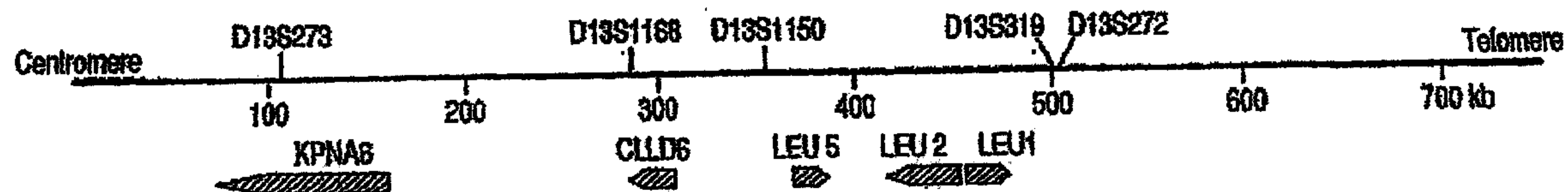




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(72) Inventeurs/Inventors:
CROCE, CARLO M., US;
CALIN, GEORGE A., US
(73) Propriétaire/Owner:
THE OHIO STATE UNIVERSITY RESEARCH
FOUNDATION, US
(74) Agent: G. RONALD BELL & ASSOCIATES

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(57) Abrégé/Abstract:

The invention provides methods and compositions for the treatment of cancers associated with overexpression of a BCL2 gene and/or gene product in a subject, and methods and compositions for the improvement of anti-cancer therapy, such as chemotherapy and radiation therapy. The invention also encompasses methods for determining the efficacy of a cancer therapy in a subject and methods for inducing apoptosis of a cell.



ABSTRACT

The invention provides methods and compositions for the treatment of cancers associated with overexpression of a BCL2 gene and/or gene product in a subject, and methods and compositions for the improvement of anti-cancer therapy, such as chemotherapy and radiation therapy. The invention also encompasses methods for determining the efficacy of a cancer therapy in a subject and methods for inducing apoptosis of a cell.

COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND THERAPY OF BCL2-ASSOCIATED CANCERS

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FIELD OF THE INVENTION

The invention relates to the diagnosis of cancers, in particular to the diagnosis of BCL2-associated cancers. The invention further encompasses methods and compositions for the treatment of cancers involving overexpression of a BCL2 gene and/or gene product. The invention additionally provides novel methods and compositions for the improvement of anti-cancer therapies, such as chemotherapy and other conventional cancer therapies.

BACKGROUND OF THE INVENTION

15 MicroRNAs (miRNAs, miRs) are found in over one hundred distinct organisms, including fruit flies, nematodes and humans. miRNAs are believed to be involved in a variety of processes that modulate development in these organisms. The miRNAs are typically processed from 60- to 70-nucleotide foldback RNA precursor structures, which are transcribed from the miRNA gene. The RNA precursor or processed miRNA products are easily
20 detected, and a lack of these molecules can indicate a deletion or loss of function of the corresponding miRNA gene.

Cancers are a significant source of mortality and morbidity in the U.S. and throughout the world. In particular, chronic lymphocytic leukemia ("CLL") and other BCL2-associated cancers (e.g., acute myeloid leukemia, multiple myeloma, melanomas, lymphomas (e.g.,

follicular lymphoma, large cell lymphoma, non-Hodgkin's lymphoma), carcinomas (e.g., brain carcinoma, breast carcinoma, prostate carcinoma, non-small cell lung carcinoma, renal carcinoma, hepatocellular carcinoma and gastric carcinoma), hematologic malignancies, solid tumors, colorectal cancer, Epstein-Barr virus-associated lymphoproliferative disease) are clinically important neoplastic diseases of adult humans. For example, CLL is the most common form of adult leukemia in the Western world, and the age-adjusted incidence of prostate cancer now surpasses that of all other cancers among men in the United States, and, after lung cancer, is the second leading cause of all male cancer deaths in the country.

Hemizygous and/or homozygous loss at 13q14 occurs in more than half of the reported CLL cases, and constitutes the most frequent chromosomal abnormality in CLL. The karyotyping of tissue samples from CLL patients identified relatively few chromosomal abnormalities, suggesting that the specificity and frequency of observed deletions at 13q14 have pathologic significance. In addition, 13q14 deletions also occur in 60% of prostate cancers, suggesting that one or more tumor suppressor genes located at 13q14 are involved in the pathogenesis of both CLL and prostate cancers.

The presence of both clonal homozygous and heterozygous deletions, and the very high frequency of 13q14 loss in CLL and prostate cancers, indicates that deletions in this region are related to the etiology of certain cancer types. Several groups have used positional cloning in order to identify the gene or genes in the deleted areas. To date, a total of eight genes from the deleted regions of 13q14 in sporadic and familial cases of CLL have been identified and screened for alterations at the DNA and/or RNA level: *Leu1* (*BCMS* or *EST70/Leu1*), *Leu 2* (*ALT1* or *1B4/Leu2*), *Leu 5* (*CAR*), *CLLD6*, *KPNA3*, *CLLD7*, *LOC51131* (putative zinc finger protein NY-REN-34 antigen) and *CLLD8*. However, detailed genetic analyses, including extensive loss of heterozygosity (LOH), mutation and expression studies, have failed to demonstrate the consistent involvement of any of these genes in carcinogenesis.

The malignant, mostly non-dividing B cells of CLL overexpress Bcl2 protein (Kitada, S., *et al.*, *Blood* 91: 3379-3389 (1998)), an apoptosis inhibitor that plays a central role in promoting survival of eukaryotic cells by inhibiting cell death (Cory, S., and Adams, J.M., *Nature Reviews* 2: 647-656 (2002)). Overexpression of Bcl2 has been associated with many

types of human cancers, including leukemias, lymphomas and carcinomas (Sanchez-Beato, M., *et al.*, *Blood* 101: 1220-1235 (2003)). In follicular lymphomas, and in a fraction of diffuse B-cell lymphomas, the mechanism of BCL2 activation was found to be a chromosomal translocation, t(14;18)(q32;q21), which places the BCL2 gene under the control of immunoglobulin heavy chain enhancers, resulting in deregulated expression of the gene (Tsujiimoto, Y., *et al.*, *Science* 226: 1097-1099 (1984); Tsujiimoto, Y., *et al.*, *Science* 228: 1440-1443 (1985)). However, the BCL2 gene is juxtaposed to immunoglobulin loci in less than 5% of CLL cases (Adachi, M., *et al.*, *J. Exp. Med.* 171: 559-564 (1990)), and the mechanism by which BCL2 is overexpressed in the majority of CLL cancers is unknown.

Current therapies for CLL typically involve chemotherapy, administered alone or in combination with autologous bone marrow transplantation. The chemotherapy agents employed are generally toxic to the patient and cause only partial remissions in a relatively large proportion of patients. Therapies for BCL2-associated cancer therapies can also involve chemotherapy, often following surgical resection of a tumor. However, as with CLL, the curative properties of the chemotherapeutic agents (with or without surgery) are limited.

Treatment with chemotherapy alone is limited in that cancer cells often become resistant to a broad spectrum of structurally unrelated chemotherapeutic agents. Such resistance, termed "multidrug resistance" (MDR), is a common problem in the treatment of patients with cancer, and the resistance of tumor cells to chemotherapeutic drugs represents a major problem in clinical oncology.

Apoptosis is an important component of the sequence of events during which chemotherapeutic drugs induce an antitumor response, and studies have implicated Bcl2 as having a critical role in anticancer drug-induced apoptosis (Kim, R. *et al.*, *Cancer* 101(11): 2491-2502 (2004)). Furthermore, tumor cells engineered to overexpress Bcl2 develop resistance to the cytotoxic effects of a number of different drugs (Kamesaki *et al.*, *Cancer Res.* 53: 4251-4256 (1993); Miyashita and Reed, *Blood* 81: 151-157 (1993)).

There is a need for a rapid, economical and accurate diagnostic test for CLL and other BCL2-associated cancers. There is also a need for an economical and effective treatment for BCL2-associated cancers, such as CLL, which does not have a significant negative impact on the patient. There is a further need for new anti-cancer therapies that are directed to inhibiting

expression of Bcl2, given that a wide variety of common cancers are associated with Bcl2 protein overexpression in addition, there is a need for improved anti-cancer therapies that display increased efficacy relative to other conventional anti-cancer treatments. Furthermore, there is a need to identify agents and methods that can increase the sensitivity of cancer cells to the cytotoxic effects of anti-cancer agents, thereby improving cancer therapies. There is also a need for methods of inducing apoptosis in a cell that overexpresses an anti-apoptotic protein, such as Bcl2.

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SUMMARY OF THE INVENTION

It has now been discovered that certain microRNAs with sequences that are complementary to nucleotide sequences in the BCL2 gene transcript are deregulated in cancer cells that overexpress Bcl2 protein.

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According to an aspect of the present invention, there is provided use of miR-15a or miR-16-1 to reduce BCL2 expression in BCL2-expressing cancer cells.

According to another aspect of the present invention, there is provided use of miR-15a or miR-16-1 to increase the efficacy of an anti-cancer treatment.

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According to yet another aspect of the present invention, there is provided use of miR-15a or miR-16-1 to increase the sensitivity of a BCL2-expressing cancer cells to the cytotoxic effects of an anti-cancer agent.

According to yet another aspect of the present invention, there is provided use of miR-15a or miR-16-1 to induce apoptosis in a BCL2-expressing cancer cell, comprising contacting the cell with at least one miR-15 or miR-16-1 gene product.

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According to further aspect of the present invention, there is provided a pharmaceutical composition for treating a BCL2-associated cancer, comprising miR-15a or miR-16-1.

According to yet further aspect of the present invention, there is provided a pharmaceutical composition for treating a BCL2-associated cancer, comprising miR-15a and miR-16-1.

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According to an aspect of the present invention, there is provided a method of increasing the efficacy of anti-cancer treatment in a subject having a BCL2-associated cancer,

comprising administering at least one anti-cancer treatment to the subject; and administering at least one miR gene product to the subject, wherein the at least one miR gene product comprises a nucleotide sequence that is complementary to a nucleotide sequence in a BCL2 gene transcript; wherein, the efficacy of the anti-cancer treatment is increased.

5 According to another aspect of the present invention, there is provided a method of increasing the efficacy of anti-cancer treatment in a human subject having a BCL2-associated cancer, comprising administering at least one anti-cancer treatment to the subject; and administering at least one miR gene product to the subject, wherein the at least one miR gene product comprises a nucleotide sequence that is complementary to a nucleotide sequence in a
10 BCL2 gene transcript; wherein, the efficacy of the anti-cancer treatment is increased.

 According to a further aspect of the present invention, there is provided a method of increasing the sensitivity of a cancer cell to the cytotoxic effects of an anti-cancer agent, comprising administering to the cancer cell at least one miR gene product comprising a nucleotide sequence that is complementary to a nucleotide sequence in a BCL2 gene

transcript, wherein the sensitivity of the cell to the anti-cancer agent is increased.

According to a still further aspect of the present invention, there is provided a method of inducing apoptosis in a cell comprising contacting the cell with at least one miR gene product, wherein the at least one miR gene product comprises a nucleotide sequence that is
5 complementary to a nucleotide sequence in a BCL2 gene transcript.

According to yet another aspect of the present invention, there is provided a method of treating a cancer associated with overexpression of a BCL2 gene product in a subject, comprising administering an effective amount of at least one miR gene product to the subject,
10 wherein the at least one miR gene product comprises a nucleotide sequence that is complementary to a nucleotide sequence in a BCL2 gene transcript, thereby treating the cancer.

According to still yet another aspect of the present invention, there is provided a method of treating a cancer associated with overexpression of a BCL2 gene product in a
15 subject, comprising administering an effective amount of at least one miR gene product to the subject, wherein the at least one miR gene product comprises a nucleotide sequence that is complementary to a nucleotide sequence in a BCL2-gene transcript, provided that the miR gene product is not miR-15a or miR-16-1.

According to a further aspect of the present invention, there is provided a method
20 of treating a cancer associated with overexpression of a BCL2 gene product in a subject, comprising administering an effective amount of at least one miR gene product to the subject, wherein the at least one miR gene product is selected from the group consisting of miR-30, miR-15b, miR-16-2, miR-217, miR-205, miR-204, miR-103, miR-107, miR-9, and miR-137.

25 According to a still further aspect of the present invention, there is provided a pharmaceutical composition for treating a Bcl2-associated cancer, comprising at least one anti-cancer agent and at least one miR gene product, wherein the at least one miR gene product comprises a nucleotide sequence that is complementary to a nucleotide sequence in a BCL2 gene transcript.

According to another aspect of the present invention, there is provided a method for determining the efficacy of a cancer therapy in a subject, comprising administering at least one therapeutic agent to the subject and subsequently measuring the expression of at least one miR gene product in a sample from the subject, wherein the miR gene product comprises a nucleotide sequence that is complementary to a nucleotide sequence in a BCL2 gene transcript.

According to yet another aspect of the present invention, there is provided a method of preventing a cancer associated with overexpression of BCL2 gene product in a subject, comprising administering an effective amount of at least one miR gene product to the subject, wherein the at least one miR gene product comprises a nucleotide sequence that is complementary to a nucleotide sequence in a BCL2 gene transcript.

According to still yet another aspect of the present invention, there is provided a method of preventing a cancer associated with overexpression of BCL2 gene product in a subject, comprising administering an effective amount of at least one miR gene product to the subject, wherein the at least one miR gene product comprises a nucleotide sequence that is complementary to a nucleotide sequence in a BCL2 gene transcript, provided that the miR gene product is not miR-15a or miR-16-1.

According to a further aspect of the present invention, there is provided a method of preventing a cancer associated with overexpression of BCL2 gene product in a subject, comprising administering an effective amount of at least one miR gene product to the subject, wherein the at least one miR gene product is selected from the group consisting of miR-30, miR-15b, miR-16-2, miR-217, miR-205, miR-204, miR-103, miR-107, miR-9, and miR-137, thereby preventing the cancer.

According to a still further aspect of the present invention, there is provided a method of diagnosing or prognosticating a BCL2-associated cancer in a subject, comprising determining the level of at least one miR gene product in a sample from the subject; and comparing the level of the at least one miR gene product in the sample to a control, wherein a decrease in the level of the at least one miR gene product in the sample from the subject,

relative to that of the control, is diagnostic or prognostic of a BCL2-associated cancer, and wherein the at least one miR gene product comprises a nucleotide sequence that is complementary to a nucleotide sequence in a BCL2 gene transcript.

5 Accordingly, the invention provides methods of preventing a cancer or treating a cancer associated with overexpression of a BCL2 gene or gene product (e.g., RNA, protein) in a subject in need of such treatment, comprising administering an effective amount of at least one miR gene product. As used herein, the term "BCL2" refers to a BCL2 nucleic acid (e.g., a BCL2 gene, cDNA, RNA transcript, DNA construct), while Bcl2" refers to the Bcl2 protein
10 product. In a particular embodiment, the at least one miR gene product comprises a nucleotide sequence that is complementary to a nucleotide sequence in a BCL2 gene transcript. In a particular embodiment, the at least one miR gene product comprises a nucleotide sequence that is complementary to nucleotides 3741 to 3749 of SEQ ID NO:55. Examples of such miR gene products include, but are not limited to, miR15, miR16, miR-15b and miR-16-2. The
15 miR15 and miR16 genes are localized at 13q14 and are commonly referred to as miR-15a and miR-16-1, respectively. As used herein, the terms "miR15" and "miR-15a" are interchangeable, as are the terms "miR16" and "miR-16-1". In a further embodiment, the miR gene product is selected from the group consisting of miR-182, miR-181, miR-30, miR-15a, miR-16-1, miR-15b, miR-16-2, miR-195, miR-34, miR-153, miR-21, miR-217,
20 miR-205, miR-204, miR-211, miR-143, miR-96, miR-103, miR-107, miR-129, miR-9, miR-137, miR-217, miR-186, and combinations thereof. In another embodiment, the miR gene product is selected from the group consisting of miR-182, miR-181, miR-30, miR-

15a, miR-16-1, miR-15b, miR-16-2, miR-195 and combinations thereof. In a particular embodiment, the miR gene product is not miR-15a or miR-16-1.

The invention further provides a pharmaceutical composition for treating a subject having a cancer associated with Bcl2 overexpression, comprising at least one
 5 chemotherapeutic agent and at least one miR gene product, wherein the at least one miR gene product comprises a nucleotide sequence that is complementary to a nucleotide sequence in a BCL2 gene transcript. In one embodiment, the at least one miR gene product is miR-15a. In another embodiment, the at least one miR gene product is miR-16-1. In yet another
 10 embodiment, the at least one miR gene product is selected from the group consisting of miR-182, miR-181, miR-30, miR-15a, miR-16-1, miR-15b, miR-16-2, miR-195, miR-34, miR-153, miR-21, miR-217, miR-205, miR-204, miR-211, miR-143, miR-96, miR-103, miR-107, miR-129, miR-9, miR-137, miR-217, miR-186, and combinations thereof. In another
 15 embodiment, the miR gene product is selected from the group consisting of miR-182, miR-181, miR-30, miR-15a, miR-16-1, miR-15b, miR-16-2, miR-195 and combinations thereof. In a particular embodiment, the miR gene product is not miR-15a or miR-16-1.

The invention also encompasses a method for determining the efficacy of a cancer therapy in a subject who has a BCL2-associated cancer, comprising administering at least one agent to the subject, and subsequently measuring the expression of a miR gene product that
 20 comprises a nucleotide sequence that is complementary to a nucleotide sequence in a BCL2 gene transcript. In a particular embodiment, an increase in the expression of the miR gene product following administration of the agent is indicative of successful treatment. In one embodiment, the at least one miR gene product is miR-15a. In another embodiment, the at
 25 least one miR gene product is miR-16-1. In yet another embodiment, the at least one miR gene product is selected from the group consisting of miR-182, miR-181, miR-30, miR-15a, miR-16-1, miR-15b, miR-16-2, miR-195, miR-34, miR-153, miR-21, miR-217, miR-205, miR-204, miR-211, miR-143, miR-96, miR-103, miR-107, miR-129, miR-9, miR-137, miR-217, miR-186, and combinations thereof. In another embodiment, the miR gene product is
 30 selected from the group consisting of miR-182, miR-181, miR-30, miR-15a, miR-16-1, miR-15b, miR-16-2, miR-195 and combinations thereof. In a particular embodiment, the miR gene product is not miR-15a or miR-16-1.

The present invention additionally provides methods for increasing the efficacy of anti-cancer treatments (e.g., chemotherapy, radiation therapy) comprising providing at least one miR gene product to a tumor cell, in combination with at least one anti-cancer treatment. In a particular embodiment, the at least one miR gene product comprises a nucleotide
5 sequence that is complementary to a nucleotide sequence in a BCL2 gene transcript. In a further embodiment, the at least one miR gene product is miR-15a or miR-16-1. In yet another embodiment, the at least one miR gene product is selected from the group consisting of miR-182, miR-181, miR-30, miR-15a, miR-16-1, miR-15b, miR-16-2, miR-195, miR-34, miR-153, miR-21, miR-217, miR-205, miR-204, miR-211, miR-143, miR-96, miR-103, miR-
10 107, miR-129, miR-9, miR-137, miR-217, miR-186, and combinations thereof. In another embodiment, the miR gene product is selected from the group consisting of miR-182, miR-181, miR-30, miR-15a, miR-16-1, miR-15b, miR-16-2, miR-195 and combinations thereof. In a certain embodiment, the miR gene product is not miR-15a or miR-16-1.

The present invention also provides a method for increasing the sensitivity of a cancer
15 cell to the cytotoxic effects of an anti-cancer agent, comprising providing at least one miR gene product to the cancer cell, wherein the at least one miR gene product comprises a nucleotide sequence that is complementary to a nucleotide sequence in a BCL2 gene transcript. In one embodiment, the at least one miR gene product is miR-15a or miR-16-1. In another embodiment, the at least one miR gene product is selected from the group consisting
20 of miR-182, miR-181, miR-30, miR-15a, miR-16-1, miR-15b, miR-16-2, miR-195, miR-34, miR-153, miR-21, miR-217, miR-205, miR-204, miR-211, miR-143, miR-96, miR-103, miR-107, miR-129, miR-9, miR-137, miR-217, miR-186, and combinations thereof. In another embodiment, the miR gene product is selected from the group consisting of miR-182, miR-181, miR-30, miR-15a, miR-16-1, miR-15b, miR-16-2, miR-195 and combinations thereof.
25 In a certain embodiment, the miR gene product is not miR-15a or miR-16-1. In a particular embodiment, the anti-cancer agent is a chemotherapeutic agent. In another embodiment, the anti-cancer agent is radiation treatment.

The invention also encompasses methods of inducing apoptosis of a cell, comprising
30 contacting a cell with at least one miR gene product that comprises a nucleotide sequence that is complementary to a nucleotide sequence in a BCL2 gene transcript. In a particular

embodiment, the miR gene product comprises a nucleotide sequence that is complementary to nucleotides 3741-3749 of SEQ ID NO:55. In a further embodiment, the at least one miR gene product is miR-15a or miR-16-1. In yet another embodiment, the at least one miR gene product is selected from the group consisting of miR-182, miR-181, miR-30, miR-15a, miR-16-1, miR-15b, miR-16-2, miR-195, miR-34, miR-153, miR-21, miR-217, miR-205, miR-204, miR-211, miR-143, miR-96, miR-103, miR-107, miR-129, miR-9, miR-137, miR-217, miR-186, and combinations thereof. In another embodiment, the miR gene product is selected from the group consisting of miR-182, miR-181, miR-30, miR-15a, miR-16-1, miR-15b, miR-16-2, miR-195 and combinations thereof. In a certain embodiment, the miR gene product is not miR-15a or miR-16-1. Suitable cells for these methods include, but are not limited to, cancer cells and other cells that express Bcl2 protein.

The invention additionally provides a method of diagnosing a BCL2-associated cancer in a subject, comprising determining the level of at least one miR gene product in a sample from the subject, relative to the level of a corresponding miR gene product in a control sample, wherein the miR gene product comprises a nucleotide sequence that is complementary to a nucleotide sequence in a BCL2 gene transcript. In a particular embodiment, the miR gene product comprises a nucleotide sequence that is complementary to nucleotides 3741-3749 of SEQ ID NO:55. In a further embodiment, the at least one miR gene product is miR-15a or miR-16-1. In yet another embodiment, the at least one miR gene product is selected from the group consisting of miR-182, miR-181, miR-30, miR-15a, miR-16-1, miR-15b, miR-16-2, miR-195, miR-34, miR-153, miR-21, miR-217, miR-205, miR-204, miR-211, miR-143, miR-96, miR-103, miR-107, miR-129, miR-9, miR-137, miR-217, miR-186, and combinations thereof. In another embodiment, the miR gene product is selected from the group consisting of miR-182, miR-181, miR-30, miR-15a, miR-16-1, miR-15b, miR-16-2, miR-195 and combinations thereof. In a certain embodiment, the miR gene product is not miR-15a or miR-16-1.

BRIEF DESCRIPTION OF THE DRAWINGS

The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawings will be provided by the Office upon request and payment of the necessary fee.

5 FIGS. 1A and 1B are schematic representations of the predicted secondary structure of the miR15 and miR16 precursor RNA, respectively. The RNA secondary structure prediction was performed using the "mfold" program, version 3.1 of Matthews, *et al.*, *J. Mol. Biol.* 288:911-940 (1999), and manually refined to accommodate G/U wobble base pairs in the helical segments. The sequence of the processed miR15 and miR16 miRNA is underlined.

10 Adapted from Lagos-Quintana, *et al.*, *Science* 294:853-858 (2001).

FIG. 2A is a map of genes within the 13q14 tumor suppressor locus in CLL showing the localization of the miR15/16 gene cluster. The position of genetic markers and the position of genes on the map are shown.

15 FIG. 2B is a map of previously reported 13q14 deletions, marked by horizontally striped boxes.

FIG. 2C is a map of the locus between the *D13S1150* and *D13S272* markers. The orientation of each gene in this locus is marked by an arrow under the gene name, and vertical bars mark the position of corresponding exons for each gene.

20 FIG. 2D is a map of the locus between the Alu 18 and *D13S272* markers. Bars and boxes mark the position of exons for *LEU2/ALT1* and *LEU1*. The short vertical arrows mark the position of *miR15* and *miR16* genes. Circles mark the position of PCR primers used to screen somatic cell hybrid clones derived from a fusion of two independent leukemia cases (CLL-A and CLL-B). Hatched boxes represent portions of chromosome 13 present in the hybrids. "←~31.4 kb→" indicates an approximately 31.4 kb deleted region in clone CLL-A, which was derived from a patient with CLL carrying a t(2;13)(q12;q13) translocation, 25 bilateral retinoblastoma, and ulcerative colitis. The long vertical arrow represents the position of the breakpoint in clone CLL-B carrying a t(2;13)(q32;q14) translocation, and "←~29 kb→" indicates an approximately 29 kb deleted region from this CLL clone.

FIG. 3A is a Northern blot analysis of *miR15* and *miR16* gene expression in normal human kidney, prostate, liver, pancreas, skeletal muscle ("Sk muscle"), testicle, CD5+ B cells (CD5+), leukemia cells ("Per B1 Leuk"), and bone marrow ("BM").

FIG. 3B is a loss of heterozygosity ("LOH") analysis of microsatellite makers
 5 *D13S272* and *D13S273* in 18 CLL patients. DNA from normal human CD5+ cells was used as a control. The LOH status for the samples is shown as "+/+", "+/-", "-/-", "NI" (not informative), "?" (not enough material) and "ND" (not done). Ethidium bromide-stained Northern gels were used as normalization controls.

FIG. 4A depicts the regions of miR::mRNA complementarity (red nucleotides)
 10 between human miRNAs, *miR-15a* (Hsa_miR-15; SEQ ID NO:58) or *miR-16-1* (Hsa_miR-16; SEQ ID NO:59), and human BCL2 cDNA (Hsa_BCL2; SEQ ID NO:57), as well as mouse miRNAs, *miR-15a* (Mmu_miR-15; SEQ ID NO:61) or *miR-16-1* (Mmu_miR-16; SEQ ID NO:62), and mouse BCL2 cDNA (Mmu_BCL2; SEQ ID NO:60). The sites of targeted deletions in miR-15a and miR-16-1 are indicated for two different 3'UTR mutant constructs:
 15 3'M1, which lacks all 9 bp responsible for the miRNA::mRNA interaction, and 3'M2, which lacks the first 5 bp in the region of complementarity.

FIG. 4B is a Western blot depicting levels of Bcl2 protein in each of 5 different CLL samples (CLL), as well as a pooled sample of CD5 positive B-lymphocytes from normal patients (CD5 pool). Jurkat cells (T-cell leukemia cell line) were used as a control for Bcl2
 20 protein expression. β -actin (Actin) levels were used for normalization. The relative expression of miR-16-1 and miR-15a microRNAs in each sample, as determined by microarray signal intensity, is shown below the corresponding lane under the blot.

FIG. 5A are Western blots depicting levels of Bcl2 protein, as well as full-length and cleaved forms of various apoptosis activators (e.g., APAF1, Pro-C9, C9, PARP and cleaved
 25 PARP), in untransfected MEG-01 cells (MEG-01 WT), as well as MEG-01 cells transfected with empty vector (MEG-01-pRS-neo-GFP), MEG-01 cells transfected with a vector containing the mir-15a/miR-16-1 cluster (MEG-01-pRS-15a/16-1 WT), or MEG-01 cells transfected with a vector containing the mir-15a/miR-16-1 cluster having a +7 (C to T) substitution in the 3' region of the miR-16a precursor (MEG-01-pRS-15a/16-1 MUT). Data
 30 were confirmed in duplicate experiments. The pRS-15a/16-1 WT transfected cells showed

cleavage of APAF1 (apoptotic protease-activating factor 1, a cytochrome c interactor), procaspase 9 (intrinsic apoptosis pathway) and poly (ADP-ribose) polymerase (PARP, a final effector of various apoptotic pathways). Actin was monitored as a loading control.

FIG. 5B are Western blots (WB) depicting levels of Bcl2 protein in MEG-01 cells transfected with miR-15a and/or miR-16-1 sense (miR-15a, miR16-1), or miR-15a and/or miR-16-1 antisense (miR-15a_AS, miR16-1_AS) RNA oligonucleotides. Untransfected cells were used as a control (MEG-01-WT). Normalization was performed using beta-actin (Actin) levels. Northern blots (NB) were performed to assess the transfection efficiency of miR-15-sense and miR-16-sense oligonucleotides. RT-PCR products represent mRNA levels of BCL2 transcripts in the same cells, which are normalized against beta-actin (Actin) mRNA levels (RT-PCR).

FIG. 6A is a bar graph depicting relative repression (Fold repression) of firefly luciferase expression, standardized to the expression of a renilla luciferase transfection control, in cells transfected with either *miR-15-a* and/or *miR-16-1* sense RNA oligonucleotides (miR15a S and miR-16-1 S, respectively), or *miR-15-a* and/or *miR-16-1* antisense RNA oligonucleotides (miR15a A and miR-16-1 A, respectively). Cells were transfected with empty control vector (pGL-3-Cont) or *miR-15-a* and/or *miR-16-1* sense or antisense RNA oligonucleotides. All the experiments were performed twice in triplicate (n=6).

FIG. 6B is a bar graph depicting relative repression of firefly luciferase expression, standardized to a renilla luciferase transfection control. Cells were transfected with empty control vector (pGL-3-Cont), *miR-15-a* and *miR-16-1* sense RNA oligonucleotides (pSR-15a/16-1 S +3'UTR) or *miR-15-a* and *miR-16-1* antisense RNA oligonucleotides (pSR-15a/16-1 A +3'UTR) RNA oligonucleotides. 3'UTR represents the luciferase reporter gene fused to a wild-type BCL2 3'UTR sequence. Two different 3'UTR mutants also were transfected, one lacking all 9 bp of the miRNA::mRNA region of complementarity in *miR-15-a* and *miR-16-1* (pSR-15a/16-1 S + 3'M1), and the other lacking the first 5 bp in the same complementarity region (pSR-15a/16-1 S +3'M2). All of the experiments were performed twice in triplicate (n=6).

The foregoing and other objects, features and advantages of the invention will be apparent from the following more particular description of embodiments of the invention.

DETAILED DESCRIPTION OF THE INVENTION

5 A description of preferred embodiments of the invention follows.

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that various changes in form and details may be made therein without departing from the scope of the invention encompassed by the appended claims.

10 As used herein interchangeably, a "miR gene product," "microRNA," "miR," or "miRNA" refers to the unprocessed or processed RNA transcript from an *miR* gene. As the miR gene products are not translated into protein, the term "miR gene products" does not include proteins. The unprocessed miR gene transcript is also called an "miR precursor," and typically comprises an RNA transcript of about 70-100 nucleotides in length. The miR
15 precursor can be processed by digestion with an RNase (for example, Dicer, Argonaut, RNase III (e.g., *E. coli* RNase III)) into an active 19-25 nucleotide RNA molecule. This active 19-25 nucleotide RNA molecule is also called the "processed" miR gene transcript or "mature" miRNA.

20 The active 19-25 nucleotide RNA molecule can be obtained from the miR precursor through natural processing routes (e.g., using intact cells or cell lysates) or by synthetic processing routes (e.g., using isolated processing enzymes, such as isolated Dicer, Argonaut, or RNase III). It is understood that the active 19-25 nucleotide RNA molecule can also be produced directly by biological or chemical synthesis, without having to be processed from the miR precursor.

25 The sequences of a large number of miR gene products are provided in Table 1. All nucleic acid sequences herein are given in the 5' to 3' direction.

Table 1- Human miR Gene Product Sequences

Name	Precursor Sequence (5' to 3')*	SEQ ID NO:
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Name	Precursor Sequence (5' to 3')*	SEQ ID NO:
<i>let-7a-1-prec</i>	CACTGTGGGATGAGGTAGTAGGTTGTATAGTTT TAGG GTCACACCCACCACTGGGAGATAACTATAACAATCTAC TGTCTTTCCTAACGTG	63
<i>let-7a-2-prec</i>	AGGTTGAGGTAGTAGGTTGTATAGTTTAGAATTACAT CAAGGGAGATAACTGTACAGCCTCCTAGCTTTCCT	64
<i>let-7a-3-prec</i>	GGGTGAGGTAGTAGGTTGTATAGTTTGGGGCTCTGCC CTGCTATGGGATAACTATAACAATCTACTGTCTTTCCT	65
<i>let-7a-4-prec</i>	GTGACTGCATGCTCCCAGGTTGAGGTAGTAGGTTGTA TAGTTTAGAATTACACAAGGGAGATAACTGTACAGC CTCCTAGCTTTCCTTGGGTCTTGCACTAAACAAC	66
<i>let-7b-prec</i>	GGCGGGGTGAGGTAGTAGGTTGTGTGGTTTCAGGGC AGTGATGTTGCCCTCGGAAGATAACTATAACAACCTA CTGCCTTCCCTG	67
<i>let-7c-prec</i>	GCATCCGGGTGAGGTAGTAGGTTGTATGGTTTAGAG TTACACCCTGGGAGTTAACTGTACAACCTTCTAGCTT TCCTTGGAGC	68
<i>let-7d-prec</i>	CCTAGGAAGAGGTAGTAGGTTGCATAGTTT TAGGGC AGGGATTTTGCCCAACAAGGAGGTA ACTATACGACCT GCTGCCTTCTTAGG	69
<i>let-7d-v1-prec</i>	CTAGGAAGAGGTAGTAGTTTGCATAGTTT TAGGGCAA AGATTTTGCCCAACAAGTAGTTAGCTATACGACCTGCA GCCTTTTGTAG	70
<i>let-7d-v2-prec</i>	CTGGCTGAGGTAGTAGTTTGTGCTGTTGGTCGGGTTG TGACATTGCCCGCTGTGGAGATAACTGCGCAAGCTAC TGCCTTGCTAG	71
<i>let-7e-prec</i>	CCCGGGCTGAGGTAGGAGGTTGTATAGTTGAGGAGG ACACCCAAGGAGATCACTATACGGCCTCCTAGCTTTC CCCAGG	72
<i>let-7f-1-prec</i>	TCAGAGTGAGGTAGTAGATTGTATAGTTGTGGGGTAG TGATTTTACCCTGTT CAGGAGATAACTATAACAATCTA TTGCCTTCCCTGA	73
<i>let-7f-2-prec-1</i>	CTGTGGGATGAGGTAGTAGATTGTATAGTTGTGGGGT AGTGATTTTACCCTGTT CAGGAGATAACTATAACAATC TATTGCCTTCCCTGA	74
<i>let-7f-2-prec-2</i>	CTGTGGGATGAGGTAGTAGATTGTATAGTTT TAGGGT CATACCCCATCTTGGAGATAACTATACAGTCTACTGT CTTCCCACGG	75
<i>let-7g-prec</i>	TTGCCTGATTCCAGGCTGAGGTAGTAGTTTGTACAGT TTGAGGGTCTATGATACCACCCGGTACAGGAGATAA CTGTACAGGCCACTGCCTTGCCAGGAACAGCGCGC	76
<i>let-7i-prec</i>	CTGGCTGAGGTAGTAGTTTGTGCTGTTGGTCGGGTTG TGACATTGCCCGCTGTGGAGATAACTGCGCAAGCTAC TGCCTTGCTAG	77

Name	Precursor Sequence (5' to 3')*	SEQ ID NO:
<i>mir-001b-1-prec-1</i>	ACCTACTCAGAGTACATACTTCTTTATGTACCCATAT GAACATACAATGCTATGGAATGTAAAGAAGTATGTA TTTTTGGTAGGC	78
<i>mir-001b-1-prec-2</i>	CAGCTAACAACCTTAGTAATACCTACTCAGAGTACATA CTTCTTTATGTACCCATATGAACATACAATGCTATGG AATGTAAAGAAGTATGTATTTTTTGGTAGGCAATA	79
<i>mir-001b-2-prec</i>	GCCTGCTTGGGAAACATACTTCTTTATATGCCCATAT GGACCTGCTAAGCTATGGAATGTAAAGAAGTATGTA TCTCAGGCCGGG	80
<i>mir-001b-prec</i>	TGGGAAACATACTTCTTTATATGCCCATATGGACCTG CTAAGCTATGGAATGTAAAGAAGTATGTATCTCA	81
<i>mir-001d-prec</i>	ACCTACTCAGAGTACATACTTCTTTATGTACCCATAT GAACATACAATGCTATGGAATGTAAAGAAGTATGTA TTTTTGGTAGGC	82
<i>mir-007-1</i>	TGGATGTTGGCCTAGTTCTGTGTGGAAGACTAGTGAT TTTGTTGTTTTAGATAACTAAATCGACAACAAATCA CAGTCTGCCATATGGCACAGGCCATGCCTCTACA	83
<i>mir-007-1-prec</i>	TTGGATGTTGGCCTAGTTCTGTGTGGAAGACTAGTGA TTTTGTTGTTTTAGATAACTAAATCGACAACAAATC ACAGTCTGCCATATGGCACAGGCCATGCCTCTACAG	84
<i>mir-007-2-prec</i>	CTGGATACAGAGTGGACCGGCTGGCCCCATCTGGAA GACTAGTGATTTTGTGTTGTCTTACTGCGCTCAACA ACAAATCCCAGTCTACCTAATGGTGCCAGCCATCGCA	85
<i>mir-007-3-prec</i>	AGATTAGAGTGGCTGTGGTCTAGTGCTGTGTGGAAGA CTAGTGATTTTGTGTTCTGATGTACTACGACAACAA GTCACAGCCGGCCTCATAGCGCAGACTCCCTTCGAC	86
<i>mir-009-1</i>	CGGGGTTGGTTGTTATCTTTGGTTATCTAGCTGTATGA GTGGTGTGGAGTCTTCATAAAGCTAGATAACCGAAA GTAAAAATAACCCCA	87
<i>mir-009-2</i>	GGAAGCGAGTTGTTATCTTTGGTTATCTAGCTGTATG AGTGTATTGGTCTTCATAAAGCTAGATAACCGAAAGT AAAAACTCCTTCA	88
<i>mir-009-3</i>	GGAGGCCCGTTTCTCTCTTTGGTTATCTAGCTGTATGA GTGCCACAGAGCCGTCATAAAGCTAGATAACCGAAA GTAGAAATGATTCTCA	89
<i>mir-010a-prec</i>	GATCTGTCTGTCTTCTGTATATACCCTGTAGATCCGA ATTGIGTAAGGAATTTTGTGGTCACAAATTCGTATC TAGGGGAATATGTAGTTGACATAAACACTCCGCTCT	90
<i>mir-010b-prec</i>	CCAGAGGTTGTAACGTTGTCTATATATACCCTGTAGA ACCGAATTTGTGTGGTATCCGTATAGTCACAGATTCTG ATTCTAGGGGAATATATGGTCGATGCAAAAACCTTCA	91

Name	Precursor Sequence (5' to 3')*	SEQ ID NO:
<i>mir-015a-2-prec</i>	GCGCGAATGTGTGTTTAAAAAAATAAAACCTTGGA GTAAAGTAGCAGCACATAATGGTTTGTGGATTTTGAA AAGGTGCAGGCCATATTGTGCTGCCTCAAAAATAC	92
<i>mir-015a-prec</i>	CCTTGGAGTAAAGTAGCAGCACATAATGGTTTGTGGA TTTGAAGGTGCAGGCCATATTGTGCTGCCTCAAA AATACAAGG	93
<i>mir-015b-prec-1</i>	CTGTAGCAGCACATCATGGTTTACATGCTACAGTCAA GATGCGAATCATTATTGCTGCTCTAG	94
<i>mir-015b-prec-2</i>	TTGAGGCCTTAAAGTACTGTAGCAGCACATCATGGTT TACATGCTACAGTCAAGATGCGAATCATTATTGCTG CTCTAGAAATTTAAGGAAATTCAT	95
<i>mir-016a-chr13</i>	GTCAGCAGTGCCTTAGCAGCACGTAAATATTGGCGTT AAGATTCTAAAATTATCTCCAGTATTAAGTGTGCTGC TGAAGTAAGGTTGAC	96
<i>mir-016b-chr3</i>	GTTCCACTCTAGCAGCACGTAAATATTGGCGTAGTGA AATATATATTAAACACCAATATTACTGTGCTGCTTTA GTGTGAC	97
<i>mir-016-prec-13</i>	GCAGTGCCTTAGCAGCACGTAAATATTGGCGTTAAGA TTCTAAAATTATCTCCAGTATTAAGTGTGCTGCTGAA GTAAGGT	98
<i>mir-017-prec</i>	GTCAGAATAATGTCAAAGTGCTTACAGTGCAGGTAGT GATATGTGCATCTACTGCAGTGAAGGCACTTGTAGCA TTATGGTGAC	99
<i>mir-018-prec</i>	TGTTCTAAGGTGCATCTAGTGCAGATAGTGAAGTAGA TTAGCATCTACTGCCCTAAGTGCTCCTTCTGGCA	100
<i>mir-018-prec-13</i>	TTTTTGTCTAAGGTGCATCTAGTGCAGATAGTGAAG TAGATTAGCATCTACTGCCCTAAGTGCTCCTTCTGGC ATAAGAA	101
<i>mir-019a-prec</i>	GCAGTCCTCTGTAGTTTTCATAGTTGCACTACAAG AAGAATGTAGTTGTGCAAATCTATGCAAAACTGATG GTGGCCTGC	102
<i>mir-019a-prec-13</i>	CAGTCCTCTGTAGTTTTCATAGTTGCACTACAAGA AGAATGTAGTTGTGCAAATCTATGCAAAACTGATGGT GGCCTG	103
<i>mir-019b-1-prec</i>	CACTGTTCTATGGTTAGTTTTCAGGTTTGCATCCAGC TGTGTGATATTCTGCTGTGCAAATCCATGCAAAACTG ACTGTGGTAGTG	104
<i>mir-019b-2-prec</i>	ACATTGCTACTTACAATTAGTTTTCAGGTTTGCATTT CAGCGTATATATGTATATGTGGCTGTGCAAATCCATG CAAACTGATTGTGATAATGT	105
<i>mir-019b-prec-13</i>	TTCTATGGTTAGTTTTCAGGTTTGCATCCAGCTGTGT GATATTCTGCTGTGCAAATCCATGCAAACTGACTGT GGTAG	106

mir-019b-prec-X

Name	Precursor Sequence (5' to 3')*	SEQ ID NO:
<i>mir-019b-prec-X</i>	TTACAATTAGTTTTGCAGGTTTGCATTTTCAGCGTATAT ATGTATATGTGGCTGTGCAAATCCATGCAAAACTGAT TGTGAT	107
<i>mir-020-prec</i>	GTAGCACTAAAGTGCTTATAGTGCAGGTAGTGTTTAG TTATCTACTGCATTATGAGCACTTAAAGTACTGC	108
<i>mir-021-prec</i>	TGTCGGGTAGCTTATCAGACTGATGTTGACTGTTGAA TCTCATGGCAACACCAGTCGATGGGCTGTCTGACA	109
<i>mir-021-prec-17</i>	ACCTTGTCGGGTAGCTTATCAGACTGATGTTGACTGT TGAATCTCATGGCAACACCAGTCGATGGGCTGTCTGA CATTTTG	110
<i>mir-022-prec</i>	GGCTGAGCCGCGAGTAGTTCTTCAGTGGCAAGCTTTAT GTCCTGACCCAGCTAAAGCTGCCAGTTGAAGAACTGT TGCCCTCTGCC	111
<i>mir-023a-prec</i>	GGCCGGCTGGGGTTCCTGGGGATGGGATTTGCTTCCT GTCACAAATCACATTGCCAGGGATTCCAACCGACC	112
<i>mir-023b-prec</i>	CTCAGGTGCTCTGGCTGCTTGGGTTCCTGGCATGCTG ATTGTGACTTAAGATTAAAATCACATTGCCAGGGAT TACCACGCAACCACGACCTTGGC	113
<i>mir-023-prec-19</i>	CCACGGCCGGCTGGGGTTCCTGGGGATGGGATTTGCT TCCTGTCAAAATCACATTGCCAGGGATTCCAACCG ACCCTGA	114
<i>mir-024-1-prec</i>	CTCCGGTGCCTACTGAGCTGATATCAGTTCTCATTTA CACACTGGCTCAGTTCAGCAGGAACAGGAG	115
<i>mir-024-2-prec</i>	CTCTGCCTCCCGTGCCTACTGAGCTGAAACACAGTTG GTTTGTGTACACTGGCTCAGTTCAGCAGGAACAGGG	116
<i>mir-024-prec-19</i>	CCCTGGGCTCTGCCTCCCGTGCCTACTGAGCTGAAAC ACAGTTGGTTTGTGTACACTGGCTCAGTTCAGCAGGA ACAGGGG	117
<i>mir-024-prec-9</i>	CCCTCCGGTGCCTACTGAGCTGATATCAGTTCTCATTT TACACACTGGCTCAGTTCAGCAGGAACAGCATC	118
<i>mir-025-prec</i>	GGCCAGTGTTGAGAGGCGGAGACTTGGGCAATTGCT GGACGCTGCCCTGGGCATTGCACCTTGCTCTCGGTCTGA CAGTGCCGGCC	119
<i>mir-026a-prec</i>	AGGCCGTGGCCTCGTTCAAGTAATCCAGGATAGGCTG TGCAGGTCCCAATGGCCTATCTTGGTTACTTGCACGG GGACGCGGGCCT	120
<i>mir-026b-prec</i>	CCGGGACCCAGTTCAAGTAATTCAGGATAGGTTGTGT GCTGTCCAGCCTGTTCTCCATTACTTGGCTCGGGGAC CGG	121
<i>mir-027a-prec</i>	CTGAGGAGCAGGGCTTAGCTGCTTGTGAGCAGGGTC CACACCAAGTCGTGTTACAGTGGCTAAGTTCCGCCC CCCAG	122

Name	Precursor Sequence (5' to 3')*	SEQ ID NO:
<i>mir-027b-prec-1</i>	AGGTGCAGAGCTTAGCTGATTGGTGAACAGTGATTG GTTCCGCTTTGTTACAGTGGCTAAGTTCTGCACCT	123
<i>mir-027b-prec-2</i>	ACCTCTCTAACAAGGTGCAGAGCTTAGCTGATTGGTG AACAGTGATTGGTTTCCGCTTTGTTACAGTGGCTAA GTTCTGCACCTGAAGAGAAGGTG	124
<i>mir-027-prec-19</i>	CCTGAGGAGCAGGGCTTAGCTGCTTGTGAGCAGGGT CCACACCAAGTCGTGTTACAGTGGCTAAGTTCCGCC CCCCAGG	125
<i>mir-028-prec</i>	GGTCCTTGCCCTCAAGGAGCTCACAGTCTATTGAGTT ACCTTTCTGACTTTCCCACTAGATTGTGAGCTCCTGG AGGGCAGGCACT	126
<i>mir-029a-2</i>	CCTTCTGTGACCCCTTAGAGGATGACTGATTTCTTTTG GTGTTACAGAGTCAATATAATTTTCTAGCACCATCTGA AATCGGTTATAATGATTGGGGAAGAGCACCATG	127
<i>mir-029a-prec</i>	ATGACTGATTTCTTTTGGTGTTCAGAGTCAATATAATT TTCTAGCACCATCTGAAATCGGTTAT	128
<i>mir-029c-prec</i>	ACCACTGGCCCATCTCTTACACAGGCTGACCGATTTC TCCTGGTGTTCAGAGTCTGTTTTTGTCTAGCACCATTI GAAATCGGTTATGATGTAGGGGGAAAAGCAGCAGC	129
<i>mir-030a-prec</i>	GCGACTGTAAACATCCTCGACTGGAAGCTGTGAAGC CACAGATGGGCTTTCAGTCGGATGTTTGCAGCTGC	130
<i>mir-030b-prec-1</i>	ATGTAAACATCCTACACTCAGCTGTAATACATGGATT GGCTGGGAGGTGGATGTTTACGT	131
<i>mir-030b-prec-2</i>	ACCAAGTTTCAGTTCATGTAAACATCCTACACTCAGC TGTAATACATGGATTGGCTGGGAGGTGGATGTTTACT TCAGCTGACTTGA	132
<i>mir-030c-prec</i>	AGATACTGTAAACATCCTACACTCTCAGCTGTGGAAA GTAAGAAAGCTGGGAGAAGGCTGTTTACTCTTTCT	133
<i>mir-030d-prec</i>	GTTGTTGTAAACATCCCCGACTGGAAGCTGTAAGACA CAGCTAAGCTTTCAGTCAGATGTTTGCTGCTAC	134
<i>mir-031-prec</i>	GGAGAGGAGGCAAGATGCTGGCATAGCTGTTGAACT GGGAACCTGCTATGCCAACATATTGCCATCTTTCC	135
<i>mir-032-prec</i>	GGAGATATTGCACATTACTAAGTTGCATGTTGTCACG GCCTCAATGCAATTTAGTGTGTGTGATATTTTC	136
<i>mir-033b-prec</i>	GGGGGCGGAGAGAGGCGGGCGGCCCGCGGTGCATT GCTGTTGCATTGCACGTGTGTGAGGCGGGTGCAGTGC CTCGGCAGTGCAGCCCGGAGCCGGCCCCCTGGCACCA C	137
<i>mir-033-prec</i>	CTGTGGTGCATTGTAGTTGCATTGCATGTTCTGGTGG TACCCATGCAATGTTTCCACAGTGCATCACAG	138
<i>mir-034-prec</i>	GGCCAGCTGTGAGTGTTTCTTTGGCAGTGTCTTAGCT GGTGTGTGTGAGCAATAGTAAGGAAGCAATCAGCAA GTATACTGCCCTAGAAGTCTCTCACGTTGTGGGGCCC	139

Name	Precursor Sequence (5' to 3')*	SEQ ID NO:
<i>mir-091-prec-13</i>	TCAGAATAATGTCAAAGTGCTTACAGTGCAGGTAAGT ATATGTGCATCTACTGCAGTGAAGGCACTTGTAGCAT TATGGTGA	140
<i>mir-092-prec-13=092-1</i>	CTTTCTACACAGGTTGGGATCGGTTGCAATGCTGTGT TTCTGTATGGTATTGCACTTGTCCCGGCCTGTTGAGTT TGG	141
<i>mir-092-prec-X=092-2</i>	TCATCCCTGGGTGGGGATTGTTGCATTACTTGTGTTT TATATAAAGTATTGCACTTGTCCCGGCCTGTGGAAGA	142
<i>mir-093-prec-7.1=093-1</i> (<i>mir-093-prec-7.2=093-2</i>)	CTGGGGGCTCCAAAGTGCTGTTTCGTGCAGGTAAGTGT ATTACCCAACCTACTGCTGAGCTAGCACTTCCCGAGC CCCCGG	143
<i>mir-095-prec-4</i>	AACACAGTGGGCACTCAATAAATGTCTGTTGAATTGA AATGCGTTACATTCAACGGGTATTATTGAGCACCCA CTCTGTG	144
<i>mir-096-prec-7</i>	TGGCCGATTTTGGCACTAGCACATTTTGTCTTGTGTCT CTCCGCTCTGAGCAATCATGTGCAGTGCCAATATGGG AAA	145
<i>mir-098-prec-X</i>	GTGAGGTAGTAAGTTGTATTGTTGTGGGGTAGGGATA TTAGGCCCCAATTAGAAGATAACTATACAACTTACTA CTTTCC	146
<i>mir-099b-prec-19</i>	GGCACCCACCCGTAGAACCGACCTTGCGGGGGCCTTCG CCGCACACAAGCTCGTGTCTGTGGGTCCGTGTC	147
<i>mir-099-prec-21</i>	CCCATTTGGCATAAACCCGTAGATCCGATCTTGTGGTG AAGTGGACCGCACAAAGCTCGCTTCTATGGGTCTGTGT CAGTGTG	148
<i>mir-100-1/2-prec</i>	AAGAGAGAAGATATTGAGGCCTGTTGCCACAAACCC GTAGATCCGAACCTTGTGGTATTAGTCCGCACAAGCTT GTATCTATAGGTATGTGTCTGTTAGGCAATCTCAC	149
<i>mir-100-prec-11</i>	CCTGTTGCCACAAACCCGTAGATCCGAACCTTGTGGTA TTAGTCCGCACAAGCTTGTATCTATAGGTATGTGTCT GTTAGG	150
<i>mir-101-1/2-prec</i>	AGGCTGCCCTGGCTCAGTTATCACAGTGCTGATGCTG TCTATTCTAAAGGTACAGTACTGTGATAACTGAAGGA TGGCAGCCATCTTACCTTCCATCAGAGGAGCCTCAC	151
<i>mir-101-prec</i>	TCAGTTATCACAGTGCTGATGCTGTCCATTCTAAAGG TACAGTACTGTGATAACTGA	152
<i>mir-101-prec-1</i>	TGCCCTGGCTCAGTTATCACAGTGCTGATGCTGTCTA TTCTAAAGGTACAGTACTGTGATAACTGAAGGATGGC A	153
<i>mir-101-prec-9</i>	TGTCCTTTTTCGGTTATCATGGTACCGATGCTGTATAT CTGAAAGGTACAGTACTGTGATAACTGAAGAATGGT G	154

Name	Precursor Sequence (5' to 3')*	SEQ ID NO:
<i>mir-102-prec-1</i>	CTTCTGGAAGCTGGTTTCACATGGTGGCTTAGATTTT CCATCTTTGTATCTAGCACCATTGAAATCAGTGTTT AGGAG	155
<i>mir-102-prec-7.1</i> (<i>mir-102-prec-7.2</i>)	CTTCAGGAAGCTGGTTTCATATGGTGGTTTAGATTTA AATAGTGATTGTCTAGCACCATTGAAATCAGTGTTT TTGGGGG	156
<i>mir-103-2-prec</i> (<i>mir-103-prec-20</i>)	TTGTGCTTTCAGCTTCTTTACAGTGCTGCCTTGTAGCA TTCAGGTCAAGCAACATTGTACAGGGCTATGAAAGA ACCA	157
<i>mir-103-prec-5=103-1</i>	TACTGCCCTCGGCTTCTTTACAGTGCTGCCTTGTGCA TATGGATCAAGCAGCATTGTACAGGGCTATGAAGGC ATTG	158
<i>mir-104-prec-17</i>	AAATGTCAGACAGCCCATCGACTGGTGTGCCATGAG ATTCAACAGTCAACATCAGTCTGATAAGCTACCCGAC AAGG	159
<i>mir-105-prec-X.1</i> (<i>mir-105-1</i> ; <i>mir-105-prec-X.2</i> ; <i>mir-105-2</i>)	TGTGCATCGTGGTCAAATGCTCAGACTCCTGTGGTGG CTGCTCATGCACCACGGATGTTTGAGCATGTGCTACG GTGTCTA	160
<i>mir-106-prec-X</i>	CCTTGGCCATGTAAAAGTGCTTACAGTGCAGGTAGCT TTTGTAGATCTACTGCAATGTAAGCACTTCTTACATT ACCATGG	161
<i>mir-107-prec-10</i>	CTCTCTGCTTTCAGCTTCTTTACAGTGTTGCCTTGTGG CATGGAGTTCAAGCAGCATTGTACAGGGCTATCAA GCACAGA	162
<i>mir-122a-prec-1</i>	CCTTAGCAGAGCTGTGGAGTGTGACAATGGTGTGTTGT GTCTAAACTATCAAACGCCATTATCACACTAAATAGC TACTGCTAGGC	163
<i>mir-122a-prec-2</i>	AGCTGTGGAGTGTGACAATGGTGTGTTGTGTCCTAACT ATCAAACGCCATTATCACACTAAATAGCT	164
<i>mir-123-prec</i>	ACATTATTACTTTTGGTACGCGCTGTGACACTTCAA CTCGTACCGTGAGTAATAATGCGC	165
<i>mir-124a-1-prec-1</i>	tccttcctCAGGAGAAAGGCCTCTCTCTCCGTGTTACAGC GGACCTTGATTAAATGTCCATACAATTAAGGCACGC GGTGAATGCCAAGAATGGGGCT	166
<i>mir-124a-1-prec-2</i>	AGGCCTCTCTCTCCGTGTTACAGCGGACCTTGATT AAATGTCCATACAATTAAGGCACGCGGTGAATGCCA AGAATGGGGCTG	167
<i>mir-124a-2-prec</i>	ATCAAGATTAGAGGCTCTGCTCTCCGTGTTACAGCG GACCTTGATTAAATGTCCATACAATTAAGGCACGCGGT GAATGCCAAGAGCGGAGCCTACGGCTGCACTTGAAG	168

Name	Precursor Sequence (5' to 3')*	SEQ ID NO:
<i>mir-124a-3-prec-1</i>	CCCGCCCCAGCCCTGAGGGCCCCTCTGCGTGTTTCA GCGGACCTTGATTTAATGTCTATACAATTAAGGCACG CGGTGAATGCCAAGAGAGGGCGCCTCCGCCGCTCCTT	169
<i>mir-124a-3-prec-2</i>	TGAGGGCCCCTCTGCGTGTTTCAAGCGGACCTTGATT TAATGTCTATACAATTAAGGCACGCGGTGAATGCCAA GAGAGGGCGCCTCC	170
<i>mir-124a-prec</i>	CTCTGCGTGTTTCAAGCGGACCTTGATTTAATGTCTA TACAATTAAGGCACGCGGTGAATGCCAAGAG	171
<i>mir-124b-prec</i>	CTCTCCGTGTTTCAAGCGGACCTTGATTTAATGTCTA ACAATTAAGGCACGCGGTGAATGCCAAGAG	172
<i>mir-125a-prec-1</i>	TGCCAGTCTCTAGGTCCCTGAGACCCTTTAACCTGTG AGGACATCCAGGGTCAAGGTGAGGTTCTTGGGAGC CTGGCGTCTGGCC	173
<i>mir-125a-prec-2</i>	GGTCCCTGAGACCCTTTAACCTGTGAGGACATCCAGG GTCACAGGTGAGGTTCTTGGGAGCCTGG	174
<i>mir-125b-1-1</i>	ACATTGTTGCGCTCCTCTCAGTCCCTGAGACCCTAAC TTGTGATGTTTACCGTTTAAATCCACGGGTAGGCTC TTGGGAGCTGCGAGTCGTGCTTTTGCATCCTGGA	175
<i>mir-125b-1-2</i>	TGCGCTCCTCTCAGTCCCTGAGACCCTAACTTGTGAT GTTTACCGTTTAAATCCACGGGTAGGCTCTTGGGAG CTGCGAGTCGTGCT	176
<i>mir-125b-2-prec-1</i>	ACCAGACTTTTCCTAGTCCCTGAGACCCTAACTTGTG AGGTATTTTAGTAACATCACAAGTCAGGCTCTTGGGA CCTAGGCGGAGGGGA	177
<i>mir-125b-2-prec-2</i>	CCTAGTCCCTGAGACCCTAACTTGTGAGGTATTTTAG TAACATCACAAGTCAGGCTCTTGGGACCTAGGC	178
<i>mir-126-prec-1</i>	CGCTGGCGACGGGACATTATTACTTTTGGTACGCGCT GTGACACTTCAAACCTCGTACCGTGAGTAATAATGCGC CGTCCACGGCA	179
<i>mir-126-prec-2</i>	ACATTATTACTTTTGGTACGCGCTGTGACACTTCAAA CTCGTACCGTGAGTAATAATGCGC	180
<i>mir-127-prec-1</i>	TGTGATCACTGTCTCCAGCCTGCTGAAGCTCAGAGGG CTCTGATTCAGAAAGATCATCGGATCCGTCTGAGCTT GGCTGGTCGGAAGTCTCATCATC	181
<i>mir-127-prec-2</i>	CCAGCCTGCTGAAGCTCAGAGGGCTCTGATTCAGAA AGATCATCGGATCCGTCTGAGCTTGGCTGGTCGG	182
<i>mir-128a-prec</i>	TGAGCTGTTGGATTCCGGGGCCGTAGCACTGTCTGAGA GGTTTACATTTCTCACAGTGAACCGGTCTCTTTTTCAG CTGCTTC	183
<i>mir-128b-prec</i>	GCCCGGCAGCCACTGTGCAGTGGGAAGGGGGGGCCGA TAACTGTACGAGAGTGAGTAGCAGGTCTCACAGTG AACCGGTCTCTTTCCCTACTGTGTACACTCCTAATG G	184

Name	Precursor Sequence (5' to 3')*	SEQ ID NO:
<i>mir-128-prec</i>	GTTGGATTCTGGGGCCGTAGCACTGTCTGAGAGGTTTACATTTCTCACAGTGAACCGGTCTCTTTTTCAGC	185
<i>mir-129-prec</i>	TGGATCTTTTGGCGGTCTGGGCTTGCTGTTCTCTCAA CAGTAGTCAGGAAGCCCTTACCCCAAAAAGTATCTA	186
<i>mir-130a-prec</i>	TGCTGCTGGCCAGAGCTCTTTTCACATTGTGCTACTGT CTGCACCTGTCACTAGCAGTGCAATGTTAAAAGGGCA TTGGCCGTGTAGTG	187
<i>mir-131-1-prec</i>	gccaggaggcggGGTTGGTTGTTATCTTTGGTTATCTAGCT GTATGAGTGGTGTGGAGTCTTCATAAAGCTAGATAAC CGAAAGTAAAAATAACCCCATACACTGCGCAG	188
<i>mir-131-3-prec</i>	CACGGCGCGGCAGCGGCACTGGCTAAGGGAGGCCCCG TTTCTCTCTTTGGTTATCTAGCTGTATGAGTGCCACAG AGCCGTCATAAAGCTAGATAACCGAAAGTAGAAATG	189
<i>mir-131-prec</i>	GTTGTTATCTTTGGTTATCTAGCTGTATGAGTGTATTG GTCTTCATAAAGCTAGATAACCGAAAGTAAAAAC	190
<i>mir-132-prec-1</i>	CCGCCCCCGCGTCTCCAGGGCAACCGTGGCTTTTCGAT TGTTACTGTGGGAAGTGGAGGTAACAGTCTACAGCCA TGGTCGCCCCGCAGCACGCCACGCGC	191
<i>mir-132-prec-2</i>	GGGCAACCGTGGCTTTTCGATTGTTACTGTGGGAAGTGT GAGGTAACAGTCTACAGCCATGGTCGCCC	192
<i>mir-133a-1</i>	ACAATGCTTTGCTAGAGCTGGTAAAATGGAACCAAA TCGCCTCTTCAATGGATTTGGTCCCCTTCAACCAGCT GTAGCTATGCATTGA	193
<i>mir-133a-2</i>	GGGAGCCAAATGCTTTGCTAGAGCTGGTAAAATGGA ACCAAATCGACTGTCCAATGGATTTGGTCCCCTTCAA CCAGCTGTAGCTGTGCATTGATGGCGCCG	194
<i>mir-133-prec</i>	GCTAGAGCTGGTAAAATGGAACCAAAATCGCCTCTTCA ATGGATTTGGTCCCCTTCAACCAGCTGTAGC	195
<i>mir-134-prec-1</i>	CAGGGTGTGTGACTGGTTGACCAGAGGGGCATGCAC TGTGTTCAACCCTGTGGGCCACCTAGTCACCAACCCTC	196
<i>mir-134-prec-2</i>	AGGGTGTGTGACTGGTTGACCAGAGGGGCATGCACT GTGTTCAACCCTGTGGGCCACCTAGTCACCAACCCT	197
<i>mir-135-1-prec</i>	AGGCCTCGCTGTTCTCTATGGCTTTTATTCTATGTG ATTCTACTGCTCACTCATATAGGGATTGGAGCCGTGG CGCACGGCGGGGACA	198
<i>mir-135-2-prec</i>	AGATAAATTCACTCTAGTGCTTTATGGCTTTTATTCC TATGTGATAGTAATAAAGTCTCATGTAGGGATGGAA GCCATGAAATACATTGTGAAAAATCA	199
<i>mir-135-prec</i>	CTATGGCTTTTATTCTATGTGATTCTACTGCTCACT CATATAGGGATTGGAGCCGTGG	200

Name	Precursor Sequence (5' to 3')*	SEQ ID NO:
<i>mir-136-prec-1</i>	TGAGCCCTCGGAGGACTCCATTTGTTTTGATGATGGA TTCTTATGCTCCATCATCGTCTCAAATGAGTCTTCAGA GGGTTCT	201
<i>mir-136-prec-2</i>	GAGGACTCCATTTGTTTTGATGATGGATTCTTATGCTC CATCATCGTCTCAAATGAGTCTTC	202
<i>mir-137-prec</i>	CTTCGGTGACGGGTATTCTTGGGTGGATAATACGGAT TACGTTGTTATTGCTTAAGAATACGCGTAGTCGAGG	203
<i>mir-138-1-prec</i>	CCCTGGCATGGTGTGGTGGGGCAGCTGGTGTGTGAA TCAGGCCGTTGCCAATCAGAGAACGGCTACTTCACAA CACAGGGGCCACACCACACTACAGG	204
<i>mir-138-2-prec</i>	CGTTGCTGCAGCTGGTGTGTGAATCAGGCCGACGAG CAGCGCATCCTCTTACCCGGCTATTTACGACACCAG GGTTGCATCA	205
<i>mir-138-prec</i>	CAGCTGGTGTGTGAATCAGGCCGACGAGCAGCGCA TCCTCTTACCCGGCTATTTACGACACCAGGGTTG	206
<i>mir-139-prec</i>	GTGTATTCTACAGTGCACGTGTCTCCAGTGTGGCTCG GAGGCTGGAGACGCGGCCCTGTTGGAGTAAC	207
<i>mir-140</i>	TGTGTCTCTCTCTGTGTCCTGCCAGTGGTTTTACCCTA TGGTAGGTTACGTCATGCTGTTCTACCACAGGGTAGA ACCACGGACAGGATAACGGGGGCACC	208
<i>mir-140as-prec</i>	TCCTGCCAGTGGTTTTACCCTATGGTAGGTTACGTCA TGCTGTTCTACCACAGGGTAGAACCACGGACAGGA	209
<i>mir-140s-prec</i>	CCTGCCAGTGGTTTTACCCTATGGTAGGTTACGTCAT GCTGTTCTACCACAGGGTAGAACCACGGACAGG	210
<i>mir-141-prec-1</i>	CGGCCGGCCCTGGGTCCATCTTCCAGTACAGTGTGG ATGGTCTAATTGTGAAGCTCCTAACACTGTCTGGTAA AGATGGCTCCCGGGTGGGTTTC	211
<i>mir-141-prec-2</i>	GGGTCCATCTTCCAGTACAGTGTGGATGGTCTAATT GTGAAGCTCCTAACACTGTCTGGTAAAGATGGCCC	212
<i>mir-142as-prec</i> (<i>mir-142s-prec</i>)	ACCCATAAAGTAGAAAGCACTACTAACAGCACTGGA GGGTGTAGTGTTCCTACTTTATGGATG	213
<i>mir-142s-pres</i>	ACCCATAAAGTAGAAAGCACTACTAACAGCACTGGA GGGTGTAGTGTTCCTACTTTATGGATG	214
<i>mir-143-prec-1</i>	GCGCAGCGCCCTGTCTCCCAGCCTGAGGTGCAGTGCT GCATCTCTGGTCAGTTGGGAGTCTGAGATGAAGCACT GTAGCTCAGGAAGAGAGAAGTTGTTCTGCAGC	215
<i>mir-143-prec-2</i>	CCTGAGGTGCAGTGCTGCATCTCTGGTCAGTTGGGAG TCTGAGATGAAGCACTGTAGCTCAGG	216
<i>mir-144-prec-1</i>	TGGGGCCCTGGCTGGGATATCATCATATACTGTAAGT TTGCGATGAGACACTACAGTATAGATGATGTACTAGT CCGGGCACCCCC	217
<i>mir-144-prec-2</i>	GGCTGGGATATCATCATATACTGTAAGTTTGCGATGA GACACTACAGTATAGATGATGTACTAGTC	218

Name	Precursor Sequence (5' to 3')*	SEQ ID NO:
<i>mir-145-prec-1</i>	CACCTTGTCTCACGGTCCAGTTTTCCAGGAATCCC TTAGATGCTAAGATGGGGATTCTTGGAAATACTGTTT TTGAGGTCATGGTT	219
<i>mir-145-prec-2</i>	CTCACGGTCCAGTTTTCCAGGAATCCCTTAGATGCT AAGATGGGGATTCTTGGAAATACTGTTCTTGAG	220
<i>mir-146-prec-1</i>	CCGATGTGTATCCTCAGCTTTGAGAACTGAATTCCAT GGGTTGTGTCAAGTGTGACACCTCTGAAATTCAGTTCT TCAGCTGGGATATCTCTGTCTCATCGT	221
<i>mir-146-prec-2</i>	AGCTTTGAGAACTGAATTCCATGGGTTGTGTCAAGTGT CAGACCTGTGAAATTCAGTTCTTCAGCT	222
<i>mir-147-prec</i>	AATCTAAAGACAACATTTCTGCACACACACCAGACTA TGGAAGCCAGTGTGTGGAAATGCTTCTGCTAGATT	223
<i>mir-148-prec</i>	GAGGCAAAGTTCTGAGACACTCCGACTCTGAGTATG ATAGAAGTCAGTGCACACTACAGAACTTTGTCTC	224
<i>mir-149-prec-1</i>	GCCGGCGCCCGAGCTCTGGCTCCGTGTCTTCACTCCC GTGCTTGTCCGAGGAGGGAGGGAGGGACGGGGGCTG TGCTGGGGCAGCTGGA	225
<i>mir-149-prec-2</i>	GCTCTGGCTCCGTGTCTTCACTCCCGTGCTTGTCCGAG GAGGGAGGGAGGGAC	226
<i>mir-150-prec-1</i>	CTCCCCATGGCCCTGTCTCCCAACCCTTGTACCAGTG CTGGGCTCAGACCCTGGTACAGGCCTGGGGGACAGG GACCTGGGGAC	227
<i>mir-150-prec-2</i>	CCCTGTCTCCCAACCCTTGTACCAGTGCTGGGCTCAG ACCCTGGTACAGGCCTGGGGGACAGGG	228
<i>mir-151-prec</i>	CCTGCCCTCGAGGAGCTCACAGTCTAGTATGTCTCAT CCCCTACTAGACTGAAGCTCCTTGAGGACAGG	229
<i>mir-152-prec-1</i>	TGTCCCCCGGCCAGGTTCTGTGATACACTCCGAC TCGGGCTCTGGAGCAGTCAGTGCATGACAGAACTTG GGCCCGGAAGGACC	230
<i>mir-152-prec-2</i>	GGCCAGGTTCTGTGATACACTCCGACTCGGGCTCTG GAGCAGTCAGTGCATGACAGAACTTGGGCCCCGG	231
<i>mir-153-1-prec-1</i>	CTCACAGCTGCCAGTGTCAATTTTGTGATCTGCAGCT AGTATTCTCACTCCAGTTGCATAGTCACAAAAGTGAT CATTGGCAGGTGTGGC	232
<i>mir-153-1-prec-2</i>	tctctctctcctcACAGCTGCCAGTGTCAATGTCAAAAAGT GATCAATTGGCAGGTGTGGCTGCTGCATG	233
<i>mir-153-2-prec-1</i>	AGCGGTGGCCAGTGTCAATTTTGTGATGTTGCAGCTA GTAATATGAGCCAGTTGCATAGTCACAAAAGTGATC ATTGGAAACTGTG	234
<i>mir-153-2-prec-2</i>	CAGTGTCAATTTTGTGATGTTGCAGCTAGTAATATGA GCCAGTTGCATAGTCACAAAAGTGATCATTG	235

Name	Precursor Sequence (5' to 3')*	SEQ ID NO:
<i>mir-154-prec-1</i>	GTGGTACTTGAAGATAGGTTATCCGTGTTGCCTTCGC TTTATTTGTGACGAATCATACACGGTTGACCTATTTT CAGTACCAA	236
<i>mir-154-prec-2</i>	GAAGATAGGTTATCCGTGTTGCCTTCGCTTTATTTGTG ACGAATCATACACGGTTGACCTATTTT	237
<i>mir-155-prec</i>	CTGTTAATGCTAATCGTGATAGGGGTTTTTGCCTCCA ACTGACTCCTACATATTAGCATTAACAG	238
<i>mir-16-2-prec</i>	CAATGTCAGCAGTGCCTTAGCAGCACGTAAATATTGG CGTTAAGATTCTAAAATTATCTCCAGTATTAAGTGTG CTGCTGAAGTAAGGTTGACCATACTCTACAGTTG	239
<i>mir-181a-prec</i>	AGAAGGGCTATCAGGCCAGCCTTCAGAGGACTCCAA GGAACATTCAACGCTGTCGGTGAGTTTGGGATTTGAA AAAACCACTGACCGTTGACTGTACCTTGGGGTCCCTA	240
<i>mir-181b-prec</i>	TGAGTTTTGAGGTTGCTTCAGTGAACATTCAACGCTG TCGGTGAGTTTGGGAATTAATAAATCAAACCATCGACCG TTGATTGTACCCTATGGCTAACCATCATCTACTCCA	241
<i>mir-181c-prec</i>	CGGAAAATTTGCCAAGGGTTTGGGGGAACATTCAAC CTGTCGGTGAGTTTGGGCAGCTCAGGCAAACCATCGA CCGTTGAGTGGACCCTGAGGCCTGGAATTGCCATCCT	242
<i>mir-182-as-prec</i>	GAGCTGCTTGCCTCCCCCGTTTTTGGCAATGGTAGA ACTCACACTGGTGAGGTAACAGGATCCGGTGGTTCTA GACTTGCCAACTATGGGGCGAGGACTCAGCCGGCAC	243
<i>mir-182-prec</i>	TTTTTGGCAATGGTAGAACTCACACTGGTGAGGTAAC AGGATCCGGTGGTTCTAGACTTGCCAACTATGG	244
<i>mir-183-prec</i>	CCGCAGAGTGTGACTCCTGTTCTGTGTATGGCACTGG TAGAATTCAGTGTGAACAGTCTCAGTCAGTGAATTAC CGAAGGGCCATAAACAGAGCAGAGACAGATCCACGA	245
<i>mir-184-prec-1</i>	CCAGTCACGTCCCCTTATCACTTTTCCAGCCCAGCTTT GTGACTGTAAGTGTGGACGGAGAACTGATAAGGGT AGGTGATTGA	246
<i>mir-184-prec-2</i>	CCTTATCACTTTTCCAGCCCAGCTTTGTGACTGTAAGT GTTGGACGGAGAACTGATAAGGGTAGG	247
<i>mir-185-prec-1</i>	AGGGGGCGAGGGATTGGAGAGAAAGGCAGTTCCTGA TGGTCCCCTCCCCAGGGGCTGGCTTTCCTCTGGTCCTT CCCTCCCA	248
<i>mir-185-prec-2</i>	AGGGATTGGAGAGAAAGGCAGTTCCTGATGGTCCCC TCCCCAGGGGCTGGCTTTCCTCTGGTCCTT	249
<i>mir-186-prec-1</i>	TGCTTGTAACTTTCCAAAGAATTCTCCTTTTGGGCTTT CTGGTTTTATTTTAAGCCCAAAGGTGAATTTTTTGGG AAGTTTGAGCT	250
<i>mir-186-prec-2</i>	ACTTTCCAAAGAATTCTCCTTTTGGGCTTTCTGGTTTT ATTTTAAGCCCAAAGGTGAATTTTTTGGGAAGT	251

Name	Precursor Sequence (5' to 3')*	SEQ ID NO:
<i>mir-187-prec</i>	GGTCGGGCTCACCATGACACAGTGTGAGACTCGGGC TACAACAAGGACCCGGGGCGCTGCTCTGACCCCTCG TGTCTTGTGTTGCAGCCGGAGGGACGCAGGTCCGCA	252
<i>mir-188-prec-1</i>	TGCTCCCTCTCTCACATCCCTTGCATGGTGGAGGGTG AGCTTTCTGAAAACCCCTCCCACATGCAGGGTTTGCA GGATGGCGAGCC	253
<i>mir-188-prec-2</i>	TCTCACATCCCTTGCATGGTGGAGGGTGAGCTTTCTG AAAACCCCTCCCACATGCAGGGTTTGACAGGA	254
<i>mir-189-prec-1</i>	CTGTCGATTGGACCCGCCCTCCGGTGCCTACTGAGCT GATATCAGTTCTCATTTTACACACTGGCTCAGTTCAG CAGGAACAGGAGTCGAGCCCTTGAGCAA	255
<i>mir-189-prec-2</i>	CTCCGGTGCCTACTGAGCTGATATCAGTTCTCATTTTA CACACTGGCTCAGTTCAGCAGGAACAGGAG	256
<i>mir-190-prec-1</i>	TGCAGGCCTCTGTGTGATATGTTTGATATATTAGGTT GTTATTTAATCCAACCTATATCAAACATATTCCTAC AGTGTCTTGCC	257
<i>mir-190-prec-2</i>	CTGTGTGATATGTTTGATATATTAGGTTGTTATTTAAT CCAACCTATATCAAACATATTCCTACAG	258
<i>mir-191-prec-1</i>	CGGCTGGACAGCGGGCAACGGAATCCCAAAGCAGC TGTTGTCTCCAGAGCATTCCAGCTGCGCTTGGATTTC GTCCCCTGCTCTCCTGCCT	259
<i>mir-191-prec-2</i>	AGCGGGCAACGGAATCCCAAAGCAGCTGTTGTCTC CAGAGCATTCCAGCTGCGCTTGGATTTCGTCCCCTGC T	260
<i>mir-192-2/3</i>	CCGAGACCGAGTGCACAGGGCTCTGACCTATGAATT GACAGCCAGTGCTCTCGTCTCCCCTCTGGCTGCCAAT TCCATAGGTCACAGGTATGTTTCGCCTCAATGCCAG	261
<i>mir-192-prec</i>	GCCGAGACCGAGTGCACAGGGCTCTGACCTATGAAT TGACAGCCAGTGCTCTCGTCTCCCCTCTGGCTGCCAA TTCCATAGGTCACAGGTATGTTTCGCCTCAATGCCAGC	262
<i>mir-193-prec-1</i>	CGAGGATGGGAGCTGAGGGCTGGGTCTTTGCGGGCG AGATGAGGGTGTCGGATCAACTGGCCTACAAAGTCC CAGTTCTCGGCCCCCG	263
<i>mir-193-prec-2</i>	GCTGGGTCTTTGCGGGCGAGATGAGGGTGTCGGATC AACTGGCCTACAAAGTCCCAGT	264
<i>mir-194-prec-1</i>	ATGGTGTTATCAAGTGTAACAGCAACTCCATGTGGAC TGTGTACCAATTTCCAGTGGAGATGCTGTTACTTTTG ATGGTTACCAA	265
<i>mir-194-prec-2</i>	GTGTAACAGCAACTCCATGTGGACTGTGTACCAATTT CCAGTGGAGATGCTGTTACTTTTGAT	266
<i>mir-195-prec-1</i>	AGCTTCCCTGGCTCTAGCAGCACAGAAATATTGGCAC AGGGAAGCGAGTCTGCCAATATTGGCTGTGCTGCTCC AGGCAGGGTGGTG	267

Name	Precursor Sequence (5' to 3')*	SEQ ID NO:
<i>mir-195-prec-2</i>	<u>TAGCAGCACAGAAATATTGGCACAGGGAAGCGAGTC</u> <u>TGCCAATATTGGCTGTGCTGCT</u>	268
<i>mir-196-1-prec</i>	<u>CTAGAGCTTGAATTGGAAGTCTGAGTGAATTAGGTA</u> <u>GTTTCATGTTGTTGGGCCTGGGTTTCTGAACACAACA</u> <u>ACATTAAACCACCCGATTACGGCAGTTACTGCTCC</u>	269
<i>mir-196-1-prec</i>	<u>GTGAATTAGGTAGTTTCATGTTGTTGGGCCTGGGTTT</u> <u>CTGAACACAACAACATTAAACCACCCGATTAC</u>	270
<i>mir-196-2-prec</i>	<u>TGCTCGCTCAGCTGATCTGTGGCTTAGGTAGTTTCAT</u> <u>GTTGTTGGGATTGAGTTTGAAGTCTGGCAACAAGAAA</u> <u>CTGCCTGAGTTACATCAGTCGGTTTTCTCGTCGAGGGC</u>	271
<i>mir-196-prec</i>	<u>GTGAATTAGGTAGTTTCATGTTGTTGGGCCTGGGTTT</u> <u>CTGAACACAACAACATTAAACCACCCGATTAC</u>	272
<i>mir-197-prec</i>	<u>GGCTGTGCCGGGTAGAGAGGGCAGTGGGAGGTAAGA</u> <u>GCTCTTCACCCTTCACCACCTTCTCCACCCAGCATGG</u> <u>CC</u>	273
<i>mir-198-prec</i>	<u>TCATTGGTCCAGAGGGGAGATAGGTTCCTGTGATTTT</u> <u>TCCTTCTTCTCTATAGAATAAATGA</u>	274
<i>mir-199a-1-prec</i>	<u>GCCAACCCAGTGTTTCAGACTACCTGTTTCAGGAGGCTC</u> <u>TCAATGTGTACAGTAGTCTGCACATTGGTTAGGC</u>	275
<i>mir-199a-2-prec</i>	<u>AGGAAGCTTCTGGAGATCCTGCTCCGTCGCCCCAGTG</u> <u>TTCAGACTACCTGTTTCAGGACAATGCCGTTGTACAGT</u> <u>AGTCTGCACATTGGTTAGACTGGGCAAGGGAGAGCA</u>	276
<i>mir-199b-prec</i>	<u>CCAGAGGACACCTCCACTCCGTCTACCCAGTGTTTAG</u> <u>ACTATCTGTTTCAGGACTCCCAAATTGTACAGTAGTCT</u> <u>GCACATTGGTTAGGCTGGGCTGGGTTAGACCCTCGG</u>	277
<i>mir-199s-prec</i>	<u>GCCAACCCAGTGTTTCAGACTACCTGTTTCAGGAGGCTC</u> <u>TCAATGTGTACAGTAGTCTGCACATTGGTTAGGC</u>	278
<i>mir-200a-prec</i>	<u>GCCGTGGCCATCTTACTGGGCAGCATTGGATGGAGTC</u> <u>AGGTCTCTAATACTGCCTGGTAATGATGACGGC</u>	279
<i>mir-200b-prec</i>	<u>CCAGCTCGGGCAGCCGTGGCCATCTTACTGGGCAGCA</u> <u>TTGGATGGAGTCAGGTCTCTAATACTGCCTGGTAATG</u> <u>ATGACGGCGGAGCCCTGCACG</u>	280
<i>mir-202-prec</i>	<u>GTTCTTTTTCTATGCATATACTTCTTTGAGGATCTG</u> <u>GCCTAAAGAGGTATAGGGCATGGGAAGATGGAGC</u>	281
<i>mir-203-prec</i>	<u>GTGTTGGGGACTCGCGCGCTGGGTCCAGTGGTTCTTA</u> <u>ACAGTTCAACAGTTCTGTAGCGCAATTGTGAAATGTT</u> <u>TAGGACCACTAGACCCGGCGGGCGCGGCGACAGCGA</u>	282
<i>mir-204-prec</i>	<u>GGCTACAGTCTTTCTTCATGTGACTCGTGGACTTCCCT</u> <u>TTGTCATCCTATGCCTGAGAATATATGAAGGAGGCTG</u> <u>GGAAGGCAAAGGGACGTTCAATTGTCATCACTGGC</u>	283
<i>mir-205-prec</i>	<u>AAAGATCCTCAGACAATCCATGTGCTTCTCTTGTCCT</u> <u>TCATTCCACCGGAGTCTGTCTCATACCCAACCAGATT</u> <u>TCAGTGGAGTGAAGTTCAGGAGGCATGGAGCTGACA</u>	284

Name	Precursor Sequence (5' to 3')*	SEQ ID NO:
<i>mir-206-prec-1</i>	TGCTTCCCGAGGCCACATGCTTCTTTATATCCCCATAT GGATTACTTTGCTATGGAATGTAAGGAAGTGTGTGGT TTCGGCAAGTG	285
<i>mir-206-prec-2</i>	AGGCCACATGCTTCTTTATATCCCCATATGGATTACTT TGCTATGGAATGTAAGGAAGTGTGTGGTTTT	286
<i>mir-208-prec</i>	TGACGGGCGAGCTTTTGGCCCGGGTTATACCTGATGC TCACGTATAAGACGAGCAAAAAGCTTGTTGGTCA	287
<i>mir-210-prec</i>	ACCCGGCAGTGCCTCCAGGCGCAGGGCAGCCCCTGC CCACCGCACACTGCGCTGCCCCAGACCCACTGTGCGT GTGACAGCGGCTGATCTGTGCCTGGGCAGCGCGACC C	288
<i>mir-211-prec</i>	TCACCTGGCCATGTGACTTGTGGGCTTCCCTTTGTCAT CCTTCGCCTAGGGCTCTGAGCAGGGCAGGGACAGCA AAGGGGTGCTCAGTTGTCACTTCCCACAGCACGGAG	289
<i>mir-212-prec</i>	CGGGGCACCCCGCCCGGACAGCGCGCCGGCACCTTG GCTCTAGACTGCTTACTGCCCGGGCCGCCCTCAGTAA CAGTCTCCAGTCACGGCCACCGACGCCTGGCCCCGCC	290
<i>mir-213-prec</i>	CCTGTGCAGAGATTATTTTAAAGGTCACAATCAA CATTCAATTGCTGTGCGGTGGGTTGAACTGTGTGGACAA GCTCACTGAACAATGAATGCAACTGTGGCCCCGCTT	291
<i>mir-213-prec-LIM</i>	GAGTTTTGAGGTTGCTTCAGTGAACATTCAACGCTGT CGGTGAGTTTGGAATTAATAAATCAAAACCATCGACCGT TGATTGTACCCTATGGCTAACCATCATCTACTCC	292
<i>mir-214-prec</i>	GGCCTGGCTGGACAGAGTTGTCATGTGTCTGCCTGTC TACACTTGCTGTGCAGAACATCCGCTCACCTGTACAG CAGGCACAGACAGGCAGTCACATGACAACCCAGCCT	293
<i>mir-215-prec</i>	ATCATTCAAGAAATGGTATACAGGAAAATGACCTATG AATTGACAGACAATATAGCTGAGTTTGTCTGTCATTT CTTTAGGCCAATATTCTGTATGACTGTGCTACTTCAA	294
<i>mir-216-prec</i>	GATGGCTGTGAGTTGGCTTAATCTCAGCTGGCAACTG TGAGATGTTTACATAAATCCCTCACAGTGGTCTCTGGG ATTATGCTAAACAGAGCAATTCCTAGCCCTCACGA	295
<i>mir-217-prec</i>	AGTATAATTATTACATAGTTTTTGATGTCGCAGATAC TGCATCAGGAAGTATTGGATAAGAATCAGTCACCAT CAGTTCCTAATGCATTGCCCTCAGCATCTAAACAAG	296
<i>mir-218-1-prec</i>	GTGATAATGTAGCGAGATTTTCTGTTGTGCTTGATCT AACCATGTGGTTGCGAGGTATGAGTAAACATGGTTC CGTCAAGCACCATGGAACGTCACGCAGCTTTCTACA	297
<i>mir-218-2-prec</i>	GACCAGTCGCTGCGGGGCTTTCCTTTGTGCTTGATCT AACCATGTGGTGGAAACGATGGAAACGGAACATGGTT CTGTCAAGCACCGCGGAAAGCACCGTGCTCTCCTGCA	298

Name	Precursor Sequence (5' to 3')*	SEQ ID NO:
<i>mir-219-prec</i>	CCGCCCCGGGCGCGGCTCCTGATTGTCCAAACGCAA TTCTCGAGTCTATGGCTCCGGCCGAGAGTTGAGTCTG GACGTCCCGAGCCGCCGCCCCCAAACCTCGAGCGGG	299
<i>mir-220-prec</i>	GACAGTGTGGCATTGTAGGGCTCCACACCGTATCTGA CACTTTGGGCGAGGGCACCATGCTGAAGGTGTTTCATG ATGCGGTCTGGGAACCTCACGGATCTTACTGATG	300
<i>mir-221-prec</i>	TGAACATCCAGGTCTGGGGCATGAACCTGGCATAACA ATGTAGATTCTGTGTTTCGTTAGGCAACAGCTACATT GTCTGCTGGGTTTCAGGCTACCTGGAAACATGTTCTC	301
<i>mir-222-prec</i>	GCTGCTGGAAGGTGTAGGTACCCTCAATGGCTCAGTA GCCAGTGTAGATCCTGTCTTTTCGTAATCAGCAGCTAC ATCTGGCTACTGGGTCTCTGATGGCATCTTCTAGCT	302
<i>mir-223-prec</i>	CCTGGCCTCCTGCAGTGCCACGCTCCGTGTATTTGAC AAGCTGAGTTGGACACTCCATGTGGTAGAGTGTGAGT TTGTCAAATACCCCAAGTGCGGCACATGCTTACCAG	303
<i>mir-224-prec</i>	GGGCTTTCAAGTCACTAGTGGTTCCGTTTAGTAGATG ATTGTGCATTGTTTCAAATGGTGCCCTAGTGACTAC AAAGCCC	304
<i>mir-29b-1=102-prec1</i>	CTTCTGGAAGCTGGTTTCACATGGTGGCTTAGATTTTT CCATCTTTGTATCTAGCACCATTGAAATCAGTGTTTT AGGAG	305
<i>mir-29b-2 (miR-29b-3) =102prec7.1=7.2</i>	CTTCAGGAAGCTGGTTTCATATGGTGGTTTAGATTTA AATAGTGATTGTCTAGCACCATTGAAATCAGTGTTT TTGGGGG	306
<i>mir-30*=mir-097-prec-6</i>	GTGAGCGACTGTAAACATCCTCGACTGGAAGCTGTG AAGCCACAGATGGGCTTTCAGTCGGATGTTTGCAGCT GCCTACT	307
<i>mir-033b</i>	ACCAAGTTTCAGTTCATGTAAACATCCTACACTCAGC TGTAATACATGGATTGGCTGGGAGGTGGATGTTTACT TCAGCTGACTTGGA	308
<i>mir-101-precursor-9 (mir-101-3)</i>	TGCCCTGGCTCAGTTATCACAGTGCTGATGCTGTCTA TTCTAAAGGTACAGTACTGTGATAACTGAAGGATGGC A	309
<i>mir-108-1-small</i>	AACTGCAAGAACAATAAGGATTTTTAGGGGCATTAT GACTGAGTCAGAAAACACAGCTGCCCTGAAAGTCC CTCATTTTTCTTGCTGT	310
<i>mir-108-2-small</i>	ACTGCAAGAGCAATAAGGATTTTTAGGGGCATTATG ATAGTGGAATGGAAACACATCTGCCCCCAAAGTCC CTCATTTT	311
<i>mir-123-prec-1 (mir-126-prec-1)</i>	CGCTGGCGACGGGACATTATTACTTTTGGTACGCGCT GTGACACTTCAAACCTCGTACCGTGAGTAATAATGCGC CGTCCACGGCA	312

<i>mir-123-prec-2</i> (<i>mir-126-prec-2</i>)	ACATTATTACTTTTGGGTACGCGCTGTGACACTTCAAA CTCGTACCGTGAGTAATAATGCGC	313
<i>mir-129-1-prec</i>	TGGATCTTTTGGCGGTCTGGGCTTGCTGTTCTCTCAA CAGTAGTCAGGAAGCCCTTACCCCAAAAAGTATCTA	314
<i>mir-129-2</i>	TGCCCTTCGCGAATCTTTTGGCGGTCTGGGCTTGCTGT ACATAACTCAATAGCCGGAAGCCCTTACCCCAAAA GCATTTGCGGAGGGCG	315
<i>mir-133b-small</i>	GCCCCCTGCTCTGGCTGGTCAAACGGAACCAAGTCCG TCTTCCTGAGAGGTTTGGTCCCCTTCAACCAGCTACA GCAGGG	316
<i>mir-135-small-2</i>	AGATAAATTCACCTCTAGTGCTTTATGGCTTTTATTCC TATGTGATAGTAATAAAGTCTCATGTAGGGATGGAA GCCATGAAATACATTGTGAAAAATCA	317
<i>mir-148b-small</i>	AAGCACGATTAGCATTTGAGGTGAAGTTCTGTTATAC ACTCAGGCTGTGGCTCTCTGAAAGTCAGTGCAT	318
<i>mir-151-prec</i>	CCTGTCCTCAAGGAGCTTCAGTCTAGTAGGGGATGAG ACATACTAGACTGTGAGCTCCTCGAGGGCAGG	319
<i>mir-155-prec(BIC)</i>	CTGTTAATGCTAATCGTGATAGGGGTTTTTGCCTCCA ACTGACTCCTACATATTAGCATTAAACAG	320
<i>mir-156 = mir-157=overlap</i> <i>mir-141</i>	CCTAACACTGTCTGGTAAAGATGGCTCCCGGGTGGGT TCTCTCGGCAGTAACCTTCAGGGAGCCCTGAAGACCA TGGAGGAC	321
<i>mir-158-small = mir-192</i>	GCCGAGACCGAGTGCACAGGGCTCTGACCTATGAAT TGACAGCCAGTGCTCTCGTCTCCCCTCTGGCTGCCAA TTCCATAGGTCACAGGTATGTTTCGCCTCAATGCCAGC	322
<i>mir-159-1-small</i>	TCCCGCCCCCTGTAAACAGCAACTCCATGTGGAAGTGC CCACTGGTTCCAGTGGGGCTGCTGTTATCTGGGGCGA GGGCCA	323
<i>mir-161-small</i>	AAAGCTGGGTTGAGAGGGCGAAAAAGGATGAGGTGA CTGGTCTGGGCTACGCTATGCTGCGGCGCTCGGG	324
<i>mir-163-1b-small</i>	CATTGGCCTCCTAAGCCAGGGATTGTGGGTTTCGAGTC CCACCCGGGGTAAAGAAAGGCCGAATT	325
<i>mir-163-3-small</i>	CCTAAGCCAGGGATTGTGGGTTTCGAGTCCCACCTGGG GTAGAGGTGAAAGTTCTTTTACGGAATTTTTT	326
<i>mir-175-small=mir-224</i>	GGGCTTTCAAGTCACTAGTGGTTCCGTTTAGTAGATG ATTGTGCATTGTTTCAAAATGGTGCCCTAGTGACTAC AAAGCCC	327
<i>mir-177-small</i>	ACGCAAGTGTCTAAGGTGAGCTCAGGGAGCACAGA AACCTCCAGTGGAACAGAAGGGCAAAAGCTCATT	328
<i>mir-180-small</i>	CATGTGTCACTTTCAGGTGGAGTTTCAAGAGTCCCTT CCTGGTTCACCGTCTCCTTTGCTCTTCCACAAC	329
<i>mir-187-prec</i>	GGTCGGGCTCACCATGACACAGTGTGAGACTCGGGC TACAACACAGGACCCGGGGCGCTGCTCTGACCCCTCG TGTCTTGTGTTGCAGCCGGAGGGACGCAGGTCCGCA	330

<i>mir-188-prec</i>	TGCTCCCTCTCTCACATCCCTTGCATGGTGGAGGGTG AGCTTTCTGAAAACCCCTCCACATGCAGGGTTTGCA GGATGGCGAGCC	331
<i>mir-190-prec</i>	TGCAGGCCTCTGTGTGATATGTTTGATATATTAGGTT GTTATTTAATCCAACATATATCAAACATATTCCTAC AGTGTCTTGCC	332
<i>mir-197-2</i>	GTGCATGTGTATGTATGTGTGCATGTGCATGTGTATG TGTATGAGTGCATGCGTGTGTGC	333
<i>mir-197-prec</i>	GGCTGTGCCGGGTAGAGAGGGCAGTGGGAGGTAAGA GCTCTTCACCCCTTACCACCTTCTCCACCCAGCATGG CC	334
<i>mir-202-prec</i>	GTTCTTTTTCCTATGCATATACTTCTTTGAGGATCTG GCCTAAAGAGGGTATAGGGCATGGGAAGATGGAGC	335
<i>mir-294-1</i> (chr16)	CAATCTTCCTTTATCATGGTATTGATTTTTCAGTGCTT CCCTTTTGTGTGAGAGAAGATA	336
<i>mir-hes1</i>	ATGGAGCTGCTCACCTGTGGGCCTCAAATGTGGAGG AACTATTCTGATGTCCAAGTGGAAAGTGCTGCGACAT TTGAGCGTCACCGGTGACGCCCATATCA	337
<i>mir-hes2</i>	GCATCCCCTCAGCCTGTGGCACTCAAACCTGTGGGGGC ACTTTCTGCTCTCTGGTGAAAGTGCCGCCATCTTTTGA GTGTTACCGCTTGAGAAGACTCAACC	338
<i>mir-hes3</i>	CGAGGAGCTCATACTGGGATACTCAAATGGGGGGCG CTTTCCTTTTGTCTGTTACTGGGAAGTGCTTCGATTT TGGGGTGTCCCTGTTTGAGTAGGGCATC	339
<i>mir-29b-1</i>	CTTCAGGAAGCTGGTTTCATATGGTGGTTTAGATTTA AATAGTGATTGTCTAGCACCATTTGAAATCAGTGTTT TTGGGGG	340

* An underlined sequence within a precursor sequence represents a processed miR transcript (mature microRNA). All sequences are human.

Methods of Diagnosis and Prognosis

5 According to the invention, BCL2-associated cancers can be diagnosed or
prognosticated by detecting a reduction in the amount of miR gene product in a sample
relative to a control sample, a reduction in miR gene copy number, or by detecting mutations
in one or more copies of a miR gene, wherein the miR gene comprises a nucleotide sequence
that is complementary to the nucleotide sequence in a BCL2 gene transcript (e.g., as described
10 herein). A reduction in miR gene copy number of a miR gene that comprises a nucleotide
sequence that is complementary to the nucleotide sequence in a BCL2 gene transcript, from

diploid to haploid, or to no copies, is diagnostic or prognostic of BCL2-associated cancers. Likewise, a mutation in one or both copies of a miR gene that comprises a nucleotide sequence that is complementary to the nucleotide sequence in a BCL2 gene transcript implies a loss of gene function, and is diagnostic or prognostic of BCL2-associated cancers.

5 As used herein, a "CLL cell" can be a lymphocyte from a subject who has, or is suspected of having, CLL, wherein the lymphocyte has a "CLL Score" of at least 4, as determined according to the scoring system of Matutes *et al.*, *Leukemia* 8(10):1640-1645 (1994). As used herein, a "prostate cancer cell" can be a neoplastic or tumorigenic cell of prostate origin, whether or not located in the prostate. Other BCL2-
10 associated cancer cells are known in those of skill in the art and/or are described herein.

The nucleic acid sequences of the miR15 and miR16 genes are contained within clone 317g11, the nucleotide sequence of which is given in GenBank Accession No.: AC069475.

15 A deletion or mutation in a miR gene that comprises a nucleotide sequence that is complementary to the nucleotide sequence in a BCL2 gene transcript can be detected by determining the structure or sequence of the gene in tissue from a subject suspected of having a BCL2-associated cancer (e.g., CLL, acute myeloid leukemia multiple myeloma, melanoma, follicular lymphoma, large cell
20 lymphoma, non-Hodgkin's lymphoma, non-small cell lung carcinoma, hematologic malignancies, solid tumors, colorectal cancer, brain carcinoma, breast carcinoma, prostate carcinoma, Epstein-Barr virus-associated lymphoproliferative disease, renal carcinoma, hepatocellular carcinoma and gastric carcinoma), and comparing this with the structure or sequence of these genes in a sample of unaffected tissue from the subject, or in a sample of tissue from a normal control. Such a comparison can be made by any suitable
25 technique (e.g., as described herein).

In one embodiment, to diagnose a BCL2-associated cancer, a tissue sample is derived from a subject. The sample is then prepared for determination of miR gene product expression or deletion or mutation of one or more miR genes. Suitable tissue samples include, but are not limited to, a biopsy of interest, as well as a blood and/or fluid sample.

As used herein, a "BCL2-associated cancer" is a cancer that is associated with overexpression of a BCL2 gene or gene product, which can be any cancer that is characterized by cells that express a higher level of one or more BCL2 gene products, relative to suitable control cells. Suitable control cells, according to the methods of the present invention, can be
5 cells from an individual who is not affected with a Bcl2 over-expressing cancer, or they may be non-cancerous cells from either the subject in need, or they may be non-cancerous cells from another individual who is affected with a Bcl2 over-expressing cancer.

The presence of miR gene deletions or mutations can be detected by Southern blot hybridization of the genomic DNA from a subject, using probes for miR genes, *e.g.*, as
10 described herein. For example, a sample of tissue can be removed from a subject suspected of having a BCL2-associated cancer by conventional biopsy techniques. Alternatively, a blood sample can be removed from a subject suspected of having a BCL2-associated cancer, and white blood cells isolated for DNA extraction. The blood or tissue sample can be obtained from the patient prior to initiation of radiotherapy or chemotherapy. A corresponding tissue
15 or blood sample can be obtained from unaffected tissues of the subject, or from a normal human individual, for use as a control.

Southern blot hybridization techniques are within the skill in the art. For example, genomic DNA isolated from a tissue or fluid (*e.g.*, blood) from a subject suspected of having a BCL2-associated cancer can be digested with restriction endonucleases. This digestion
20 generates restriction fragments of the genomic DNA, which can be separated by electrophoresis, for example, on an agarose gel. The restriction fragments are then blotted onto a hybridization membrane (*e.g.*, nitrocellulose, nylon), and hybridized with labeled probes specific for one or more miR genes (*e.g.*, a miR gene that comprises a nucleotide sequence that is complementary to the nucleotide sequence in a BCL2 gene transcript). A
25 deletion or mutation of the one or more genes is indicated by an alteration of the restriction fragment patterns on the hybridization membrane, as compared to a control DNA sample that has been treated identically to the DNA sample from the subject. Probe labeling and hybridization conditions suitable for detecting the gene copy number of a miR gene or mutations within a miR gene can be readily determined by one of ordinary skill in the art.

The term "deletion," as used herein, refers to partial deletion of a gene or to deletion of the entire gene.

For example, miR-15a and miR-16-1 nucleic acid probes for Southern blot hybridization can be designed based upon the published sequence of the miR-15a and miR-16-1 microRNAs, as described in Lagos-Quintana *et al.*, *Science* 294:853-858 (2001).

The nucleotide sequence of the miR-15a microRNA is uagcagcacauaaugguuugug (SEQ ID NO:3). The nucleotide sequence of the miR-16-1 microRNA is uagcagcacguaaaauuuggcg (SEQ ID NO:4). Suitable probes for detecting miR-15a and miR-16-1 DNA are, respectively:

CACAAACCATTATGTGCTTGCTA (SEQ ID NO:5)

GCCAATATTTACGTGCTGCTA (SEQ ID NO:6)

The complements of SEQ ID NO:5 and SEQ ID NO:6 can also be used to probe for miR-15a or miR-16-1 DNA. Other suitable probes for detecting miR-15a, miR-16-1 or other miR genes (e.g., miR genes that comprise a nucleotide sequence that is complementary to the nucleotide sequence in a BCL2 gene transcript) can easily be determined by one of skill in the art.

Methods for preparation of labeled DNA and RNA probes, and the conditions for hybridization thereof to target nucleotide sequences, are described in Molecular Cloning: A Laboratory Manual, J. Sambrook *et al.*, eds., 2nd edition, Cold Spring Harbor Laboratory Press, 1989, Chapters 10 and 11.

For example, the nucleic acid probe can be labeled with, e.g., a radionuclide, such as ^3H , ^{32}P , ^{33}P , ^{14}C , or ^{35}S ; a heavy metal; or a ligand capable of functioning as a specific binding pair member for a labeled ligand (e.g., biotin, avidin or an antibody), a fluorescent molecule, a chemiluminescent molecule, an enzyme or the like.

Probes can be labeled to high specific activity by either the nick translation method of Rigby *et al.*, *J. Mol. Biol.* 113:237-251 (1977) or by the random priming method of Fienberg *et al.*, *Anal. Biochem.* 132:6-13 (1983).

The latter is the method of choice for synthesizing ^{32}P -labeled probes of high specific activity from single-stranded DNA or from RNA templates. For example, by replacing preexisting nucleotides with highly radioactive nucleotides according to the nick translation method, it is possible to prepare ^{32}P -labeled nucleic acid probes with a specific activity well in excess of 10^8 cpm/microgram. Autoradiographic detection of hybridization can then be performed by exposing hybridized filters to photographic film. Densitometric scanning of the photographic films exposed by the hybridized filters provides an accurate measurement of miR15 or miR16 gene copy number. Alternatively, miR15 or miR16 gene copy number can be quantified by computerized imaging systems, such as the Molecular Dynamics 400-B™ 2D Phosphorimager that is available from Amersham Biosciences, Piscataway, NJ.

Where radionuclide labeling of DNA or RNA probes is not practical, the random-primer method can be used to incorporate a nucleotide analogue (e.g., the dTTP analogue, 5-(N-(N-biotinyl-epsilon-aminocaproyl)-3-aminoallyl)deoxyuridine triphosphate) into the probe molecule. The biotinylated probe oligonucleotide can be detected by reaction with biotin-binding proteins, such as avidin, streptavidin, or anti-biotin antibodies, coupled to fluorescent dyes or enzymes that produce color reactions.

Deletions or mutations of miR genes can also be detected by amplifying a fragment of these genes by polymerase chain reaction (PCR), and analyzing the amplified fragment by sequencing or by electrophoresis to determine if the sequence and/or length of the amplified fragment from a subject's DNA sample is different from that of a control DNA sample. Suitable reaction and cycling conditions for PCR amplification of DNA fragments can be readily determined by one of ordinary skill in the art. Exemplary PCR reaction and cycling conditions are provided in the methods described in the Examples below.

Diagnosis of a BCL2-associated cancer can be performed by detecting deletions of miR genes (e.g., miR genes that comprises a nucleotide sequence that is complementary to the nucleotide sequence in a BCL2 gene transcript). For example, detection of miRs between various chromosome markers, such as the markers indicated in FIGS. 2A-2D. For example, a deletion in the region of 13q14 between microsatellite markers D13S272 and D13S273 comprising miR-15a and miR-16-1, can indicate the presence of a BCL2-associated cancer.

In addition, when the deletion in 13q14 is between microsatellite markers D13S1150 and D13S272 or between locus Alu18 and microsatellite marker D13S272, where miR15 or miR16 are deleted, the presence of a BCL2-associated cancer can be indicated.

An alternative method of determining the copy number of a miR gene that comprises a nucleotide sequence complementary to the nucleotide sequence in a BCL2 gene transcript (for example, miR-15a or miR-16-1 genes) per diploid genome in a sample of tissue relies on the fact that the miR-15a/miR-16-1 gene cluster is located in 13q14, and is linked to the markers *D13S272* and *D13S273*. The loss of a copy of the miR-15a or miR-16-1 genes in an individual who is heterozygous at a locus linked to the *D13S272* and *D13S273* markers can be inferred from the loss of heterozygosity in these markers. Methods for determining loss of heterozygosity of chromosomal markers are within the skill in the art. An exemplary loss of heterozygosity study is described in Example 3 below.

Another technique for determining whether one or more miR genes in a subject suspected of having a BCL2-associated cancer is mutated is single strand conformational polymorphism (SSCP), for example, as described in Orita, *et al.*, *Genomics* 5:1474-879 (1989) and Hayashi, *PCR Methods and Applic.* 1:34-38 (1991). The SSCP technique consists of amplifying a fragment of the gene of interest (e.g., a miR gene) by PCR; denaturing the fragment and electrophoresing the two denatured single strands under non-denaturing conditions. The single strands assume a complex sequence-dependent intrastrand secondary structure that affects the strands electrophoretic mobility.

A deletion or mutation in one or more miR genes can also cause a reduction in expression of those miR genes. Thus, a BCL2-associated cancer can also be diagnosed by detecting expression levels of the RNA produced from one or more miR genes (e.g., a miR gene that comprises a nucleotide sequence that is complementary to the nucleotide sequence in a BCL2 gene transcript), where a reduction in miR gene expression is diagnostic of a BCL2-associated cancer.

miR genes are transcribed to produce a precursor RNA which forms a stem-loop structure. The precursor RNA is not translated into a protein, but is rather processed into a "micro RNA" or "miRNA," which is believed to be the functional gene product.

As used herein, a "miR gene product" means the processed or unprocessed RNA transcripts from a miR gene, as described more fully below. The terms "RNA," RNA transcripts," and "gene product," are used interchangeably herein in the context of miR gene expression.

5 For example, the miR-15a and miR-16-1 precursor RNAs are described in Lagos-Quintana, *et al.*, *Science* 294, 853-858 (2001). The sequences of the miR-15a and miR-16-1 precursor RNAs are given as SEQ ID NO:1 and SEQ ID NO:2. The predicted stem-loop structures of SEQ ID NO:1 and SEQ ID NO:2, are shown in FIGS. 1A and 1B, respectively.

10 [SEQ ID NO:1]:

ccuuggaguaaaguagcagcacauaauggguuuguggauuuugaaaaggugcaggccauauugugcug
ccucaaaaauacaagg

[SEQ ID NO:2]:

gucagcagugccuuagcagcacguaaaauuuggcguaaagauucuaaaaauauaucuccaguauuaacug
15 ugcugcugaaguaagguugac

Without wishing to be bound by any theory, it is believed that the miR-15a and miR16-1 precursor RNAs are co-expressed from the miR-15a/miR-16-1 gene cluster, and are processed by the Dicer/Argonaute complex into the functional miRNA products. See, *e.g.*,
20 Lee *et al.*, *Science* 294:862 (2001). Both functional miRNA products from these genes are single-stranded RNA molecules of 22 nucleotides in length which have a 5' terminal monophosphate and a 3' terminal hydroxyl group. The nucleotide sequence of the processed miR-15a microRNA is uagcagcacauaauggguuugug (SEQ ID NO:3). The nucleotide sequence of the processed miR-16-1 microRNA is uagcagcacguaaaauuuggcg (SEQ ID NO:4). In the
25 practice of the invention, the 60-70 nt RNA precursor molecules produced from the miR-15a or miR-16-1 genes can be detected. Alternatively, the shorter miR-15a and miR-16-1 microRNA gene products, which are produced through processing of the precursor RNAs by the Dicer and Argonaute proteins, can be detected.

Methods for determining RNA expression levels are within the level of skill in the art.
30 For example, a sample of tissue or blood from a subject suspected of having a BCL2-

associated cancer is obtained as described herein. As a control, a corresponding tissue or blood sample can be obtained from unaffected tissues of the subject, or from a normal human individual, as described herein. The control tissue or blood sample is then processed along with the sample from the subject. The levels of miR gene expression (e.g., a miR gene that
5 comprises a nucleotide sequence that is complementary to the nucleotide sequence in a BCL2 gene transcript) in the subject can then be compared to those from unaffected tissue from the subject, or to the miR expression level in tissue or blood from the normal control. For example, the relative miR expression level in BCL2-associated cancer cells are conveniently determined with respect to one or more standards. The standards may comprise, for example,
10 a zero expression level on the one hand and the expression level of the gene in normal tissue of the same patient, or the expression level in the tissue of a normal control group on the other hand. The standard may also comprise the miR expression level in a standard cell line. In one embodiment, the magnitude of the decrement in miR expression, as compared to normal expression levels, is indicative of the future clinical outcome following treatment.

15 Alternatively, the levels of miR gene expression (e.g., a miR gene that comprises a nucleotide sequence that is complementary to the nucleotide sequence in a BCL2 gene transcript) in a subject suspected of having a BCL2-associated cancer can be compared to average levels of miR gene expression previously obtained for a population of normal human controls.

20 Suitable techniques for determining the level of RNA transcripts of a particular gene in cells are well known to those skilled in the art. According to one such method, total cellular RNA can be purified from cells by homogenization in the presence of nucleic acid extraction buffer, followed by centrifugation. Nucleic acids are precipitated, and DNA is removed by treatment with DNase and precipitation. The RNA molecules are then separated
25 by gel electrophoresis on agarose gels according to standard techniques, and transferred to nitrocellulose filters, e.g., using the so-called "Northern" blotting technique. The RNA is then immobilized on the filters by heating. Detection and quantification of specific RNA is accomplished using appropriately labeled DNA or RNA probes complementary to the RNA in question. See, for example, Molecular Cloning: A Laboratory Manual, J. Sambrook *et al.*,
30 eds., 2nd edition, Cold Spring Harbor Laboratory Press, 1989, Chapter 7.

Suitable probes for Northern blot hybridization of miR-15a or miR-16-1 include, e.g., SEQ ID NO:5 and SEQ ID NO:6.

5 Autoradiographic detection of probe hybridization to miR RNA can be performed by exposing hybridized filters to photographic film. Densitometric scanning of the photographic films exposed by the hybridized filters provides an accurate measurement of RNA transcript levels. Alternatively, RNA transcript levels can be quantified by computerized imaging of the hybridization blot, for example, with the Molecular Dynamics 400-B 2D Phosphorimager that is available from Amersham Biosciences, Piscataway, NJ.

10 In addition to Northern and other RNA blotting hybridization techniques, the levels of RNA transcripts can be carried out according to the technique of *in situ* hybridization. This technique requires fewer cells than the Northern blotting technique, and involves depositing whole cells onto a microscope cover slip and probing the nucleic acid content of the cell with a solution containing radioactive or otherwise labeled oligonucleotide (e.g., cDNA or cRNA) probes. This technique is particularly well-suited for analyzing 15 tissue biopsy samples from subjects suspected of having a BCL2-associated cancer (e.g., CLL, prostate cancer). The practice of the *in situ* hybridization technique is described in more detail in U.S. Patent No. 5,427,916. Suitable probes for *in situ* hybridization of miR-15a or miR-16-1 RNA include, e.g., SEQ ID NO:5 and SEQ ID NO:6.

20 The relative number of a particular miR transcript can also be determined by reverse transcription of the miR transcript, followed by amplification in a polymerase chain reaction (RT-PCR). The levels of a miR transcript can be by comparing with an internal standard, for example, levels of mRNA from a "housekeeping" gene present in the same sample. Suitable "housekeeping" genes for use as an internal standard include, e.g., myosin and 25 glyceraldehyde-3-phosphate dehydrogenase (G3PDH). The methods for quantitative RT-PCR and variations thereof are well known to those of skill in the art.

Other techniques for measuring expression of a miR gene transcript are also known to those of skill in the art and include various techniques for measuring the rates of RNA transcription and degradation.

Methods of Treatment

A BCL2-associated cancer can be treated by administering the isolated gene product of one or more miR genes (e.g., a miR gene that comprises a nucleotide sequence that is complementary to the nucleotide sequence in a BCL2 gene transcript), either alone or in
5 combination, to a BCL2-associated cancer cell. Without wishing to be bound by any theory, it is believed that the miR gene products suppress the neoplastic or tumorigenic growth of such cancer cells.

In particular, a BCL2-associated cancer can be treated by administering the isolated gene product of one or more miR genes, either alone or in combination, to a cancer cell.

10 As used herein, a "BCL2-associated cancer cell" is a tumorigenic or neoplastic cell, which can be isolated from a subject suffering from a BCL2-associated cancer. A BCL2-associated cancer cell can be identified by detecting an increase in the expression level of a BCL2 gene product in a cell, relative to a normal control cell, or by detecting a cancerous or neoplastic phenotype in the cell. One skilled in the art can readily identify cells with a
15 cancerous or neoplastic phenotype. For example, such cells are insensitive to contact-induced growth inhibition in culture, and will form foci when cultured for extended periods. Cancerous or neoplastic cells also exhibit characteristic morphological changes, disorganized patterns of colony growth and acquisition of anchorage-independent growth. Cancerous or neoplastic cells also have the ability to form invasive tumors in susceptible animals, which
20 can be evaluated by injecting the cells, for example, into athymic mice using techniques within the skill in the art.

As used herein, an "isolated" gene product is one which is altered or removed from the natural state through human intervention. For example, an RNA naturally present in a living animal is not "isolated." A synthetic RNA, or an RNA partially or completely separated from
25 the coexisting materials of its natural state, is "isolated." An isolated RNA can exist in substantially purified form, or can exist in a cell into which the RNA has been delivered. Thus, a miR gene product that is deliberately delivered to, or expressed in, a cell, (e.g., a BCL2-associated cancer cell) is considered an "isolated" gene product.

miR gene products can be obtained using a number of standard techniques. For
30 example, the gene products can be chemically synthesized or recombinantly produced using

methods known in the art. In one embodiment, the RNA products are chemically synthesized using appropriately protected ribonucleoside phosphoramidites and a conventional DNA/RNA synthesizer. Commercial suppliers of synthetic RNA molecules or synthesis reagents include, e.g., Proligo (Hamburg, Germany), Dharmacon Research (Lafayette, CO, USA), Pierce Chemical (part of Perbio Science, Rockford, IL, USA), Glen Research (Sterling, VA, USA), ChemGenes (Ashland, MA, USA) and Cruachem (Glasgow, UK).

Alternatively, one or more miR gene products can be expressed from recombinant circular or linear DNA plasmids using any suitable promoter. Suitable promoters for expressing RNA from a plasmid include the U6 or H1 RNA pol III promoter sequences, or the cytomegalovirus (CMV) promoters. Selection of other suitable promoters is within the skill in the art. Such recombinant plasmids can also comprise inducible or regulatable promoters for expression of one or more miR gene products in cells (e.g., BCL2-associated cancer cells (e.g., CLL cells, prostate cancer cells, other cancer cells)).

miR gene products that are expressed from recombinant plasmids can be isolated from cultured cell expression systems by standard techniques. miR gene products that are expressed from recombinant plasmids can also be delivered to, and expressed directly in, cancer cells (e.g., BCL2-associated cancer cells (e.g., CLL cells, prostate cancer cells, other cancer cells)). The use of recombinant plasmids to deliver the miR gene products to cancer cells is discussed in more detail below.

Multiple miR gene products can be expressed from a separate recombinant plasmid, or can be expressed from the same recombinant plasmid. In one embodiment, the one or more miR gene products are expressed as the RNA precursor molecules from a single plasmid, and the precursor molecules are processed into functional miRNA molecules by a suitable processing system. Suitable processing systems include, e.g., the *in vitro* Drosophila cell lysate system described in U.S. Published Application No.: 2002/0086356, by Tuschl *et al.*

Selection of plasmids suitable for expressing a miR gene product, methods for inserting nucleic acid sequences that express a miR gene product into a plasmid, and methods of delivering a recombinant plasmid to the cells of interest are within the skill in the art. See, for example, Zeng, *et al.*, *Molecular Cell* 9:1327-1333 (2002); Tuschl, *Nat. Biotechnol.*,

20:446-448 (2002); Brummelkamp, *et al.*, *Science* 296:550-553 (2002); Miyagishi, *et al.*, *Nat. Biotechnol.* 20:497-500 (2002); Paddison, *et al.*, *Genes Dev.* 16:948-958 (2002); Lee, *et al.*, *Nat. Biotechnol.* 20:500-505 (2002); and Paul, *et al.*, *Nat. Biotechnol.* 20:505-508 (2002).

5 In a particular embodiment, a plasmid expressing a miR gene product(s) comprises a sequence encoding the miR precursor RNA under the control of the cytomegalovirus (CMV) intermediate-early promoter. As used herein, "under the control" of a promoter means that the nucleic acid sequences encoding the miRNA product are located 3' of the promoter, so that the promoter can initiate transcription of the miRNA coding sequences.

10 miR gene products can also be expressed from recombinant viral vectors. It is contemplated that the miR gene product(s) can be expressed from two separate recombinant viral vectors, or from the same viral vector. The RNA expressed from the recombinant viral vectors can either be isolated from cultured cell expression systems by standard techniques, or can be expressed directly in BCL2-associated cancer cells. The use of recombinant viral
15 vectors to deliver the miR gene product(s) to BCL2-associated cancer cells is discussed in more detail below.

The recombinant viral vectors of the invention comprise sequences encoding the one or more miR gene products and any suitable promoter for expressing the RNA sequences. As described herein, suitable promoters include, for example, the U6 or H1 RNA pol III promoter
20 sequences, or the cytomegalovirus promoters. Selection of other suitable promoters is within the skill in the art. The recombinant viral vectors of the invention can also comprise inducible or regulatable promoters for expression of the one or more miR gene products in a BCL2-associated cancer cell.

Any viral vector capable of accepting a nucleotide sequence encoding a miR gene
25 product can be used; for example, vectors derived from adenovirus (AV); adeno-associated virus (AAV); retroviruses (*e.g.*, lentiviruses (LV), Rhabdoviruses, murine leukemia virus); herpes virus, and the like. The tropism of the viral vectors can also be modified by pseudotyping the vectors with envelope proteins or other surface antigens from other viruses. For example, an AAV vector of the invention can be pseudotyped with surface proteins from
30 vesicular stomatitis virus (VSV), rabies, Ebola, Mokola, and the like. Selection of

recombinant viral vectors suitable for use in the invention, methods for inserting nucleic acid sequences for expressing RNA into the vector, methods of delivering the viral vector to the cells of interest, and recovery of the expressed RNA products are all within the skill in the art. See, for example, Dornburg, *Gene Therap.* 2:301-310 (1995); Eglitis, *Biotechniques* 6:608-614 (1988); Miller, *Hum. Gene Therap.* 1:5-14 (1990); and Anderson, *Nature* 392:25-30 (1998).

Preferred viral vectors are those derived from AV and AAV. A suitable AV vector for expressing the miRNA of the invention, a method for constructing the recombinant AV vector, and a method for delivering the vector into target cells, are described in Xia, *et al.*, *Nat. Biotech.* 20:1006-1010 (2002). Suitable AAV vectors for expressing the miRNA of the invention, methods for constructing the recombinant AAV vector, and methods for delivering the vectors into target cells are described in Samulski, *et al.*, *J. Virol.* 61:3096-3101 (1987); Fisher, *et al.*, *J. Virol.* 70:520-532 (1996); Samulski, *et al.*, *J. Virol.* 63:3822-3826 (1989); U.S. Patent No. 5,252,479; U.S. Patent No. 5,139,941; International Patent Application No. WO 94/13788; and International Patent Application No. WO 93/24641. In a particular embodiment, one or more miR gene products are expressed from a single recombinant AAV vector comprising the CMV intermediate early promoter.

In one embodiment, a recombinant AAV viral vector of the invention comprises a nucleic acid sequence encoding a miR precursor RNA in operable connection with a polyT termination sequence under the control of a human U6 RNA promoter. As used herein, "in operable connection with a polyT termination sequence" means that the nucleic acid sequences encoding the sense or antisense strands are immediately adjacent to the polyT termination signal in the 5' direction. During transcription of the miR sequences from the vector, the polyT termination signals act to terminate transcription.

In particular embodiments, one or more miR gene products are used to inhibit the neoplastic or tumorigenic growth of BCL2-associated cancer cells (e.g., CLL cells, prostate cancer cells, other cancer cells). Without wishing to be bound by any one theory, it is believed that the processed miRNAs bind to complementary sequences in one or more target

mRNAs that are necessary to initiate and/or maintain neoplastic or tumorigenic growth in these cells. Thus, the invention provides a method of treating a BCL2-associated cancer, for example, CLL, acute myeloid leukemia, multiple myeloma, melanoma, follicular lymphoma, large cell lymphoma, non-Hodgkin's lymphoma, non-small cell lung carcinoma, hematologic malignancies, solid tumors, colorectal cancer, brain carcinoma, breast carcinoma, prostate carcinoma, Epstein-Barr virus-associated lymphoproliferative disease, renal carcinoma, hepatocellular carcinoma and gastric carcinoma, in a subject in need of such treatment. The method comprises administering an effective amount of one or more miR gene products to the subject, such that proliferation of BCL2-associated cancer cells is inhibited. In one embodiment, one or more miR gene products comprise a nucleotide sequence that is complementary to a nucleotide sequence within a BCL2 transcript.

For example, the expression of one or more miR genes may be reduced or absent in primary or metastatic tumor or neoplastic cells from cancers of at least the following histologic subtypes: sarcoma (cancers of the connective and other tissue of mesodermal origin); melanoma (cancers deriving from pigmented melanocytes); carcinoma (cancers of epithelial origin); adenocarcinoma (cancers of glandular epithelial origin); cancers of neural origin (glioma/glioblastoma and astrocytoma); and hematological neoplasias, such as leukemias and lymphomas (*e.g.*, acute lymphoblastic leukemia, chronic myelocytic leukemia, CLL).

Expression of the one or more miR genes may also be reduced or absent in cancers having their origin in at least the following organs or tissues, regardless of histologic subtype: breast; tissues of the male and female urogenital system (*e.g.* ureter, bladder, prostate, testis, ovary, cervix, uterus, vagina); lung; tissues of the gastrointestinal system (*e.g.*, stomach, large and small intestine, colon, rectum); exocrine glands such as the pancreas and adrenals; tissues of the mouth and esophagus; brain and spinal cord; kidney (renal); pancreas; hepatobiliary system (*e.g.*, liver, gall bladder); lymphatic system; smooth and striated muscle; bone and bone marrow; skin; and tissues of the eye.

Expression of the one or more miR genes may also be reduced or absent in cancers or tumors in any prognostic stage of development, for example, as measured by the "Overall Stage Groupings" (also called "Roman Numeral") or the "Tumor, Nodes, and Metastases"

(TNM) staging systems. Appropriate prognostic staging systems and stage descriptions for a given cancer are known in the art, for example, as described in the National Cancer Institute's "CancerNet" Internet website.

A subject in need of treatment for a BCL2-associated cancer can be identified by obtaining a sample of tumor or neoplastic cells (or cells suspected of being tumor or neoplastic) from the subject, and determining whether the expression of one or more miR genes (e.g., miR genes that comprise a nucleotide sequence that is complementary to a nucleotide sequence within a BCL2 transcript) is reduced or absent in at least a portion of the cells, as compared to cells from normal tissue obtained from the subject (e.g., control cells). Methods for detecting miR gene expression levels in cells are within the skill in the art and are described herein. Alternatively, the expression of one or more miR gene products in cells obtained from a subject can be compared to average expression levels of these genes in cells obtained from a population of normal subjects. A subject in need of treatment for a BCL2-associated cancer can be readily identified by a physician using standard diagnostic techniques. See, e.g., "Chronic lymphocytic leukemia: recommendations for diagnosis, staging, and response criteria. International Workshop on Chronic Lymphocytic Leukemia," (1989) *Annals of Internal Medicine* 110(3):236-238. For example, subjects with CLL exhibit circulating CLL cells lymphocytosis (*i.e.*, lymphocyte counts in the blood equal to or higher than 10,000 cells per cubic millimeter), and a progressive accumulation of CLL cells in the bone marrow and lymphatic tissues.

The identity of BCL2-associated cancer cells in a subject's blood or other tissue can be confirmed by direct visual observation of a blood sample, and/or, in the case of CLL, by determining the "CLL Score" of lymphocytes. The CLL Score indicates the presence or absence of five lymphocyte surface markers characteristic of CLL cells: CD5+, CD23+, FMC7-, and weak expression (+/-) of surface immunoglobulin (SmIg) and CD22. This scoring system gives a value of 1 or 0 for each of these five markers according to whether it is typical or atypical for CLL. CLL cells have a CLL Score of 4 or 5, while lymphocytes from other leukemias have a CLL Score of <1 to 3. See Matutes, *et al.*, *Leukemia* 8(10):1640-1645 (1994) and Moreau, *et al.*, *American Journal of Clinical Pathology*, 108:378-82 (1997), the

CLL cells also have relatively low levels of surface-membrane immunoglobulin as compared with normal peripheral blood B cells. Surface-membrane immunoglobulin levels on lymphocytes can be readily detected according to standard techniques; see, e.g., Rozman, *et al.*, *New England Journal of Medicine* 333:1052-1057 (1995).

As used herein, an "effective amount" of a miR gene product is an amount sufficient to inhibit proliferation of a BCL2-associated cancer cell in a subject suffering from a BCL2-associated cancer. As used herein, "to inhibit the proliferation of a BCL2-associated cancer cell" means to kill the cell, or permanently or temporarily arrest the growth of the cell. Inhibition of a BCL2-associated cancer cell can be inferred if the number of such cells in the subject remains constant or decreases after administration of a miR gene product. An inhibition of BCL2-associated cancer cell proliferation can also be inferred if the absolute number of such cells increases, but the rate of tumor growth decreases.

The number of BCL2-associated cancer cells in a subject's body can be determined by direct measurement, or by estimation from the size of primary or metastatic tumor masses.

For example, the number of BCL2-associated cancer cells in a subject can be readily determined using a whole blood or white blood cell count. The number of BCL2-associated cancer cells can also be readily determined by immunohistological methods, flow cytometry, or other techniques designed to detect the characteristic surface markers of BCL2-associated cancer cells.

The size of a tumor mass can be ascertained by direct visual observation, or by diagnostic imaging methods, such as X-ray, magnetic resonance imaging (MRI), ultrasound, and scintigraphy. Diagnostic imaging methods used to ascertain the size of a tumor mass can be employed with or without contrast agents, as is known in the art. The size of a tumor mass can also be ascertained by physical means, such as palpation of the tissue mass or measurement of the tissue mass with a measuring instrument, such as a caliper.

One skilled in the art can readily determine an effective amount of the one or more miR gene products to be administered to a given subject, by taking into account factors, such as the

size and weight of the subject; the extent of disease penetration; the age, health and sex of the subject; the route of administration; and whether the administration is regional or systemic.

For example, an effective amount of a miR gene product can be based on the approximate weight of a tumor mass to be treated. The approximate weight of a tumor mass can be determined by calculating the approximate volume of the mass, wherein one cubic centimeter of volume is roughly equivalent to one gram. An effective amount of the one or more miR gene products, based on the weight of a tumor mass, can be at least about 10 micrograms/gram of tumor mass, and can be between about 10-500 micrograms/gram of tumor mass. In addition, the effective amount can be at least about 60 micrograms/gram of tumor mass or at least about 100 micrograms/gram of tumor mass. In a particular embodiment, an effective amount, based on the weight of the tumor mass, is injected directly into the tumor.

An effective amount of the one or more miR gene products can also be based on the approximate or estimated body weight of a subject to be treated. In one embodiment, such effective amounts are administered parenterally or enterally, as described herein. For example, an effective amount of the one or more miR gene products administered to a subject can range from about 5 – 3000 micrograms/kg of body weight, and can be between about 700 - 1000 micrograms/kg of body weight, and also can be greater than about 1000 micrograms/kg of body weight.

One skilled in the art can also readily determine an appropriate dosage regimen for the administration of one or more miR gene products to a given subject. For example, one or more miR gene products can be administered to the subject once (e.g., as a single injection or deposition). Alternatively, the one or more miR gene products can be administered once or twice daily to a subject for a period of from about three to about twenty-eight days, more preferably from about seven to about ten days. In a particular dosage regimen, the one or more miR gene products are administered once a day for seven days. Where a dosage regimen comprises multiple administrations, it is understood that the effective amount of the one or more miR gene products administered to the subject can comprise the total amount of gene product administered over the entire dosage regimen.

One or more miR gene products can be administered to a subject by any means suitable for delivering the gene products to cells of the subject, such as hematopoietic stem cells (HSCs) and/or BCL2-associated cancer cells (e.g., CLL cells, prostate cancer cells, other cancer cells)). For example, one or more miR gene products can be administered by methods
 5 suitable to transfect cells of the subject with a miR gene product, or with a nucleic acid comprising a sequence encoding a miR gene product. The cells can be transfected directly with one or more miR gene products (as these are nucleic acids), or can be transfected with nucleic acids comprising sequences encoding the one or more miR gene products. In one embodiment, the cells are transfected with a plasmid or viral vector comprising sequences
 10 encoding the one or more miR gene products, as described herein.

Transfection methods for eukaryotic cells are well known in the art, and include direct injection of the nucleic acid into the nucleus or pronucleus of a cell; electroporation; liposome transfer or transfer mediated by lipophilic materials; receptor mediated nucleic acid delivery, bioballistic or particle acceleration; calcium phosphate precipitation, and transfection
 15 mediated by viral vectors.

For example, cells can be transfected with a liposomal transfer compound, e.g., DOTAP (N-[1-(2,3-dioleoyloxy)propyl]-N,N,N-trimethyl-ammonium methylsulfate, Boehringer - Mannheim) or an equivalent, such as LIPOFECTIN™. The amount of nucleic acid used is not critical to the practice of the invention; acceptable results may be achieved
 20 with 0.1-100 micrograms of nucleic acid/ 10^5 cells. For example, a ratio of about 0.5 micrograms of plasmid vector in 3 micrograms of DOTAP per 10^5 cells can be used.

In one embodiment, BCL2-associated cancer cells, for example, CLL or prostate cancer cells, are isolated from the subject, transfected with a nucleic acid encoding a miR gene product, and reintroduced into the subject. In a particular embodiment, the transfected
 25 and reimplanted cells are CLL cells. In another embodiment, the transfected and reimplanted cells are HSCs from a subject who has been diagnosed with a BCL2-associated cancer.

Techniques for isolating BCL2-associated cancer cells (e.g., CLL cells) from a subject are within the skill in the art, for example, as described in the Examples below. Techniques for isolating, identifying, separating, and culturing HSCs from a subject are also within the
 30 skill in the art, for example, as disclosed in U.S. Pat. Nos. 5,635,387 and 5,643,741, and

Campana, *et al.*, *Blood* 85:1416-1434 (1995). In one embodiment, harvested bone marrow is purged of tumorigenic or neoplastic cells prior to transfection of the HSCs. Suitable purging techniques include, for example, leukopheresis of mobilized peripheral blood cells; immunoaffinity-based selection or killing of tumor cells, or the use of cytotoxic or photosensitizing agents to selectively kill tumor cells, as are known in the art. See, for example, Bone Marrow Processing and Purging, Part 5 (A. Gee, ed.), CRC Press, Boca Raton, Fla., 1991; Lydaki, *et al.*, *J. Photochem. and Photobiol.* 32:27-32 (1996); and Gazitt, *et al.*, *Blood* 86:381-389 (1995).

10 The isolated cells (e.g., HSC cells, BCL2-associated cancer cells (e.g., CLL cells, prostate cancer cells, other cancer cells)) can be transfected by any suitable technique, as discussed herein. After transfection, a portion of the cells can be examined to confirm the presence of appropriate expression levels of the gene products. Once appropriate expression of a miR gene product has been confirmed, the remaining transfected cells can then be
15 reintroduced into the subject. Transfected cells can be reintroduced into the subject by parenteral methods, including intravenous infusion or direct injection into the bone marrow. The transfected cells are preferably reintroduced into the subject in a saline solution or other pharmaceutically acceptable carrier. A suitable number of transfected cells for reintroduction is from about 10^5 to about 10^8 cells per kilogram of subject body weight. The number of
20 transfected cells available for re-introduction can be increased by expanding the cells in culture prior to transfection.

In one embodiment, the genome of the cell (e.g., HSC cells, BCL2-associated cancer cells (e.g., CLL cells, prostate cancer cells, other cancer cells)) is transfected with a nucleic acid comprising a sequence that encodes a miR gene product, e.g., a plasmid expression
25 vector, that stably integrates into the genome of the cell to provide long-term expression of the miR. Stable integration and expression can be confirmed by techniques known in the art, such as Southern blot analysis of genomic DNA using a miR gene cDNA (or fragments thereof) as a probe. Expression of a miR gene product can also be detected by standard Northern blot techniques. The cells that are stably transfected with a sequence encoding the
30 miR gene product continue to express the miR gene product once they are re-implanted into

the subject. An exemplary method of isolating HSC from a subject, transfecting them with plasmids expressing one or more miR gene products, and reimplanting the transfected HSC into the subject is described in the Examples below.

A miR gene product can also be administered to a subject by any suitable enteral or parenteral administration route. Suitable enteral administration routes for the present methods include oral, rectal, or intranasal delivery. Suitable parenteral administration routes include intravascular administration (e.g. intravenous bolus injection, intravenous infusion, intra-arterial bolus injection, intra-arterial infusion and catheter instillation into the vasculature); peri- and intra-tissue injection (e.g., peri-tumoral and intra-tumoral injection, intra-retinal injection, or subretinal injection); subcutaneous injection or deposition including subcutaneous infusion (such as by osmotic pumps); direct application to the tissue of interest, for example, by a catheter or other placement device (e.g., a retinal pellet or a suppository or an implant comprising a porous, non-porous, or gelatinous material); and inhalation. In one embodiment, a miR gene product is administered by injection or infusion. For the treatment of BCL2-associated cancers that involve solid tumors, a miR gene product can be administered by direct injection into the tumor.

In the present methods, a miR gene product can be administered to the subject either as naked RNA, in conjunction with a delivery reagent, or as a nucleic acid (e.g., a recombinant plasmid or viral vector) comprising a sequence that expresses the gene product. Suitable delivery reagents for administration of the miR gene product include, e.g., the Mirus Transit TKO™ lipophilic reagent; lipofectin; lipofectamine™; cellfectin™; polycations (e.g., polylysine); and liposomes.

Recombinant plasmids comprising sequences that express a miR gene product are discussed herein. Recombinant viral vectors comprising sequences that express a miR gene product are also discussed herein, and methods for delivering such vectors to cells (e.g., HSC cells, BCL2-associated cancer cells (e.g., CLL cells, prostate cancer cells, other cancer cells)) of a subject are within the skill in the art.

In a particular embodiment, liposomes are used to deliver a miR gene product, or a nucleic acid comprising a sequence encoding a miR gene product, to a subject. Liposomes can also increase the blood half-life of a miR gene product or nucleic acid. In the practice of

this embodiment of the invention, a miR gene product, or nucleic acid comprising a sequence encoding a miR gene product, is encapsulated in liposomes prior to administration to the subject.

Liposomes suitable for use in the invention can be formed from standard vesicle-forming lipids, which generally include neutral or negatively charged phospholipids, and a sterol, such as cholesterol. The selection of lipids is generally guided by consideration of factors, such as the desired liposome size and half-life of the liposomes in the blood stream. A variety of methods are known for preparing liposomes, for example, as described in Szoka, *et al.*, *Ann. Rev. Biophys*
 5 *Bioeng.* 9:467 (1980); and U.S. Pat. Nos. 4,235,871, 4,501, 728, 4,837,028, and
 10 5,019,369.

The liposomes encapsulating a miR gene product, or a nucleic acid comprising a sequence encoding a miR gene product, can comprise a ligand molecule that targets the liposome to a BCL2-associated cancer cell (e.g., a CLL cell, an HSC cell, a prostate cancer
 15 cell, another cancer cell). In one embodiment, a ligand that binds to a receptor that is prevalent in such cancer cells (e.g., a monoclonal antibody that binds to a tumor cell antigen or a cancer cell surface marker) is used.

The liposomes encapsulating a miR gene product, or a nucleic acid comprising a sequence encoding a miR gene product, can also be modified so as to avoid clearance by the
 20 mononuclear macrophage system ("MMS") and reticuloendothelial system ("RES"). Such modified liposomes can have opsonization-inhibition moieties on the surface or incorporated into the liposome structure. In one embodiment, a liposome of the invention can comprise both opsonization-inhibition moieties and a ligand.

Opsonization-inhibiting moieties for use in preparing the liposomes of the invention
 25 are typically large hydrophilic polymers that are bound to the liposome membrane. As used herein, an opsonization inhibiting moiety is "bound" to a liposome membrane when it is chemically or physically attached to the membrane, e.g., by the intercalation of a lipid-soluble anchor into the membrane itself, or by binding directly to active groups of membrane lipids. These opsonization-inhibiting hydrophilic polymers form a protective surface layer that
 30 significantly decreases the uptake of the liposomes by the MMS and RES; e.g., as described

in U.S. Patent No. 4,920,616.

Opsonization inhibiting moieties suitable for modifying liposomes are preferably water-soluble polymers with a number-average molecular weight from about 500 to about 40,000 daltons, and more preferably from about 2,000 to about 20,000 daltons. Such polymers include polyethylene glycol (PEG) or polypropylene glycol (PPG) derivatives; *e.g.*, methoxy PEG or PPG, and PEG or PPG stearate; synthetic polymers, such as polyacrylamide or poly N-vinyl pyrrolidone; linear, branched, or dendrimeric polyamidoamines; polyacrylic acids; polyalcohols, *e.g.*, polyvinylalcohol and polyxylitol to which carboxylic or amino groups are chemically linked, as well as gangliosides, such as ganglioside GM₁. Copolymers of PEG, methoxy PEG, or methoxy PPG, or derivatives thereof, are also suitable. In addition, the opsonization inhibiting polymer can be a block copolymer of PEG and either a polyamino acid, polysaccharide, polyamidoamine, polyethylenamine, or polynucleotide. The opsonization inhibiting polymers can also be natural polysaccharides containing amino acids or carboxylic acids, *e.g.*, galacturonic acid, glucuronic acid, mannuronic acid, hyaluronic acid, pectic acid, neuraminic acid, alginic acid, carrageenan; aminated polysaccharides or oligosaccharides (linear or branched); or carboxylated polysaccharides or oligosaccharides, *e.g.*, reacted with derivatives of carbonic acids with resultant linking of carboxylic groups. In one embodiment, the opsonization-inhibiting moiety is a PEG, PPG, or a derivative thereof. Liposomes modified with PEG or PEG-derivatives are sometimes called "PEGylated liposomes."

The opsonization inhibiting moiety can be bound to the liposome membrane by any one of numerous well-known techniques. For example, an N-hydroxysuccinimide ester of PEG can be bound to a phosphatidyl-ethanolamine lipid-soluble anchor, and then bound to a membrane. Similarly, a dextran polymer can be derivatized with a stearylamine lipid-soluble anchor via reductive amination using Na(CN)BH₃ and a solvent mixture, such as tetrahydrofuran and water in a 30:12 ratio, at 60°C.

Liposomes modified with opsonization-inhibition moieties remain in the circulation much longer than unmodified liposomes. For this reason, such liposomes are sometimes called "stealth" liposomes. Stealth liposomes are known to accumulate in tissues fed by

porous or "leaky" microvasculature. Thus, tissue characterized by such microvasculature defects, for example, solid tumors, will efficiently accumulate these liposomes; *see* Gabizon, *et al.*, *Proc. Natl. Acad. Sci., USA*, 18: 6949-53 (1988). In addition, the reduced uptake by the RES lowers the toxicity of stealth liposomes by preventing significant accumulation of the liposomes in the liver and spleen. Thus, liposomes that are modified with opsonization-inhibition moieties are particularly suited to deliver the miR gene products, or nucleic acids comprising sequences encoding the gene products, to tumor cells.

As described herein, in one embodiment, the invention is a method of preventing or treating a cancer associated with overexpression of a BCL2 gene or gene product (e.g., RNA, protein) in a subject in need of such treatment, comprising administering an effective amount of at least one miR gene product to the subject. The Bcl2 protein and members of the Bcl2 family, as well as their role in cancer, are described in Cory, S., and Adams, J.M., *Nature Reviews* 2:647-656 (2002) and Sanchez-Beato, M., *et al.*, *Blood* 101:1220-1235 (2003). The nucleotide and amino acid sequences for a human BCL2 cDNA and protein are shown in Table 2.

Table 2. BCL2 cDNA and protein sequences.

Name	Sequence	SEQ ID NO:
BCL2 cDNA (Genbank Acc. No. NM_000633)	TTTCTGTGAAGCAGAAAGTCTGGGAATCGATCTGGAAATCCTCCTAATTTTACTCCCTCTCCCGGACTCCTGATTCT ATTGGGAAGTTTCAAATCAGCTATAACTGGAGAGTCTGAAGATTGATGGGATCGTTGCCCTTATGCAATTTGTTTGGT TTTACAAAAGGAAACTTGACAGAGGATCATGCTGTACTTAAATAAATAACAACATCACAGAGGAAGTAGACTGATATTA ACAATACTTACTAATAATAACGTGCTCATGAATAAAGATCCGAAAGGAATTGGAATAAAATTTCTGCACTCTCAT GCCAAGGGGAAAACACCAGAAATCAAGTGTTCGCCGTGATTGAAGACACCCCTCTGTCCAAGAAATGCAAGCACATCCA ATAAATAGCTGGATTATTAACCTCTTCTTCTGCGGCCGTGGGTGGGAGCTGGGGCGAGAGTGCCTGTTGGC CCCCCTGCTTTCTCTGGGAAGGATGGCGCAGCTGGGAGAACAGGTAACCCGGGAGATAGTGATGAAGTA CATCCATTATAAGCTGTCCGAGAGGGGCTACGAGTGGGATGCGGGAGATGTGGGCGCCGCCCGGGGGCCGCCCC CGCACCGGGCATCTTCTCCAGCCCGGGCACACGCCCATCCAGCCGATCCCGGGACCCGGTCCGCCAGGACCTC GCCGCTGCAGACCCCGGCGCCCGGGCCGTCCGCTCAGCCCGGTGCCACCTGTGTGGTCCACCTGAC CCTCCGCCAGGCCGGCAGACTTCTCCGCCGCTACCGCCGACTTCGCCGAGATGTCCAGCCAGCTGCACCTGAC GCCCTTCAACCGCGGGACGCTTTGCCACGGTGTGGAGGAGCTCTTCAGGGACGGGTGAACCTGGGGGAGGATTGT GGCCCTTCTTTGAGTTCGGTGGGTCAATGTGTGTGGAGAGCGTCAACCGGAGATGTGCCCTGGTGGACAAACATCCG CCTGTGGATGACTGAGTACCTGAACCGGCACCTGCACACCTGGATCCAGGATAACGGAGGCTGGGATGCCCTTTGTGGA ACTGTACGGCCCCAGCATGCGGCCCTGTGTTGATTTCTCTGGCTGTCTCTGAAGACTCTGCTCAGTTTGGCCCCCTGGT GGGAGCTTGCATCACCCCTGGTGCCTATCTGGGCCACAAGTGAAGTCAACATGCCCTGCCCAAACAATAATGCAAAAG GTTCACTAAAGCAGTAGAAATAATATGCATTGTCAGTGATGTACCATGAACAAGCTGCAGGCTGTGTTAAGAAAAAA TAACACACATATAACATCACACACACAGACACACACACACAAATTAACAGTCTTCAGGCCAAAACGTCGA ATCAGCTATTTACTGCCAAAGGGAATAATATCATTTATTTTACATTATTAAGAAAAAAGATTTATTTATTTAAGACA GTCCCATCAAAACTCCTGTCTTTGGAAATCCGACCACCTAATTGCCAAGCACCCGCTTCGTGTGGCTCCACCTGGATGTT CTGTGCCCTGTAAACATAGATTCCGCTTTCTGGCTGTCTGGAGGCTGGGGAGAGGTGTTCACTTCACTTGCATTTCTTTGCC CCTGATCATTTGGGAAGCTGGCTTTCTGGCTGTCTGGAGGCTGGGGAGAGGTCCATGCCCTCCCTGAGAGAGAGACTCTT TGGGGCTGTGATTAACAGAGGGAGGGTTCCTGTGGGGGAAAGTCCATGCCCTCCCTGAGAGAGAGAGACTCTT TGCATATGACTCACATGATGCATACCTGTGGGAGGAAAGAGTTGGGAACTTCAGATGGAACCTAGTACCCACTGAGA TTTCCACGCCGGAAGGACAGCGATGGGAAAAATGCCCTTAAATCATAGGAAAGTATTTTTTTAAGCTACCAATTGTGCC GAGAAAAGCATTTTAGCAATTTATACAAATATCATCCAGTACCCTTAAGCCCTGATTGTGTATATTCATATATTTTGGAT ACGCACCCCCCAACTCCCAATACTGGCTCTGTCTGAGTAAGAAACAGAAATCCTCTGGAACTTGAGGAAAGTGAACATTT CGGTGACTTCCGCATCAGGAAGGCTAGAGTTACCCAGAGCATCAGGCCGCCACAAAGTGCCTGTCTTTTAGGAGACCCGAA	55

GTCCGCAGAAACCTGCTGTGTCCTCCAGCTTGGAGCCCTGGTCTGGAACTGAGCCGGGGCCCTCACTGGCCCTCCTCCAG
GGATGATCAACAGGGCAGTGTGGTCTCCGAATGTCTGGAAGCTGATGGAGCTCAGAATTCCTACTGTCAAGAAAGAGCA
GTAGAGGGGTGTGGCTGGCCCTGTCAACCTGGGCCCTCCAGGTAGGCCCGTTTTCAGGTGGAGCATGGGAGCCACGA
CCCTTCTTAAGACATGTATCACTGTAGAGGGAAGGAACAGAGGCCCTGGGCCCTTCCCTATCAGAGGACATGGTGAAG
GCTGGGAAACGTGAGGAGAGGCAATGGCCACGGCCCATTTTGGCTGTAGCACATGGCACGTTGGCTGTGTGGCCCTTGGC
CCACCTGTGAGTTTAAAGCAAGGCTTTAAATGACTTTGGAGAGGGTCACAAAATCCCTAAAGAGCATTTGAAGTGAGGT
GTATGGATTAATTGACCCCTGTCTATGGAATTACATGTAAACATATCTGTCACTGTAGTTTGGTTTATTTGAA
AACCCTGACAAAAGTTCCAGGTGTGGAATATGGGGTTATCTGTACATCTGGGGCATTAATAAAATCAAT
GGTGGGGAACCTATAAAGAAAGTAACAAGAGTGCATCTTCAGCAATAAATAAGGAAATTTTTTTTCTTCCAGTT
TAGAATCAGCCCTTGAAACATTTGATGGAATAACTCTGTGGCATTTTGCATTAATATACCATTTATCTGTATTAACCTTG
GAACTACTCTGTCTCAATGTAAAGCTGTGTGATATTTCCGAAGCTGTCTTAATAAAATATACATGCTCATCTCAGCGT
TTTTTTTGTTTTAAATTGTAATTTAGTTATGGCCCTAATACACTAATTTGTGAGCAAAAGGTGATCGTTTCTGTGTGAGATT
TTATCTCTGTGATTTCTCAAAAGCATTTCTGAGAAAGTGAGATAAGCCCTGAGTCTCAGCTACCTAAGAAAACCTGGAT
GTCACTGGCCACTGAGGAGCTTTGTCTCAACCAAGTCAAGTGCATTTCCAGTCAACAGAAATGTATTATGTGACAGT
TATATCTGTGTGCCCTTTTGACCTTTGTCTGTGAAGGTTTCCCTGGTCCCTGGGCAATTCGCCATTTAATTCATGGTATT
CAGGATTACATGCTGTTTGGTTAAACCCATGAGATTTCATTCAGTTAAATAATCCAGATGGCAATAATGACCAGAGATT
AAATCTATGGTGGTTTGACCTTTAGAGAGTTGCTTTACGTGGCCCTTTTCAACACAGACCCACCCAGAGCCCTCCCTGC
CTCCTTCCGGGGGCTTTCTCAAGGCTGTCTTCAAGGCTTCCCTGAATATGCAAGTGGTGTCTTACGCTCCACCAAGA
AAGCAGGAAACCTGTGGTAAGAAGCCAGACCTCCCGGGGGCTCAGGGGAACAGAAATGATCAGACCTTTTGAATGATT
CTAATTTTAAAGCAAAATATATTTTATGAAGGTTTACATTTGTCAAAAGTGAATATATGGAATATCCAAATCCTGTGC
TGCTATCCTGCCAAATCATTTTATGGAGTCAAGTTTGCAGTATGCTCCACGTGGTAAGATCCTCCAAAGCTGCTTTAG
AAGTAACAATGAAGAACGTGGAGCTTTTAAATAAAGCCGTCTTGTCTTTTGTGTGTCTTCAAAACGGGATTCACAG
AGTATTTGAAAATGTATATATTAAGAGGTCAAGGGGGCTAATTTGCTGGCTGGCTGCTTTTGTGTGGGGTTTGTG
TTACCTGGTTTAAATAACAGTAAATGTGCCCCAGCCCTTTGGCCCCAGAACTGTACAGTATTTGTGGCTGCACCTTGTCT
AAGAGTAGTTGATGTGCTTTTCTTATTTTAAACAAGTTAGAAAGCAATGAATGTATATATAAAGCCCTCAACTAG
TCATTTTCTCTCTCTCTCTTTTCTTCTATTAATTTTGCAGTTTGGGCAACAGAGAACCATCCCTATTTT
GTATTGAAGAGGATTCACATCTGCATCTTAACTGCTCTTTATGAATGAATAACAGTCCCTCTGTATGTACTCCTCTT
TACACTGGCCAGGGTCAGAGTTAAATAGAGTATATGCACTTTGCAATTTGGGACAAAGGCTCTAATAAAAGCCCCAA
AAGGAGAAGAACTCTGAGAACCTCCCTGGCCCTCCAGTCCCTGCTGCACAAATACTCCGCAAGAGAGGCCAGAAAT
GACAGCTGACAGGCTCTATGGCCATCGGGTCTCTCCGAAGATTTTGGCAGGGGCAAAACTCTGGCAGGCTTAAAGAT
TTGGAATAAAGTCACAGAAATTAAGGAAGCACCTCAATTTAGTTCAAAACAAGAGCCCAACATTTCTCTCCACAGCTCACT
TACCTCTCTGTGTTCAGATGTGGCCCTTCCATTTATATGATGATGATCTTTTATTTAGTAAATGCTTATCATCTAAAGAT

	GTAGCTCTGGCCAGTGGGAAAATTAGGAAGTGATTATAAATCGAGAGGAGTTATAATAATCAAGATTAAATGTAAAT TAATCAGGGCAATCCCAACACATGCTTAGCTTTCACCTCCAGGATCTATTGAGTGAACAGAAATTGCAAAATAGTCTCTA TTTGTAATTGAACCTTATCCTAAACAAATAGTTTATAAATGTGAACCTTAAACTCTAATTAAATCCAACTGTACTTTTA AGGCAGTGGCGTGTCTTAGACTTTCTTATCCTTATAGTATAGTAAATGTACACCTACTCTATCAGAGAAAACAGGAAA GGCTCGAAATACAAAGCCATTCTAAGGAAATTAGGGAGTCAGTTGAAATTCATATTCGATCTTATTCGTGGTGTCTTT TGCAGCCCAGACAAATGTGGTTACACACTTTTAAAGAAATACAAATTCATATTGTCAAGCTTATGAAGGTTCCAAATCA GATCTTTATTGTTATCAATTTGGATCTTTCAGGGATTTTTCAGGATTTTAAATTTATATGGGACAAAGGACATTTGTTGGA GGGTGGGAGGAGGAAGAAATTTTAAATGTAAACATTCCTCAAGTTTGGATCAGGGAGTTGGAAGTTTTCAGAAATAA CCAGAACTAAGGGTATGAAGGACCTGTATTCGGGTCTGATGTGAATGCTCTGCGAAGAACCTTGTGTGACAAATGAGAA ACATTTTGAAAGTTTGGGTAGGACCTTTTAGATTCAGAGACATCAGCATGGCTCAAAAGTGCAGCTCCGTTTGGCAGTG CAATGGTATAAATTTCAAGCTGGATATGCTAATGGGTATTTAAACAATAAATGTCAGTTTAACTAACAGGATATT TAAAGACAACCTCTGGTTGGTAGGGACATCTGTTTCTAAATGTTTATTAATGTACAAATACAGAAAATAATTTATAAA ATTAAGCAATGTGAACCTGAATTTGGAGAGTGTATAATACAAAGTCTTTAGTCTTAGCCAGTGAATCATCTGTTCCATG TCTTTGGACACACCATGACCTTGGACAAATCATGAATAATATGCATCTCACTGGATGCAAAAGAAATCAGATGGAGCATGAA TGGTACTGTACCGGTTCACTTGGACTGGCCAGAAAATAAATCACTCAAGCAACATCTCTATCAACAACAAGGTGTTCT GCATACCAAGCTGAGCACAGAAAGATGGGAACACACTGGTGAGGATGGAAAGGCTCGCTCAATCAAGAAAATCTTGAGAC TATTAATAAATAAGACTGTAGTGTAGATACAGTAAATCCATGCACCTAAAGCTTTTGGAAAATCTGCCGTGGGCCC TCCAGATAGCTCATTTTCAATTAAGTTTTCCTCCAAAGGTAGAAATTTGCAAGAGTGCAGTGGATTTGCATTTCTTTTGG GGAAGCTTTCCTTTTGGTGGTTTGTATTAATTAACCTCTTAAGTTTTCAGCAAGGTTTGTCTTTTGTGAGTTACT GGGTTTATTTTGTGTTTAAATAAATAAGTGTACAAATAAGTGTGTTTGTGTAATGAAAGCTTTTGTGTTATCAAGATTTTC ATACTTTTACCTTCCATGGCTCTTTTAAAGATTGATACTTTTAAAGAGGTGGCTGATATTCTGCAACACTGTACACATA AAAAATAAGGTAAGGATACCTTTACATGGTTAAGGTAAGTCTCCAGTTGGCCACCATTAGCTATAATGGCATT TGTTTGTGTTGTTGGAAAAGATCACATTTGCCATTTAAACTTTCCCTTGTCTGTCTAGTTAAATAATTGTGAAGAAAATAAA GTACAGTGTGAGATACTG	56
Bcl2 Protein (Genbank Acc. No. NM_0006 24)	MAHAGRTGYDNREIVMKYIHYKLISORGYENDAGDVGAAPPAPGIFSSQPGHTPEHPAASRDPVARTSPLOTPAAP GAAAGPALSPVPPVVHLTLRQAGDDFSRRYRRRDEAEMSSQLHLTPFTARGREATVVEELFRDGVNWNWGRIVAEFFGGV MCVESVNRMSPLVDNIALWMTLEYLNRHLHTWIQDNGGWDAFVELYGPSMRPLEDFESWLSLKTLLSLALVGACITLGA YLGHK	

Methods for detecting the expression level of a BCL2 gene product are well known in the art. For example, the expression level of a BCL2 gene transcript in a sample of cells can be detected using techniques already described herein (e.g., Northern blotting, *in situ* hybridization, RT-PCR). Detection of the expression level of a Bcl2 protein can be
 5 accomplished using commonly-applied techniques, for example, immunostaining or Western blotting, which is described in Current Protocols in Molecular Biology, F. Ausubel *et al.*, eds., Vol. 2, John Wiley and Sons, Inc., 1998, Chapter 10.

Bcl2 over-expressing cancers are known to those of skill in the art and include, but are not limited to, leukemias, lymphomas and carcinomas (see Kim, R., *et al.*,
 10 *Cancer* 101(11):2491-2502 (2004); U.S. Patent No.: 5,789,389; and U.S. Patent No: 6,800,639). Particular cancers known to be associated with over-expression of Bcl2 include CLL, acute myeloid leukemia, multiple myeloma, melanoma, follicular lymphoma, large cell lymphoma, non-Hodgkin's lymphoma, non-small cell lung carcinoma, hematologic malignancies, solid tumors, colorectal cancer, brain
 15 carcinoma, breast carcinoma, prostate carcinoma, Epstein-Barr virus-associated lymphoproliferative disease, renal carcinoma, hepatocellular carcinoma and gastric carcinoma, among others.

In a particular embodiment, the at least one miR gene product that is administered to the subject in need of treatment comprises a nucleotide sequence that is complementary to a
 20 nucleotide sequence in a BCL2 gene transcript.

As used herein, the term "complementary nucleotide sequence" means a polynucleotide sequence that is capable of forming base pairs via hydrogen bonds with another nucleotide sequence to which it is complementary. Such hydrogen bonds are formed between a purine and pyrimidine (e.g., between adenine and thymine or uracil, between
 25 guanine and cytosine) through standard Watson-Crick base pairs. As used herein, "Watson-Crick base pair" refers to a pair of hydrogen-bonded bases on opposite antiparallel strands of a nucleic acid. The rules of base pairing, which were first elaborated by Watson and Crick, are well known to those of skill in the art. For example, these rules require that adenine (A) pairs with thymine (T) or uracil (U), and guanine (G) pairs with cytosine (C), with the
 30 complementary strands anti-parallel to one another. As used herein, the term "Watson-Crick

base pair" encompasses not only the standard AT, AU or GC base pairs, but also base pairs formed between non-standard or modified bases of nucleotide analogs capable of hydrogen bonding to a standard base or to another complementary non-standard base. One example of such non-standard Watson-Crick base pairing is the base pairing which involves the

5 nucleotide analog inosine, wherein its hypoxanthine base can form two hydrogen bonds with adenine, cytosine or uracil.

In one embodiment, the at least one miR gene product comprises a nucleotide sequence that is 100% complementary (i.e., exactly complementary) to a nucleotide sequence in a BCL2 gene transcript. In other embodiments, the at least one miR gene product

10 comprises a nucleotide sequence that is at least about 70%, at least about 80%, at least about 90%, at least about 95%, or at least about 99%, complementary to a nucleotide sequence in a BCL2 gene transcript. The region of complementarity can be from about 5 to about 25 nucleotides in length, from about 5 to about 15 nucleotides in length, or more particularly, from about 7 to about 12 nucleotides in length. Examples of miR gene products having

15 complementary to a nucleotide sequence in a BCL2 gene transcript include, but are not limited to, miR-182, miR-181, miR-30, miR-15a, miR-16-1, miR-15b, miR-16-2, miR-195, miR-34, miR-153, miR-21, miR-217, miR-205, miR-204, miR-211, miR-143, miR-96, miR-103, miR-107, miR-129, miR-9, miR-137, miR-217, and miR-186 (*see, e.g.*, Table 5). In one embodiment, the miR gene product comprises a nucleotide sequence that is complementary to

20 nucleotides 3741-3749 of SEQ ID NO: 55. Examples of such miR gene products include, but are not limited to, miR-15a, miR-16-1, miR-15b and miR-16-2. In a particular embodiment, the miR gene product is not miR-15a or miR-16-1. Methods for administering a miR gene product to a subject, several of which are described herein, are well known in the art.

The invention also encompasses a method for increasing the efficacy of an anti-cancer

25 treatment in a subject having a cancer, comprising administering to the subject at least one miR gene product that comprises a nucleotide sequence that is complementary to a nucleotide sequence in a BCL2 gene transcript, and additionally administering at least one anti-cancer treatment to the subject. According to the invention, the anti-cancer treatment can be any anti-cancer treatment known to those of skill in the art. Suitable anti-cancer treatments include,

30 but are not limited to, chemotherapy, radiation therapy and combinations thereof (e.g.,

chemoradiation). The invention also contemplates methods of increasing the efficacy of non-conventional cancer therapies as well.

As used herein, chemotherapy refers to the administration of one or more chemical substances or drugs for the treatment of cancer. A suitable chemotherapeutic agent for the methods of the invention can be any chemical substance known to be useful for treating cancer, for example, DNA-alkylating agents, anti-tumor antibiotic agents, anti-metabolic agents, tubulin stabilizing agents, tubulin destabilizing agents, hormone antagonist agents, topoisomerase inhibitors, protein kinase inhibitors, HMG-CoA inhibitors, CDK inhibitors, cyclin inhibitors, caspase inhibitors, metalloproteinase inhibitors, antisense nucleic acids, triple-helix DNAs, nucleic acids aptamers, and molecularly-modified viral, bacterial or exotoxic agents. Examples of particularly suitable agents for use in the methods of the present invention include, but are not limited to, cytidine arabinoside, methotrexate, vincristine, etoposide (VP-16), doxorubicin (adriamycin), cisplatin (CDDP), dexamethasone, arglabin, cyclophosphamide, sarcolysin, methylnitrosourea, fluorouracil, 5-fluorouracil (5FU), vinblastine, camptothecin, actinomycin-D, mitomycin C, hydrogen peroxide, oxaliplatin, irinotecan, topotecan, leucovorin, carmustine, streptozocin, CPT-11, taxol™ and derivatives thereof, tamoxifen, dacarbazine, rituximab, daunorubicin, 1-β-D-arabinofuranosylcytosine, imatinib, fludarabine, docetaxel and FOLFOLX4.

As used herein, radiation therapy refers to the use of high energy radiation for the treatment of cancer. High energy radiation for use in radiation therapy may be provided by X-rays, gamma ray and neutrons, among others. Different methods of radiation therapy are well known in the art and are suitable for the methods of the invention. These methods include, but are not limited to, external beam radiation, brachytherapy, intensity-modulated radiotherapy (IMRT), implant radiation, systemic radiation and stereotactic radiotherapy.

25

The terms “subject”, “individual” and “patient” are defined herein to include animals such as mammals, including but not limited to, primates, cows, sheep, goats, horses, dogs, cats, rabbits, guinea pigs, rats, mice or other bovine, ovine, equine, canine, feline, rodent, or murine species. In a preferred embodiment, the animal is a human. In one embodiment, the subject is a mammal (e.g., a human) afflicted with one or more BCL2-associated cancers. As

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described herein, suitable BCL2-associated cancers for treatment by the methods of the invention include lymphomas, carcinomas and leukemias, among others. In a particular embodiment, the BCL2-associated cancer is a cancer that is characterized by increased expression (e.g., overexpression, up-regulation) of a BCL2 gene or gene product (e.g., RNA, protein). Examples of particularly suitable BCL2-associated cancers include CLL, acute myeloid leukemia, multiple myeloma, melanoma, follicular lymphoma, large cell lymphoma, non-Hodgkin's lymphoma, non-small cell lung carcinoma, hematologic malignancies, solid tumors, colorectal cancer, brain carcinoma, breast carcinoma, prostate carcinoma, Epstein-Barr virus-associated lymphoproliferative disease, renal carcinoma, hepatocellular carcinoma and gastric carcinoma, among others. In one embodiment, the cancer is CLL. In another embodiment the cancer is lymphoma. In yet another embodiment, the cancer is lung cancer. In still another embodiment, the cancer is prostate cancer.

According to the methods of this embodiment of the invention, the efficacy of a cancer treatment is increased by administering at least one miR gene product to a subject. The miR gene product may be co-administered (i.e., simultaneously) with a chemotherapeutic agent, or it may be administered separately. In one embodiment, the miR gene product is complementary to a nucleotide sequence in a BCL2 gene transcript. Examples of such miR gene products include, but are not limited to, miR-182, miR-181, miR-30, miR-15a, miR-16-1, miR-15b, miR-16-2, miR-195, miR-34, miR-153, miR-21, miR-217, miR-205, miR-204, miR-211, miR-143, miR-96, miR-103, miR-107, miR-129, miR-9, miR-137, miR-217, and miR-186 (see Table 5). In a further embodiment, the miR gene product comprises a nucleotide sequence that is complementary to nucleotides 3741 to 3749 of SEQ ID NO: 55, for example, miR-15a, miR-16-1, miR-15b and miR-16-2. In one embodiment, the miR gene product is not miR-15a or miR-16-1.

An increase in the efficacy of an anti-cancer treatment can be evidenced by increased remission of the cancer in the subject relative to a suitable control. Cancer remission can be determined according to accepted clinical standards, such as a decrease in the number of cancer cells in the subject and/or a decrease in tumor mass and/or size. The number of BCL2-associated cancer cells in a subject can be determined by direct measurement, or by estimation from the size of primary or metastatic tumor masses.

The invention also provides a method of increasing the sensitivity of a cancer cell to the cytotoxic effects of an anti-cancer agent, comprising providing at least one miR gene product comprising a nucleotide sequence that is complementary to a nucleotide sequence in a BCL2 gene transcript to the cell. By providing the at least one miR gene product to the cell,
5 the sensitivity of the cell to the anti-cancer agent is increased.

In one embodiment, the invention is a method of increasing the sensitivity of a cancer cell to the cytotoxic effects of an anti-cancer agent, comprising providing at least one anti-cancer agent to a cancer cell and additionally providing at least one miR gene product to the cancer cell, wherein the at least one miR gene product comprises a nucleotide sequence that is
10 complementary to a nucleotide sequence in a BCL2 gene transcript. The anti-cancer agent may be any agent known to be useful for treating cancer. Such agents include, but are not limited to chemotherapeutic agents and radiation. Examples of suitable chemotherapeutic agents are described hereinabove.

As used herein, the phrase "cytotoxic effects of an anti-cancer agent" refers to any cell
15 damage and/or death that results from the administration of the agent. An increase in the sensitivity of a cancer cell to the cytotoxic effects of an anti-cancer agent can be evidenced by an increase in the severity of cell damage and/or an increase in the quantity or rate of cell death that results from administration of at least one anti-cancer agent and at least one miR gene product, relative to a control cell in which only an anti-cancer agent is provided.
20 Techniques for assessing cytotoxicity (e.g., cell damage and/or death) are well known in the art and include, but are not limited to, assays that monitor cell proliferation, cell growth and cell death (e.g., apoptosis, necrosis).

Suitable cells for use in this embodiment of the invention include cancer cells. In a particular embodiment, the cancer cell overexpresses a BCL2 gene product (e.g., RNA,
25 protein). In one embodiment, the cancer cell is an *in vivo* cell (e.g., a BCL2-associated cancer cell in a mammal (e.g., a human)). In other embodiments, the cancer cell is obtained from a patient sample (e.g., biopsy, blood) or it may be obtained from an established cancer cell line or a cell line derived from a cancer cell of a patient sample. In certain embodiments, the cancer cell is from a patient sample that was obtained from a subject who has a cancer
30 associated with overexpression of Bcl2. Examples of such cancers include, among others,

CLL, acute myeloid leukemia, multiple myeloma, melanoma, follicular lymphoma, large cell lymphoma, non-Hodgkin's lymphoma, non-small cell lung carcinoma, hematologic malignancies, solid tumors, colorectal cancer, brain carcinoma, breast carcinoma, prostate carcinoma, Epstein-Barr virus-associated lymphoproliferative disease, renal carcinoma, hepatocellular carcinoma and gastric carcinoma, among others. In one embodiment, the cancer is CLL. In another embodiment the cancer is lymphoma. In yet another embodiment, the cancer is lung cancer.

According to the methods of the invention, the sensitivity of a cancer cell to the cytotoxic effects of a chemotherapeutic agent is increased by providing the cancer cell with at least one miR gene product. In a particular embodiment, the miR gene product is complementary to a nucleotide sequence in a BCL2 gene transcript. Examples of such miR gene products include, but are not limited to, miR-182, miR-181, miR-30, miR-15a, miR-16-1, miR-15b, miR-16-2, miR-195, miR-34, miR-153, miR-21, miR-217, miR-205, miR-204, miR-211, miR-143, miR-96, miR-103, miR-107, miR-129, miR-9, miR-137, miR-217, and miR-186 (see Table 5). In a further embodiment, the miR gene product comprises a nucleotide sequence that is complementary to nucleotides 3741 to 3749 of SEQ ID NO: 55, for example, miR-15a, miR-16-1, miR-15b and miR-16-2. In another embodiment, the miR gene product is not miR-15a or miR-16-1.

The miR gene products used in the methods of the invention are preferably formulated as pharmaceutical compositions prior to administering to a subject, according to techniques known in the art. Accordingly, the present invention encompasses pharmaceutical compositions comprising at least one miR gene product. In one embodiment, the miR gene product is miR15 or miR16 (e.g., miR-15a or miR-16-1). In other embodiments, the miR gene product comprises a nucleotide sequence that is complementary to a nucleotide sequence in a BCL2 gene transcript. Examples of suitable miR gene products for the methods of the present invention include, but are not limited to, miR-182, miR-181, miR-30, miR-15a, miR-16-1, miR-15b, miR-16-2, miR-195, miR-34, miR-153, miR-21, miR-217, miR-205, miR-204, miR-211, miR-143, miR-96, miR-103, miR-107, miR-129, miR-9, miR-137, miR-217, and miR-186 (see Table 5). In one embodiment, the miR gene product is not miR-15a or miR-16-1.

In a related embodiment, the compositions of the invention further comprise at least one chemotherapeutic agent. Many chemotherapeutic agents that are useful for the treatment of cancer are well known in the art. Suitable chemotherapeutic agents for use in the compositions of the invention are described herein. In certain embodiments, the amount of
5 chemotherapeutic agent administered per dose is from about 0.0001 to 1000 mg/kg, about 0.5 to 70 mg/kg or about 1 to 50 mg/kg.

Pharmaceutical compositions of the present invention are characterized as being sterile and pyrogen-free. As used herein, "pharmaceutical compositions" include compositions for human and veterinary use. Methods for preparing pharmaceutical
10 compositions of the invention are within the skill in the art, for example, as described in *Remington's Pharmaceutical Science*, 17th ed., Mack Publishing Company, Easton, Pa. (1985).

In one embodiment, the present pharmaceutical compositions comprise the miR gene product, or a nucleic acid comprising a sequence encoding the gene product (e.g., 0.1 to 90%
15 by weight), or a physiologically acceptable salt thereof, mixed with a pharmaceutically-acceptable carrier. The pharmaceutical compositions of the invention can also comprise the miR gene product, or nucleic acid comprising a sequence encoding the gene product, which are encapsulated by liposomes and a pharmaceutically-acceptable carrier.

Preferred pharmaceutically-acceptable carriers are water, buffered water, normal
20 saline, 0.4% saline, 0.3% glycine, hyaluronic acid and the like.

In a preferred embodiment, the pharmaceutical compositions of the invention can comprise a miR gene product that is resistant to degradation by nucleases. One skilled in the art can readily synthesize a miR gene product that is nuclease resistant, for example, by incorporating one or more ribonucleotides that are modified at the 2' position into the miR
25 gene product. Suitable 2'-modified ribonucleotides include those modified at the 2'-position with fluoro, amino, alkyl, alkoxy, and O-allyl.

For example, the pharmaceutical compositions of the invention comprise a miR gene product incorporating one or more 2'-modified ribonucleotides of the formulae 2'AR-nucleotide, wherein:

30 A is oxygen or a halogen (preferably fluorine, chlorine or bromine); and

R is hydrogen or straight or branched chain C₁₋₆ alkyl;

provided that when A is a halogen, then R is omitted. A preferred modified 2-ribonucleotide is 2'-O methyl ribonucleotide. In one embodiment, pharmaceutical compositions of the invention comprise a miR gene product in which each ribonucleotide is a 2'-modified ribonucleotide.

Pharmaceutical compositions of the invention can also comprise conventional pharmaceutical excipients and/or additives. Suitable pharmaceutical excipients include stabilizers, antioxidants, osmolality adjusting agents, buffers, and pH adjusting agents.

Suitable additives include physiologically biocompatible buffers (*e.g.*, tromethamine hydrochloride), chelants (such as, *e.g.*, DTPA or DTPA-bisamide) or calcium chelate complexes (*e.g.*, calcium DTPA, CaNaDTPA-bisamide), or, optionally, additions of calcium or sodium salts (*e.g.*, calcium chloride, calcium ascorbate, calcium gluconate or calcium lactate). Pharmaceutical compositions of the invention can be packaged for use in liquid form, or can be lyophilized.

For solid pharmaceutical compositions of the invention, conventional nontoxic solid pharmaceutically-acceptable carriers can be used; for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharin, talcum, cellulose, glucose, sucrose, magnesium carbonate, and the like.

For example, a solid pharmaceutical composition for oral administration can comprise any of the carriers and excipients listed above and 10-95%, preferably 25%-75%, of the miR gene product. A pharmaceutical composition for aerosol (inhalational) administration can comprise 0.01-20% by weight, preferably 1%-10% by weight, of the miR gene product encapsulated in a liposome, as described above, and a propellant. A carrier can also be included as desired, *e.g.*, lecithin for intranasal delivery.

The invention also encompasses a method for determining the efficacy of a cancer therapy in a subject, comprising administering at least one test agent to the subject, and subsequently measuring the expression of a miR gene product in a sample from the subject. In one embodiment, the miR gene product is complementary to a nucleotide sequence in a BCL2 gene transcript. Examples of such miR gene products include, but are not limited to,

miR-182, miR-181, miR-30, miR-15a, miR-16-1, miR-15b, miR-16-2, miR-195, miR-34, miR-153, miR-21, miR-217, miR-205, miR-204, miR-211, miR-143, miR-96, miR-103, miR-107, miR-129, miR-9, miR-137, miR-217, and miR-186 (see Table 5). In a further embodiment, the miR gene product comprises a nucleotide sequence that is complementary to nucleotides 3741 to 3749 of SEQ ID NO: 55, for example, miR-15a, miR-16-1, miR-15b and miR-16-2. In another embodiment, the miR gene product is not miR-15a or miR-16-1.

In a particular embodiment, an increase in the expression of a miR gene product that is complementary to a nucleotide sequence in a BCL2 gene transcript, following administration of the agent, is indicative of a favorable response to treatment. Methods for detecting the expression level of a miR gene product are well known in the art and include, but are not limited to, such techniques as those described hereinabove (e.g., Northern blotting, RT-PCR, *in situ* hybridization). Suitable agents to be tested include small organic molecules, peptides, and naturally-occurring biological macromolecules, among others. Particularly suitable subjects include individuals suffering from one or more cancers associated with Bcl2 overexpression.

The invention will now be illustrated by the following non-limiting examples.

Examples

The following techniques were used in the Examples 1-4:

Patient Samples and Cell Lines

Patient samples were obtained after informed consent from patients diagnosed with CLL at the CLL Research Consortium institutions. Briefly, peripheral blood was obtained from CLL patients, and mononuclear cells were isolated through Ficoll-Hypaque™ gradient centrifugation (Amersham Pharmacia Biotech, Piscataway, NJ) and then processed for RNA and DNA extraction according to standard protocols as described in Sambrook, J., *et al.* (1989), *Molecular Cloning: A Laboratory Manual* (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY). As normal controls for LOH studies, DNA from buccal

mucosa from the corresponding patients was included on small (1-2 mm²) pieces of paper.

Thirty human cell lines were obtained from the American Type Culture Collection (ATCC; Manassas, VA) and maintained according to ATCC instructions. These cell lines
 5 were AS283, BL2, Bla, BJAB, CA46, Namalva, P3HRI, PAPB 682, PABm, Raji (Burkitt's lymphoma), Del1, SKDHL, ST486 (T-cell lymphoma), JM (immunoblastic B cell lymphoma), MC116 (undifferentiated lymphoma), Molt3, Supt 11 (T-ALL), U266 (multiple myeloma), A549, H1299 (lung carcinoma), TE2, TE10 (esophageal carcinoma), HeLa (cervical carcinoma), RC48 (kidney carcinoma) and 2220, 2221, 11609, 11611, LNCAP,
 10 TSUR (prostate carcinoma).

CD5+ B-cell Separation

Tonsils were obtained from patients in the pediatric age group (3-9 years) undergoing routine tonsillectomies. Purified B cells were obtained by rosetting the mononuclear cells
 15 with neuraminidase treated sheep erythrocytes. The B cells were further fractionated by discontinuous Percoll gradients (Pharmacia Biotech, Uppsala, Sweden) as described in Dono, M. *et al.*, *J. Immunol* 164:5596-5604 (2000). The B cells collected from the 50% Percoll fraction were incubated with anti CD5 mAB followed by goat anti mouse Ig conjugated with magnetic microbeads. CD5+ B cells were obtained by positive selection
 20 by collecting the cells retained on the magnetic column MS using the MiniMACS™ system (Miltenyi Biotech).

Somatic Cell Hybrids

Somatic cell hybrids were generated following conventional methods and
 25 selected in hypoxanthine-aminopterin-thymidine (HAT) medium as described in Negrini, M., *et al.*, *Cancer Res.* 54:1818-1824 (1994). DNA derived from single cell clones and subclones was isolated with the DNeasy™ tissue kit (Qiagen) and screened by PCR for the presence or absence of chromosome 13 and chromosome 2 markers (see Table 3 below for primer sequences). Fifteen clones were
 30 isolated from fusion of a CLL case (CLL-B) carrying a t(2;13)(q32; q14) translocation, and

one clone was isolated from fusion of another CLL case (CLL-A) carrying a t(2;13)(q12; q13) translocation. Twelve CLL-B derived clones carried a full complement of both chromosomes 13 and 2, whereas three carried the del(13q) and a full complement of chromosome 2. The single clone from CLL-A carried a chromosome 13 with a small deletion at 13q14 and no part
 5 of chromosome 2.

Northern Blotting

Total RNA isolation was performed using the Tri-Reagent™ protocol (Molecular Research Center, Inc). RNA samples (30 µg each) were run on 15% acrylamide denaturing
 10 (urea) Criterion™ precast gels (Bio-Rad Laboratories, Hercules, CA) and then transferred onto Hybond-N+™ membrane (Amersham Pharmacia Biotech). The hybridization with α -³²P ATP was performed at 42°C in 7% SDS, 0.2M Na₂PO₄ pH 7.0 overnight. Membranes were washed at 42°C, twice in 2x SSPE, 0.1% SDS and twice with 0.5x SSPE, 0.1% SDS. The probes used to detect miR15 and miR16 RNA were, respectively:

15 CACAAACCATTATGTGCTTGCTA (SEQ ID NO:5); and
 GCCAATATTTACGTGCTGCTA (SEQ ID NO:6)

Blots were stripped by boiling in 0.1% aqueous SDS/0.1x SSC for 10 minutes, and
 20 were reprobed several times. As a loading control, 5S rRNA stained with ethidium bromide was used.

Reverse Transcriptase Polymerase Chain Reaction (RT-PCR)

RT-PCR was performed to analyze the levels of gene expression in normal CD5+ cells
 25 and 23 B-CLL samples. One microliter of cDNA was used for each amplification reaction using the Advantage2™ PCR kit (Clontech), with 10 pmol of each gene-specific primer for 35 cycles of 94°C for 20 seconds, 65°C for 30 seconds, 68°C for 1 minute (for a list of primers used, see Table 3 below). To ensure that the RNA was of sufficient purity for RT-PCR, a PCR assay with primers specific for G3PDH cDNA (Clontech, Palo Alto, CA) was used. RT-
 30 PCR products were separated by agarose gel electrophoresis following standard procedures as described in Sambrook, J., *et al.* (1989), *supra*.

Western Blotting

SDS/PAGE gels of cell lysates from 9 B-CLL patients were probed with GST-SLUG Middle™ antibody (a gift from Dr. Thomas Look - Harvard, MA) and SNX2 (N17) antibody
 5 (Santa Cruz Biotechnology, CA). Detection was performed using an ECL™ Western Blotting detection kit (Amersham Pharmacia, UK) according to the manufacturer's instructions.

Database Analysis

Searches against the "nr" and "dbEST" databases, and a search for short, nearly exact
 10 matches were performed with the BLAST alignment tool accessed through the National Center for Biotechnology Information website, maintained by the National Institutes of Health and the National Library of Medicine. See also Altschul, *et al.*, *J. Mol. Biol.* 215: 403-
 10 (1990) and Altschul, *et al.*, *Nucleic Acids Res.* 25:3389-3402 (1997). Searches for homology of short sequences were also performed with the FASTA alignment tool provided
 15 by the Biology workBench website.

Table 3 - Primers Used for Screening Somatic Cell Hybrids

Name	Primer Sequence	SEQ ID NO:
D2S396L	ATA CAC CTC TAA ATA TCT GTT CCA G	7
D2S396R	AAG TAG GAC CAT TCT AAT AGC C	8
D2S112L	GAG TGG CGG TGA GAA GGT AT	9
D2S112R	AGC CAT TGC TAT CTT TGA GG	10
D2S2243L	TGG GAT ATG CTT CAG GGA C	11
D2S2243R	AGC TGA CCT TGG AAT CTG GTT	12
D13S260L	AGA TAT TGT CTC CGT TCC ATG A	13
D13S260R	CCC AGA TAT AAG GAC CTG GCT A	14
D13S263L	CCT GGC CTG TTA GTT TTT ATT GTT A	15

D13S263R	CCC AGT CTT GGG TAT GTT TTT A	16
D13S165L	GTT TCG CCA AGC CTG TT	17
D13S165R	GTT GAC AAT AAA ATA CGC CAC A	18
D13S273L	CTG NGG CAA AAA CAA CTC TT	19
D13S273R	ATC TGT ATG TCC TCC TTT CAA TG	20
D13S1168L	AAC CTC ATT TAA ATG TAA AGC ATC A	21
D13S1168R	GTA ATG TCA TTG CTT TTG ATT TGC	22
D13S1150L	CTC TTG AGG GAA AAA AAA AAT CA	23
D13S1150R	CCA GGC AAC CAA CCA GTC	24
D13S272L	ATA CAG ACT TCC CAG TGG CT	25
D13S272R	AGC TAT TAA AGT TCC CTG GAT AAA T	26
GCT16C05L	AAG GAA TCA GAG AAA TGG GG	27
GCT16C05R	GCT GAG TCA GAG GGA TTT GA	28
D13S25FOR	AGA GGT AAA CAA ACC AAA CCC	29
D13S25REV	GCT GAC AAT CAA GAG AAG ATG	30
D13S284L	AAA ATC AGG TGG AAA CAG AAT	31
D13S284R	AAA GGC TAA CAT CGA AGG GA	32
01ALU18	CAG AAC CAG AGA AAC AGC	33
02ALU18	ATG GCA CAA CAG CTT AAC	34
AFMA301WB5	GAA TGC AGG TGT ACC TAT CAA C	35
AFMA301WB5	ACT GAG TGA CTG CTA CCC AG	36
D13S272L1	AGC TAG CCC TAT CAG GGT	37
D13S272R1	GTA AGT GGA GGT TAC CTG	38
5279F	GAA TCA TTC GTG CTA AGT GGA T	39
5451R	TGC CAA CTG CTT GAA GAA TCT C	40
7130F	ACA CCT AAC TCC TGG GTT GTT C	41

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7371R	ACT AAA TGC CAG CGT TTG CAT G	42
9530F	GGT CTT ACT CTG GTT AAA TCT	43
9757R	CAT TGG TAG CTA AGG AAA CAC	44
11521F	CCA TTC AAG CCT GGA CAA TCT T	45
11802R	GAA ACT TGA GAC AAT AAG GAG C	46
12440F	CAT GTA ACC AAG ATA AAT CCG T	47
12558R	CTG GAA AAT GTA TGT GAT GAG G	48
17261F	CTG TTG CTA TCT GTA ATA ACA C	49
17494R	CTT GGA ATT TTC CAC TGA ATC	50
18701R	TCA TCA GAA GAA ATC AAG GCA G	51
18560F	CAG TGT TAG GAA TAC GCA TTC A	52
GSP2F4	CCT TGC CAG TAC GCC CAC AAG CTG	53
GSP1R1	CCC CAC CTA TGG TTG TAG TGA GCA TCC	54

Example 1: A 30 kb Deletion Region in Somatic Cell Hybrids of CLL Patients

- 5 The minimal region of loss at 13q14 in CLL patients has been unclear. Previously, various and relatively large (between 130 to 550 kb) regions deleted in 13q14 have been described in CLL (see FIG. 2B). LOH and Southern blot analyses were used to identify the centromeric boundary of homozygous loss at the Alu18 locus (FIG. 2D), which is located between *D13S1150* and *D13S272* less than 65 kb centromeric to exon 5 of the *LEU2* gene.
- 10 However, no small or overlapping homozygous deletions were found that allowed a better localization of the target tumor suppressor.

- 15 To better define the region of loss in CLL, somatic cell hybrids of mouse LM-TK⁻ and CLL cells carrying 13q14 translocations and/or deletions were generated. PCR screening of resulting hybrid clones allowed the segregation of the two copies of chromosome 13 present in the tumors. In this manner, a 31.4 kb deletion was identified in one case, and the chromosomal breakpoint was precisely localized in the other (FIG. 2D). These results indicated that the 13q14 tumor suppressor genes lay within a 29 kb region between exons 2

and 5 of the *LEU2* gene. The primers used to screen the somatic cell hybrids are given in Table 3.

As shown in FIG. 2, the region deleted in the somatic cell hybrids was consistent with all reported regions of loss, including a 10 kb region reported several years ago by Liu, *et al.*, *Oncogene* 15:2463-2473 (1997). Exons 1 and 2 of *LEU2* also lay within that region, and within the one defined here. However, *LEU2* has been excluded as a likely candidate tumor suppressor gene for B-CLL (see Bullrich, *et al.*, *Cancer Res.* 61:6640-6648 (2001); Migliazza, *et al.*, *Blood* 97:2098-2104 (2001); Wolf, *et al.*, *Hum. Mol. Genet.* 10:1275-1285 (2001); and Mertens, *et al.*, *Blood* 99:4116-4121(2002)).

Example 2: The miR15 and miR16 Genes Are Localized in the Minimally Deleted Region of Chromosome 13 and Are Highly Expressed in CD5+ Cells

Publicly available sequence information and databases were screened for new regulatory genes in the minimal region of loss at 13q14. A cluster of two recently cloned miRNA genes, miR15 and miR16, were located exactly in the deleted region (FIG. 2A). To evaluate the level of expression of miR15 and miR16 in normal tissues, Northern blot analysis of miR15 and miR16 RNA was performed on a panel of normal tissues, including CD5+ B cells isolated from tonsils of normal individuals (FIG. 3A). CD5+ B cells were used as controls, because B-CLL is characterized by a progressive accumulation of CD5+ B-lymphocytes. Ubiquitous expression of both miR15 and miR16 genes was found, with the highest level in normal CD5+ lymphocytes. In addition, miR16 was consistently expressed at higher levels than miR15 in normal tissues. These data indicated that the miR15 and miR16 genes play an important role in normal CD5+ B-cell homeostasis.

Example 3: The miR15 and miR16 Genes are Frequently Deleted or Downregulated in CLL Samples with Deletions at 13q14

To investigate whether the miR15 and miR16 genes were involved in CLL pathogenesis, 60 CLL samples and 30 human cancer cell lines were analyzed for miR15 and miR16 expression by Northern blotting (FIG. 3B). 68% of CLL patients (41/60), as well as 5 out of 6 analyzed prostate cancer cell lines, showed a significant reduction in expression when

compared with their normal tissue counterparts. These findings demonstrated that the miR15 and miR16 genes are down-regulated in the majority of B-CLL and prostate cancer cases tested.

5 In addition, 23 out of 60 CLL samples (38%) presented a clearly identifiable band of about 70 nt representing the miR15 precursor RNA. The 70 nt miR15 band was not found in any normal tissue analyzed except for bone marrow (FIG. 3A), which indicated that miR15 precursor RNA could be inefficiently processed in CLL.

To determine whether the observed down-regulation of expression correlated with allelic loss in CLL, LOH studies were performed with microsatellite makers *D13S272* and *D13S273* on 46 CLL patients from whom normal DNA was available (FIG. 3B). We found that 68% of informative samples displayed LOH in at least one marker (24 out of 35 cases). In all but four samples (75%), expression of the miR15/16 gene products was reduced. For 12 samples, reproducible results were not obtained due to the poor quality of the starting material. Additionally, expression levels were reduced in 6 out of 11 cases (55%) without apparent LOH. In these cases, deletions may have been too small to be detected with the markers analyzed.

Northern blot analysis indicated that both miR15 and miR16 gene products were expressed in cases with known large homozygous deletions at 13q14 and with less than 5% normal cells, pointing to the presence of other highly similar micro RNA genes in the genome. Indeed, a cluster very similar to miR15/miR16 gene cluster (but with different precursors) has been reported on chromosome 3q25-26.1 (see Lagos-Quintana, *et al.*, *Curr. Biol.* 12:735-739(2002)). To show that the variation in miR15/16 gene expression was strictly related to deletions on chromosome 13q, probes specific for miR16 precursor RNA on chromosome 13 and for the miRNA precursor RNA produced from the gene on chromosome 3 were designed and used to probe Northern blots.

While the miR16 precursor RNA from chromosome 13 was detected at low levels, no specific hybridization with the chromosome 3 probe was found in the same samples. In addition, an LOH study was performed with two microsatellite markers spanning a region of 2 Mb located immediately centromeric to this cluster. Four of 17 informative samples showed LOH in at least one marker, and no correlation with the levels of expression of miR15/16 was

found. These data clearly demonstrated that down-regulation of miR15 and miR16 gene expression in CLL correlates with allelic loss at 13q14, and provide evidence of a role for miR15 and miR16 gene products in CLL pathogenesis.

5 Example 4: miR15 and miR16 are Also Involved in CLL Pathogenesis in Mice

To further investigate whether the miR15 and miR16 genes were involved in CLL pathogenesis, studies were extended to E μ -TCL1 transgenic mice, which develop CLL (Bichi, *et al.*, *Proc. Natl. Acad. Sci. USA* 99(10):6955-6960(2002)). Cytogenetic and genetic alterations were examined in E μ -TCL1 transgenic mice. Northern blot analyses were
10 performed as described above (see Examples- "Northern blotting," and Example 3).

In approximately 80% of the transgenic mice, there was a decrease in expression of the mouse homologues of miR15 and miR16 in CLL cells, as compared to normal mouse spleen lymphocytes. These results are similar to those described in Example 3 for miR15 and miR16 expression in human CLL and normal samples.

15 Comparisons were made between mouse chromosome 15 and human chromosome 12. Comparative gene hybridization (CGH) of the transgenic mouse leukemias showed that approximately 35% had an amplification of a region of mouse chromosome 15, which corresponds to a region of human chromosome 12. Cytogenetic analyses of these mouse leukemias also showed trisomies or tetrasomies of mouse chromosome 15. Trisomies of
20 chromosome 12 are known to occur in approximately 25% of human CLLs.

Comparative gene hybridization also showed a loss of a region of mouse chromosome 14 (51.6-78.5 Mb), which corresponds to region 13q14 in humans.

The results of the studies indicate that the CLL mouse model recapitulates events occurring in the pathogenesis of human CLL.

25 Taken together, the data presented in Examples 1-4 provide evidence of a role for miR15 and miR16 in CLL pathogenesis in mammals.

The following techniques were used in Examples 5-8:

Patient Samples

Twenty-six CLL samples were obtained, after informed consent, from patients diagnosed with CLL at the CLL Research Consortium institutions. Briefly, blood was obtained from CLL patients, and mononuclear cells were isolated through Ficoll/Hypaque gradient centrifugation (Amersham Pharmacia Biotech) and processed for RNA extraction according to described protocols (Sambrook J., *et al.* Molecular Cloning: A Laboratory Manual (Cold Spring Harbor Lab, Press, Plainview, NY (1989)). Two normal pools containing CD5 positive cells from each of two different normal individuals were used as controls. CD5+ B cells were prepared from tonsillar lymphocytes. Briefly, tonsils were obtained from patients in the pediatric age group (less than 18 years old), who were undergoing routine tonsillectomies, after informed consent. Purified B cell populations were prepared by rosetting T cells from mononuclear cells (MNCs) with neuraminidase-treated sheep erythrocytes (SRBCs). In order to obtain CD5+ B cells, purified B cells were incubated with anti-CD5 monoclonal antibodies (mAb), followed by goat anti mouse Ig conjugated with magnetic microbeads (Miltenyi Biotec, Auburn, CA), as described. CD5+ B cells were positively selected by collecting the cells retained on the magnetic column MS by Mini MACS™ system (Miltenyi Biotec, Auburn, CA). The degree of purification of the cell preparations was greater than 95%, as assessed by flow cytometry.

Western Blotting for BCL2

The levels of BCL2 protein were quantified using a mouse monoclonal anti-BCL2 antibody (Dako) and confirmed by using a second mouse monoclonal anti-BCL2 antibody (Santa Cruz Biotechnology, Santa Cruz, CA) using standard procedures for Western blotting (Sambrook, J., *et al.* Molecular Cloning: A Laboratory Manual (Cold Spring Harbor Lab, Press, Plainview, NY (1989))). Normalization was performed with mouse monoclonal anti-Actin antibody (Sigma). The band intensities were quantified using ImageQuantTL™ (Nonlinear Dynamics Ltd.).

RNA Extraction, Northern Blots, and miRNACHIP Experiments

Procedures were performed as described (Calin, G. A., *et al.* *Proc. Natl. Acad. Sci. U.S.A.* 99: 15524-15529 (2002); Liu, C.G., *et al.*, *Proc Natl. Acad. Sci U.S.A.* 101:9740-9744

(2004); Calin, G. A., *et al. Proc. Natl. Acad. Sci. U.S.A. 101*: 11755-11760 (2004)). Briefly, labeled targets from 5 µg of total RNA were used for hybridization on each miRNACHIP microarray chip containing 368 probes in triplicate, corresponding to 245 human and mouse miRNA genes. Raw data were normalized and analyzed in GeneSpring® software version 5 7.2 (Silicon Genetics, Redwood City, CA). Expression data were median centered using both GeneSpring® normalization option or Global Median normalization of the Bioconductor package without any substantial difference. Statistical comparisons were performed using both GeneSpring® ANOVA tool and SAM software (Significance Analysis of Microarray). The microarray data were confirmed by Northern blottings for *mir-16-1* and *mir-15a*, as reported in 10 Calin, G.A., *et al., Proc. Natl. Acad. Sci. USA 101*: 11755-11760 (2004).

mir-16-1/mir-15a Expression Vectors

Wild-type (mir-16-1-WT) and mutant (mir-16-1-MUT) *mir-16-1/mir-15a* expression 15 vectors were constructed by ligating the relevant open reading frame in a sense orientation into the mammalian expression vector, pSR-GFP-Neo (OligoEngine, Seattle, WA). Each construct contained an 832 bp genomic sequence that included both *mir-16-1* and *mir-15a*. The mutant construct contained a C to T substitution at +7 base pairs in the 3' region of *mir-16-1*. After confirmation by sequencing, each construct was transfected into 293 cells using 20 Lipofectamine2000, according to the manufacturer's instructions (Invitrogen, Carlsbad, CA). The expression of both constructs was assessed by Northern blot analysis, as described in Example 5. Western blot analysis of GFP levels was used to show that both wild-type and mutant pRS-neo-GFP constructs were transfected with equal efficiency.

25 Transfection Assays

Human megakaryocytic cells (MEG-01) were grown in 10% FBS in RPMI-1640 medium, supplemented with 1X non-essential amino acid and 1 mmol sodium pyruvate, at 37°C in a humidified atmosphere containing 5% CO₂. The cells were cotransfected in 12-well plates using siPORT neoFX (Ambion), according to the manufacturer's instructions, 30 using 0.4 µg of the firefly luciferase reporter vector (Promega) and 0.08 µg of control vector

containing Renilla luciferase, pRLTK (Promega). For each well, 10nM of mir-16-1-sense (5'-uagcagcacguaaaauuuggcg-3'; SEQ ID NO:341) and/or mir-15a-sense (5'-uagcagcacauaaugguuugug-3'; SEQ ID NO:342) (Dharmacon), or miR-15a-anti-sense and/or miR-16-1 anti-sense precursor miRNA inhibitor (Ambion) were used. Firefly and Renilla luciferase activities were measured, consecutively, using a Dual-luciferase assay (Promega), 24 hr after transfection.

Luciferase Reporter Experiments

To generate luciferase reporter constructs, a 546 base pair segment of the 3' UTR of the BCL2 gene was amplified from human genomic DNA by PCR and inserted into the pGL3 control vector (Promega), using the XbaI site immediately downstream from the stop codon of luciferase. The following primer set was used to generate specific fragments:

BCL2-UTRF2

5'-CTAGTCTAGAGCCTCAGGGAACAGAATGATCAG-3' (SEQ ID NO:343); and

BCL2-UTRR2

(5'-CTAGTCTAGAAAGCGTCCACGTTCTTCATTG-3' (SEQ ID NO:344).

Two BCL2 inserts with deletions of 5 bp and 9 bp from the site of complementarity with *miR-15a* and *miR-16-1*, respectively (see FIG. 4A), were also generated using the QuikChange XL™ Site-Directed Mutagenesis Kit (Stratagene). Wild-type and mutant inserts were confirmed by sequencing.

Example 5: *miR-15a* and *miR-16-1* Display Complementarity to a Region of the BCL2 Transcript and Show Expression Patterns that are Inversely Correlated with Those of BCL2 Protein

Two microRNAs, *mir-16-1* and *mir-15a*, were identified as having homology to the BCL2 mRNA sequence by homology searching. Specifically, the first 9 nucleotides at the 5'-end of both miRNAs were found to be complementary to bases 3741 to 3749 of a human Bcl2

cDNA clone, NM_000633 (FIG. 4A). This region of nucleotides in the BCL2 transcript is conserved in mice (FIG. 4A). *miR-15b* and *miR-16-2*, both members of a second cluster from chromosome 3q26, were also identified as having complementarity to the same region of Bcl2 transcripts.

- 5 To evaluate whether *mir-16-1* and/or *mir-15a* miRNAs interact with BCL2 transcript, we first determined whether a correlation exists between the expression levels of *miR-15a/miR-16-1* and Bcl2 protein levels in both CLL cells and normal CD5 positive lymphocytes. In normal CD5 positive B lymphocytes, the cluster from chromosome 13q14 is highly expressed, while the *miR-15b* and *miR-16-2* precursors are barely detectable by
- 10 Northern blot analysis (Calin, G.A., *et al.*, *Proc. Natl. Acad. Sci. USA* 99: 15524-15529 (2002)). By miRNACHIP analysis and Western blotting, a set of 30 samples was analyzed, comprising 26 CLL samples and 4 normal CD5 positive lymphocytes from tonsils of unaffected individuals. In normal CD5 positive lymphoid cells, the levels of both *miR-15a* and *miR-16-1* miRNAs were high. In contrast, Bcl2 protein was expressed at low levels.
- 15 However, in the majority of leukemic cells, both *miR-15a* and *miR-16-1* were expressed at low levels, while Bcl2 protein was overexpressed (FIG. 4B and Table 4). Moreover, in all leukemia samples that were analyzed, we found an inverse correlation between the expression levels of *miR-15a/miR-16-1* and those of Bcl2 (Table 4). Thus, in CLL samples, a downregulation of *miR-15a* and *miR-16-1* expression and an overexpression of Bcl2 protein
- 20 was generally observed.

Table 4 -- Normalized values of BCL2 protein expression by Western blot and miR-15a and miR-16-1 expression by miRNACHIP in a set of 26 CLL samples and two pools of normal CD5 cells*.

Sa name	Bcl2/ACT	mir-16-1 chip	mir-15a chip	mir16/Bcl2/ACT	mir15/Bcl2/ACT
N1-N2	0.06	9	3.5	142.08	55.25
N1-N2	0.05	9	3.5	169.27	65.83
N3-N4	0.07	6.24	2.3	83.58	30.81
CLL1	0.61	4.28	1.11	7.04	1.82
CLL2	1.02	2.65	1.17	2.61	1.15
CLL3	0.17	3.08	1.12	18.40	6.69
CLL4	0.67	2.65	1.17	3.96	1.75
CLL5	0.67	3.27	1.3	4.88	1.94
CLL6	2.95	1.42	1.02	0.48	0.35
CLL7	1.92	3.53	1.51	1.84	0.79
CLL8	1.27	4.34	1.24	3.43	0.98
CLL8	1.50	4.3	1.26	2.86	0.84
CLL9	2.26	2.5	1.1	1.11	0.49
CLL10	3.53	1.17	0.91	0.33	0.26
CLL11	2.50	1.2	1.01	0.48	0.40
CLL12	10.26	1.57	1.16	0.15	0.11
CLL13	7.85	1.8	1.17	0.23	0.15
CLL14	2.86	3.28	0.99	1.15	0.35
CLL15	1.28	9.1	2.62	7.09	2.04
CLL16	14.60	2.2	1.15	0.15	0.08
CLL17	0.99	1.54	1.08	1.55	1.09
CLL18	7.00	1.46	1.07	0.21	0.15
CLL19	1.97	2.71	1.22	1.37	0.62
CLL20	0.56	3.08	1.12	5.50	2.00
CLL21	0.65	2.43	1.26	3.71	1.93

CLL22	0.79	3.08	1.13	3.92	1.44
CLL23	1.30	2.2	1.15	1.69	0.88
CLL24	1.88	0.92	0.87	0.49	0.46
CLL25	8.48	5.03	1.66	0.59	0.20
CLL26	0.17	7.64	1.69	43.70	9.67

* - N1, N2, N3 and N4 = normal CD5 samples; CLL1-CLL26 = chronic lymphocytic leukemia samples. Data are presented as arbitrary units. Two samples, e.g., one normal pool and sample CLL 8, were tested in duplicate to assess data reproducibility. The Western blot (WB) band intensities were quantified using ImageQuantTL (Nonlinear Dynamics Ltd.). Expression data were median-centered using both the GeneSpring normalization option and Global Median normalization of the Bioconductor package (www.bioconductor.org) without any substantial difference.

10 Example 6: Expression of microRNAs, *miR-15a* and *miR-16-1*, Reduces Expression of BCL2 Protein in Transfected MEG-01 Cells

To investigate the effects of expressing the full cluster containing *miR-15a/miR-16-1* on Bcl2 expression, MEG-01 cells, an acute leukemia-derived cell line that expresses high levels of Bcl2 but does not express either *miR-15a* or *miR-16-1* due to a deletion of one allele and alteration of the other allele of the *miR-15a/16-1* locus, were used. MEG-01 cells that were transiently transfected with the pSR-miR-15/16-WT vector displayed highly reduced levels of Bcl2 (about 7% of normalized expression), relative to wild-type MEG-01 cells (MEG-01 WT) and MEG-01 cells that were transfected with the empty vector (MEG-01-pRS-neo-GFP) (FIG. 5A). To confirm this effect, the same expression vector containing a +7(C to T) germline substitution in *miR-16-1* (pSR-miR-15/16-MUT), which was detected in a case of familial CLL (Calin, G.C., *et al.*, *N. Engl. J. Med.*, in press) and strongly reduces the expression of both miRNAs, was transfected. As expected, Bcl2 levels were comparable (75% normalized expression) with those in WT cells or control cells that were transfected with empty vector (FIG. 5A). Furthermore, the cells transfected with pSR-miR-15a/16-1 WT showed activation of an intrinsic apoptosis pathway (as determined by activation of the APAF1 – caspase 9 – PARP pathway). None of the control samples, including the sample of cells transfected with the mutant construct (pSR-miR-15/16-MUT), showed changes in the levels of these pro-apoptotic proteins (FIG. 5A).

To determine if both *miR-15a* and *miR-16-1* miRNAs affect Bcl2 protein expression, we transiently transfected *miR-15a* and *miR-16-1* sense or antisense oligonucleotide RNAs into the MEG-01 cells. As shown in FIG. 5B, separate transfections of *miR-15a*-sense and *miR-16-1*-sense oligonucleotides completely abolished Bcl2 expression, while transfection of antisense RNAs for both miRNAs did not affect Bcl2 expression. Similar results were obtained when both sense RNAs or both antisense RNAs were cotransfected (FIG. 5B), confirming that both *miR-15a* and *miR-16-1* miRNAs influence Bcl2 protein expression.

Example 7: Evidence for a Direct Interaction Between microRNAs, *miR-15a* and *miR-16-1*, and the 3' UTR of BCL2 Transcripts

Downregulation of Bcl2 protein levels following expression of *miR-15a* and *miR-16-1* could be explained by a direct effect (i.e., hybridization of the miRNAs directly to the Bcl2 transcript via miRNA::mRNA complementarity), or by an indirect interaction (i.e., interaction of *miR-15a* and *miR-16-1* with another target(s), thereby resulting in downregulation of Bcl2 levels). To distinguish between these possibilities, a 536 bp sequence from the 3'UTR of human Bcl2 (nucleotides 3064 to 3599 of SEQ ID NO: 55), which shows complementarity to the *miR-15a* and *miR-16-1* microRNAs, was fused to a luciferase reporter gene. Interaction between either miRNA and the BCL2 mRNA should reduce the firefly luciferase activity (normalized to Renilla luciferase activity of the transfection control plasmid), whereas failure of either miRNA to interact with BCL2 mRNA should not affect reporter gene expression. The data presented in FIGS. 6A and 6B are consistent with a direct interaction between *miR-15a*/*miR-16-1* miRNAs and BCL2 transcript, as significant repression of luciferase activity was observed following transfection with either or both microRNAs, relative to control vectors. A control experiment was performed using two types of mutated target mRNA sequences that lacked either 9 (3'M1) or 5 (3'M2) of the bases in *miR-15a* and *miR-16-1* that are complementary to BCL2 cDNA. As expected, both mutants completely abolished the interaction between *miR-15a* and *miR-16-1* and the 3'UTR of BCL2 (FIG. 6B). These data indicate that both *miR-15a* and *miR-16-1* microRNAs directly interact with the 3'UTR of BCL2.

Translocations affecting the Bcl2 gene increase both messenger and protein levels (Tsujimoto, Y., *et al.*, *Science* 228: 1440-1443 (1985)). Because it was recently shown that miRNAs can downregulate a specific target by affecting mRNA translation or mRNA stability (Lim, L.P., *et al.*, *Nature* 433: 769-773 (2005)), the possibility that BCL2 was
 5 downregulated by miR15a/16-1 interaction via mRNA stability was tested. Levels of BCL2 mRNA were evaluated by RT-PCR amplification using extracts from cells that were transfected with either pSR-miR-15/16-WT or specific *miR-15a* and *miR-16-1* RNA oligonucleotides. No differences in the level of Bcl2 expression were observed between control cells (e.g., untransfected cells or cells transfected with empty vector) and cells
 10 transfected with any of these constructs (FIG. 6A). These results indicate that *miR-15a* and *miR-16-1* do not affect mRNA stability, but are likely to affect translation of Bcl2 mRNA.

Example 8: Identification of Putative microRNA/BCL2 Interactions

In the human genome, four members of the mir15/16 family of miRNAs are present
 15 and all have the same 9 bp sequence that is complementary to a region of Bcl2 transcripts. This functional redundancy suggests the existence of a very fine mechanism to regulate Bcl2 expression. Moreover, using a target prediction software (TargetScan™ (Lewis, B.P., *et al.*, *Cell* 120: 15-20 (2005)), BCL2 was identified as a potential target for 14 different miRNAs, including *mir15* and *mir16* (Table 5). These findings suggest that other microRNAs can
 20 regulate Bcl2 protein expression in various cell types.

Table 5. Predicted miRNA::BCL2 interactions by different target prediction programs.*

Rank	microRNA	TargetScanS (p value)	PicTar (score)	Miranda (prediction)
1	mir-182	0.031	4.79	N/A
2	mir-181	0.041	N/A	N/A
3	mir-30	0.065	N/A	N/A
4	mir-15	0.091	2.08	N/A
5	mir-16	0.091	2.08	N/A
6	mir-195	0.091	2.12	N/A
7	mir-34	0.15	1.34	Yes
8	mir-153	0.24	0.64	N/A
9	mir-21	0.33	0.64	N/A
10	mir-217	0.36	2.37	N/A
11	mir-205	0.37	N/A	N/A
12	mir-204	0.4	0.73	Yes
13	mir-211	0.4	0.73	Yes
14	mir-143	0.41	3.86	N/A
15	mir-96	N/A	1.77	N/A
16	mir-103	N/A	1.23	N/A
17	mir-107	N/A	1.23	N/A
18	mir-129	N/A	N/A	Yes
19	mir-9	N/A	N/A	Yes
20	mir-137	N/A	N/A	Yes
21	mir-217	N/A	N/A	Yes
22	mir-186	N/A	N/A	Yes

* Note: TargetScan (MIT) at genes.mit.edu/targetscan/, PicTar (New York University) at pictar.bio.nyu.edu/ and Miranda (Memorial Sloan-Kettering Cancer Center) at www.microrna.org/. N/A - prediction not available.

5

The data provided herein indicate that Bcl2 overexpression as a consequence of microRNA (e.g., *miR-15a*, *miR-16-1*) downregulation is an important mechanism contributing to the pathogenesis of human B-CLL. Notably, downregulation of *miR-15a* and *miR-16-1*

also has been reported in cases of diffuse large B cell lymphomas (DLBCL) (Eis, P.S., *et al.*, *Proc Natl. Acad. Sci. USA* 102: 3627-3632 (2005)). Therefore, Bcl2 overexpression as a consequence of microRNA (e.g., *miR-15a*, *miR-16-1*) downregulation is likely to be involved in other human malignancies.

5

Example 9: Expression of miR Gene Products in Human Cells

The cDNA sequences encoding one or more entire miR precursor RNAs are separately cloned into the context of an irrelevant mRNA expressed under the control of the cytomegalovirus immediate early (CMV-IE) promoter, according to the procedure of Zeng, *et al.*, *Mol. Cell* 9:1327-1333 (2002).

Briefly, Xho I linkers are placed on the end of double-stranded cDNA sequences encoding the miR precursors, and these constructs are separately cloned into the Xho I site present in the pBCL2/CMV plasmid. The pBCL2/CMV plasmid is described in Cullen, (1986), *Cell* 46:973-982. The plasmid containing the miR precursor RNA sequences is called pCMV-miR (e.g., pCMV-miR16 for miR-16-1).

One or more pCMV-miR constructs are separately transfected into cultured human 293T cells by standard techniques using the FuGene 6 reagent (Roche). Total RNA is extracted as described above, and the presence of processed microRNA is detected by Northern blot analysis with miR-specific probes.

One or more pCMV-miR constructs are also separately transfected into cultured human cancer cell lines (e.g., carcinoma cell lines 2220, 2221, 11609, 11611, LNCAP, TSUR). Total RNA is extracted as described above, and the presence of processed microRNA in the cancer cells is detected by Northern blot analysis with miR-specific probes. The transfected cancer cells are also evaluated for changes in morphology, the ability to overcome contact inhibition, and other markers indicative of a transformed phenotype.

Example 10: Transfection of BCL2-associated Cancer Cells with miR Gene Products

BCL2-associated cancer cells from a subject diagnosed with a BCL2-associated cancer are isolated and transfected with plasmids encoding one or more microRNAs as follows.

CD5+ B cells are isolated as described above and BCL2-associated cancer cells (e.g., CLL cells) are identified by visual inspection or, if the cancer is CLL, by determining the CLL Score according to the scoring system of Matutes, *et al.*, *Leukemia* 8(10):1640-1645 (1994). CD5+ B cells with a CLL Score of at least 4 are considered CLL cells.

The isolated BCL2-associated cancer cells are transfected with miR expression constructs (e.g., pCMV-miR15, pCMV-miR16) by standard techniques. Total RNA is extracted as described above, and the presence of processed microRNA is detected by Northern blot analysis with probes specific for particular miRs (e.g., miR-15a, miR-16-1). Stable integration of miR gene sequences is also confirmed by Southern blot hybridization using probes specific for certain miR gene sequences.

15

Example 11: Transfection of Hematopoietic Stem Cells with miR Gene Products

Hematopoietic stem cells (HSC) from subjects diagnosed with a BCL2-associated cancer (e.g., CLL) are obtained from bone marrow as follows.

Bone marrow is harvested from the iliac bones of a subject under general anesthesia in an operating room using standard techniques. Multiple aspirations are taken into heparinized syringes for a total of about 750 to 1000 ml bone marrow. The aspirated marrow is transferred immediately into a transport medium (TC-199, Gibco, Grand Island, New York) containing 10,000 units of preservative-free heparin per 100 ml of medium. The aspirated marrow is filtered through three progressively finer meshes to obtain a cell suspension devoid of cellular aggregates, debris and bone particles. The filtered marrow is then processed further into an automated cell separator (e.g., Cobe 2991 Cell Processor™) to obtain the “buffy coat” (*i.e.*, leukocytes devoid of red cells and platelets).

The buffy coat preparation is partially enriched for hematopoietic stem cells (HSC) by positively selecting for CD34⁺ cells with immunomagnetic beads (Dynal A.S., Oslo, Norway) as follows. The buffy coat preparation is suspended in supplemented alpha medium and

incubated with mouse anti-HPCA-I antibody in 1:20 dilution, 45 minutes, at 4°C with gentle inverting of tubes. The cells are washed 3X in supplemented alpha medium, and then incubated with beads coated with the Fc fragment of goat anti-mouse IgG₁ (75 µl of immunobeads/10⁷ CD34⁺ cells). After 45 minutes of incubation at 4°C, cells adherent to the
 5 beads are positively selected using a magnetic particle concentrator, as directed by the manufacturer.

2 x 10⁴ cells from the preparation enriched for HSC are incubated in 5 ml polypropylene tubes (Fisher Scientific, Pittsburgh, PA) in a total volume of 0.4 ml of Iscove's modified Dulbecco's medium (IMDM) containing 2% human AB serum and 10 mM Hepes
 10 buffer, and are transfected with miR-expressing constructs (e.g., pCMV-miR15, pCMV-miR16) by standard techniques. Expression of microRNA is confirmed in a portion of the transfected HSC by Northern blot analysis, and stable integration of miR gene sequences in a portion of the HSC is confirmed by Southern blot analysis. Approximately 4 x 10⁸/kg body weight to about 8 x 10⁸/kg body weight of the remaining transfected cells are reimplanted into
 15 the subject according to standard bone marrow transplant techniques.

The experiment is repeated, but the bone marrow is purged of neoplastic cells with ionizing radiation prior to transfection and reimplantation, as follows. Cells in the buffy coat preparation are adjusted to a cell concentration of about 2 x 10⁷/ml in TC-199 containing about 20% autologous plasma. Recombinant human hematopoietic growth factors rH IL-3 or
 20 rH GM-CSF are added to the cell suspension to stimulate growth of hematopoietic neoplasms and thereby increase their sensitivity to ionizing radiation. The cells are then exposed to 5 - 10 Gy ionizing radiation, washed once at 4°C in TC-199 containing about 20% autologous plasma, and transfected with miR-expressing constructs (e.g., pCMV-miR15, pCMV-miR16) as above.

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Example 12: Preparation of Liposomes Encapsulating microRNAs

Liposome Preparation 1 - Liposomes composed of lactosyl cerebroside, phosphatidylglycerol, phosphatidylcholine and cholesterol in molar ratios of 1:1:4:5 are prepared by the reverse phase evaporation method described in U.S. Patent No.: 4,235,871.

5 The liposomes are prepared in an aqueous solution of 100 µg/ml processed microRNA or 500 µg/ml (e.g., pCMV-miR15, pCMV-miR16). The liposomes thus prepared encapsulate either the processed microRNA (e.g., miR-15a, miR-16-1 RNA), or the constructs expressing microRNA (e.g., pCMV-miR15, pCMV-miR16 plasmids).

10 The liposomes are then passed through a 0.4 polycarbonate membrane and suspended in saline, and are separated from non-encapsulated material by column chromatography in 135 mM sodium chloride, 10 mM sodium phosphate pH 7.4. The liposomes are used without further modification, or are modified as described below.

A quantity of the liposomes prepared above are charged to an appropriate reaction
15 vessel to which is added, with stirring, a solution of 20 mM sodium metaperiodate, 135 mM sodium chloride and 10 mM sodium phosphate (pH 7.4). The resulting mixture is allowed to stand in darkness for 90 minutes at a temperature of about 20°C. Excess periodate is removed by dialysis of the reaction mixture against 250 ml of buffered saline (135 mM sodium chloride, 10 mM sodium phosphate, pH 7.4) for 2 hours. The product is a liposome having a
20 surface modified by oxidation of carbohydrate hydroxyl groups to aldehyde groups. Targeting groups or opsonization inhibiting moieties are conjugated to the liposome surface via these aldehyde groups.

Liposome Preparation 2 - A second liposome preparation composed of maleimidobenzoyl-phosphatidylethanolamine (MBPE), phosphatidylcholine and cholesterol
25 is obtained as follows. MBPE is an activated phospholipid for coupling sulfhydryl-containing compounds, including proteins, to the liposomes.

Dimyristoylphosphatidylethanolamine (DMPE) (100 mmoles) is dissolved in 5 ml of anhydrous methanol containing 2 equivalents of triethylamine and 50 mg of m-
maleimidobenzoyl N-hydroxysuccinimide ester, as described in Kitagawa, *et al.*, *J. Biochem.*
30 79:233-236 (1976). The resulting reaction is allowed to proceed under a nitrogen gas

atmosphere overnight at room temperature, and is subjected to thin layer chromatography on Silica gel H in chloroform/methanol/water (65/25/4), which reveals quantitative conversion of the DMPE to a faster migrating product. Methanol is removed under reduced pressure and the products re-dissolved in chloroform. The chloroform phase is extracted twice with 1% sodium chloride and the maleimidobenzoyl-phosphatidylethanolamine (MBPE) purified by silicic acid chromatography with chloroform/methanol (4/1) as the solvent. Following purification, thin-layer chromatography indicates a single phosphate containing spot that is ninhydrin negative.

Liposomes are prepared with MBPE, phosphatidylcholine and cholesterol in molar ratios of 1:9:8 by the reverse phase evaporation method of U.S. Patent No.: 4,235,871, *supra*, in an aqueous solution of 100 µg/ml processed microRNA or a solution of microRNA-encoding plasmid. Liposomes are separated from non-encapsulated material by column chromatography in 100 mM sodium chloride-2 mM sodium phosphate (pH 6.0).

15 Example 13: Attachment of Anti-CD5+ or Anti-Prostate Tumor Antibodies to Liposomes Encapsulating miR Gene Products

An appropriate vessel is charged with 1.1 ml (containing about 10 mmoles) of Liposome Preparation 1 carrying reactive aldehyde groups, or Liposome Preparation 2 above. 0.2 ml of a 200 mM sodium cyanoborohydride solution and 1.0 ml of a 3 mg/ml solution of a monoclonal antibody directed against the CD5+ cell surface marker or a prostate tumor cell antigen is added to the preparation, with stirring. The resulting reaction mixture is allowed to stand overnight while maintained at a temperature of 4°C. The reaction mixture is separated on a Biogel A5M agarose column (Biorad, Richmond, Ca.; 1.5 X 37 cm).

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Example 14: Inhibition of Human Prostate Tumor Growth In Vivo with miR Gene Products

A hormone refractory human prostate adenocarcinoma cell line (PC-3) is inoculated into nude mice, and the mice are divided into treatment and control groups. When tumors in the mice reach 100 to 250 cubic millimeters, one or more processed microRNAs (e.g., miR-15a, miR-16-1) encapsulated in liposomes are injected directly into the tumors of the control group. The tumors of the control group are injected with liposomes encapsulating carrier

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solution only. Tumor volume is measured throughout the study. The efficacy of miR gene products in inhibiting prostate tumor growth in the Dunning R-3327 rat prostate adenocarcinoma model is also evaluated, as follows. A highly metastatic and malignant clone (RT-3.1) of Dunning R-3327 prostate adenocarcinoma cells is inoculated into Copenhagen
5 rats, which are then divided into treatment and control groups. Both groups form solid tumor masses in approximately one week. The tumors of rats in the treatment group are then injected with processed microRNA encapsulated in liposomes twice a week for 5 weeks. The tumors of the control group are injected with liposomes encapsulating carrier solution only. Tumor volume is measured throughout the study.

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THE EMBODIMENTS OF THE PRESENT INVENTION IN WHICH AN EXCLUSIVE PROPERTY OR PRIVILEGE IS CLAIMED ARE DEFINED AS FOLLOWS:

1. Use of miR-15a and/or miR-16-1 to reduce BCL2 expression in BCL2-expressing cancer cells.
2. Use of miR-15a and/or miR-16-1 according to claim 1, wherein the cancer cells are lymphoma cells.
3. Use of miR-15a and/or miR-16-1 according to claim 2, wherein the lymphoma cells are selected from the group consisting of follicular lymphoma cells, small cell lymphoma cells, large cell lymphoma cells, and non-Hodgkin's lymphoma cells.
4. Use of miR-15a and/or miR-16-1 according to claim 1, wherein the cancer cells are lung cancer cells.
5. Use of miR-15a and/or miR-16-1 to increase the efficacy of an anti-cancer treatment of a BCL2-associated cancer, wherein the anti-cancer treatment comprises:
 - a) treatment with one or more chemotherapeutic agent; or
 - b) treatment with one or more radiation treatment;
 wherein the BCL2-associated cancer is selected from the group consisting of acute myeloid leukemia, multiple myeloma, melanoma, lymphomas, follicular lymphoma, large cell lymphoma, non-Hodgkin's lymphoma, carcinoma, brain carcinoma, breast carcinoma, prostate carcinoma, non-small cell lung carcinoma, renal carcinoma, hepatocellular carcinoma and gastric carcinoma, hematologic malignancies, solid tumors, colorectal cancer and Epstein-Barr virus-associated lymphoproliferative disease.
6. Use of miR-15a and/or miR-16-1 according to claim 5, wherein the one or more chemotherapeutic agent is selected from the group consisting of DNA-alkylating agents, anti-tumor antibiotic agents, anti-metabolic agents, tubulin stabilizing agents, tubulin destabilizing agents, hormone antagonist agents, topoisomerase inhibitors, protein kinase inhibitors, HMG-CoA inhibitors, cyclin-dependent kinase (CDK) inhibitors, cyclin inhibitors, caspase inhibitors, metalloproteinase inhibitors, antisense nucleic acids, triple-

helix DNAs, nucleic acids aptamers, and molecularly-modified viral, bacterial or exotoxic agents.

7. Use of miR-15a and/or miR-16-1 according to claim 5, wherein the one or more chemotherapeutic agent is selected from the group consisting of cytidine arabinoside, methotrexate, vincristine, etoposide, doxorubicin, cisplatin, dexamethasone, arglabin, cyclophosphamide, sarcolysin, methylnitrosourea, fluorouracil, 5-fluorouracil, vinblastine, camptothecin, actinomycin-D, mitomycin C, hydrogen peroxide, oxaliplatin, irinotecan, topotecan, leucovorin, carmustine, streptozocin, CPT-11, taxol™ and derivatives thereof, tamoxifen, dacarbazine, rituximab, daunorubicin, 1-β-D-arabinofuranosylcytosine, imatinib, fludarabine, docetaxel and FOLFOX4.
8. Use according to any one of claims 5 to 7, wherein the radiation treatment includes one or more of high energy radiation provided by X-rays, gamma ray and neutrons; external beam radiation; brachytherapy; intensity-modulated radiotherapy (IMRT); implant radiation; systemic radiation; and stereotactic radiotherapy.
9. Use of miR-15a and/or miR-16-1 according to any one of claims 5 to 8, wherein the miR-15a and/or miR-16-1 are formulated for co-administration with the one or more chemotherapeutic agent.
10. Use of miR-15a and/or miR-16-1 to increase the sensitivity of a BCL2-expressing cancer cells to the cytotoxic effects of an anti-cancer agent selected from one or more of DNA-alkylating agents, anti-tumor antibiotic agents, anti-metabolic agents, tubulin stabilizing agents, tubulin destabilizing agents, hormone antagonist agents, topoisomerase inhibitors, protein kinase inhibitors, HMG-CoA inhibitors, cyclin-dependent kinase (CDK) inhibitors, cyclin inhibitors, caspase inhibitors, metalloproteinase inhibitors, antisense nucleic acids, triple-helix DNAs, nucleic acids aptamers, and molecularly-modified viral, bacterial or exotoxic agents.
11. Use of miR-15a and/or miR-16-1 according to claim 10, wherein the one or more of DNA-alkylating agents, anti-tumor antibiotic agents, anti-metabolic agents, tubulin stabilizing agents, tubulin destabilizing agents, hormone antagonist agents, topoisomerase inhibitors,

protein kinase inhibitors, HMG-CoA inhibitors, cyclin-dependent kinase (CDK) inhibitors, cyclin inhibitors, caspase inhibitors, metalloproteinase inhibitors, antisense nucleic acids, triple-helix DNAs, nucleic acids aptamers, and molecularly-modified viral, bacterial or exotoxic agents are selected from the group consisting of cytidine arabinoside, methotrexate, vincristine, etoposide, doxorubicin, cisplatin, dexamethasone, arglabin, cyclophosphamide, sarcolysin, methylnitrosourea, fluorouracil, 5-fluorouracil, vinblastine, camptothecin, actinomycin-D, mitomycin C, hydrogen peroxide, oxaliplatin, irinotecan, topotecan, leucovorin, carmustine, streptozocin, CPT-11, taxol™ and derivatives thereof, tamoxifen, dacarbazine, rituximab, daunorubicin, 1-β-D-arabinofuranosylcytosine, imatinib, fludarabine, docetaxel and FOLFOX4.

12. Use of miR-15a and/or miR-16-1 according to claim 10 or 11, wherein the cancer cells are selected from the group consisting of chronic lymphocytic leukemia (CLL) cells, lung cancer cells and lymphoma cells.
13. Use of miR-15a and/or miR-16-1 according to claim 10 or 11, wherein the cancer cells are lymphoma cells selected from the group consisting of follicular lymphoma cells, small cell lymphoma cells, large cell lymphoma cells and non-Hodgkin's lymphoma cells.
14. Use of miR-15a and/or miR-16-1 according to claim 10 or 11, wherein the cancer cells are lung cancer cells.
15. Use of miR-15a and/or miR-16-1 according to claim 14, wherein the lung cancer cells are non-small cell lung carcinoma cells.
16. Use of miR-15a or miR-16-1 according to claim 10 or 11, wherein the cancer cells are from a cancer selected from the group consisting of acute myeloid leukemia, multiple myeloma, melanoma, a hematologic malignancy, a solid tumor, colorectal cancer, brain carcinoma, breast carcinoma, prostate carcinoma, Epstein-Barr virus-associated lymphoproliferative disease, renal carcinoma, hepatocellular carcinoma and gastric carcinoma.
17. Use of miR-15a and/or miR-16-1 to induce apoptosis in a BCL2-expressing cancer cell.

18. Use of miR-15a and/or miR-16-1 according to claim 17, wherein the cancer cell is selected from the group consisting of a chronic lymphocytic leukemia (CLL) cell, a lung cancer cell and a lymphoma cell.
19. Use of miR-15a and/or miR-16-1 according to claim 17, wherein the cancer cell is a lymphoma cell selected from the group consisting of a follicular lymphoma cell, a small cell lymphoma cell, a large cell lymphoma cell and a non-Hodgkin's lymphoma cell.
20. Use of miR-15a and/or miR-16-1 according to claim 17, wherein the cancer cell is a lung cancer cell.
21. Use of miR-15a and/or miR-16-1 according to claim 20, wherein the lung cancer cell is a non-small cell lung carcinoma cell.
22. Use of miR-15a and/or miR-16-1 according to claim 17, wherein the cancer cell is from a cancer selected from the group consisting of acute myeloid leukemia, multiple myeloma, melanoma, a hematologic malignancy, a solid tumor, colorectal cancer, brain carcinoma, breast carcinoma, prostate carcinoma, Epstein-Barr virus-associated lymphoproliferative disease, renal carcinoma, hepatocellular carcinoma and gastric carcinoma.
23. Use according to any one of claims 1 to 22, which further comprises the use of at least one additional miR gene product selected from the group consisting of miR-182, miR-181, miR-30, miR-15b, miR-16-2, miR-195, miR-34, miR-153, miR-21, miR-217, miR-205, miR-204, miR-211, miR-143, miR-96, miR-103, miR-107, miR-129, miR-9, miR-137, miR-217 and miR-186.
24. Use according to any one of claims 1 to 22, which further comprises the use of at least one additional miR gene product selected from the group consisting of miR-182, miR-181, miR-30, miR-15b, miR-16-2 and miR-195.
25. A pharmaceutical composition for treating a BCL2-associated cancer, comprising miR-15a and/or miR-16-1, wherein the BCL2-associated cancer is selected from the group consisting of acute myeloid leukemia, multiple myeloma, melanoma, lymphomas, follicular lymphoma,

large cell lymphoma, non-Hodgkin's lymphoma, carcinoma, brain carcinoma, breast carcinoma, prostate carcinoma, non-small cell lung carcinoma, renal carcinoma, hepatocellular carcinoma and gastric carcinoma, hematologic malignancies, solid tumors, colorectal cancer and Epstein-Barr virus-associated lymphoproliferative disease.

26. The pharmaceutical composition according to claim 25, further comprising at least one chemotherapeutic agent.
27. The pharmaceutical composition according to claim 26, wherein the amount of the chemotherapeutic agent in the composition provides for an administration thereof of from about 0.0001 to 1000 mg/kg of agent per dose.
28. The pharmaceutical composition according to claim 27, wherein the range is from about 0.5 to 70 mg/kg.
29. The pharmaceutical composition according to claim 27 or 28, wherein the range is from about 1 to 50 mg/kg.
30. The pharmaceutical composition according to any one of claims 25 to 29, which further comprises at least one additional miR gene product selected from the group consisting of miR-182, miR-181, miR-30, miR-15b, miR-16-2, miR-195, miR-34, miR-153, miR-21, miR-217, miR-205, miR-204, miR-211, miR-143, miR-96, miR-103, miR-107, miR-129, miR-9, miR-137, miR-217 and miR-186.
31. The pharmaceutical composition according to any one of claims 25 to 29, which further comprises at least one additional miR gene product selected from the group consisting of miR-182, miR-181, miR-30, miR-15b, miR-16-2 and miR-195.

Application number / numéro de demande: 2,621,441

Figures: 3A, 3B, 4A, 4B, 5A, 5B, 6A, 6B

Pages: _____

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GAGUAAAGUA UA GA U
 5' CCUUG GCAGCACA AUGGUUUGUG UUU \
 GGAAC CGUCGUGU UACCGGACGU AAA G
 AUAAAAACUC UA GG A

FIG. 1A

 AG C A CGUUA UCUA
 5' GUCAGC UGC UUAGCAGCAC GU AAUAUUGG AGAU \
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 GA A U A - - - - - UUA

FIG. 1B

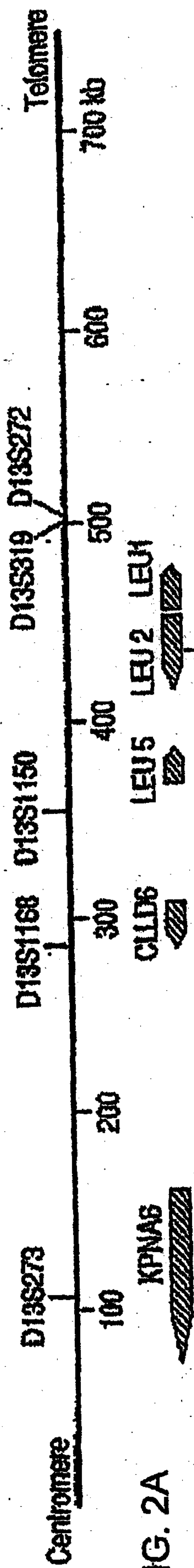


FIG. 2A

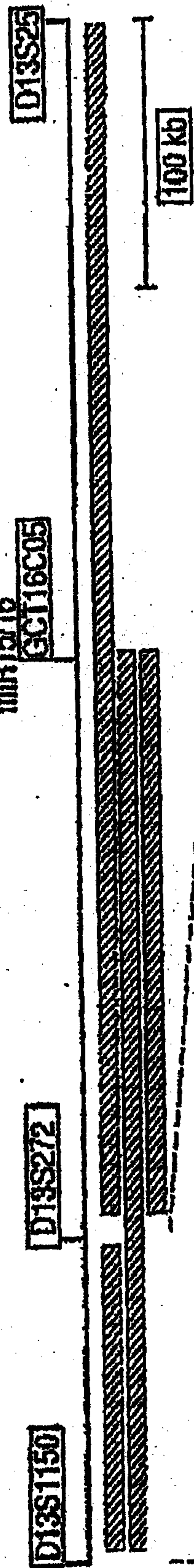


FIG. 2B

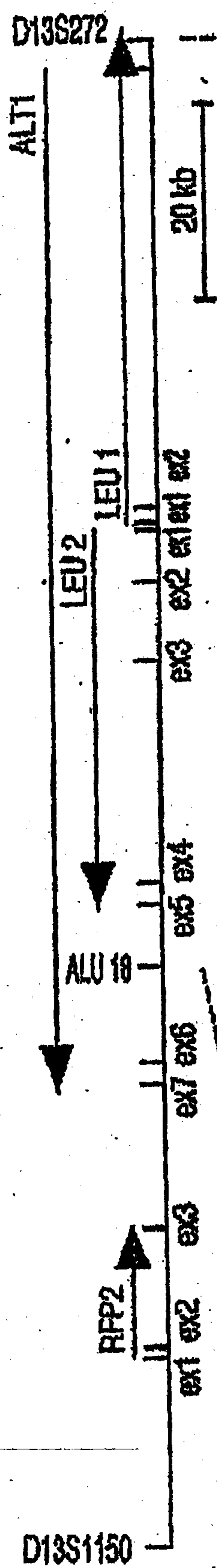


FIG. 2C

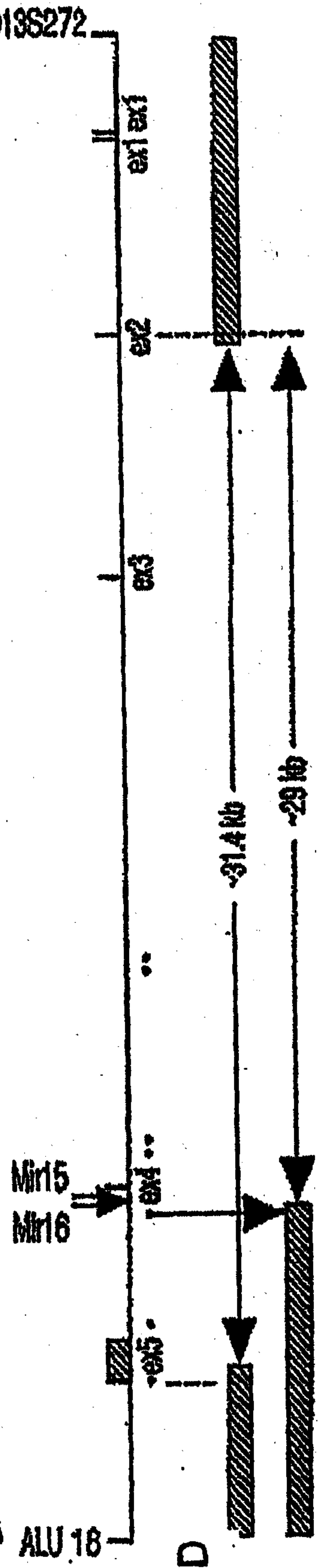


FIG. 2D

