME NKLEAGIRRD GLLLRVLDDF LLVTPHLTHA 2460
KTFLRTLVRG VPEYGCVVNL RKTVVNFVE DEALGGTAFV QMPAHGLFPW CGLLLDTRTL 2520
EVQSDYSSYA RTSIRASLTF NRGFKAGRNM RRKLFGLVRL KCHSLFLDLQ VNSLQTVCTN 2580
IYKILLQAY RFHACHQLP FHQQVWKNPT FFLRVISDTA SLCYSILKAK NAGMSLGAKG 2640
AAGPLPSEAV QWLCHQAFLL KLTRHRVTYV PLLGSLRTAQ TQLSRKLPST TLTALEAAAN 2700
PALPSDEKTI LD 2712

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(SEQ ID NO:2)

FIG. 3



INTERNATIONAL SEARCH REPORT

International application No
PCT/US2015/040557

A. CLASSIFICATION OF SUBJECT MATTER
INV. C12Q1/68
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

EPO-Internal, BIOSIS, Sequence Search, EMBASE, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

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X	D. T. BREAU LT ET AL: "Generation of mTert-GFP mice as a model to identify and study tissue progenitor cells", PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES, vol. 105, no. 30, 29 July 2008 (2008-07-29), pages 10420-10425, XP055224207, US ISSN: 0027-8424, DOI: 10.1073/pnas.0804800105 figure 2	1,3-8, 16-20
X	WO 2013/173912 A1 (HOSPITAL FOR SICK CHILDREN [CA]) 28 November 2013 (2013-11-28) paragraph [0061] - paragraph [0062]; claim 1 ----- -/-	2-11,14, 16-20



Further documents are listed in the continuation of Box C.



See patent family annex.

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"&" document member of the same patent family

Date of the actual completion of the international search

3 November 2015

Date of mailing of the international search report

09/11/2015

Name and mailing address of the ISA/

European Patent Office, P.B. 5818 Patentlaan 2
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Authorized officer

Santagati, Fabio

INTERNATIONAL SEARCH REPORT

International application No

PCT/US2015/040557

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INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No

PCT/US2015/040557

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