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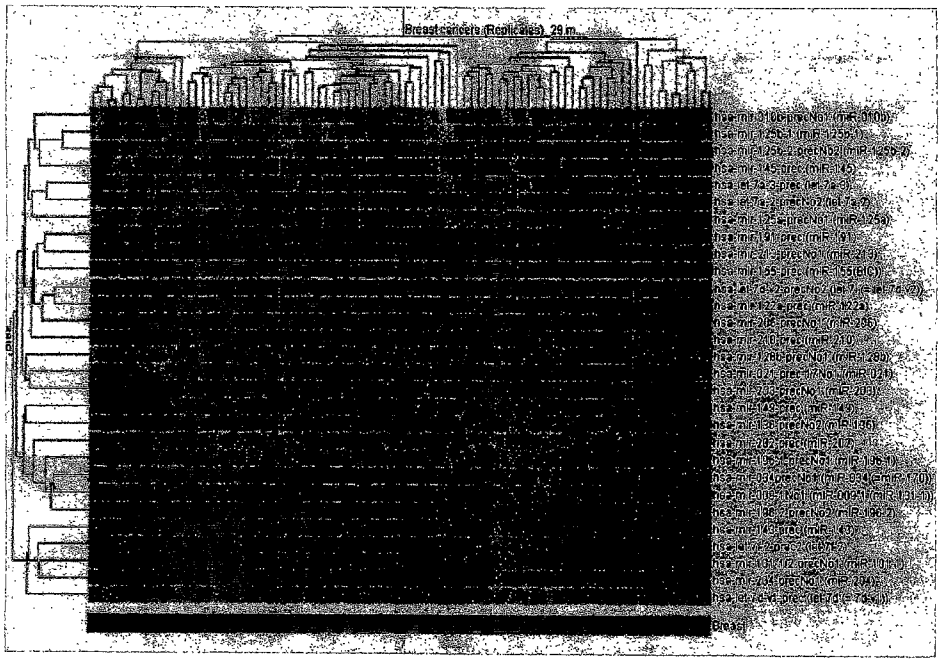
(54) **Title:** MICRO-RNA-BASED METHODS AND COMPOSITIONS FOR THE DIAGNOSIS, PROGNOSIS AND TREATMENT OF BREAST CANCER



(57) **Abstract:** The present invention provides novel methods and compositions for the diagnosis, prognosis and treatment of breast cancer. The invention also provides methods of identifying anti-breast cancer agents.

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TITLE

MicroRNA-BASED METHODS AND COMPOSITIONS FOR THE DIAGNOSIS, PROGNOSIS AND TREATMENT OF BREAST CANCER

Inventors: George A. Calin and Carlo M. Croce

GOVERNMENT SUPPORT

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BACKGROUND OF THE INVENTION

Breast cancer is a significant health problem for women in the United States and throughout the world. Although advances have been made in the detection and treatment of the disease, breast cancer remains the second leading cause of cancer-related deaths in women, affecting more than 180,000 women in the United States each year. For women in North America, the life-time odds of getting breast cancer are now one in eight.

No universally successful method for the treatment or prevention of breast cancer is currently available. Management of breast cancer currently relies on a combination of early diagnosis (e.g., through routine breast screening procedures) and aggressive treatment, which may include one or more of a variety of treatments, such as surgery, radiotherapy, chemotherapy and hormone therapy. The course of treatment for a particular breast cancer is often selected based on a variety of prognostic parameters including an analysis of specific tumor markers. *See, e.g.*, Porter-Jordan and Lippman, *Breast Cancer 8*:73-100 (1994).

Although the discovery of BRCA1 and BRCA2 were important steps in identifying key genetic factors involved in breast cancer, it has become clear that mutations in BRCA1 and BRCA2 account for only a fraction of inherited susceptibility to breast cancer (Nathanson, K.L. *et al.*, *Human Mol. Gen. 10(7)*:715-720 (2001); Anglican Breast Cancer Study Group. *Br. J. Cancer 83(10)*:1301-08 (2000); and Syrjakoski K., *et al.*, *J. Natl. Cancer Inst. 92*:1529-31 (2000)). In spite of considerable research into therapies for breast cancer,

breast cancer remains difficult to diagnose and treat effectively, and the high mortality observed in breast cancer patients indicates that improvements are needed in the diagnosis, treatment and prevention of the disease.

MicroRNAs are a class of small, non-coding RNAs that control gene expression by hybridizing to and triggering either translational repression or, less frequently, degradation of a messenger RNA (mRNA) target. The discovery and study of miRNAs has revealed miRNA-mediated gene regulatory mechanisms that play important roles in organismal development and various cellular processes, such as cell differentiation, cell growth and cell death (Cheng, A.M., *et al.*, *Nucleic Acids Res. 33*:1290-1297 (2005)). Recent studies suggest that aberrant expression of particular miRNAs may be involved in human diseases, such as neurological disorders (Ishizuka, A., *et al.*, *Genes Dev. 16*:2497-2508 (2002)) and cancer. In particular, misexpression of miR-16-1 and/or miR-15a has been found in human chronic lymphocytic leukemias (Calin, G.A., *et al.*, *Proc. Natl. Acad. Sci. U.S.A. 99*:15524-15529 (2002)).

The development and use of microarrays containing all known human microRNAs has permitted a simultaneous analysis of the expression of every miRNA in a sample (Liu, C.G., *et al.*, *Proc Natl. Acad. Sci U.S.A. 101*:9740-9744 (2004)). These microRNA microarrays have not only been used to confirm that miR-16-1 is deregulated in human CLL cells, but also to generate miRNA expression signatures that are associated with well-defined clinico-pathological features of human CLL (Calin, G.A., *et al.*, *Proc. Natl. Acad. Sci. U.S.A. 101*:1175-11760 (2004)).

The use of microRNA microarrays to identify a group of microRNAs, which are differentially-expressed between normal cells and breast cancer cells (i.e., an expression signature or expression profile), may help pinpoint specific miRNAs that are involved in breast cancer. Furthermore, the identification of putative targets of these miRNAs may help to unravel their pathogenic role. The present invention provides novel methods and compositions for the diagnosis, prognosis and treatment of breast cancer.

SUMMARY OF THE INVENTION

The present invention is based, in part, on the identification of a breast cancer-specific signature of miRNAs that are differentially-expressed in breast cancer cells, relative to normal control cells.

Accordingly, the invention encompasses methods of diagnosing whether a subject has, or is at risk for developing, breast cancer, comprising measuring the level of at least one miR gene product in a test sample from the subject and comparing the level of the miR gene product in the test sample to the level of a corresponding miR gene product in a control sample. An alteration (e.g., an increase, a decrease) in the level of the miR gene product in the test sample, relative to the level of a corresponding miR gene product in a control sample, is indicative of the subject either having, or being at risk for developing, breast cancer. In certain embodiments, the at least one miR gene product is selected from the group consisting of miR-125b-1, miR125b-2, miR-145, miR-21, miR-155, miR-10b and combinations thereof.

The level of the at least one miR gene product can be measured using a variety of techniques that are well known to those of skill in the art. In one embodiment, the level of the at least one miR gene product is measured using Northern blot analysis. In another embodiment, the level of the at least one miR gene product is measured by reverse transcribing RNA from a test sample obtained from the subject to provide a set of target oligodeoxynucleotides, hybridizing the target oligodeoxynucleotides to a microarray that comprises miRNA-specific probe oligonucleotides to provide a hybridization profile for the test sample, and comparing the test sample hybridization profile to a hybridization profile generated from a control sample. An alteration in the signal of at least one miRNA in the test sample relative to the control sample is indicative of the subject either having, or being at risk for developing, breast cancer. In a particular embodiment, the microarray comprises miRNA-specific probe oligonucleotides for a substantial portion of the human miRNome. In a further embodiment, the microarray comprises miRNA-specific probe oligonucleotides for one or more miRNAs selected from the group consisting of miR-145, miR-21, miR-155, miR-10b, miR-009-1 (miR131-1), miR-34 (miR-170), miR-102 (miR-29b), miR-123 (miR-126), miR-140-as, miR-125a, miR-125b-1, miR-125b-2, miR-194, miR-204, miR-213, let-7a-

2, let-7a-3, let-7d (let-7d-v1), let-7f-2, let-7i (let-7d-v2), miR-101-1, miR-122a, miR-128b, miR-136, miR-143, miR-149, miR-191, miR-196-1, miR-196-2, miR-202, miR-203, miR-205, miR-206, miR-210 and combinations thereof.

The invention also provides methods of diagnosing a breast cancer associated with one or more prognostic markers, comprising measuring the level of at least one miR gene product in a breast cancer test sample from a subject and comparing the level of the at least one miR gene product in the breast cancer test sample to the level of a corresponding miR gene product in a control sample. The breast cancer can be associated with one or more adverse prognostic markers associated with breast cancer, such as, but not limited to, estrogen receptor expression, progesterone receptor expression, positive lymph node metastasis, high proliferative index, detectable p53 expression, advanced tumor stage, and high vascular invasion. In one embodiment, the level of the at least one miR gene product is measured by reverse transcribing RNA from a test sample obtained from the subject to provide a set of target oligodeoxynucleotides, hybridizing the target oligodeoxynucleotides to a microarray that comprises miRNA-specific probe oligonucleotides to provide a hybridization profile for the test sample, and comparing the test sample hybridization profile to a hybridization profile generated from a control sample. An alteration in the signal of at least one miRNA in the test sample relative to the control sample is indicative of the subject either having, or being at risk for developing, a breast cancer associated with the one or more prognostic markers. In a particular embodiment, the microarray comprises at least one miRNA-specific probe oligonucleotide for a miRNA selected from the group consisting of miR-26a, miR-26b, miR-102 (miR-29b), miR-30a-5p, miR-30b, miR-30c, miR-30d, miR-185, miR-191, miR-206, miR-212, let-7c, miR-9-2, miR-15-a, miR-21, miR-30a-s, miR-133a-1, miR-137, miR-153-2, miR-154, miR-181a, miR-203, miR-213, let-7f-1, let-7a-3, let-7a-2, miR-9-3, miR-10b, miR-27a, miR-29a, miR-123, miR-205, let-7d, miR-145, miR-16a, miR-128b and combinations thereof.

The invention also encompasses methods of treating breast cancer in a subject, wherein at least one miR gene product is de-regulated (e.g., down-regulated, up-regulated) in the cancer cells of the subject. When the at least one isolated miR gene product is down-regulated in the breast cancer cells, the method comprises administering an effective amount

of the at least one isolated miR gene product, such that proliferation of cancer cells in the subject is inhibited. In one embodiment, the method comprises administering an effective amount of the at least one isolated miR gene product, provided that the *miR* gene is not *miR-15a* or *miR-16-1*, such that proliferation of cancer cells in the subject is inhibited. When the at least one isolated miR gene product is up-regulated in the cancer cells, the method comprises administering to the subject an effective amount of at least one compound for inhibiting expression of the at least one *miR* gene, such that proliferation of breast cancer cells is inhibited.

In related embodiments, the invention provides methods of treating breast cancer in a subject, comprising determining the amount of at least one miR gene product in breast cancer cells from the subject, relative to control cells. If expression of the miR gene product is deregulated in breast cancer cells, the methods further comprise altering the amount of the at least one miR gene product expressed in the breast cancer cells. If the amount of the miR gene product expressed in the cancer cells is less than the amount of the miR gene product expressed in control cells, the method comprises administering an effective amount of at least one isolated miR gene product. In one embodiment, the miR gene product is not *miR-15a* or *miR-16-1*. If the amount of the miR gene product expressed in the cancer cells is greater than the amount of the miR gene product expressed in control cells, the method comprises administering to the subject an effective amount of at least one compound for inhibiting expression of the at least one miR gene. In one embodiment, the miR gene product is not *miR-15a* or *miR-16-1*.

The invention further provides pharmaceutical compositions for treating breast cancer. In one embodiment, the pharmaceutical compositions comprise at least one isolated miR gene product and a pharmaceutically-acceptable carrier. In a particular embodiment, the at least one miR gene product corresponds to a miR gene product that has a decreased level of expression in breast cancer cells relative to suitable control cells. In certain embodiments the isolated miR gene product is selected from the group consisting of miR-145, miR-10b, miR-123 (miR-126), miR-140-as, miR-125a, miR-125b-1, miR-125b-2, miR-194, miR-204, let-7a-2, let-7a-3, let-7d (let-7d-v1), let-7f-2, miR-101-1, miR-143 and combinations thereof.

In another embodiment, the pharmaceutical compositions of the invention comprise at least one miR expression inhibition compound. In a particular embodiment, the at least one miR expression inhibition compound is specific for a miR gene whose expression is greater in breast cancer cells than control cells. In certain embodiments, the miR expression inhibition compound is specific for one or more miR gene products selected from the group consisting of miR-21, miR-155, miR-009-1 (miR131-1), miR-34 (miR-170), miR-102 (miR-29b), miR-213, let-7i (let-7d-v2), miR-122a, miR-128b, miR-136, miR-149, miR-191, miR-196-1, miR-196-2, miR-202, miR-203, miR-206, miR-210, miR-213 and combinations thereof.

The invention also encompasses methods of identifying an anti-breast cancer agent, comprising providing a test agent to a cell and measuring the level of at least one miR gene product in the cell. In one embodiment, the method comprises providing a test agent to a cell and measuring the level of at least one miR gene product associated with decreased expression levels in breast cancer cells. An increase in the level of the miR gene product in the cell, relative to a suitable control cell, is indicative of the test agent being an anti-breast cancer agent. In a particular embodiment, the at least one miR gene product associated with decreased expression levels in breast cancer cells is selected from the group consisting of miR-145, miR-10b, miR-123 (miR-126), miR-140-as, miR-125a, miR-125b-1, miR-125b-2, miR-194, miR-204, let-7a-2, let-7a-3, let-7d (let-7d-v1), let-7f-2, miR-101-1, miR-143 and combinations thereof.

In other embodiments the method comprises providing a test agent to a cell and measuring the level of at least one miR gene product associated with increased expression levels in breast cancer cells. A decrease in the level of the miR gene product in the cell, relative to a suitable control cell, is indicative of the test agent being an anti-breast cancer agent. In a particular embodiment, at least one miR gene product associated with increased expression levels in breast cancer cells is selected from the group consisting of miR-21, miR-155, miR-009-1 (miR131-1), miR-34 (miR-170), miR-102 (miR-29b), miR-213, let-7i (let-7d-v2), miR-122a, miR-128b, miR-136, miR-149, miR-191, miR-196-1, miR-196-2, miR-202, miR-203, miR-206, miR-210, miR-213 and combinations thereof.

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 drawing(s) will be provided by the Office upon request and payment of the necessary fee.

FIG. 1 depicts a tree generated by cluster analysis showing a separation of breast cancer from normal tissues on the basis of differential microRNA expression ($P<0.05$). The bar at the bottom of the figure indicates the group of cancer (red) or normal breast tissues (yellow).

FIG. 2 is a graph depicting the probability (0.0 to 1.0) of each sample being a cancerous or normal tissue based on PAM analysis. All breast cancer and normal tissues were correctly predicted by the miR signature shown in Table 2.

FIG. 3A is a Northern blot depicting the expression level of miR-125b, using a miR-125b complementary probe, in a normal sample, as well as several tumor samples from breast cancer patients (P). The U6 probe was used for normalization of expression levels for each sample.

FIG. 3B is a Northern blot depicting the expression level of miR-145, using a miR-145 complementary probe, in a normal sample, as well as several tumor samples from breast cancer patients (P). The U6 probe was used for normalization of expression levels for each sample.

FIG. 3C is a Northern blot depicting the expression level of miR-21, using a miR-21 complementary probe, in a normal sample, as well as several tumor samples from breast cancer patients (labeled as numbered patients). The U6 probe was used for normalization of expression levels for each sample.

FIG. 3D is a Northern blot depicting the expression levels of microRNAs miR-125b, miR-145 and miR-21 in various breast cancer cell lines. The expression level of each microRNA was also determined in a sample from normal tissues. The U6 probe was used for normalization of expression levels for each sample.

FIG. 4A is a table listing miRNAs that are differentially-expressed in breast cancer samples associated with the presence (ER+) or absence (ER-) of estrogen receptor.

FIG. 4B is a table listing miRNAs that are differentially-expressed in breast cancer samples associated with the presence (PR+) or absence (PR-) of progesterone receptor.

FIG. 4C is a table listing miRNAs that are differentially-expressed in breast cancer samples associated with stage 1 (pT1) or stage 2 or 3 (pT2-3) tumors.

FIG. 4D is a table listing miRNAs that are differentially-expressed in breast cancer samples associated with the presence (pN0) or absence (pN10+) of lymph node metastasis.

FIG. 4E is a table listing miRNAs that are differentially-expressed in breast cancer samples associated with the presence or absence of vascular invasion.

FIG. 4F is a table listing miRNAs that are differentially-expressed in breast cancer samples associated with a high (MIB-1>30) or low (MIB-1<20) proliferative index (PI).

FIG. 4G is a table listing miRNAs that are differentially-expressed in breast cancer samples associated with positive (p53+) or negative (p53-) immunostaining of p53.

DETAILED DESCRIPTION OF THE INVENTION

The present invention is based, in part, on the identification of particular miRNAs whose expression is altered in breast cancer cells relative to normal control cells, and microRNAs whose expression is altered in breast cancer cells associated with particular prognostic features, relative to breast cancer cells lacking such features.

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 precursor can be processed by digestion with an RNAse (for example, Dicer, Argonaut, or 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.

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 RNAase III). It is understood that the active 19-25 nucleotide RNA molecule can also be produced directly by biological or chemical synthesis, without having been processed from the miR precursor.

The sequences of 187 miR gene products are provided in Table 1. All nucleic acid sequences herein are given in the 5' to 3' direction. In addition, genes are represented by italics, and gene products are represented by normal type; *e.g.*, *mir-17* is the gene and miR-17 is the gene product.

The present invention encompasses methods of diagnosing whether a subject has, or is at risk for developing, breast cancer, comprising measuring the level of at least one miR gene product in a test sample from the subject and comparing the level of the miR gene product in the test sample to the level of a corresponding miR gene product in a control sample. As used herein, a "subject" can be any mammal that has, or is suspected of having, breast cancer. In a particular embodiment, the subject is a human who has, or is suspected of having, breast cancer.

The breast cancer can be any form of breast cancer and may be associated with one or more prognostic markers or features, including, but not limited to, estrogen receptor expression, progesterone receptor expression, lymph node metastasis, high proliferative index, detectable p53 expression, advanced tumor stage, and high vascular invasion. The prognostic marker can be associated with an adverse or negative prognosis, or it may be associated with a good or positive prognosis.

Table 1- Human miR Gene Product Sequences

Name	Precursor Sequence (5' to 3')*	SEQ ID NO.
hsa-let-7a-1-prec	CACTGTGGGATGAGGTAGTAGGTTGTATAGTTTTAGG GTCACACCCACCACTGGGAGATAACTATACAATCTAC TGTCTTTCCTAACGTG	1
hsa-let-7a-2-prec	AGGTTGAGGTAGTAGGTTGTATAGTTTAGAATTACAT CAAGGGAGATAACTGTACAGCCTCCTAGCTTTCCT	2
hsa-let-7a-3-prec	GGGTGAGGTAGTAGGTTGTATAGTTTGGGGCTCTGCC CTGCTATGGGATAACTATACAATCTACTGTCTTTCCT	3
hsa-let-7a-4-prec	GTGACTGCATGCTCCCAGGTTGAGGTAGTAGGTTGTA TAGTTTAGAATTACACAAGGGAGATAACTGTACAGC CTCCTAGCTTTCCTTGGGTCTTGCACTAAACAAC	4

Name	Precursor Sequence (5' to 3')*	SEQ ID NO.
hsa-let-7b-prec	GGCGGGGTGAGGTAGTAGGTTGTGTGGTTTCAGGGC AGTGATGTTGCCCCTCGGAAGATAACTATACAACCTA CTGCCTTCCCTG	5
hsa-let-7c-prec	GCATCCGGGTTGAGGTAGTAGGTTGTATGGTTTAGAG TTACACCCTGGGAGTTAACTGTACAACCTTCTAGCTT TCCTTGGAGC	6
hsa-let-7d-prec	CCTAGGAAGAGGTAGTAGGTTGCATAGTTTTAGGGC AGGGATTTTGCCCACAAGGAGGTAACTATACGACCT GCTGCCTTTCTTAGG	7
hsa-let-7d-v1-prec	CTAGGAAGAGGTAGTAGTTTGCATAGTTTTAGGGCAA AGATTTTGCCCACAAGTAGTTAGCTATACGACCTGCA GCCTTTTGTAG	8
hsa-let-7d-v2-prec	CTGGCTGAGGTAGTAGTTTGTGCTGTTGGTCGGGTTG TGACATTGCCCGCTGTGGAGATAACTGCGCAAGCTAC TGCCTTGCTAG	9
hsa-let-7e-prec	CCCGGGCTGAGGTAGGAGGTTGTATAGTTGAGGAGG ACACCCAAGGAGATCACTATACGGCCTCCTAGCTTTC CCCAGG	10
hsa-let-7f-1-prec	TCAGAGTGAGGTAGTAGATTGTATAGTTGTGGGGTAG TGATTTTACCCTGTTCAGGAGATAACTATACAATCTA TTGCCTTCCCTGA	11
hsa-let-7f-2-prec	CTGTGGGATGAGGTAGTAGATTGTATAGTTGTGGGGT AGTGATTTTACCCTGTTCAGGAGATAACTATACAATC TATTGCCTTCCCTGA	12
hsa-let-7f-2-prec	CTGTGGGATGAGGTAGTAGATTGTATAGTTTTAGGGT CATACCCCATCTTGGAGATAACTATACAGTCTACTGT CTTTCCCACGG	13
hsa-let-7g-prec	TTGCCTGATTCCAGGCTGAGGTAGTAGTTTGTACAGT TTGAGGGTCTATGATACCACCCGGTACAGGAGATAA CTGTACAGGCCACTGCCTTGCCAGGAACAGCGCGC	14
hsa-let-7i-prec	CTGGCTGAGGTAGTAGTTTGTGCTGTTGGTCGGGTTG TGACATTGCCCGCTGTGGAGATAACTGCGCAAGCTAC TGCCTTGCTAG	15
hsa-mir-001b-1-prec	ACCTACTCAGAGTACATACTTCTTTATGTACCCATAT GAACATACAATGCTATGGAATGTAAAGAAGTATGTA TTTTTGGTAGGC	16
hsa-mir-001b-1-prec	CAGCTAACAACTTAGTAATACCTACTCAGAGTACATA CTTCTTTATGTACCCATATGAACATACAATGCTATGG AATGTAAAGAAGTATGTATTTTTGGTAGGCAATA	17
hsa-mir-001b-2-prec	GCCTGCTTGGGAAACATACTTCTTTATATGCCCATAT GGACCTGCTAAGCTATGGAATGTAAAGAAGTATGTA TCTCAGGCCGGG	18

Name	Precursor Sequence (5' to 3')*	SEQ ID NO.
hsa-mir-001b-prec	TGGGAAACATACTTCTTTATATGCCCATATGGACCTG CTAAGCTATGGAATGTAAAGAAGTATGTATCTCA	19
hsa-mir-001d-prec	ACCTACTCAGAGTACATACTTCTTTATGTACCCATAT GAACATACAATGCTATGGAATGTAAAGAAGTATGTA TTTTTGGTAGGC	20
hsa-mir-007-1	TGGATGTTGGCCTAGTTCTGTGTGGAAGACTAGTGAT TTTGTTGTTTTTAGATAACTAAATCGACAACAAATCA CAGTCTGCCATATGGCACAGGCCATGCCTCTACA	21
hsa-mir-007-1-prec	TTGGATGTTGGCCTAGTTCTGTGTGGAAGACTAGTGA TTTTGTTGTTTTTAGATAACTAAATCGACAACAAATC ACAGTCTGCCATATGGCACAGGCCATGCCTCTACAG	22
hsa-mir-007-2	CTGGATACAGAGTGGACCGGCTGGCCCCATCTGGAA GACTAGTGATTTTGTTGTTGTCTTACTGCGCTCAACA ACAAATCCCAGTCTACCTAATGGTGCCAGCCATCGCA	23
hsa-mir-007-2-prec	CTGGATACAGAGTGGACCGGCTGGCCCCATCTGGAA GACTAGTGATTTTGTTGTTGTCTTACTGCGCTCAACA ACAAATCCCAGTCTACCTAATGGTGCCAGCCATCGCA	24
hsa-mir-007-3	AGATTAGAGTGGCTGTGGTCTAGTGCTGTGTGGAAGA CTAGTGATTTTGTTGTTCTGATGTACTACGACAACAA GTCACAGCCGGCCTCATAGCGCAGACTCCCTTCGAC	25
hsa-mir-007-3-prec	AGATTAGAGTGGCTGTGGTCTAGTGCTGTGTGGAAGA CTAGTGATTTTGTTGTTCTGATGTACTACGACAACAA GTCACAGCCGGCCTCATAGCGCAGACTCCCTTCGAC	26
hsa-mir-009-1	CGGGGTTGGTTGTTATCTTTGGTTATCTAGCTGTATGA GTGGTGTGGAGTCTTCATAAAGCTAGATAACCGAAA GTAAAAATAACCCCA	27
hsa-mir-009-2	GGAAGCGAGTTGTTATCTTTGGTTATCTAGCTGTATG AGTGTATTGGTCTTCATAAAGCTAGATAACCGAAAGT AAAAACTCCTTCA	28
hsa-mir-009-3	GGAGGCCCGTTTCTCTCTTTGGTTATCTAGCTGTATGA GTGCCACAGAGCCGTCATAAAGCTAGATAACCGAAA GTAGAAATGATTCTCA	29
hsa-mir-010a-prec	GATCTGTCTGTCTTCTGTATATACCCTGTAGATCCGA ATTTGTGTAAGGAATTTTGTGGTCACAAATTCGTATC TAGGGGAATATGTAGTTGACATAAACACTCCGCTCT	30
hsa-mir-010b-prec	CCAGAGGTTGTAACGTTGTCTATATATACCCTGTAGA ACCGAATTTGTGTGGTATCCGTATAGTCACAGATTCG ATTCTAGGGGAATATATGGTCGATGCAAAAACTTCA	31
hsa-mir-015a-2-prec	GCGCGAATGTGTGTTTAAAAAAAATAAAACCTTGGA GTAAAGTAGCAGCACATAATGGTTTGTGGATTTTGAA AAGGTGCAGGCCATATTGTGCTGCCTCAAAAATAC	32

Name	Precursor Sequence (5' to 3')*	SEQ ID NO.
hsa-mir-015a-prec	CCTTGGAGTAAAGTAGCAGCACATAATGGTTTGTGGATTTTGAAAAGGTGCAGGCCATATTGTGCTGCCTCAAAAATACAAGG	33
hsa-mir-015b-prec	CTGTAGCAGCACATCATGGTTTACATGCTACAGTCAAGATGCGAATCATTATTTGCTGCTCTAG	34
hsa-mir-015b-prec	TTGAGGCCTTAAAGTACTGTAGCAGCACATCATGGTTTACATGCTACAGTCAAGATGCGAATCATTATTTGCTGCTCTAGAAATTTAAGGAAATTCAT	35
hsa-mir-016a-chr13	GTCAGCAGTGCCTTAGCAGCACGTAAATATTGGCGTTAAGATTCTAAAATTATCTCCAGTATTAACTGTGCTGCTGAAGTAAGGTTGAC	36
hsa-mir-016b-chr3	GTTCCACTCTAGCAGCACGTAAATATTGGCGTAGTGAAATATATATTAAACACCAATATTACTGTGCTGCTTTAGTGTGAC	37
hsa-mir-016-prec-13	GCAGTGCCTTAGCAGCACGTAAATATTGGCGTTAAGATTCTAAAATTATCTCCAGTATTAACTGTGCTGCTGAAGTAAGGT	38
hsa-mir-017-prec	GTCAGAATAATGTCAAAGTGCTTACAGTGCAGGTAGTGATATGTGCATCTACTGCAGTGAAGGCACTTGTAGCATTATGGTGAC	39
hsa-mir-018-prec	TGTTCTAAGGTGCATCTAGTGCAGATAGTGAAGTAGATTAGCATCTACTGCCCTAAGTGCTCCTTCTGGCA	40
hsa-mir-018-prec-13	TTTTTGTTCTAAGGTGCATCTAGTGCAGATAGTGAAGTAGATTAGCATCTACTGCCCTAAGTGCTCCTTCTGGCATAAGAA	41
hsa-mir-019a-prec	GCAGTCCTCTGTTAGTTTTGCATAGTTGCACTACAAGAAGAATGTAGTTGTGCAAATCTATGCAAAACTGATGGTGGCCTGC	42
hsa-mir-019a-prec-13	CAGTCCTCTGTTAGTTTTGCATAGTTGCACTACAAGAAGAATGTAGTTGTGCAAATCTATGCAAAACTGATGGTGGCCTG	43
hsa-mir-019b-1-prec	CACTGTTCTATGGTTAGTTTTGCAGGTTTGCATCCAGCTGTGTGATATTCTGCTGTGCAAATCCATGCAAAACTGACTGTGGTAGTG	44
hsa-mir-019b-2-prec	ACATTGCTACTTACAATTAGTTTTGCAGGTTTGCATTTCAGCGTATATATGTATATGTGGCTGTGCAAATCCATGCAAAACTGATTGTGATAATGT	45
hsa-mir-019b-prec-13	TTCTATGGTTAGTTTTGCAGGTTTGCATCCAGCTGTGTGATATTCTGCTGTGCAAATCCATGCAAAACTGACTGTGGTAG	46

Name	Precursor Sequence (5' to 3')*	SEQ ID NO.
hsa-mir-019b-prec-X	TTACAATTAGTTTTGCAGGTTTGCATTTCAGCGTATAT ATGTATATGTGGCTGTGCAAATCCATGCAAAACTGAT TGTGAT	47
hsa-mir-020-prec	GTAGCACTAAAGTGCTTATAGTGCAGGTAGTGTTTAG TTATCTACTGCATTATGAGCACTTAAAGTACTGC	48
hsa-mir-021-prec	TGTCGGGTAGCTTATCAGACTGATGTTGACTGTTGAA TCTCATGGCAACACCAGTCGATGGGCTGTCTGACA	49
hsa-mir-021-prec-17	ACCTTGTCGGGTAGCTTATCAGACTGATGTTGACTGT TGAATCTCATGGCAACACCAGTCGATGGGCTGTCTGA CATTTTG	50
hsa-mir-022-prec	GGCTGAGCCGCAGTAGTTCTTCAGTGGCAAGCTTTAT GTCCTGACCCAGCTAAAGCTGCCAGTTGAAGAACTGT TGCCCTCTGCC	51
hsa-mir-023a-prec	GGCCGGCTGGGGTTCCTGGGGATGGGATTTGCTTCCT GTCACAAATCACATTGCCAGGGATTTCCAACCGACC	52
hsa-mir-023b-prec	CTCAGGTGCTCTGGCTGCTTGGGTTCCTGGCATGCTG ATTTGTGACTTAAGATTAAAATCACATTGCCAGGGAT TACCACGCAACCACGACCTTGGC	53
hsa-mir-023-prec-19	CCACGGCCGGCTGGGGTTCCTGGGGATGGGATTTGCT TCCTGTCACAAATCACATTGCCAGGGATTTCCAACCG ACCCTGA	54
hsa-mir-024-1-prec	CTCCGGTGCCTACTGAGCTGATATCAGTTCTCATTTTA CACACTGGCTCAGTTCAGCAGGAACAGGAG	55
hsa-mir-024-2-prec	CTCTGCCTCCCGTGCCTACTGAGCTGAAACACAGTTG GTTTGTGTACACTGGCTCAGTTCAGCAGGAACAGGG	56
hsa-mir-024-prec-19	CCCTGGGCTCTGCCTCCCGTGCCTACTGAGCTGAAAC ACAGTTGGTTTGTGTACACTGGCTCAGTTCAGCAGGA ACAGGGG	57
hsa-mir-024-prec-9	CCCTCCGGTGCCTACTGAGCTGATATCAGTTCTCATTT TACACACTGGCTCAGTTCAGCAGGAACAGCATC	58
hsa-mir-025-prec	GGCCAGTGTTGAGAGGCGGAGACTTGGGCAATTGCT GGACGCTGCCCTGGGCATTGCACTTGTCTCGGTCTGA CAGTGCCGGCC	59
hsa-mir-026a-prec	AGGCCGTGGCCTCGTTCAAGTAATCCAGGATAGGCTG TGCAGGTCCCAATGGCCTATCTTGGTTACTTGCACGG GGACGCGGGCCT	60
hsa-mir-026b-prec	CCGGGACCCAGTTCAAGTAATTCAGGATAGGTTGTGT GCTGTCCAGCCTGTTCTCCATTACTTGGCTCGGGGAC CGG	61
hsa-mir-027a-prec	CTGAGGAGCAGGGCTTAGCTGCTTGTGAGCAGGGTC CACACCAAGTCGTGTTCACAGTGGCTAAGTTCCGCCC CCCAG	62

Name	Precursor Sequence (5' to 3')*	SEQ ID NO.
hsa-mir-027b-prec	AGGTGCAGAGCTTAGCTGATTGGTGAACAGTGATTG GTTTCCGCTTTGTTCACAGTGGCTAAGTTCTGCACCT	63
hsa-mir-027b-prec	ACCTCTCTAACAAGGTGCAGAGCTTAGCTGATTGGTG AACAGTGATTGGTTTCCGCTTTGTTCACAGTGGCTAA GTTCTGCACCTGAAGAGAAGGTG	64
hsa-mir-027-prec-19	CCTGAGGAGCAGGGCTTAGCTGCTTGTGAGCAGGGT CCACACCAAGTCGTGTTCACAGTGGCTAAGTTCCGCC CCCCAGG	65
hsa-mir-028-prec	GGTCCTTGCCCTCAAGGAGCTCACAGTCTATTGAGTT ACCTTTCTGACTTTCCCACTAGATTGTGAGCTCCTGG AGGGCAGGCACT	66
hsa-mir-029a-2	CCTTCTGTGACCCCTTAGAGGATGACTGATTTCTTTTG GTGTTCAGAGTCAATATAATTTTCTAGCACCATCTGA AATCGGTTATAATGATTGGGGAAGAGCACCATG	67
hsa-mir-029a-prec	ATGACTGATTTCTTTTGGTGTTCAGAGTCAATATAATT TTCTAGCACCATCTGAAATCGGTTAT	68
hsa-mir-029c-prec	ACCACTGGCCCATCTCTTACACAGGCTGACCGATTTC TCCTGGTGTTCAGAGTCTGTTTTTGTCTAGCACCATTT GAAATCGGTTATGATGTAGGGGGAAAAGCAGCAGC	69
hsa-mir-030a-prec	GCGACTGTAAACATCCTCGACTGGAAGCTGTGAAGC CACAGATGGGCTTTCAGTCGGATGTTTGCAGCTGC	70
hsa-mir-030b-prec	ATGTAAACATCCTACACTCAGCTGTAATACATGGATT GGCTGGGAGGTGGATGTTTACGT	71
hsa-mir-030b-prec	ACCAAGTTTCAGTTCATGTAAACATCCTACACTCAGC TGTAATACATGGATTGGCTGGGAGGTGGATGTTTACT TCAGCTGACTTGGA	72
hsa-mir-030c-prec	AGATACTGTAAACATCCTACACTCTCAGCTGTGGAAA GTAAGAAAGCTGGGAGAAGGCTGTTTACTCTTTCT	73
hsa-mir-030d-prec	GTTGTTGTAAACATCCCCGACTGGAAGCTGTAAGACA CAGCTAAGCTTTCAGTCAGATGTTTGCTGCTAC	74
hsa-mir-031-prec	GGAGAGGAGGCAAGATGCTGGCATAGCTGTTGAACT GGGAACCTGCTATGCCAACATATTGCCATCTTTCC	75
hsa-mir-032-prec	GGAGATATTGCACATTACTAAGTTGCATGTTGTCACG GCCTCAATGCAATTTAGTGTGTGTGATATTTTC	76
hsa-mir-033b-prec	GGGGGCCGAGAGAGGCGGGCGGCCCCGCGGTGCATT GCTGTTGCATTGCACGTGTGTGAGGCGGGTGCAGTGC CTCGGCAGTGCAGCCCGGAGCCGGCCCCTGGCACCA C	77
hsa-mir-033-prec	CTGTGGTGCATTGTAGTTGCATTGCATGTTCTGGTGG TACCCATGCAATGTTTCCACAGTGCATCACAG	78

Name	Precursor Sequence (5' to 3')*	SEQ ID NO.
hsa-mir-034-prec	GGCCAGCTGTGAGTGTTTCTTTGGCAGTGTCTTAGCT GGTTGTTGTGAGCAATAGTAAGGAAGCAATCAGCAA GTATACTGCCCTAGAAGTGCTGCACGTTGTGGGGCCC	79
hsa-mir-091-prec-13	TCAGAATAATGTCAAAGTGCTTACAGTGCAGGTAGTG ATATGTGCATCTACTGCAGTGAAGGCACTTGTAGCAT TATGGTGA	80
hsa-mir-092-prec-13=092-1	CTTTCTACACAGGTTGGGATCGGTTGCAATGCTGTGT TTCTGTATGGTATTGCACTTGTCCCGGCCTGTTGAGTT TGG	81
hsa-mir-092-prec-X=092-2	TCATCCCTGGGTGGGGATTTGTTGCATTACTTGTGTTC TATATAAAGTATTGCACTTGTCCCGGCCTGTGGAAGA	82
hsa-mir-093-prec-7.1=093-1	CTGGGGGCTCCAAAGTGCTGTTCGTGCAGGTAGTGTG ATTACCCAACCTACTGCTGAGCTAGCACTTCCCGAGC CCCCGG	83
hsa-mir-093-prec-7.2=093-2	CTGGGGGCTCCAAAGTGCTGTTCGTGCAGGTAGTGTG ATTACCCAACCTACTGCTGAGCTAGCACTTCCCGAGC CCCCGG	84
hsa-mir-095-prec-4	AACACAGTGGGCACTCAATAAATGTCTGTTGAATTGA AATGCGTTACATTCAACGGGTATTTATTGAGCACCCA CTCTGTG	85
hsa-mir-096-prec-7	TGGCCGATTTTGGCACTAGCACATTTTTGCTTGTGTCT CTCCGCTCTGAGCAATCATGTGCAGTGCCAATATGGG AAA	86
hsa-mir-098-prec-X	GTGAGGTAGTAAGTTGTATTGTTGTGGGGTAGGGATA TTAGGCCCCAATTAGAAGATAACTATACAACTTACTA CTTTCC	87
hsa-mir-099b-prec-19	GGCACCCACCCGTAGAACCGACCTTGCGGGGCCTTCG CCGCACACAAGCTCGTGTCTGTGGGTCCGTGTC	88
hsa-mir-099-prec-21	CCCATTGGCATAAACCCGTAGATCCGATCTTGTGGTG AAGTGGACCGCACAAGCTCGCTTCTATGGGTCTGTGT CAGTGTG	89
hsa-mir-100-1/2-prec	AAGAGAGAAGATATTGAGGCCTGTTGCCACAAACCC GTAGATCCGAACTTGTGGTATTAGTCCGCACAAGCTT GTATCTATAGGTATGTGTCTGTTAGGCAATCTCAC	90
hsa-mir-100-prec-11	CCTGTTGCCACAAACCCGTAGATCCGAACTTGTGGTA TTAGTCCGCACAAGCTTGTATCTATAGGTATGTGTCT GTTAGG	91
hsa-mir-101-1/2-prec	AGGCTGCCCTGGCTCAGTTATCACAGTGCTGATGCTG TCTATTCTAAAGGTACAGTACTGTGATAACTGAAGGA TGGCAGCCATCTTACCTTCCATCAGAGGAGCCTCAC	92
hsa-mir-101-prec	TCAGTTATCACAGTGCTGATGCTGTCCATTCTAAAGG TACAGTACTGTGATAACTGA	93

Name	Precursor Sequence (5' to 3')*	SEQ ID NO.
hsa-mir-101-prec-1	TGCCCTGGCTCAGTTATCACAGTGCTGATGCTGTCTATTCTAAAGGTACAGTACTGTGATAACTGAAGGATGGCA	94
hsa-mir-101-prec-9	TGTCCTTTTTCGGTTATCATGGTACCGATGCTGTATATCTGAAAGGTACAGTACTGTGATAACTGAAGAATGGTG	95
hsa-mir-102-prec-1	CTTCTGGAAGCTGGTTTCACATGGTGGCTTAGATTTTTCCATCTTTGTATCTAGCACCATTTGAAATCAGTGTTTTAGGAG	96
hsa-mir-102-prec-7.1	CTTCAGGAAGCTGGTTTCATATGGTGGTTTAGATTTAAATAGTGATTGTCTAGCACCATTTGAAATCAGTGTTCTTGGGGG	97
hsa-mir-102-prec-7.2	CTTCAGGAAGCTGGTTTCATATGGTGGTTTAGATTTAAATAGTGATTGTCTAGCACCATTTGAAATCAGTGTTCTTGGGGG	98
hsa-mir-103-2-prec	TTGTGCTTTCAGCTTCTTTACAGTGCTGCCTTGTAGCATTCAGGTCAAGCAACATTGTACAGGGCTATGAAAGAACCA	99
hsa-mir-103-prec-20	TTGTGCTTTCAGCTTCTTTACAGTGCTGCCTTGTAGCATTCAGGTCAAGCAACATTGTACAGGGCTATGAAAGAACCA	100
hsa-mir-103-prec-5=103-1	TACTGCCCTCGGCTTCTTTACAGTGCTGCCTTGTTGCATATGGATCAAGCAGCATTGTACAGGGCTATGAAGGCATTG	101
hsa-mir-104-prec-17	AAATGTCAGACAGCCCATCGACTGGTGTTGCCATGAGATTCAACAGTCAACATCAGTCTGATAAGCTACCCGACAAGG	102
hsa-mir-105-prec-X.1=105-1	TGTGCATCGTGGTCAAATGCTCAGACTCCTGTGGTGGCTGCTCATGCACCACGGATGTTTGAGCATGTGCTACGGTGTCTA	103
hsa-mir-105-prec-X.2=105-2	TGTGCATCGTGGTCAAATGCTCAGACTCCTGTGGTGGCTGCTCATGCACCACGGATGTTTGAGCATGTGCTACGGTGTCTA	104
hsa-mir-106-prec-X	CCTTGGCCATGTAAAAGTGCTTACAGTGCAGGTAGCTTTTTGAGATCTACTGCAATGTAAGCACTTCTTACATTACCATGG	105
hsa-mir-107-prec-10	CTCTCTGCTTTCAGCTTCTTTACAGTGTTGCCTTGTGGCATGGAGTTCAAGCAGCATTGTACAGGGCTATCAAAGCACAGA	106
hsa-mir-122a-prec	CCTTAGCAGAGCTGTGGAGTGTGACAATGGTGTTTGTGTCTAAACTATCAAACGCCATTATCACACTAAATAGCTACTGCTAGGC	107

Name	Precursor Sequence (5' to 3')*	SEQ ID NO.
hsa-mir-122a-prec	AGCTGTGGAGTGTGACAATGGTGTTTGTGTCCAAACT ATCAAACGCCATTATCACACTAAATAGCT	108
hsa-mir-123-prec	ACATTATTACTTTTGGTACGCGCTGTGACACTTCAAA CTCGTACCGTGAGTAATAATGCGC	109
hsa-mir-124a-1-prec	tccttcctCAGGAGAAAGGCCTCTCTCTCCGTGTTCACAGC GGACCTTGATTTAAATGTCCATACAATTAAGGCACGC GGTGAATGCCAAGAATGGGGCT	110
hsa-mir-124a-1-prec	AGGCCTCTCTCTCCGTGTTCACAGCGGACCTTGATTT AAATGTCCATACAATTAAGGCACGCGGTGAATGCCA AGAATGGGGCTG	111
hsa-mir-124a-2-prec	ATCAAGATTAGAGGCTCTGCTCTCCGTGTTCACAGCG GACCTTGATTTAATGTCATACAATTAAGGCACGCGGT GAATGCCAAGAGCGGAGCCTACGGCTGCACTTGAAG	112
hsa-mir-124a-3-prec	CCCGCCCCAGCCCTGAGGGCCCCTCTGCGTGTTCACA GCGGACCTTGATTTAATGTCTATACAATTAAGGCACG CGGTGAATGCCAAGAGAGGCGCCTCCGCCGCTCCTT	113
hsa-mir-124a-3-prec	TGAGGGCCCCTCTGCGTGTTCACAGCGGACCTTGATT TAATGTCTATACAATTAAGGCACGCGGTGAATGCCAA GAGAGGCGCCTCC	114
hsa-mir-124a-prec	CTCTGCGTGTTCACAGCGGACCTTGATTTAATGTCTA TACAATTAAGGCACGCGGTGAATGCCAAGAG	115
hsa-mir-124b-prec	CTCTCCGTGTTCACAGCGGACCTTGATTTAATGTCAT ACAATTAAGGCACGCGGTGAATGCCAAGAG	116
hsa-mir-125a-prec	TGCCAGTCTCTAGGTCCCTGAGACCCTTTAACCTGTG AGGACATCCAGGGTCACAGGTGAGGTTCTTGGGAGC CTGGCGTCTGGCC	117
hsa-mir-125a-prec	GGTCCCTGAGACCCTTTAACCTGTGAGGACATCCAGG GTCACAGGTGAGGTTCTTGGGAGCCTGG	118
hsa-mir-125b-1	ACATTGTTGCGCTCCTCTCAGTCCCTGAGACCCTAAC TTGTGATGTTTACCGTTTAAATCCACGGGTTAGGCTC TTGGGAGCTGCGAGTCGTGCTTTTGCATCCTGGA	119
hsa-mir-125b-1	TGCGCTCCTCTCAGTCCCTGAGACCCTAACTTGTGAT GTTTACCGTTTAAATCCACGGGTTAGGCTCTTGGGAG CTGCGAGTCGTGCT	120
hsa-mir-125b-2-prec	ACCAGACTTTTCCTAGTCCCTGAGACCCTAACTTGTG AGGTATTTTAGTAACATCACAAGTCAGGCTCTTGGGA CCTAGGCGGAGGGGA	121
hsa-mir-125b-2-prec	CCTAGTCCCTGAGACCCTAACTTGTGAGGTATTTTAG TAACATCACAAGTCAGGCTCTTGGGACCTAGGC	122
hsa-mir-126-prec	CGCTGGCGACGGGACATTATTACTTTTGGTACGCGCT GTGACACTTCAAACTCGTACCGTGAGTAATAATGCGC CGTCCACGGCA	123

Name	Precursor Sequence (5' to 3')*	SEQ ID NO.
hsa-mir-126-prec	ACATTATTACTTTTGGTACGCGCTGTGACACTTCAAA CTCGTACCGTGAGTAATAATGCGC	124
hsa-mir-127-prec	TGTGATCACTGTCTCCAGCCTGCTGAAGCTCAGAGGG CTCTGATTCAGAAAGATCATCGGATCCGTCTGAGCTT GGCTGGTCGGAAGTCTCATCATC	125
hsa-mir-127-prec	CCAGCCTGCTGAAGCTCAGAGGGCTCTGATTCAGAA AGATCATCGGATCCGTCTGAGCTTGGCTGGTCGG	126
hsa-mir-128a-prec	TGAGCTGTTGGATTCGGGGCCGTAGCACTGTCTGAGA GGTTTACATTTCTCACAGTGAACCGGTCTCTTTTTCAG CTGCTTC	127
hsa-mir-128b-prec	GCCCGGCAGCCACTGTGCAGTGGGAAGGGGGGCCGA TACACTGTACGAGAGTGAGTAGCAGGTCTCACAGTG AACCGGTCTCTTTCCCTACTGTGTCACACTCCTAATG G	128
hsa-mir-128-prec	GTTGGATTCGGGGCCGTAGCACTGTCTGAGAGGTTTA CATTTCTCACAGTGAACCGGTCTCTTTTTCAGC	129
hsa-mir-129-prec	TGGATCTTTTTGCGGTCTGGGCTTGCTGTTCCTCTCAA CAGTAGTCAGGAAGCCCTTACCCCAAAAAGTATCTA	130
hsa-mir-130a-prec	TGCTGCTGGCCAGAGCTCTTTTCACATTGTGCTACTGT CTGCACCTGTCACTAGCAGTGCAATGTTAAAAGGGCA TTGGCCGTGTAGTG	131
hsa-mir-131-1-prec	gccaggaggcggGGTTGGTTGTTATCTTTGGTTATCTAGCT GTATGAGTGGTGTGGAGTCTTCATAAAGCTAGATAAC CGAAAGTAAAAATAACCCCATACACTGCGCAG	132
hsa-mir-131-3-prec	CACGGCGCGGCAGCGGCACTGGCTAAGGGAGGCCCG TTTCTCTCTTTGGTTATCTAGCTGTATGAGTGCCACAG AGCCGTCATAAAGCTAGATAACCGAAAGTAGAAATG	133
hsa-mir-131-prec	GTTGTTATCTTTGGTTATCTAGCTGTATGAGTGTATTG GTCTTCATAAAGCTAGATAACCGAAAGTAAAAAC	134
hsa-mir-132-prec	CCGCCCCCGCGTCTCCAGGGCAACCGTGGCTTTCGAT TGTTACTGTGGGAACTGGAGGTAACAGTCTACAGCCA TGGTCGCCCCGCAGCACGCCCACGCGC	135
hsa-mir-132-prec	GGGCAACCGTGGCTTTCGATTGTTACTGTGGGAACTG GAGGTAACAGTCTACAGCCATGGTCGCCC	136
hsa-mir-133a-1	ACAATGCTTTGCTAGAGCTGGTAAAATGGAACCAAA TCGCCTCTTCAATGGATTTGGTCCCCTTCAACCAGCT GTAGCTATGCATTGA	137
hsa-mir-133a-2	GGGAGCCAAATGCTTTGCTAGAGCTGGTAAAATGGA ACCAAATCGACTGTCCAATGGATTTGGTCCCCTTCAA CCAGCTGTAGCTGTGCATTGATGGCGCCG	138

Name	Precursor Sequence (5' to 3')*	SEQ ID NO.
hsa-mir-133-prec	GCTAGAGCTGGTAAAATGGAACCAAATCGCCTCTTCA ATGGATTTGGTCCCCTTCAACCAGCTGTAGC	139
hsa-mir-134-prec	CAGGGTGTGTGACTGGTTGACCAGAGGGGCATGCAC TGTGTTCACCCTGTGGGCCACCTAGTCACCAACCCTC	140
hsa-mir-134-prec	AGGGTGTGTGACTGGTTGACCAGAGGGGCATGCACT GTGTTCACCCTGTGGGCCACCTAGTCACCAACCCT	141
hsa-mir-135-1-prec	AGGCCTCGCTGTTCTCTATGGCTTTTTATTCCTATGTG ATTCTACTGCTCACTCATATAGGGATTGGAGCCGTGG CGCACGGCGGGGACA	142
hsa-mir-135-2-prec	AGATAAATTCACTCTAGTGCTTTATGGCTTTTTATTCC TATGTGATAGTAATAAAGTCTCATGTAGGGATGGAA GCCATGAAATACATTGTGAAAAATCA	143
hsa-mir-135-prec	CTATGGCTTTTTATTCCTATGTGATTCTACTGCTCACT CATATAGGGATTGGAGCCGTGG	144
hsa-mir-136-prec	TGAGCCCTCGGAGGACTCCATTTGTTTTGATGATGGA TTCTTATGCTCCATCATCGTCTCAAATGAGTCTTCAGA GGGTTCT	145
hsa-mir-136-prec	GAGGACTCCATTTGTTTTGATGATGGATTCTTATGCTC CATCATCGTCTCAAATGAGTCTTC	146
hsa-mir-137-prec	CTTCGGTGACGGGTATTCTTGGGTGGATAATACGGAT TACGTTGTTATTGCTTAAGAATACGCGTAGTCGAGG	147
hsa-mir-138-1-prec	CCCTGGCATGGTGTGGTGGGGCAGCTGGTGTTGTGAA TCAGGCCGTTGCCAATCAGAGAACGGCTACTTCACAA CACCAGGGCCACACCACACTACAGG	148
hsa-mir-138-2-prec	CGTTGCTGCAGCTGGTGTTGTGAATCAGGCCGACGAG CAGCGCATCCTCTTACCCGGCTATTTCACGACACCAG GGTTGCATCA	149
hsa-mir-138-prec	CAGCTGGTGTTGTGAATCAGGCCGACGAGCAGCGCA TCCTCTTACCCGGCTATTTCACGACACCAGGGTTG	150
hsa-mir-139-prec	GTGTATTCTACAGTGCACGTGTCTCCAGTGTGGCTCG GAGGCTGGAGACGCGGCCCTGTTGGAGTAAC	151
hsa-mir-140	TGTGTCTCTCTCTGTGTCCTGCCAGTGGTTTTACCCTA TGGTAGGTTACGTCATGCTGTTCTACCACAGGGTAGA ACCACGGACAGGATACCGGGGCACC	152
hsa-mir-140as-prec	TCCTGCCAGTGGTTTTACCCTATGGTAGGTTACGTCA TGCTGTTCTACCACAGGGTAGAACCACGGACAGGA	153
hsa-mir-140s-prec	CCTGCCAGTGGTTTTACCCTATGGTAGGTTACGTCAT GCTGTTCTACCACAGGGTAGAACCACGGACAGG	154
hsa-mir-141-prec	CGGCCGGCCCTGGGTCCATCTTCCAGTACAGTGTTGG ATGGTCTAATTGTGAAGCTCCTAACACTGTCTGGTAA AGATGGCTCCCGGGTGGGTTC	155

Name	Precursor Sequence (5' to 3')*	SEQ ID NO.
hsa-mir-141-prec	GGGTCCATCTTCCAGTACAGTGTTGGATGGTCTAATT GTGAAGCTCCTAACACTGTCTGGTAAAGATGGCCC	156
hsa-mir-142as-prec	ACCCATAAAGTAGAAAGCACTACTAACAGCACTGGA GGGTGTAGTGTTTCCTACTTTATGGATG	157
hsa-mir-142-prec	GACAGTGCAGTCACCCATAAAGTAGAAAGCACTACT AACAGCACTGGAGGGTGTAGTGTTTCCTACTTTATGG ATGAGTGTACTGTG	158
hsa-mir-142s-pres	ACCCATAAAGTAGAAAGCACTACTAACAGCACTGGA GGGTGTAGTGTTTCCTACTTTATGGATG	159
hsa-mir-143-prec	GCGCAGCGCCCTGTCTCCCAGCCTGAGGTGCAGTGCT GCATCTCTGGTCAGTTGGGAGTCTGAGATGAAGCACT GTAGCTCAGGAAGAGAGAAGTTGTTCTGCAGC	160
hsa-mir-143-prec	CCTGAGGTGCAGTGCTGCATCTCTGGTCAGTTGGGAG TCTGAGATGAAGCACTGTAGCTCAGG	161
hsa-mir-144-prec	TGGGGCCCTGGCTGGGATATCATCATATACTGTAAGT TTGCGATGAGACACTACAGTATAGATGATGTACTAGT CCGGGCACCCCC	162
hsa-mir-144-prec	GGCTGGGATATCATCATATACTGTAAGTTTGCGATGA GACACTACAGTATAGATGATGTACTAGTC	163
hsa-mir-145-prec	CACCTTGTCCTCACGGTCCAGTTTTCCCAGGAATCCCT TTAGATGCTAAGATGGGGATTCCTGGAAATACTGTTC TTGAGGTCATGGTT	164
hsa-mir-145-prec	CTCACGGTCCAGTTTTCCCAGGAATCCCTTAGATGCT AAGATGGGGATTCCTGGAAATACTGTTCTTGAG	165
hsa-mir-146-prec	CCGATGTGTATCCTCAGCTTTGAGAACTGAATTCCAT GGGTTGTGTCAGTGTCAGACCTCTGAAATTCAGTTCT TCAGCTGGGATATCTCTGTCATCGT	166
hsa-mir-146-prec	AGCTTTGAGAACTGAATTCCATGGGTTGTGTCAGTGT CAGACCTGTGAAATTCAGTTCTTCAGCT	167
hsa-mir-147-prec	AATCTAAAGACAACATTTCTGCACACACACCAGACTA TGGAAGCCAGTGTGTGGAAATGCTTCTGCTAGATT	168
hsa-mir-148-prec	GAGGCAAAGTTCTGAGACACTCCGACTCTGAGTATG ATAGAAGTCAGTGCACTACAGAACTTTGTCTC	169
hsa-mir-149-prec	GCCGGCGCCCGAGCTCTGGCTCCGTGTCTTCACTCCC GTGCTTGTCCGAGGAGGGAGGGAGGGACGGGGGCTG TGCTGGGGCAGCTGGA	170
hsa-mir-149-prec	GCTCTGGCTCCGTGTCTTCACTCCCGTGCTTGTCCGAG GAGGGAGGGAGGGAC	171
hsa-mir-150-prec	CTCCCCATGGCCCTGTCTCCCAACCCTTGTACCAGTG CTGGGCTCAGACCCTGGTACAGGCCTGGGGGACAGG GACCTGGGGAC	172

Name	Precursor Sequence (5' to 3')*	SEQ ID NO.
hsa-mir-150-prec	CCCTGTCTCCCAACCCTTGTACCAGTGCTGGGCTCAG ACCCTGGTACAGGCCTGGGGGACAGGG	173
hsa-mir-151-prec	CCTGCCCTCGAGGAGCTCACAGTCTAGTATGTCTCAT CCCCTACTAGACTGAAGCTCCTTGAGGACAGG	174
hsa-mir-152-prec	TGTCCCCCCCGGCCCAGGTTCTGTGATACACTCCGAC TCGGGCTCTGGAGCAGTCAGTGCATGACAGAACTTG GGCCCGGAAGGACC	175
hsa-mir-152-prec	GGCCCAGGTTCTGTGATACACTCCGACTCGGGCTCTG GAGCAGTCAGTGCATGACAGAACTTGGGCCCCGG	176
hsa-mir-153-1-prec	CTCACAGCTGCCAGTGTCATTTTTGTGATCTGCAGCT AGTATTCTCACTCCAGTTGCATAGTCACAAAAGTGAT CATTGGCAGGTGTGGC	177
hsa-mir-153-1-prec	tctctctctccctcACAGCTGCCAGTGTCATTGTCACAAAAGT GATCATTGGCAGGTGTGGCTGCTGCATG	178
hsa-mir-153-2-prec	AGCGGTGGCCAGTGTCATTTTTGTGATGTTGCAGCTA GTAATATGAGCCCAGTTGCATAGTCACAAAAGTGATC ATTGGAAACTGTG	179
hsa-mir-153-2-prec	CAGTGTCATTTTTGTGATGTTGCAGCTAGTAATATGA GCCCAGTTGCATAGTCACAAAAGTGATCATTG	180
hsa-mir-154-prec	GTGGTACTTGAAGATAGGTTATCCGTGTTGCCTTCGC TTTATTTGTGACGAATCATACACGGTTGACCTATTTTT CAGTACCAA	181
hsa-mir-154-prec	GAAGATAGGTTATCCGTGTTGCCTTCGCTTTATTTGTG ACGAATCATACACGGTTGACCTATTTTT	182
hsa-mir-155-prec	CTGTTAATGCTAATCGTGATAGGGGTTTTTGCCTCCA ACTGACTCCTACATATTAGCATTAACAG	183
hsa-mir-16-2-prec	CAATGTCAGCAGTGCCTTAGCAGCACGTAAATATTGG CGTTAAGATTCTAAAATTATCTCCAGTATTAACTGTG CTGCTGAAGTAAGGTTGACCATACTCTACAGTTG	184
hsa-mir-181a-prec	AGAAGGGCTATCAGGCCAGCCTTCAGAGGACTCCAA GGAACATTCAACGCTGTCGGTGAGTTTGGGATTTGAA AAAACCACTGACCGTTGACTGTACCTTGGGGTCCTTA	185
hsa-mir-181b-prec	TGAGTTTTGAGGTTGCTTCAGTGAACATTCAACGCTG TCGGTGAGTTTGGAATTAAAATCAAAACCATCGACCG TTGATTGTACCCTATGGCTAACCATCATCTACTCCA	186
hsa-mir-181c-prec	CGGAAAATTTGCCAAGGGTTTGGGGGAACATTCAAC CTGTCGGTGAGTTTGGGCAGCTCAGGCAAACCATCGA CCGTTGAGTGGACCCTGAGGCCTGGAATTGCCATCCT	187
hsa-mir-182-as-prec	GAGCTGCTTGCCTCCCCCCGTTTTTGGCAATGGTAGA ACTCACACTGGTGAGGTAACAGGATCCGGTGGTTCTA GACTTGCCAACTATGGGGCGAGGACTCAGCCGGCAC	188

Name	Precursor Sequence (5' to 3')*	SEQ ID NO.
hsa-mir-182-prec	TTTTTGGCAATGGTAGAACTCACACTGGTGAGGTAAC AGGATCCGGTGGTTCTAGACTTGCCAACTATGG	189
hsa-mir-183-prec	CCGCAGAGTGTGACTCCTGTTCTGTGTATGGCACTGG TAGAATTCACTGTGAACAGTCTCAGTCAGTGAATTAC CGAAGGGCCATAAACAGAGCAGAGACAGATCCACGA	190
hsa-mir-184-prec	CCAGTCACGTCCCCTTATCACTTTTCCAGCCCAGCTTT GTGACTGTAAGTGTTGGACGGAGAACTGATAAGGGT AGGTGATTGA	191
hsa-mir-184-prec	CCTTATCACTTTTCCAGCCCAGCTTTGTGACTGTAAGT GTTGGACGGAGAACTGATAAGGGTAGG	192
hsa-mir-185-prec	AGGGGGCGAGGGATTGGAGAGAAAGGCAGTTCCTGA TGGTCCCCTCCCCAGGGGCTGGCTTTCCTCTGGTCCTT CCCTCCCA	193
hsa-mir-185-prec	AGGGATTGGAGAGAAAGGCAGTTCCTGATGGTCCCC TCCCCAGGGGCTGGCTTTCCTCTGGTCCTT	194
hsa-mir-186-prec	TGCTTGTAACTTTCCAAAGAATTCTCCTTTTGGGCTTT CTGGTTTTATTTTAAGCCCAAAGGTGAATTTTTTGGG AAGTTTGAGCT	195
hsa-mir-186-prec	ACTTTCCAAAGAATTCTCCTTTTGGGCTTTCTGGTTTT ATTTTAAGCCCAAAGGTGAATTTTTTGGGAAGT	196
hsa-mir-187-prec	GGTCGGGCTCACCATGACACAGTGTGAGACTCGGGC TACAACACAGGACCCGGGGCGCTGCTCTGACCCCTCG TGTCTTGTGTTGCAGCCGGAGGGACGCAGGTCCGCA	197
hsa-mir-188-prec	TGCTCCCTCTCTCACATCCCTTGCATGGTGGAGGGTG AGCTTTCTGAAAACCCCTCCCACATGCAGGGTTTGCA GGATGGCGAGCC	198
hsa-mir-188-prec	TCTCACATCCCTTGCATGGTGGAGGGTGAGCTTTCTG AAAACCCCTCCCACATGCAGGGTTTGCAGGA	199
hsa-mir-189-prec	CTGTCGATTGGACCCGCCCTCCGGTGCCTACTGAGCT GATATCAGTTCTCATTTTACACACTGGCTCAGTTCAG CAGGAACAGGAGTCGAGCCCTTGAGCAA	200
hsa-mir-189-prec	CTCCGGTGCCTACTGAGCTGATATCAGTTCTCATTTTA CACACTGGCTCAGTTCAGCAGGAACAGGAG	201
hsa-mir-190-prec	TGCAGGCCTCTGTGTGATATGTTTGATATATTAGGTT GTTATTTAATCCAACTATATATCAAACATATTCCTAC AGTGTCTTGCC	202
hsa-mir-190-prec	CTGTGTGATATGTTTGATATATTAGGTTGTTATTTAAT CCAACTATATATCAAACATATTCCTACAG	203
hsa-mir-191-prec	CGGCTGGACAGCGGGCAACGGAATCCCAAAAGCAGC TGTTGTCTCCAGAGCATTCCAGCTGCGCTTGGATTTC GTCCCCTGCTCTCCTGCCT	204

Name	Precursor Sequence (5' to 3')*	SEQ ID NO.
hsa-mir-191-prec	AGCGGGCAACGGAATCCCAAAAGCAGCTGTTGTCTC CAGAGCATTCCAGCTGCGCTTGGATTTCGTCCCCTGC T	205
hsa-mir-192-2/3	CCGAGACCGAGTGCACAGGGCTCTGACCTATGAATT GACAGCCAGTGCTCTCGTCTCCCCTCTGGCTGCCAAT TCCATAGGTCACAGGTATGTTCGCCTCAATGCCAG	206
hsa-mir-192-prec	GCCGAGACCGAGTGCACAGGGCTCTGACCTATGAAT TGACAGCCAGTGCTCTCGTCTCCCCTCTGGCTGCCAA TTCCATAGGTCACAGGTATGTTCGCCTCAATGCCAGC	207
hsa-mir-193-prec	CGAGGATGGGAGCTGAGGGCTGGGTCTTTGCGGGCG AGATGAGGGTGTCGGATCAACTGGCCTACAAAGTCC CAGTTCTCGGCCCCCG	208
hsa-mir-193-prec	GCTGGGTCTTTGCGGGCGAGATGAGGGTGTCGGATC AACTGGCCTACAAAGTCCCAGT	209
hsa-mir-194-prec	ATGGTGTTATCAAGTGTAACAGCAACTCCATGTGGAC TGTGTACCAATTTCCAGTGGAGATGCTGTTACTTTTG ATGGTTACCAA	210
hsa-mir-194-prec	GTGTAACAGCAACTCCATGTGGACTGTGTACCAATTT CCAGTGGAGATGCTGTTACTTTTGAT	211
hsa-mir-195-prec	AGCTTCCCTGGCTCTAGCAGCACAGAAATATTGGCAC AGGGAAGCGAGTCTGCCAATATTGGCTGTGCTGCTCC AGGCAGGGTGGTG	212
hsa-mir-195-prec	TAGCAGCACAGAAATATTGGCACAGGGAAGCGAGTC TGCCAATATTGGCTGTGCTGCT	213
hsa-mir-196-1-prec	CTAGAGCTTGAATTGGAACTGCTGAGTGAATTAGGTA GTTTCATGTTGTTGGGCCTGGGTTTCTGAACACAACA ACATTAAACCACCCGATTCACGGCAGTTACTGCTCC	214
hsa-mir-196-1-prec	GTGAATTAGGTAGTTTCATGTTGTTGGGCCTGGGTTT CTGAACACAACAACATTAAACCACCCGATTCAC	215
hsa-mir-196-2-prec	TGCTCGCTCAGCTGATCTGTGGCTTAGGTAGTTTCAT GTTGTTGGGATTGAGTTTTGAACTCGGCAACAAGAAA CTGCCTGAGTTACATCAGTCGGTTTTCGTCGAGGGC	216
hsa-mir-196-prec	GTGAATTAGGTAGTTTCATGTTGTTGGGCCTGGGTTT CTGAACACAACAACATTAAACCACCCGATTCAC	217
hsa-mir-197-prec	GGCTGTGCCGGGTAGAGAGGGCAGTGGGAGGTAAGA GCTCTTCACCCTTCACCACCTTCTCCACCCAGCATGG CC	218
hsa-mir-198-prec	TCATTGGTCCAGAGGGGAGATAGGTTCCTGTGATTTT TCCTTCTTCTCTATAGAATAAATGA	219
hsa-mir-199a-1-prec	GCCAACCCAGTGTTCAGACTACCTGTTCAGGAGGCTC TCAATGTGTACAGTAGTCTGCACATTGGTTAGGC	220

Name	Precursor Sequence (5' to 3')*	SEQ ID NO.
hsa-mir-199a-2-prec	AGGAAGCTTCTGGAGATCCTGCTCCGTCGCCCCAGTG TTCAGACTACCTGTTCAGGACAATGCCGTTGTACAGT AGTCTGCACATTGGTTAGACTGGGCAAGGGAGAGCA	221
hsa-mir-199b-prec	CCAGAGGACACCTCCACTCCGTCTACCCAGTGTTTAG ACTATCTGTTCAGGACTCCCAAATTGTACAGTAGTCT GCACATTGGTTAGGCTGGGCTGGGTTAGACCCTCGG	222
hsa-mir-199s-prec	GCCAACCCAGTGTTCAGACTACCTGTTCAGGAGGCTC TCAATGTGTACAGTAGTCTGCACATTGGTTAGGC	223
hsa-mir-200a-prec	GCCGTGGCCATCTTACTGGGCAGCATTGGATGGAGTC AGGTCTCTAATACTGCCTGGTAATGATGACGGC	224
hsa-mir-200b-prec	CCAGCTCGGGCAGCCGTGGCCATCTTACTGGGCAGCA TTGGATGGAGTCAGGTCTCTAATACTGCCTGGTAATG ATGACGGCGGAGCCCTGCACG	225
hsa-mir-202-prec	GTTCCTTTTTCCTATGCATATACTTCTTTGAGGATCTG GCCTAAAGAGGTATAGGGCATGGGAAGATGGAGC	226
hsa-mir-203-prec	GTGTTGGGGACTCGCGCGCTGGGTCCAGTGGTTCTTA ACAGTTCAACAGTTCTGTAGCGCAATTGTGAAATGTT TAGGACCACTAGACCCGGCGGGCGCGGCGACAGCGA	227
hsa-mir-204-prec	GGCTACAGTCTTTCTTCATGTGACTCGTGGACTTCCCT TTGTCATCCTATGCCTGAGAATATATGAAGGAGGCTG GGAAGGCAAAGGGACGTTCAATTGTCATCACTGGC	228
hsa-mir-205-prec	AAAGATCCTCAGACAATCCATGTGCTTCTCTTGTCCT TCATTCCACCGGAGTCTGTCTCATACCCAACCAGATT TCAGTGGAGTGAAGTTCAGGAGGCATGGAGCTGACA	229
hsa-mir-206-prec	TGCTTCCCGAGGCCACATGCTTCTTTATATCCCCATAT GGATTACTTTGCTATGGAATGTAAGGAAGTGTGTGGT TTCGGCAAGTG	230
hsa-mir-206-prec	AGGCCACATGCTTCTTTATATCCCCATATGGATTACTT TGCTATGGAATGTAAGGAAGTGTGTGGTTTT	231
hsa-mir-208-prec	TGACGGGCGAGCTTTTGGCCCGGGTTATACCTGATGC TCACGTATAAGACGAGCAAAAAGCTTGTTGGTCA	232
hsa-mir-210-prec	ACCCGGCAGTGCCTCCAGGCGCAGGGCAGCCCCTGC CCACCGCACACTGCGCTGCCCCAGACCCACTGTGCGT GTGACAGCGGCTGATCTGTGCCTGGGCAGCGCGACC C	233
hsa-mir-211-prec	TCACCTGGCCATGTGACTTGTGGGCTTCCCTTTGTCAT CCTTCGCCTAGGGCTCTGAGCAGGGCAGGGACAGCA AAGGGGTGCTCAGTTGTCACTTCCCACAGCACGGAG	234
hsa-mir-212-prec	CGGGGCACCCCGCCCGGACAGCGCGCCGGCACCTTG GCTCTAGACTGCTTACTGCCCGGGCCGCCCTCAGTAA CAGTCTCCAGTCACGGCCACCGACGCCTGGCCCCGCC	235

Name	Precursor Sequence (5' to 3')*	SEQ ID NO.
hsa-mir-213-prec	CCTGTGCAGAGATTATTTTTTAAAAGGTCACAATCAA CATTCATTGCTGTCGGTGGGTTGAACTGTGTGGACAA GCTCACTGAACAATGAATGCAACTGTGGCCCCGCTT	236
hsa-mir-213-prec-LIM	GAGTTTTGAGGTTGCTTCAGTGAACATTCAACGCTGT CGGTGAGTTTGGAATTAAAATCAAAACCATCGACCGT TGATTGTACCCTATGGCTAACCATCATCTACTCC	237
hsa-mir-214-prec	GGCCTGGCTGGACAGAGTTGTCATGTGTCTGCCTGTC TACACTTGCTGTGCAGAACATCCGCTCACCTGTACAG CAGGCACAGACAGGCAGTCACATGACAACCCAGCCT	238
hsa-mir-215-prec	ATCATTCAGAAATGGTATACAGGAAAATGACCTATG AATTGACAGACAATATAGCTGAGTTTGTCTGTCATTT CTTTAGGCCAATATTCTGTATGACTGTGCTACTTCAA	239
hsa-mir-216-prec	GATGGCTGTGAGTTGGCTTAATCTCAGCTGGCAACTG TGAGATGTTCATACAATCCCTCACAGTGGTCTCTGGG ATTATGCTAAACAGAGCAATTTCCTAGCCCTCACGA	240
hsa-mir-217-prec	AGTATAATTATTACATAGTTTTTGATGTCGCAGATAC TGCATCAGGAACTGATTGGATAAGAATCAGTCACCAT CAGTTCCTAATGCATTGCCTTCAGCATCTAAACAAG	241
hsa-mir-218-1-prec	GTGATAATGTAGCGAGATTTTCTGTTGTGCTTGATCT AACCATGTGGTTGCGAGGTATGAGTAAAACATGGTTC CGTCAAGCACCATGGAACGTCACGCAGCTTTCTACA	242
hsa-mir-218-2-prec	GACCAGTCGCTGCGGGGCTTTCCTTTGTGCTTGATCT AACCATGTGGTGGAACGATGGAAACGGAACATGGTT CTGTCAAGCACCGCGGAAAGCACCGTGCTCTCCTGCA	243
hsa-mir-219-prec	CCGCCCCGGGCCGCGGCTCCTGATTGTCCAAACGCAA TTCTCGAGTCTATGGCTCCGGCCGAGAGTTGAGTCTG GACGTCCCGAGCCGCCGCCCCCAAACCTCGAGCGGG	244
hsa-mir-220-prec	GACAGTGTGGCATTGTAGGGCTCCACACCGTATCTGA CACTTTGGGCGAGGGCACCATGCTGAAGGTGTTCATG ATGCGGTCTGGGAACTCCTCACGGATCTTACTGATG	245
hsa-mir-221-prec	TGAACATCCAGGTCTGGGGCATGAACCTGGCATACA ATGTAGATTTCTGTGTTCGTTAGGCAACAGCTACATT GTCTGCTGGGTTTCAGGCTACCTGGAAACATGTTCTC	246
hsa-mir-222-prec	GCTGCTGGAAGGTGTAGGTACCCTCAATGGCTCAGTA GCCAGTGTAGATCCTGTCTTTCGTAATCAGCAGCTAC ATCTGGCTACTGGGTCTCTGATGGCATCTTCTAGCT	247
hsa-mir-223-prec	CCTGGCCTCCTGCAGTGCCACGCTCCGTGTATTTGAC AAGCTGAGTTGGACACTCCATGTGGTAGAGTGTCAGT TTGTCAAATACCCCAAGTGCGGCACATGCTTACCAG	248
hsa-mir-224-prec	GGGCTTTCAAGTCACTAGTGGTTCCGTTTAGTAGATG ATTGTGCATTGTTTCAAAATGGTGCCCTAGTGACTAC AAAGCCC	249

Name	Precursor Sequence (5' to 3')*	SEQ ID NO.
hsA-mir-29b-1=102-prec1	CTTCTGGAAGCTGGTTTCACATGGTGGCTTAGATTTTTCCATCTTTGTATCTAGCACCATTTGAAATCAGTGTTTTAGGAG	250
hsA-mir-29b-2=102prec7.1=7.2	CTTCAGGAAGCTGGTTTCATATGGTGGTTTAGATTTAAATAGTGATTGTCTAGCACCATTTGAAATCAGTGTTCTTGGGGG	251
hsA-mir-29b-3=102prec7.1=7.2	CTTCAGGAAGCTGGTTTCATATGGTGGTTTAGATTTAAATAGTGATTGTCTAGCACCATTTGAAATCAGTGTTCTTGGGGG	252
hsa-mir-30*=mir-097-prec-6	GTGAGCGACTGTAAACATCCTCGACTGGAAGCTGTGAAGCCACAGATGGGCTTTCAGTCGGATGTTTGCAGCTGCCTACT	253
mir-033b	ACCAAGTTTCAGTTCATGTAAACATCCTACACTCAGCTGTAATACATGGATTGGCTGGGAGGTGGATGTTTACTTCAGCTGACTTGGA	254
mir-101-precursor-9=mir-101-3	TGCCCTGGCTCAGTTATCACAGTGCTGATGCTGTCTATTCTAAAGGTACAGTACTGTGATAACTGAAGGATGGCA	255
mir-108-1-small	ACACTGCAAGAACAATAAGGATTTTTAGGGGCATTATGACTGAGTCAGAAAACACAGCTGCCCCTGAAAGTCCCTCATTTTTCTTGCTGT	256
mir-108-2-small	ACTGCAAGAGCAATAAGGATTTTTAGGGGCATTATGATAGTGGAATGGAAACACATCTGCCCCCAAAAGTCCCTCATTTT	257
mir-123-prec = mir-126-prec	CGCTGGCGACGGGACATTATTACTTTTGGTACGCGCTGTGACACTTCAAACTCGTACCGTGAGTAATAATGCGCCGTCCACGGCA	258
mir-123-prec = mir-126-prec	ACATTATTACTTTTGGTACGCGCTGTGACACTTCAAACTCGTACCGTGAGTAATAATGCGC	259
mir-129-1-prec	TGGATCTTTTTGCGGTCTGGGCTTGCTGTTCCTCTCAACAGTAGTCAGGAAGCCCTTACCCCAAAAAGTATCTA	260
mir-129-small-2=129b?	TGCCCTTCGCGAATCTTTTTGCGGTCTGGGCTTGCTGTACATAACTCAATAGCCGGAAGCCCTTACCCCAAAAAGCATTTGCGGAGGGCG	261
mir-133b-small	GCCCCCTGCTCTGGCTGGTCAAACGGAACCAAGTCCGTCTTCCTGAGAGGTTTGGTCCCCTTCAACCAGCTACAGCAGGG	262
mir-135-small-2	AGATAAATTCACTCTAGTGCTTTATGGCTTTTTATTCCTATGTGATAGTAATAAAGTCTCATGTAGGGATGGAAGCCATGAAATACATTGTGAAAAATCA	263
mir-148b-small	AAGCACGATTAGCATTTGAGGTGAAGTTCTGTTATACACTCAGGCTGTGGCTCTCTGAAAGTCAGTGCAT	264

mir-151-prec	CCTGTCCTCAAGGAGCTTCAGTCTAGTAGGGGATGAG ACATACTAGACTGTGAGCTCCTCGAGGGCAGG	265
mir-155-prec(BIC)	CTGTTAATGCTAATCGTGATAGGGGTTTTTGCCTCCA ACTGACTCCTACATATTAGCATTAACAG	266
mir-156 = mir-157=overlap mir-141	CCTAACACTGTCTGGTAAAGATGGCTCCCGGGTGGGT TCTCTCGGCAGTAACCTTCAGGGAGCCCTGAAGACCA TGGAGGAC	267
mir-158-small = mir-192	GCCGAGACCGAGTGCACAGGGCTCTGACCTATGAAT TGACAGCCAGTGCTCTCGTCTCCCCTCTGGCTGCCAA TTCCATAGGTCACAGGTATGTTCGCCTCAATGCCAGC	268
mir-159-1-small	TCCCGCCCCCTGTAACAGCAACTCCATGTGGAAGTGC CCACTGGTTCCAGTGGGGCTGCTGTTATCTGGGGCGA GGGCCA	269
mir-161-small	AAAGCTGGGTTGAGAGGGCGAAAAAGGATGAGGTGA CTGGTCTGGGCTACGCTATGCTGCGGCGCTCGGG	270
mir-163-1b-small	CATTGGCCTCCTAAGCCAGGGATTGTGGGTTCGAGTC CCACCCGGGGTAAAGAAAGGCCGAATT	271
mir-163-3-small	CCTAAGCCAGGGATTGTGGGTTCGAGTCCCACCTGGG GTAGAGGTGAAAGTTCCTTTTACGGAATTTTTT	272
mir-175-small=mir-224	GGGCTTTCAAGTCACTAGTGGTTCCGTTTAGTAGATG ATTGTGCATTGTTTCAAAATGGTGCCCTAGTGACTAC AAAGCCC	273
mir-177-small	ACGCAAGTGTCCTAAGGTGAGCTCAGGGAGCACAGA AACCTCCAGTGGAACAGAAGGGCAAAAGCTCATT	274
mir-180-small	CATGTGTCACTTTCAGGTGGAGTTTCAAGAGTCCCTT CCTGGTTCACCGTCTCCTTTGCTCTTCCACAAC	275
mir-187-prec	GGTCGGGCTCACCATGACACAGTGTGAGACTCGGGC TACAACACAGGACCCGGGGCGCTGCTCTGACCCCTCG TGTCTTGTGTTGCAGCCGGAGGGACGCAGGTCCGCA	276
mir-188-prec	TGCTCCCTCTCTCACATCCCTTGCATGGTGGAGGGTG AGCTTTCTGAAAACCCCTCCCACATGCAGGGTTTGCA GGATGGCGAGCC	277
mir-190-prec	TGCAGGCCTCTGTGTGATATGTTTGATATATTAGGTT GTTATTTAATCCAACTATATATCAAACATATTCCTAC AGTGTCTTGCC	278
mir-197-2	GTGCATGTGTATGTATGTGTGCATGTGCATGTGTATG TGTATGAGTGCATGCGTGTGTGC	279
mir-197-prec	GGCTGTGCCGGGTAGAGAGGGCAGTGGGAGGTAAGA GCTCTTCACCCTTCACCACCTTCTCCACCCAGCATGG CC	280
mir-202-prec	GTTCCTTTTTCCTATGCATATACTTCTTTGAGGATCTG GCCTAAAGAGGTATAGGGCATGGGAAGATGGAGC	281
mir-294-1 (chr16)	CAATCTTCCTTTATCATGGTATTGATTTTTCAGTGCTT CCCTTTTGTGTGAGAGAAGATA	282

mir-hes1	ATGGAGCTGCTCACCCTGTGGGCCTCAAATGTGGAGG AACTATTCTGATGTCCAAGTGGAAAGTGCTGCGACAT TTGAGCGTCACCGGTGACGCCCATATCA	283
mir-hes2	GCATCCCCTCAGCCTGTGGCACTCAAACTGTGGGGGC ACTTTCTGCTCTCTGGTGAAAGTGCCGCCATCTTTTGA GTGTTACCGCTTGAGAAGACTCAACC	284
mir-hes3	CGAGGAGCTCATACTGGGATACTCAAAATGGGGGCG CTTTCCTTTTTGTCTGTTACTGGGAAGTGCTTCGATTT TGGGGTGTCCCTGTTTGAGTAGGGCATC	285
hsa-mir-29b-1	CTTCAGGAAGCTGGTTTCATATGGTGGTTTAGATTTA AATAGTGATTGTCTAGCACCATTTGAAATCAGTGTTC TTGGGGG	286

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

The level of at least one miR gene product can be measured in cells of a biological sample obtained from the subject. For example, a tissue sample can be removed from a subject suspected of having breast cancer associated with by conventional biopsy techniques. In another example, a blood sample can be removed from the subject, and white blood cells can be isolated for DNA extraction by standard techniques. The blood or tissue sample is preferably obtained from the subject prior to initiation of radiotherapy, chemotherapy or other therapeutic treatment. A corresponding control tissue or blood sample can be obtained from unaffected tissues of the subject, from a normal human individual or population of normal individuals, or from cultured cells corresponding to the majority of cells in the subject's sample. The control tissue or blood sample is then processed along with the sample from the subject, so that the levels of miR gene product produced from a given miR gene in cells from the subject's sample can be compared to the corresponding miR gene product levels from cells of the control sample.

An alteration (*i.e.*, an increase or decrease) in the level of a miR gene product in the sample obtained from the subject, relative to the level of a corresponding miR gene product in a control sample, is indicative of the presence of breast cancer in the subject. In one embodiment, the level of the at least one miR gene product in the test sample is greater than the level of the corresponding miR gene product in the control sample (i.e., expression of the miR gene product is "up-regulated"). As used herein, expression of an miR gene product is

"up-regulated" when the amount of miR gene product in a cell or tissue sample from a subject is greater than the amount the same gene product in a control cell or tissue sample. In another embodiment, the level of the at least one miR gene product in the test sample is less than the level of the corresponding miR gene product in the control sample (i.e., expression of the miR gene product is "down-regulated"). As used herein, expression of an miR gene is "down-regulated" when the amount of miR gene product produced from that gene in a cell or tissue sample from a subject is less than the amount produced from the same gene in a control cell or tissue sample. The relative miR gene expression in the control and normal samples can be determined with respect to one or more RNA expression standards. The standards can comprise, for example, a zero miR gene expression level, the miR gene expression level in a standard cell line, or the average level of miR gene expression previously obtained for a population of normal human controls.

The level of a miR gene product in a sample can be measured using any technique that is suitable for detecting RNA expression levels in a biological sample. Suitable techniques for determining RNA expression levels in cells from a biological sample (e.g., Northern blot analysis, RT-PCR, *in situ* hybridization) are well known to those of skill in the art. In a particular embodiment, the level of at least one miR gene product is detected using Northern blot analysis. For example, 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 by gel electrophoresis on agarose gels according to standard techniques, and transferred to nitrocellulose filters. 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.*, eds., 2nd edition, Cold Spring Harbor Laboratory Press, 1989, Chapter 7, the entire disclosure of which is incorporated by reference.

Suitable probes for Northern blot hybridization of a given miR gene product can be produced from the nucleic acid sequences provided in Table 1. 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, the disclosures of which are incorporated herein by reference.

For example, the nucleic acid probe can be labeled with, *e.g.*, a radionuclide, such as ^{3}H, ^{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.* (1977), *J. Mol. Biol.* 113:237-251 or by the random priming method of Fienberg *et al.* (1983), *Anal. Biochem.* 132:6-13, the entire disclosures of which are incorporated herein by reference. 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 miR gene transcript levels. Using another approach, miR gene transcript levels can be quantified by computerized imaging systems, such the Molecular Dynamics 400-B 2D Phosphorimager 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 an analogue, for example, 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, and antibodies (e.g., anti-biotin antibodies) coupled to fluorescent dyes or enzymes that produce color reactions.

In addition to Northern and other RNA hybridization techniques, determining the levels of RNA transcripts can be accomplished using 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 nucleic acid (e.g., cDNA or RNA) probes. This technique is particularly well-suited for analyzing tissue biopsy samples from subjects. The practice of the *in situ* hybridization technique is described in more detail in U.S. Pat. No. 5,427,916, the entire disclosure of which is incorporated herein by reference. Suitable probes for *in situ* hybridization of a given miR gene product can be produced from the nucleic acid sequences provided in Table 1, as described above.

The relative number of miR gene transcripts in cells can also be determined by reverse transcription of miR gene transcripts, followed by amplification of the reverse-transcribed transcripts by polymerase chain reaction (RT-PCR). The levels of miR gene transcripts can be quantified in comparison with an internal standard, for example, the level of mRNA from a "housekeeping" gene present in the same sample. A suitable "housekeeping" gene for use as an internal standard includes, e.g., myosin or glyceraldehyde-3-phosphate dehydrogenase (G3PDH). The methods for quantitative RT-PCR and variations thereof are within the skill in the art.

In some instances, it may be desirable to simultaneously determine the expression level of a plurality of different miR gene products in a sample. In other instances, it may be desirable to determine the expression level of the transcripts of all known miR genes correlated with a cancer. Assessing cancer-specific expression levels for hundreds of miR genes is time consuming and requires a large amount of total RNA (at least 20 μg for each Northern blot) and autoradiographic techniques that require radioactive isotopes.

To overcome these limitations, an oligolibrary, in microchip format (i.e., a microarray), may be constructed containing a set of probe oligodeoxynucleotides that are specific for a set of miR genes. Using such a microarray, the expression level of multiple microRNAs in a biological sample can be determined by reverse transcribing the RNAs to generate a set of target oligodeoxynucleotides, and hybridizing them to probe oligodeoxynucleotides on the microarray to generate a hybridization, or expression, profile. The hybridization profile of the test sample can then be compared to that of a control sample to determine which microRNAs have an altered expression level in breast cancer cells. As used herein, "probe oligonucleotide" or "probe oligodeoxynucleotide" refers to an oligonucleotide that is capable of hybridizing to a target oligonucleotide. "Target

oligonucleotide" or "target oligodeoxynucleotide" refers to a molecule to be detected (e.g., via hybridization). By "miR-specific probe oligonucleotide" or "probe oligonucleotide specific for an miR" is meant a probe oligonucleotide that has a sequence selected to hybridize to a specific miR gene product, or to a reverse transcript of the specific miR gene product.

An "expression profile" or "hybridization profile" of a particular sample is essentially a fingerprint of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is unique to the state of the cell. That is, normal tissue may be distinguished from breast cancer tissue, and within breast cancer tissue, different prognosis states (good or poor long term survival prospects, for example) may be determined. By comparing expression profiles of breast cancer tissue in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. The identification of sequences that are differentially expressed in breast cancer tissue or normal breast tissue, as well as differential expression resulting in different prognostic outcomes, allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated (e.g., to determine whether a chemotherapeutic drug act to improve the long-term prognosis in a particular patient). Similarly, diagnosis may be done or confirmed by comparing patient samples with the known expression profiles. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates that suppress the breast cancer expression profile or convert a poor prognosis profile to a better prognosis profile.

Accordingly, the invention provides methods of diagnosing whether a subject has, or is at risk for developing, breast cancer, comprising reverse transcribing RNA from a test sample obtained from the subject to provide a set of target oligo-deoxynucleotides, hybridizing the target oligo-deoxynucleotides to a microarray comprising miRNA-specific probe oligonucleotides to provide a hybridization profile for the test sample, and comparing the test sample hybridization profile to a hybridization profile generated from a control sample, wherein an alteration in the signal of at least one miRNA is indicative of the subject either having, or being at risk for developing, breast cancer. In one embodiment, the

microarray comprises miRNA-specific probe oligonucleotides for a substantial portion of the human miRNome. In a particular embodiment, the microarray comprises miRNA-specific probe oligo-nucleotides for one or more miRNAs selected from the group consisting of miR-125b, miR-145, miR-21, miR-155, miR-10b, miR-009-1 (miR131-1), miR-34 (miR-170), miR-102 (miR-29b), miR-123 (miR-126), miR-140-as, miR-125a, miR-125b-1, miR-125b-2, miR-194, miR-204, miR-213, let-7a-2, let-7a-3, let-7d (let-7d-v1), let-7f-2, let-7i (let-7d-v2), miR-101-1, miR-122a, miR-128b, miR-136, miR-143, miR-149, miR-191, miR-196-1, miR-196-2, miR-202, miR-203, miR-206, miR-210 and combinations thereof. In a further embodiment, the at least one miR gene product is selected from the group consisting of miR-125b, miR-145, miR-21, miR-155, miR-10b and combinations thereof.

The microarray can be prepared from gene-specific oligonucleotide probes generated from known miRNA sequences. The array may contain two different oligonucleotide probes for each miRNA, one containing the active, mature sequence and the other being specific for the precursor of the miRNA. The array may also contain controls, such as one or more mouse sequences differing from human orthologs by only a few bases, which can serve as controls for hybridization stringency conditions. tRNAs from both species may also be printed on the microchip, providing an internal, relatively stable, positive control for specific hybridization. One or more appropriate controls for non-specific hybridization may also be included on the microchip. For this purpose, sequences are selected based upon the absence of any homology with any known miRNAs.

The microarray may be fabricated using techniques known in the art. For example, probe oligonucleotides of an appropriate length, e.g., 40 nucleotides, are 5'-amine modified at position C6 and printed using commercially available microarray systems, e.g., the GeneMachine OmniGrid^{TM} 100 Microarrayer and Amersham CodeLink^{TM} activated slides. Labeled cDNA oligomer corresponding to the target RNAs is prepared by reverse transcribing the target RNA with labeled primer. Following first strand synthesis, the RNA/DNA hybrids are denatured to degrade the RNA templates. The labeled target cDNAs thus prepared are then hybridized to the microarray chip under hybridizing conditions, e.g., 6X SSPE/30% formamide at 25°C for 18 hours, followed by washing in 0.75X TNT at 37°C for 40 minutes. At positions on the array where the immobilized probe DNA recognizes a

complementary target cDNA in the sample, hybridization occurs. The labeled target cDNA marks the exact position on the array where binding occurs, allowing automatic detection and quantification. The output consists of a list of hybridization events, indicating the relative abundance of specific cDNA sequences, and therefore the relative abundance of the corresponding complementary miRs, in the patient sample. According to one embodiment, the labeled cDNA oligomer is a biotin-labeled cDNA, prepared from a biotin-labeled primer. The microarray is then processed by direct detection of the biotin-containing transcripts using, e.g., Streptavidin-Alexa647 conjugate, and scanned utilizing conventional scanning methods. Image intensities of each spot on the array are proportional to the abundance of the corresponding miR in the patient sample.

The use of the array has several advantages for miRNA expression detection. First, the global expression of several hundred genes can be identified in the same sample at one time point. Second, through careful design of the oligonucleotide probes, expression of both mature and precursor molecules can be identified. Third, in comparison with Northern blot analysis, the chip requires a small amount of RNA, and provides reproducible results using 2.5 μg of total RNA. The relatively limited number of miRNAs (a few hundred per species) allows the construction of a common microarray for several species, with distinct oligonucleotide probes for each. Such a tool would allow for analysis of trans-species expression for each known miR under various conditions.

In addition to use for quantitative expression level assays of specific miRs, a microchip containing miRNA-specific probe oligonucleotides corresponding to a substantial portion of the miRNome, preferably the entire miRNome, may be employed to carry out miR gene expression profiling, for analysis of miR expression patterns. Distinct miR signatures can be associated with established disease markers, or directly with a disease state.

According to the expression profiling methods described herein, total RNA from a sample from a subject suspected of having a cancer (e.g., breast cancer) is quantitatively reverse transcribed to provide a set of labeled target oligodeoxynucleotides complementary to the RNA in the sample. The target oligodeoxynucleotides are then hybridized to a microarray comprising miRNA-specific probe oligonucleotides to provide a hybridization profile for the sample. The result is a hybridization profile for the sample representing the

expression pattern of miRNA in the sample. The hybridization profile comprises the signal from the binding of the target oligodeoxynucleotides from the sample to the miRNA-specific probe oligonucleotides in the microarray. The profile may be recorded as the presence or absence of binding (signal vs. zero signal). More preferably, the profile recorded includes the intensity of the signal from each hybridization. The profile is compared to the hybridization profile generated from a normal, i.e., noncancerous, control sample. An alteration in the signal is indicative of the presence of the cancer in the subject.

Other techniques for measuring miR gene expression are also within the skill in the art, and include various techniques for measuring rates of RNA transcription and degradation.

The invention also provides methods of diagnosing a breast cancer associated with one or more prognostic markers, comprising measuring the level of at least one miR gene product in a breast cancer test sample from a subject and comparing the level of the at least one miR gene product in the breast cancer test sample to the level of a corresponding miR gene product in a control sample. An alteration (e.g., an increase, a decrease) in the signal of at least one miRNA in the test sample relative to the control sample is indicative of the subject either having, or being at risk for developing, breast cancer associated with the one or more prognostic markers.

The breast cancer can be associated with one or more prognostic markers or features, including, a marker associated with an adverse (i.e., negative) prognosis, or a marker associated with a good (i.e., positive) prognosis. In certain embodiments, the breast cancer that is diagnosed using the methods described herein is associated with one or more adverse prognostic features selected from the group consisting of estrogen receptor expression, progesterone receptor expression, positive lymph node metastasis, high proliferative index, detectable p53 expression, advanced tumor stage, and high vascular invasion. Particular microRNAs whose expression is altered in breast cancer cells associated with each of these prognostic markers are described herein (see, for example, Example 3 and Figure 4). In one embodiment, the level of the at least one miR gene product is measured by reverse transcribing RNA from a test sample obtained from the subject to provide a set of target oligodeoxynucleotides, hybridizing the target oligodeoxynucleotides to a microarray that comprises miRNA-specific probe oligonucleotides to provide a hybridization profile for the

test sample, and comparing the test sample hybridization profile to a hybridization profile generated from a control sample.

Without wishing to be bound by any one theory, it is believed that alterations in the level of one or more miR gene products in cells can result in the deregulation of one or more intended targets for these miRs, which can lead to the formation of breast cancer. Therefore, altering the level of the miR gene product (e.g., by decreasing the level of a miR that is up-regulated in breast cancer cells, by increasing the level of a miR that is down-regulated in cancer cells) may successfully treat the breast cancer. Examples of putative gene targets for miRNAs that are deregulated in breast cancer tissues are described herein (*see, e.g.*, Example 2 and Table 4).

Accordingly, the present invention encompasses methods of treating breast cancer in a subject, wherein at least one miR gene product is de-regulated (e.g., down-regulated, up-regulated) in the cancer cells of the subject. When the at least one isolated miR gene product is down-regulated in the breast cancer cells, the method comprises administering an effective amount of the at least one isolated miR gene product, provided that the *miR* gene is not *miR15* or *miR16*, such that proliferation of cancer cells in the subject is inhibited. When the at least one isolated miR gene product is up-regulated in the cancer cells, the method comprises administering to the subject an effective amount of at least one compound for inhibiting expression of the at least one *miR* gene, referred to herein as miR gene expression inhibition compounds, such that proliferation of breast cancer cells is inhibited.

The terms "treat", "treating" and "treatment", as used herein, refer to ameliorating symptoms associated with a disease or condition, for example, breast cancer, including preventing or delaying the onset of the disease symptoms, and/or lessening the severity or frequency of symptoms of the disease or condition. The terms "subject" and "individual" 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.

As used herein, an "effective amount" of an isolated miR gene product is an amount sufficient to inhibit proliferation of a cancer cell in a subject suffering from breast cancer.

One skilled in the art can readily determine an effective amount of an miR gene product 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 an isolated 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 isolated miR gene product based on the weight of a tumor mass can be in the range of about 10-500 micrograms/gram of tumor mass. In certain embodiments, the tumor mass can be at least about 10 micrograms/gram of tumor mass, at least about 60 micrograms/gram of tumor mass or at least about 100 micrograms/gram of tumor mass.

An effective amount of an isolated miR gene product can also be based on the approximate or estimated body weight of a subject to be treated. Preferably, such effective amounts are administered parenterally or enterally, as described herein. For example, an effective amount of the isolated miR gene product is administered to a subject can range from about 5 – 3000 micrograms/kg of body weight, from about 700 - 1000 micrograms/kg of body weight, or 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 an isolated miR gene product to a given subject. For example, an miR gene product can be administered to the subject once (*e.g.*, as a single injection or deposition). Alternatively, an miR gene product can be administered once or twice daily to a subject for a period of from about three to about twenty-eight days, more particularly from about seven to about ten days. In a particular dosage regimen, an miR gene product is administered once a day for seven days. Where a dosage regimen comprises multiple administrations, it is understood that the effective amount of the miR gene product administered to the subject can comprise the total amount of gene product administered over the entire dosage regimen.

As used herein, an "isolated" miR gene product is one which is synthesized, or altered or removed from the natural state through human intervention. For example, a synthetic miR gene product, or an miR gene product partially or completely separated from the coexisting

materials of its natural state, is considered to be "isolated." An isolated miR gene product can exist in substantially-purified form, or can exist in a cell into which the miR gene product has been delivered. Thus, an miR gene product which is deliberately delivered to, or expressed in, a cell is considered an "isolated" miR gene product. An miR gene product produced inside a cell from an miR precursor molecule is also considered to be "isolated" molecule.

Isolated miR gene products can be obtained using a number of standard techniques. For example, the miR gene products can be chemically synthesized or recombinantly produced using methods known in the art. In one embodiment, miR gene 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, U.S.A.), Pierce Chemical (part of Perbio Science, Rockford, IL, U.S.A.), Glen Research (Sterling, VA, U.S.A.), ChemGenes (Ashland, MA, U.S.A.) and Cruachem (Glasgow, UK).

Alternatively, the 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, e.g., the U6 or H1 RNA pol III promoter sequences, or the cytomegalovirus promoters. Selection of other suitable promoters is within the skill in the art. The recombinant plasmids of the invention can also comprise inducible or regulatable promoters for expression of the miR gene products in cancer cells.

The miR gene products that are expressed from recombinant plasmids can be isolated from cultured cell expression systems by standard techniques. The miR gene products which are expressed from recombinant plasmids can also be delivered to, and expressed directly in, the cancer cells. The use of recombinant plasmids to deliver the miR gene products to cancer cells is discussed in more detail below.

The miR gene products can be expressed from a separate recombinant plasmid, or they can be expressed from the same recombinant plasmid. In one embodiment, the miR gene products are expressed as RNA precursor molecules from a single plasmid, and the precursor molecules are processed into the functional miR gene product by a suitable

processing system, including, but not limited to, processing systems extant within a cancer cell. Other suitable processing systems include, e.g., the *in vitro* Drosophila cell lysate system (e.g., as described in U.S. Published Patent Application No. 2002/0086356 to Tuschl *et al.*, the entire disclosure of which are incorporated herein by reference) and the *E. coli* RNAse III system (e.g., as described in U.S. Published Patent Application No. 2004/0014113 to Yang *et al.*, the entire disclosure of which are incorporated herein by reference).

Selection of plasmids suitable for expressing the miR gene products, methods for inserting nucleic acid sequences into the plasmid to express the gene products, and methods of delivering the recombinant plasmid to the cells of interest are within the skill in the art. See, for example, Zeng *et al.* (2002), *Molecular Cell* 9:1327-1333; Tuschl (2002), *Nat. Biotechnol*, 20:446-448; Brummelkamp *et al.* (2002), *Science* 296:550-553; Miyagishi *et al.* (2002), *Nat. Biotechnol.* 20:497-500; Paddison *et al.* (2002), *Genes Dev.* 16:948-958; Lee *et al.* (2002), *Nat. Biotechnol.* 20:500-505; and Paul *et al.* (2002), *Nat. Biotechnol.* 20:505-508, the entire disclosures of which are incorporated herein by reference.

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

The miR gene products can also be expressed from recombinant viral vectors. It is contemplated that the miR gene products 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 cancer cells. The use of recombinant viral vectors to deliver the miR gene products to cancer cells is discussed in more detail below.

The recombinant viral vectors of the invention comprise sequences encoding the miR gene products and any suitable promoter for expressing the RNA sequences. Suitable promoters include, for example, the U6 or H1 RNA pol III promoter 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 miR gene products in a cancer cell.

Any viral vector capable of accepting the coding sequences for the miR gene products 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 be modified by pseudotyping the vectors with envelope proteins or other surface antigens from other viruses, or by substituting different viral capsid proteins, as appropriate.

For example, lentiviral vectors of the invention can be pseudotyped with surface proteins from vesicular stomatitis virus (VSV), rabies, Ebola, Mokola, and the like. AAV vectors of the invention can be made to target different cells by engineering the vectors to express different capsid protein serotypes. For example, an AAV vector expressing a serotype 2 capsid on a serotype 2 genome is called AAV 2/2. This serotype 2 capsid gene in the AAV 2/2 vector can be replaced by a serotype 5 capsid gene to produce an AAV 2/5 vector. Techniques for constructing AAV vectors that express different capsid protein serotypes are within the skill in the art; *see, e.g.*, Rabinowitz, J.E., *et al.* (2002), *J. Virol.* 76:791-801, the entire disclosure of which is incorporated herein by reference.

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 within the skill in the art. See, for example, Dornburg (1995), *Gene Therap.* 2:301-310; Eglitis (1988), *Biotechniques* 6:608-614; Miller (1990), *Hum. Gene Therap.* 1:5-14; and Anderson (1998), *Nature* 392:25-30, the entire disclosures of which are incorporated herein by reference.

Particularly suitable viral vectors are those derived from AV and AAV. A suitable AV vector for expressing the miR gene products, a method for constructing the recombinant AV vector, and a method for delivering the vector into target cells, are described in Xia *et al.* (2002), *Nat. Biotech.* 20:1006-1010, the entire disclosure of which is incorporated herein by reference. Suitable AAV vectors for expressing the miR gene products, methods for constructing the recombinant AAV vector, and methods for delivering the vectors into target

cells are described in Samulski *et al.* (1987), *J. Virol.* 61:3096-3101; Fisher *et al.* (1996), *J. Virol.*, 70:520-532; Samulski *et al.* (1989), *J. Virol.* 63:3822-3826; U.S. Pat. No. 5,252,479; U.S. Pat. No. 5,139,941; International Patent Application No. WO 94/13788; and International Patent Application No. WO 93/24641, the entire disclosures of which are incorporated herein by reference. In one embodiment, the miR gene products are expressed from a single recombinant AAV vector comprising the CMV intermediate early promoter.

In a certain embodiment, a recombinant AAV viral vector of the invention comprises a nucleic acid sequence encoding an 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 other embodiments of the treatment methods of the invention, an effective amount of at least one compound which inhibits miR expression can also be administered to the subject. As used herein, "inhibiting miR expression" means that the production of the active, mature form of miR gene product after treatment is less than the amount produced prior to treatment. One skilled in the art can readily determine whether miR expression has been inhibited in a cancer cell, using for example the techniques for determining miR transcript level discussed above for the diagnostic method. Inhibition can occur at the level of gene expression (i.e., by inhibiting transcription of a miR gene encoding the miR gene product) or at the level of processing (e.g., by inhibiting processing of a miR precursor into a mature, active miR).

As used herein, an "effective amount" of a compound that inhibits miR expression is an amount sufficient to inhibit proliferation of a cancer cell in a subject suffering from a cancer associated with a cancer-associated chromosomal feature. One skilled in the art can readily determine an effective amount of an miR expression-inhibiting compound 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 the expression-inhibiting compound 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 based on the weight of a tumor mass can be between about 10-500 micrograms/gram of tumor mass, at least about 10 micrograms/gram of tumor mass, at least about 60 micrograms/gram of tumor mass, and at least about 100 micrograms/gram of tumor mass.

An effective amount of a compound that inhibits miR expression can also be based on the approximate or estimated body weight of a subject to be treated. Such effective amounts are administered parenterally or enterally, among others, as described herein. For example, an effective amount of the expression-inhibiting compound administered to a subject can range from about 5 -3000 micrograms/kg of body weight, from about 700 - 1000 micrograms/kg of body weight, or it 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 administering a compound that inhibits miR expression to a given subject. For example, an expression-inhibiting compound can be administered to the subject once (*e.g.*, as a single injection or deposition). Alternatively, an expression-inhibiting compound 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, an expression-inhibiting compound is administered once a day for seven days. Where a dosage regimen comprises multiple administrations, it is understood that the effective amount of the expression-inhibiting compound administered to the subject can comprise the total amount of compound administered over the entire dosage regimen.

Suitable compounds for inhibiting miR gene expression include double-stranded RNA (such as short- or small-interfering RNA or "siRNA"), antisense nucleic acids, and enzymatic RNA molecules, such as ribozymes. Each of these compounds can be targeted to a given miR gene product and destroy or induce the destruction of the target miR gene product.

For example, expression of a given miR gene can be inhibited by inducing RNA interference of the miR gene with an isolated double-stranded RNA ("dsRNA") molecule

which has at least 90%, for example at least 95%, at least 98%, at least 99% or 100%, sequence homology with at least a portion of the miR gene product. In a particular embodiment, the dsRNA molecule is a "short or small interfering RNA" or "siRNA."

siRNA useful in the present methods comprise short double-stranded RNA from about 17 nucleotides to about 29 nucleotides in length, preferably from about 19 to about 25 nucleotides in length. The siRNA comprise a sense RNA strand and a complementary antisense RNA strand annealed together by standard Watson-Crick base-pairing interactions (hereinafter "base-paired"). The sense strand comprises a nucleic acid sequence which is substantially identical to a nucleic acid sequence contained within the target miR gene product.

As used herein, a nucleic acid sequence in an siRNA which is "substantially identical" to a target sequence contained within the target mRNA is a nucleic acid sequence that is identical to the target sequence, or that differs from the target sequence by one or two nucleotides. The sense and antisense strands of the siRNA can comprise two complementary, single-stranded RNA molecules, or can comprise a single molecule in which two complementary portions are base-paired and are covalently linked by a single-stranded "hairpin" area.

The siRNA can also be altered RNA that differs from naturally-occurring RNA by the addition, deletion, substitution and/or alteration of one or more nucleotides. Such alterations can include addition of non-nucleotide material, such as to the end(s) of the siRNA or to one or more internal nucleotides of the siRNA, or modifications that make the siRNA resistant to nuclease digestion, or the substitution of one or more nucleotides in the siRNA with deoxyribonucleotides.

One or both strands of the siRNA can also comprise a 3' overhang. As used herein, a "3' overhang" refers to at least one unpaired nucleotide extending from the 3'-end of a duplexed RNA strand. Thus, in certain embodiments, the siRNA comprises at least one 3' overhang of from 1 to about 6 nucleotides (which includes ribonucleotides or deoxyribonucleotides) in length, from 1 to about 5 nucleotides in length, from 1 to about 4 nucleotides in length, or from about 2 to about 4 nucleotides in length. In a particular embodiment, the 3' overhang is present on both strands of the siRNA, and is 2 nucleotides in

length. For example, each strand of the siRNA can comprise 3' overhangs of dithymidylic acid ("TT") or diuridylic acid ("uu").

The siRNA can be produced chemically or biologically, or can be expressed from a recombinant plasmid or viral vector, as described above for the isolated miR gene products. Exemplary methods for producing and testing dsRNA or siRNA molecules are described in U.S. Published Patent Application No. 2002/0173478 to Gewirtz and in U.S. Published Patent Application No. 2004/0018176 to Reich *et al.*, the entire disclosures of which are incorporated herein by reference.

Expression of a given miR gene can also be inhibited by an antisense nucleic acid. As used herein, an "antisense nucleic acid" refers to a nucleic acid molecule that binds to target RNA by means of RNA-RNA or RNA-DNA or RNA-peptide nucleic acid interactions, which alters the activity of the target RNA. Antisense nucleic acids suitable for use in the present methods are single-stranded nucleic acids (*e.g.*, RNA, DNA, RNA-DNA chimeras, PNA) that generally comprise a nucleic acid sequence complementary to a contiguous nucleic acid sequence in an miR gene product. The antisense nucleic acid can comprise a nucleic acid sequence that is 50-100% complementary, 75-100% complementary, or 95-100% complementary to a contiguous nucleic acid sequence in an miR gene product. Nucleic acid sequences for the miR gene products are provided in Table 1. Without wishing to be bound by any theory, it is believed that the antisense nucleic acids activate RNase H or another cellular nuclease that digests the miR gene product/antisense nucleic acid duplex.

Antisense nucleic acids can also contain modifications to the nucleic acid backbone or to the sugar and base moieties (or their equivalent) to enhance target specificity, nuclease resistance, delivery or other properties related to efficacy of the molecule. Such modifications include cholesterol moieties, duplex intercalators, such as acridine, or one or more nuclease-resistant groups.

Antisense nucleic acids can be produced chemically or biologically, or can be expressed from a recombinant plasmid or viral vector, as described above for the isolated miR gene products. Exemplary methods for producing and testing are within the skill in the art; *see, e.g.*, Stein and Cheng (1993), *Science* 261:1004 and U.S. Pat. No. 5,849,902 to Woolf *et al.*, the entire disclosures of which are incorporated herein by reference.

Expression of a given miR gene can also be inhibited by an enzymatic nucleic acid. As used herein, an "enzymatic nucleic acid" refers to a nucleic acid comprising a substrate binding region that has complementarity to a contiguous nucleic acid sequence of an miR gene product, and which is able to specifically cleave the miR gene product. The enzymatic nucleic acid substrate binding region can be, for example, 50-100% complementary, 75-100% complementary, or 95-100% complementary to a contiguous nucleic acid sequence in an miR gene product. The enzymatic nucleic acids can also comprise modifications at the base, sugar, and/or phosphate groups. An exemplary enzymatic nucleic acid for use in the present methods is a ribozyme.

The enzymatic nucleic acids can be produced chemically or biologically, or can be expressed from a recombinant plasmid or viral vector, as described above for the isolated miR gene products. Exemplary methods for producing and testing dsRNA or siRNA molecules are described in Werner and Uhlenbeck (1995), *Nucl. Acids Res.* 23:2092-96; Hammann *et al.* (1999), *Antisense and Nucleic Acid Drug Dev.* 9:25-31; and U.S. Pat. No. 4,987,071 to Cech *et al*, the entire disclosures of which are incorporated herein by reference.

Administration of at least one miR gene product, or at least one compound for inhibiting miR expression, will inhibit the proliferation of cancer cells in a subject who has a cancer associated with a cancer-associated chromosomal feature. As used herein, to "inhibit the proliferation of a cancer cell" means to kill the cell, or permanently or temporarily arrest or slow the growth of the cell. Inhibition of cancer cell proliferation can be inferred if the number of such cells in the subject remains constant or decreases after administration of the miR gene products or miR gene expression-inhibiting compounds. An inhibition of 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 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 cancer cells in a subject can be measured by immunohistological methods, flow cytometry, or other techniques designed to detect characteristic surface markers of 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, ultrasound, and scintigraphy. Diagnostic imaging methods used to ascertain size of the 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.

The miR gene products or miR gene expression-inhibiting compounds can be administered to a subject by any means suitable for delivering these compounds to cancer cells of the subject. For example, the miR gene products or miR expression inhibiting compounds can be administered by methods suitable to transfect cells of the subject with these compounds, or with nucleic acids comprising sequences encoding these compounds. In one embodiment, the cells are transfected with a plasmid or viral vector comprising sequences encoding at least one miR gene product or miR gene expression inhibiting compound.

Transfection methods for eukaryotic cells are well known in the art, and include, e.g., 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 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 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.

An miR gene product or miR gene expression inhibiting compound can also be administered to a subject by any suitable enteral or parenteral administration route. Suitable enteral administration routes for the present methods include, e.g., oral, rectal, or intranasal delivery. Suitable parenteral administration routes include, e.g., 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. Particularly suitable administration routes are injection, infusion and direct injection into the tumor.

In the present methods, an miR gene product or miR gene product expression inhibiting compound can be administered to the subject either as naked RNA, in combination with a delivery reagent, or as a nucleic acid (*e.g.*, a recombinant plasmid or viral vector) comprising sequences that express the miR gene product or expression inhibiting compound. Suitable delivery reagents include, e.g., the Mirus Transit TKO lipophilic reagent; lipofectin; lipofectamine; cellfectin; polycations (*e.g.*, polylysine), and liposomes.

Recombinant plasmids and viral vectors comprising sequences that express the miR gene products or miR gene expression inhibiting compounds, and techniques for delivering such plasmids and vectors to cancer cells, are discussed herein.

In a particular embodiment, liposomes are used to deliver an miR gene product or miR gene expression-inhibiting compound (or nucleic acids comprising sequences encoding them) to a subject. Liposomes can also increase the blood half-life of the gene products or nucleic acids. Suitable liposomes 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.* (1980), *Ann. Rev. Biophys. Bioeng.* 9:467; and U.S. Pat. Nos. 4,235,871, 4,501,728, 4,837,028, and 5,019,369, the entire disclosures of which are incorporated herein by reference.

The liposomes for use in the present methods can comprise a ligand molecule that targets the liposome to cancer cells. Ligands which bind to receptors prevalent in cancer cells, such as monoclonal antibodies that bind to tumor cell antigens, are preferred.

The liposomes for use in the present methods can also be modified so as to avoid clearance by the mononuclear macrophage system ("MMS") and reticuloendothelial system ("RES"). Such modified liposomes have opsonization-inhibition moieties on the surface or incorporated into the liposome structure. In a particularly preferred 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 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 significantly decreases the uptake of the liposomes by the MMS and RES; e.g., as described in U.S. Pat. No. 4,920,016, the entire disclosure of which is incorporated herein by reference.

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, polyethyleneamine, 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. Preferably, the opsonization-inhibiting moiety is a PEG, PPG, or derivatives 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 $Na(CN)BH_3$ 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.* (1988), Proc. Natl. Acad. Sci., U.S.A., 18:6949-53. 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 miR gene expression inhibition compounds (or nucleic acids comprising sequences encoding them) to tumor cells.

The miR gene products or miR gene expression inhibition compounds can be formulated as pharmaceutical compositions, sometimes called "medicaments," prior to administering them to a subject, according to techniques known in the art. Accordingly, the invention encompasses pharmaceutical compositions for treating breast cancer. In one embodiment, the pharmaceutical compositions comprise at least one isolated miR gene product and a pharmaceutically-acceptable carrier. In a particular embodiment, the at least one miR gene product corresponds to a miR gene product that has a decreased level of expression in breast cancer cells relative to suitable control cells. In certain embodiments the isolated miR gene product is selected from the group consisting of miR-145, miR-10b, miR-

123 (miR-126), miR-140-as, miR-125a, miR-125b-1, miR-125b-2, miR-194, miR-204, let-7a-2, let-7a-3, let-7d (let-7d-v1), let-7f-2, miR-101-1, miR-143 and combinations thereof.

In other embodiments, the pharmaceutical compositions of the invention comprise at least one miR expression inhibition compound. In a particular embodiment, the at least one miR gene expression inhibition compound is specific for a miR gene whose expression is greater in breast cancer cells than control cells. In certain embodiments, the miR gene expression inhibition compound is specific for one or more miR gene products selected from the group consisting of miR-21, miR-155, miR-009-1 (miR131-1), miR-34 (miR-170), miR-102 (miR-29b), miR-213, let-7i (let-7d-v2), miR-122a, miR-128b, miR-136, miR-149, miR-191, miR-196-1, miR-196-2, miR-202, miR-203, miR-206, miR-210, miR-213 and combinations thereof.

Pharmaceutical compositions of the present invention are characterized as being at least sterile and pyrogen-free. As used herein, "pharmaceutical formulations" include formulations for human and veterinary use. Methods for preparing pharmaceutical 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), the entire disclosure of which is incorporated herein by reference.

The present pharmaceutical formulations comprise at least one miR gene product or miR gene expression inhibition compound (or at least one nucleic acid comprising sequences encoding them) (e.g., 0.1 to 90% by weight), or a physiologically acceptable salt thereof, mixed with a pharmaceutically-acceptable carrier. The pharmaceutical formulations of the invention can also comprise at least one miR gene product or miR gene expression inhibition compound (or at least one nucleic acid comprising sequences encoding them) which are encapsulated by liposomes and a pharmaceutically-acceptable carrier. In one embodiment, the pharmaceutical compositions comprise an miR gene or gene product that is not miR-15, miR-16, miR-143 and/or miR-145.

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

In a particular embodiment, the pharmaceutical compositions of the invention comprise at least one miR gene product or miR gene expression inhibition compound (or at

least one nucleic acid comprising sequences encoding them) which is resistant to degradation by nucleases. One skilled in the art can readily synthesize nucleic acids which are nuclease resistant, for example by incorporating one or more ribonucleotides that are modified at the 2'-position into the miR gene products. Suitable 2'-modified ribonucleotides include those modified at the 2'-position with fluoro, amino, alkyl, alkoxy, and O-allyl.

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, e.g., physiologically biocompatible buffers (e.g., tromethamine hydrochloride), additions of chelants (such as, for example, DTPA or DTPA-bisamide) or calcium chelate complexes (such as, for example, calcium DTPA, CaNaDTPA-bisamide), or, optionally, additions of calcium or sodium salts (for example, 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 at least one miR gene product or miR gene expression inhibition compound (or at least one nucleic acid comprising sequences encoding them). A pharmaceutical composition for aerosol (inhalational) administration can comprise 0.01-20% by weight, preferably 1%-10% by weight, of the at least one miR gene product or miR gene expression inhibition compound (or at least one nucleic acid comprising sequences encoding them) 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 methods of identifying an anti-breast cancer agent, comprising providing a test agent to a cell and measuring the level of at least one miR gene product in the cell. In one embodiment, the method comprises providing a test agent to a cell

and measuring the level of at least one miR gene product associated with decreased expression levels in breast cancer cells. An increase in the level of the miR gene product in the cell, relative to a suitable control cell, is indicative of the test agent being an anti-breast cancer agent. In a particular embodiment, at least one miR gene product associated with decreased expression levels in breast cancer cells is selected from the group consisting of miR-145, miR-10b, miR-123 (miR-126), miR-140-as, miR-125a, miR-125b-1, miR-125b-2, miR-194, miR-204, let-7a-2, let-7a-3, let-7d (let-7d-v1), let-7f-2, miR-101-1, miR-143 and combinations thereof.

In other embodiments the method comprises providing a test agent to a cell and measuring the level of at least one miR gene product associated with increased expression levels in breast cancer cells. A decrease in the level of the miR gene product in the cell, relative to a suitable control cell, is indicative of the test agent being an anti-breast cancer agent. In a particular embodiment, at least one miR gene product associated with increased expression levels in breast cancer cells is selected from the group consisting of miR-21, miR-155, miR-009-1 (miR131-1), miR-34 (miR-170), miR-102 (miR-29b), miR-213, let-7i (let-7d-v2), miR-122a, miR-128b, miR-136, miR-149, miR-191, miR-196-1, miR-196-2, miR-202, miR-203, miR-206, miR-210, miR-213 and combinations thereof.

Suitable agents include, but are not limited to drugs (e.g., small molecules, peptides), and biological macromolecules (e.g., proteins, nucleic acids). The agent can be produced recombinantly, synthetically, or it may be isolated (i.e., purified) from a natural source. Various methods for providing such agents to a cell (e.g., transfection) are well known in the art, and several of such methods are described hereinabove. Methods for detecting the expression of at least one miR gene product (e.g., Northern blotting, *in situ* hybridization, RT-PCR, expression profiling) are also well known in the art. Several of these methods are also described hereinabove.

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

Example 1: *Identification of a microRNA expression signature that discriminates breast cancer tissues from normal tissues.*

Materials and Methods

Breast cancer samples and cell lines. RNAs from primary tumors were obtained from 76 samples collected at the University of Ferrara (Italy), Istituto Nazionale dei Tumori, Milano (Italy) and Thomas Jefferson University (Philadelphia, PA). Clinico-pathological information was available for 58 tumor samples. RNA from normal samples consisted of 6 pools of RNA from 5 normal breast tissues each, as well as RNA from 4 additional single breast tissues. Breast cancer RNAs were also obtained from the following cell lines: Hs578-T, MCF7, T47D, BT20, SK-BR-3, HBL100, HCC2218, MDA-MB-175, MDA-MB-231, MDA-MB-361, MDA-MB-435, MDA-MB-436, MDA-MB-453 and MDAMB-468.

miRNA microarray. Total RNA isolation was performed with Trizol Reagent (Invitrogen) according to the manufacturer's instructions. RNA labeling and hybridization on microRNA microarray chips was performed as previously described (Liu, C.-G., *et al., Proc. Natl. Acad. Sci. U.S.A. 101*:9740-9744 (2004)). Briefly, 5 μg of RNA from each sample was labeled with biotin during reverse transcription using random hexamers. Hybridization was carried out on a miRNA microarray chip (KCI version 1.0) (Liu, C.-G., *et al., Proc. Natl. Acad. Sci. U.S.A. 101*:9740-9744 (2004)), which contains 368 probes, including 245 human and mouse miRNA genes, in triplicate. Hybridization signals were detected by binding of biotin to a Streptavidin–Alexa647 conjugate using a Perkin-Elmer ScanArray XL5K. Scanner images were quantified by the Quantarray software (Perkin Elmer).

Statistical and bioinformatic analysis of microarray data. Raw data were normalized and analyzed using the GeneSpring® software, version 7.2 (SiliconGenetics, Redwood City, CA). Expression data were median centered. Statistical comparisons were performed by ANOVA (Analysis of Variance), using the Benjamini and Hochberg correction for reduction of false positives. Prognostic miRNAs for tumor or normal class prediction were determined using both the PAM software (Prediction Analysis of Microarrays, available at http://www.stat.stanford.edu/~tibs/PAM/index.html) (Tibshirani, R., *et al. Proc. Natl. Acad.*

Sci. U.S.A. 99:6567-6572 (2002)) and the Support Vector Machine (Furey, T.S., *et al. Bioinformatics 16*: 906-914 (2000)) software. Both algorithms were used for Cross-validation and Test-set prediction. All data were submitted using MIAMExpress to the Array Express database (accession numbers to be received upon revision).

Northern Blotting. Northern blot analysis was performed as previously described (Calin, G.A., *et al., Proc. Natl. Acad. Sci. U.S.A. 99*:15524-29 (2002)). RNA samples (10 μg each) were electrophoresed on 15% acrylamide, 7 M urea Criterion pre-casted gels (Bio-Rad) and transferred onto Hybond-N+ membrane (Amersham Pharmacia Biotech). The hybridization was performed at 37°C in 7% sodium dodecyl sulfate (SDS) / 0.2M Na_2PO_4 (pH 7.0) for 16 hours. Membranes were washed twice at 42°C with 2x standard saline phosphate (0.18 M NaCl/10 mM phosphate, pH 7.4), supplemented with 1 mM EDTA (SSPE) and 0.1% SDS, and twice with 0.5X SSPE /0.1% SDS. Oligonucleotide probes were complementary to the sequence of the corresponding mature microRNA (see miR Registry at http://www.sanger.ac.uk/Software/Rfam/mirna/): miR-21 5'- TCA ACA TCA GTC TGA TAA GCT A -3' (SEQ ID NO:287); miR-125b1: 5'- TCA CAA GTT AGG GTC TCA GGG A -3' (SEQ ID NO:288); miR-145: 5'- AAG GGA TTC CTG GGA AAA CTG GAC -3' (SEQ ID NO:289). An oligonucleotide that was complementary to the U6 RNA (5'- GCA GGG GCC ATG CTA ATC TTC TCT GTA TCG -3' (SEQ ID NO:290)) was used for normalizing expression levels. 200 ng of each probe was end labeled with 100 mCi [gamma-^{32}P]-ATP using a polynucleotide kinase (Roche). Northern Blots were stripped in a boiling 0.1% SDS solution for 10 minutes before re-hybridization.

Results

A microRNA microarray (Liu, C.-G., *et al., Proc. Natl. Acad. Sci. U.S.A. 101*:9740-9744 (2004)) was used to generate microRNA expression profiles for 10 normal and 76 neoplastic breast tissues. Each tumor sample was derived from a single specimen, while 6 of the 10 normal samples consisted of pools of RNA made from five different normal breast tissues. Hence, 34 normal breast samples were actually examined in the study.

To identify miRNAs that were differentially-expressed between normal and tumor samples, and, therefore, can be used to distinguish normal from cancerous breast tissues, analyses of variance and class prediction statistical tools were utilized. Results of the ANOVA analysis on normalized data generated a profile of differentially-expressed miRNAs ($p<0.05$) between normal and cancerous breast tissues (Table 2). Cluster analysis, based on differentially-expressed miRNA, generated a tree having a clear distinction between normal and cancer tissues (FIG. 1A).

To accurately identify a set of predictive miRNAs capable of differentiating normal from breast cancer tissues, we used Support Vector Machine (GeneSpring software) and PAM (Prediction Analysis of Microarrays) (http://wwwstat.stanford.edu/~tibs/). Results from the two class prediction analyses largely overlapped (Table 3 and FIG. 1B). Among the miRNAs listed in Table 3, 11 of 15 have an ANOVA p-value of less than 0.05. To confirm the results obtained by microarray analysis, we performed Northern blot analysis to assess expression levels for a subset of microRNAs, namely, *mir-125b*, *mir-145* and *mir-21*, that were differentially-expressed in normal and cancerous breast tissues. Northern blot analysis confirmed results obtained by microarray analysis. In many cases, expression differences appeared stronger than those anticipated by the microarray studies (FIG. 1C).

Table 2. miRNAs differentially-expressed between breast carcinoma and normal breast tissue.

		Breast Cancer				Normal Breast			
		Median	Range			Median	Range		
	P-value	Normalized	Min		Max	Normalized	Min		Max
let-7a-2	1.94E-02	1.67	0.96	-	6.21	2.30	1.34	-	5.00
let-7a-3	4.19E-02	1.26	0.81	-	3.79	1.58	1.02	-	2.91
let-7d (= 7d-v1)	4.61E-03	0.90	0.59	-	1.54	1.01	0.83	-	1.25
let-7f-2	6.57E-03	0.84	0.51	-	1.58	0.92	0.76	-	1.03
let-7i (= let-7d-v2)	3.38E-02	2.05	1.02	-	7.49	1.53	1.01	-	3.47
mir-009-1 (mir-131-1)	9.12E-03	1.36	0.69	-	4.16	1.01	0.61	-	2.44
mir-010b	4.49E-02	1.11	0.69	-	4.79	1.70	0.96	-	6.32
mir-021	4.67E-03	1.67	0.66	-	26.43	1.09	0.60	-	2.31
mir-034 (=mir-170)	1.06E-02	1.67	0.70	-	6.40	1.09	0.65	-	3.17
mir-101-1	4.15E-03	0.83	0.52	-	1.26	0.99	0.77	-	1.05
mir-122a	3.43E-03	2.21	0.93	-	8.08	1.48	1.06	-	3.67
mir-125a	3.28E-03	1.20	0.69	-	2.36	1.73	1.21	-	3.34
mir-125b-1	2.65E-02	1.30	0.55	-	8.85	2.87	1.45	-	18.38
mir-125b-2	2.33E-02	1.26	0.69	-	6.29	2.63	1.40	-	16.78
mir-126b	1.60E-02	1.12	0.68	-	7.34	1.02	0.89	-	1.27
mir-136	2.42E-03	1.32	0.74	-	10.26	1.06	0.76	-	1.47
mir-143	7.11E-03	0.87	0.68	-	1.33	0.99	0.81	-	1.17
mir-145	4.02E-03	1.52	0.92	-	8.46	3.61	1.65	-	14.45
mir-149	2.75E-02	1.11	0.53	-	1.73	1.03	0.83	-	1.22
mir-155(BIC)	1.24E-03	1.75	0.95	-	11.45	1.37	1.11	-	1.88
mir-191	4.26E-02	5.17	1.03	-	37.81	3.12	1.45	-	14.58
mir-196-1	1.07E-02	1.20	0.57	-	3.95	0.95	0.66	-	1.75
mir-196-2	1.16E-03	1.46	0.57	-	5.55	1.04	0.79	-	1.80
mir-202	1.25E-02	1.05	0.71	-	2.03	0.89	0.65	-	1.20
mir-203	4.06E-07	1.12	0.50	-	5.89	0.88	0.71	-	1.04
mir-204	2.15E-03	0.78	0.46	-	1.04	0.89	0.72	-	1.08
mir-206	1.42E-02	2.55	1.22	-	6.42	1.95	1.34	-	3.22
mir-210	6.40E-13	1.60	0.98	-	12.13	1.12	0.97	-	1.29
mir-213	1.08E-02	3.72	1.42	-	40.83	2.47	1.35	-	5.91

Table 3. Normal and tumor breast tissues class predictor microRNAs

a - Analysis of Variance (Welch t-test in Genespring software package) as calculated in Table

miRNA name	Median expression		ANOVA[a] Probability	SVM prediction strength[b]	PAM score[c]		Chromos map
	Cancer	Normal			Cancer	Normal	
mir-009-1	1.36	1.01	0,0091	8.05	0.011	-0.102	1q22
mir-010b	1.11	1.70	0,0449	8.70	-0.032	0.299	2q31
mir-021	1.67	1.08	0,0047	10.20	0.025	-0.235	17q23.2
mir-034	1.67	1.09	0,0106	8.05	0.011	-0.106	1p36.22
mir-102 (mir-29b)	1.36	1.14	> 0.10	8.92	0.000	-0.004	1q32.2-32.3
mir-123 (mir-126)	0.92	1.13	0,0940	9.13	-0.015	0.138	9q34
mir-125a	1.20	1.73	0,0033	8.99	-0.040	0.381	19q13.4
mir-125b-1	1.30	2.87	0,0265	14.78	-0.096	0.915	11q24.1
mir-125b-2	1.26	2.63	0,0233	17.62	-0.106	1.006	21q11.2
mir-140-as	0.93	1.10	0,0695	11.01	-0.005	0.050	16q22.1
mir-145	1.52	3.61	0,0040	12.93	-0.158	1.502	5q32-33
mir-155(BIC)	1.75	1.37	0,0012	10.92	0.003	-0.030	21q21
mir-194	0.96	1.09	> 0.10	11.12	-0.025	0.234	1q41
mir-204	0.78	0.89	0,0022	8.10	-0.015	0.144	9q21.1
mir-213	3.72	2.47	0,0108	9.44	0.023	-0.220	1q31.3-q32.1

2.

b - Support Vector Machine prediction analysis tool (from Genespring 7.2 software package). Prediction strengths are calculated as negative natural log of the probability to predict the observed number of samples, in one of the two classes, by chance. The higher is the score, the best is the prediction strength.

c - Centroid scores for the two classes of the Prediction Analysis of Microarrays (Tibshirani, R., *et al. Proc. Natl. Acad. Sci. U.S.A.* 99:6567-6572 (2002)).

Of the 29 miRNAs whose expression is significantly ($p<0.05$) deregulated according to the microarray analysis, a set of 15 miRNAs were able to correctly predict the nature of the sample analyzed (i.e., normal vs. tumor) with 100% accuracy. Among the differentially-expressed miRNAs, *miR-10b*, *miR-125b*, *miR145*, *miR-21* and *miR-155* were the most consistently deregulated miRNAs in breast cancer samples. Three of these, namely, *miR-10b*, *miR-125b* and *miR-145*, were down-regulated, while the remaining two, *miR-21* and *miR-155*, were up-regulated, suggesting that they might act as tumor suppressor genes or oncogenes, respectively.

Example 2: *Determination of putative gene targets of miRNAs that are deregulated in breast cancer tissues.*

At present, the lack of knowledge about *bona fide* miRNA gene targets hampers a full understanding of which biological functions are deregulated in cancers characterized by aberrant miRNA expression. To identify putative targets of the most significantly de-

regulated miRNAs from our study: *miR-10b*, *miR125b*, *miR-145*, *miR-21* and *miR-155* (see Example 1), we utilized multiple computational approaches. In particular, the analysis was performed using three algorithms, miRanda, TargetScan and PicTar, which are commonly used to predict human miRNA gene targets (Enright, A.J., *et al. Genome Biol. 5*:R1 (2003); Lewis, B.P. *et al., Cell 115*:787-798 (2003); Krek, A., *et al., Nat. Genet. 37*:495-500 (2005)). The results obtained using each of the three algorithms were cross-referenced with one another to validate putative targets and only targets that were identified by at least 2 of the 3 algorithms were considered. Results of this analysis are presented in Table 4.

Several genes with potential oncogenic functions were identified as putative targets of miRNAs that are down-regulated in breast cancer samples. Notably, oncogenes were identified as targets of *miR-10b* (e.g., *FLT1,* the v-crk homolog, the growth factor *BDNF* and the transducing factor *SHC1), miR-125b* (e.g., *YES, ETS1, TEL, AKT3,* the growth factor receptor *FGFR2* and members of the mitogen-activated signal transduction pathway *VTS58635, MAP3K10, MAP3K11, MAPK14*), and *miR-145* (e.g., *MYCN, FOS, YES* and *FLI1*, integration site of Friend leukemia virus, cell cycle promoters, such as *cyclins D2* and *L1*, MAPK transduction proteins, such as MAP3K3 and MAP4K4). The proto-oncogene, *YES,* and the core-binding transcription factor, *CBFB,* were determined to be potential targets of both *miR-125* and *miR-145.*

Consistent with these findings, multiple tumor suppressor genes were identified as targets of *miR-21* and *miR-155*, miRNAs that are up-regulated in breast cancer cells. For *miR-21*, the *TGFB* gene was predicted as target by all three methods. For *miR-155*, potential targets included the tumor suppressor genes, *SOCS1* and *APC*, and the kinase, *WEE1*, which blocks the activity of Cdc2 and prevents entry into mitosis. The hypoxia inducible factor, *HIF1A,* was also a predicted target of *miR-155.* Notably, the tripartite motif-containing protein *TRIM2*, the proto-oncogene, *SKI,* and the RAS homologs, *RAB6A* and *RAB6C,* were found as potential targets of both *miR-21* and *miR-155.*

Table 4. Putative gene targets of differentially-expressed miRNA identified by at least two prediction methods

miRNA	Genbank	Gene Symbol	Gene Name	Prediction algorithm	Gene Ontology condensed
miR-10b	AL117516	38596	strand-exchange protein 1	P+T	exonuclease activity|nucleus
miR-10b	NM_004915	ABCG1	ATP-binding cassette, sub-family G (WHITE), member 1	P+T	ATP binding|ATPase activity|ATPase activity, coupled to transmembrane movement of substances|L-tryptophan transporter activity|cholesterol homeostasis|cholesterol metabolism|detection of hormone stimulus|integral to plasma membrane|lipid transport|membrane|membrane fraction|permease activity|protein dimerization activity|purine nucleotide transporter activity|response to organic substance
miR-10b	NM_001148	ANK2	ankyrin 2, neuronal	P+T	actin cytoskeleton|membrane|metabolism|oxidoreductase activity|protein binding|signal transduction|structural constituent of cytoskeleton
miR-10b	NM_020987	ANK3	ankyrin 3, node of Ranvier (ankyrin G)	P+T	Golgi apparatus|cytoskeletal anchoring|cytoskeleton|cytoskeleton|endoplasmic reticulum|protein binding|protein targeting|signal transduction|structural constituent of cytoskeleton
miR-10b	NM_016376	ANKHZN	ANKHZN protein	P+T	endocytosis|endosome membrane|membrane|protein binding|zinc ion binding
miR-10b	NM_006380	APPBP2	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	P+T	binding|cytoplasm|intracellular protein transport|membrane|microtubule associated complex|microtubule motor activity|nucleus
miR-10b	NM_006321	ARIH2	ariadne homolog 2 (Drosophila)	P+T	development|nucleic acid binding|nucleus|protein ubiquitination|ubiquitin ligase complex|ubiquitin-protein ligase activity|zinc ion binding
miR-10b	NM_001668	ARNT	aryl hydrocarbon receptor nuclear translocator	P+T	aryl hydrocarbon receptor nuclear translocator activity|nucleus|nucleus|protein-nucleus import, translocation|receptor activity|regulation of transcription, DNA-dependent|signal transducer activity|signal transduction|transcription coactivator activity|transcription factor activity|transcription factor activity
miR-10b	AI829840	ASXL1	ESTs, Weakly similar to SFRB_HUMAN Splicing factor arginine/serine-rich 11 (Arginine-rich 54 kDa nuclear protein) (P54) [H.sapiens]	P+T	nucleus|regulation of transcription, DNA-dependent|transcription
miR-10b	NM_021813	BACH2	BTB and CNC homology 1, basic leucine zipper transcription factor 2	P+T	DNA binding|nucleus|protein binding|regulation of transcription, DNA-dependent|transcription
miR-10b	NM_013450	BAZ2B	bromodomain adjacent to zinc finger domain, 2B	P+T	DNA binding|nucleus|regulation of transcription, DNA-dependent|transcription
miR-10b	NM_001706	BCL6	B-cell CLL/lymphoma 6 (zinc finger protein 51)	P+T	inflammatory response|mediator complex|negative regulation of transcription from RNA polymerase II promoter|nucleus|positive regulation of cell proliferation|protein binding|regulation of transcription, DNA-dependent|transcription|transcription factor activity|zinc ion binding
miR-10b	NM_001709	BDNF	brain-derived neurotrophic factor	P+T	growth factor activity|growth factor activity|neurogenesis

miR-10b	NM_006624	BS69	adenovirus 5 E1A binding protein	P+T	DNA binding|cell cycle|cell proliferation|negative regulation of cell cycle|negative regulation of transcription from RNA polymerase II promoter|nucleus|regulation of transcription, DNA-dependent|transcription
miR-10b	AF101784	BTRC	beta-transducin repeat containing	P+T	Wnt receptor signaling pathway|endoplasmic reticulum|ligase activity|signal transduction|ubiquitin conjugating enzyme activity|ubiquitin cycle|ubiquitin-dependent protein catabolism
miR-10b	NM_005808	C3orf8	HYA22 protein	P+T	biological_process unknown|molecular_function unknown|nucleus
miR-10b	BF111268	CAMK2G	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma	P+T	ATP binding|ATP binding|calcium- and calmodulin-dependent protein kinase activity|calcium-dependent protein serine/threonine phosphatase activity|calmodulin binding|cellular_component unknown|insulin secretion|kinase activity|protein amino acid phosphorylation|protein amino acid phosphorylation|protein serine/threonine kinase activity|protein-tyrosine kinase activity|signal transduction|transferase activity
miR-10b	NM_020184	CNNM4	cyclin M4	P+T	
miR-10b	NM_022730	COPS7B	COP9 constitutive photomorphogenic homolog subunit 7B (Arabidopsis)	P+T	signalosome complex
miR-10b	NM_016823	CRK	v-crk sarcoma virus CT10 oncogene homolog (avian)	P+T	SH3/SH2 adaptor activity|actin cytoskeleton organization and biogenesis|cell motility|cytoplasm|intracellular signaling cascade|nucleus|regulation of transcription from RNA polymerase II promoter
miR-10b	NM_020248	CTNNBIP1	catenin, beta interacting protein 1	P+T	Wnt receptor signaling pathway|beta-catenin binding|cell proliferation|development|nucleus|regulation of transcription, DNA-dependent|signal transduction
miR-10b	NM_018959	DAZAP1	DAZ associated protein 1	P+T	RNA binding|cell differentiation|nucleotide binding|nucleus|spermatogenesis
miR-10b	AL136828	DKFZP434K0427	hypothetical protein DKFZp434K0427	P+T	cation transport|cation transporter activity
miR-10b	R20763	DKFZp547J036	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 3 (Hu antigen C)	P+T	
miR-10b	AF009204	DLGAP2	discs, large (Drosophila) homolog-associated protein 2	P+T	cell-cell signaling|membrane|nerve-nerve synaptic transmission|neurofilament|protein binding
miR-10b	NM_001949	E2F3	E2F transcription factor 3	P+T	nucleus|protein binding|regulation of cell cycle|regulation of transcription, DNA-dependent|transcription|transcription factor activity|transcription factor complex|transcription initiation from RNA polymerase II promoter
miR-10b	NM_022659	EBF2	early B-cell factor 2	P+T	DNA binding|development|nucleus|regulation of transcription, DNA-dependent|transcription
miR-10b	NM_004432	ELAVL2	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B)	P+T	RNA binding|mRNA 3'-UTR binding|nucleotide binding|regulation of transcription, DNA-dependent
miR-10b	NM_001420	ELAVL3	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 3 (Hu antigen C)	P+T	RNA binding|cell differentiation|mRNA 3'-UTR binding|neurogenesis|nucleotide binding
miR-10b	NM_004438	EPHA4	EphA4	P+T	ATP binding|ephrin receptor activity|integral to plasma membrane|membrane|protein amino acid phosphorylation|receptor activity|signal transduction|transferase activity|transmembrane receptor protein tyrosine kinase signaling pathway
miR-10b	AL035703	EPHA8; EEK; HEK3; Hek3; KIAA1459	EphA8	P+T	

miR-10b	NM_004468	FHL3	four and a half LIM domains 3	P+T	muscle development|zinc ion binding
miR-10b	NM_024679	FLJ11939	hypothetical protein FLJ11939	P+T	
miR-10b	AI742838	FLJ32122	hypothetical protein FLJ32122	P+T	GTP binding|GTPase binding|guanyl-nucleotide exchange factor activity
miR-10b	AL040935	FLJ33957	hypothetical protein FLJ33957	P+T	protein binding
miR-10b	AA058828	FLT1	ESTs	P+T	ATP binding|angiogenesis|cell differentiation|extracellular space|integral to plasma membrane|membrane|positive regulation of cell proliferation|pregnancy|protein amino acid phosphorylation|receptor activity|transferase activity|transmembrane receptor protein tyrosine kinase signaling pathway|vascular endothelial growth factor receptor activity
miR-10b	NM_004860	FXR2	fragile X mental retardation, autosomal homolog 2	P+T	RNA binding|cytoplasm|cytosolic large ribosomal subunit (sensu Eukaryota)|nucleus
miR-10b	NM_020474	GALNT1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1)	P+T	Golgi apparatus|O-linked glycosylation|integral to membrane|manganese ion binding|polypeptide N-acetylgalactosaminyltransferase activity|sugar binding|transferase activity, transferring glycosyl groups
miR-10b	D87811	GATA6	GATA binding protein 6	P+T	muscle development|nucleus|positive regulation of transcription|regulation of transcription, DNA-dependent|transcription|transcription factor activity|transcriptional activator activity|zinc ion binding
miR-10b	NM_000840	GRM3	glutamate receptor, metabotropic 3	P+T	G-protein coupled receptor protein signaling pathway|integral to plasma membrane|membrane|metabotropic glutamate, GABA-B-like receptor activity|negative regulation of adenylate cyclase activity|receptor activity|signal transduction|synaptic transmission
miR-10b	NM_005316	GTF2H1	general transcription factor IIH, polypeptide 1, 62kDa	P+T	DNA repair|[RNA-polymerase]-subunit kinase activity|general RNA polymerase II transcription factor activity|nucleus|regulation of cyclin dependent protein kinase activity|regulation of transcription, DNA-dependent|transcription|transcription factor TFIIH complex|transcription from RNA polymerase II promoter
miR-10b	AF232772	HAS3	hyaluronan synthase 3	P+T	carbohydrate metabolism|hyaluronan synthase activity|integral to plasma membrane|transferase activity, transferring glycosyl groups
miR-10b	AL023584	HIVEP2	human immunodeficiency virus type I enhancer binding protein 2	P+T	
miR-10b	S79910	HOXA1	homeo box A1	P+T	RNA polymerase II transcription factor activity|development|nucleus|regulation of transcription, DNA-dependent|transcription factor activity
miR-10b	NM_030661	HOXA3	homeo box A3	P+T	development|nucleus|regulation of transcription, DNA-dependent|transcription factor activity
miR-10b	AW299531	HOXD10	homeo box D10	P+T	RNA polymerase II transcription factor activity|development|nucleus|regulation of transcription, DNA-dependent|transcription factor activity
miR-10b	BF031714	HYA22	HYA22 protein	P+T	
miR-10b	NM_001546	ID4	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	P+T	nucleus|regulation of transcription from RNA polymerase II promoter|transcription corepressor activity
miR-10b	NM_014333	IGSF4	immunoglobulin superfamily, member 4	P+T	
miR-10b	NM_014271	IL1RAPL1	interleukin 1 receptor accessory protein-like 1	P+T	integral to membrane|learning and/or memory|membrane|signal transduction|transmembrane receptor activity
miR-10b	D87450	KIAA0261	KIAA0261 protein	P+T	
miR-10b	AL117518	KIAA0978	KIAA0978 protein	P+T	nucleus|regulation of transcription, DNA-

					dependent|transcription
miR-10b	AK025960	KIAA1255	KIAA1255 protein	P+T	endocytosis|endosome membrane|membrane|protein binding|zinc ion binding
miR-10b	AB037797	KIAA1376	KIAA1376 protein	P+T	
miR-10b	NM_004795	KL	klotho	P+T	beta-glucosidase activity|carbohydrate metabolism|extracellular space|glucosidase activity|integral to membrane|integral to plasma membrane|membrane fraction|signal transducer activity|soluble fraction
miR-10b	NM_015995	KLF13	Kruppel-like factor 13	P+T	DNA binding|RNA polymerase II transcription factor activity|nucleus|regulation of transcription, DNA-dependent|transcription|transcription from RNA polymerase II promoter|zinc ion binding
miR-10b	NM_004235	KLF4	Kruppel-like factor 4 (gut)	P+T	mesodermal cell fate determination|negative regulation of cell proliferation|negative regulation of transcription, DNA-dependent|negative regulation of transcription, DNA-dependent|nucleic acid binding|nucleus|transcription|transcription factor activity|transcription factor activity|transcriptional activator activity|transcriptional activator activity|transcriptional repressor activity|transcriptional repressor activity|zinc ion binding|zinc ion binding
miR-10b	AW511293	LOC144455	hypothetical protein BC016658	P+T	regulation of cell cycle|regulation of transcription, DNA-dependent|transcription factor activity|transcription factor complex
miR-10b	NM_014921	LPHN1	lectomedin-2	P+T	G-protein coupled receptor activity|integral to membrane|latrotoxin receptor activity|membrane|neuropeptide signaling pathway|receptor activity|signal transduction|sugar binding
miR-10b	NM_012325	MAPRE1	microtubule-associated protein, RP/EB family, member 1	P+T	cell proliferation|cytokinesis|microtubule binding|mitosis|protein C-terminus binding|regulation of cell cycle
miR-10b	AA824369	MGC4643	hypothetical protein MGC4643	P+T	Wnt receptor signaling pathway|endoplasmic reticulum|ligase activity|signal transduction|ubiquitin conjugating enzyme activity|ubiquitin cycle|ubiquitin-dependent protein catabolism
miR-10b	NM_021090	MTMR3	myotubularin related protein 3	P+T	cytoplasm|hydrolase activity|inositol or phosphatidylinositol phosphatase activity|membrane|membrane fraction|phospholipid dephosphorylation|protein amino acid dephosphorylation|protein serine/threonine phosphatase activity|protein tyrosine phosphatase activity|protein tyrosine/serine/threonine phosphatase activity|zinc ion binding
miR-10b	AI498126	NAC1	transcriptional repressor NAC1	P+T	protein binding
miR-10b	AF128458	NCOA6	nuclear receptor coactivator 6	P+T	DNA recombination|DNA repair|DNA replication|brain development|chromatin binding|embryonic development (sensu Mammalia)|estrogen receptor binding|estrogen receptor signaling pathway|glucocorticoid receptor signaling pathway|heart development|ligand-dependent nuclear receptor transcription coactivator activity|myeloid blood cell differentiation|nucleus|nucleus|positive regulation of transcription from RNA polymerase II promoter|protein binding|regulation of transcription, DNA-dependent|response to hormone stimulus|retinoid X receptor binding|thyroid hormone receptor binding|transcription|transcription factor complex|transcription initiation from RNA polymerase II promoter|transcriptional activator activity
miR-10b	NM_006312	NCOR2	nuclear receptor co-repressor 2	P+T	DNA binding|nucleus|regulation of transcription, DNA-dependent|transcription corepressor activity

miR-10b	NM_006599	NFAT5	nuclear factor of activated T-cells 5, tonicity-responsive	P+T	RNA polymerase II transcription factor activity|excretion|nucleus|regulation of transcription, DNA-dependent|signal transduction|transcription factor activity|transcription from RNA polymerase II promoter
miR-10b	NM_006981	NR4A3	nuclear receptor subfamily 4, group A, member 3	M+P+T	binding|nucleus|nucleus|regulation of transcription, DNA-dependent|steroid hormone receptor activity|steroid hormone receptor activity|thyroid hormone receptor activity|transcription|transcription factor activity
miR-10b	NM_003822	NR5A2	nuclear receptor subfamily 5, group A, member 2	P+T	RNA polymerase II transcription factor activity, enhancer binding|morphogenesis|nucleus|nucleus|regulation of transcription, DNA-dependent|steroid hormone receptor activity|transcription|transcription factor activity|transcription from RNA polymerase II promoter
miR-10b	AA295257	NRP2	neuropilin 2	P+T	angiogenesis|axon guidance|cell adhesion|cell adhesion|cell differentiation|electron transport|electron transporter activity|integral to membrane|membrane|membrane fraction|neurogenesis|receptor activity|semaphorin receptor activity|vascular endothelial growth factor receptor activity|vascular endothelial growth factor receptor activity
miR-10b	NM_000430	PAFAH1B1	platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa	P+T	astral microtubule|cell cortex|cell cycle|cell differentiation|cell motility|cytokinesis|cytoskeleton|dynein binding|establishment of mitotic spindle orientation|kinetochore|lipid metabolism|microtubule associated complex|microtubule-based process|mitosis|neurogenesis|nuclear membrane|signal transduction
miR-10b	NM_013382	POMT2	putative protein O-mannosyltransferase	P+T	O-linked glycosylation|dolichyl-phosphate-mannose-protein mannosyltransferase activity|endoplasmic reticulum|integral to membrane|magnesium ion binding|membrane|transferase activity, transferring glycosyl groups
miR-10b	BF337790	PURB	purine-rich element binding protein B	P+T	
miR-10b	AI302106	RAP2A	RAP2A, member of RAS oncogene family	P+T	GTP binding|GTPase activity|membrane|signal transduction|small GTPase mediated signal transduction
miR-10b	NM_002886	RAP2B	RAP2B, member of RAS oncogene family	P+T	GTP binding|protein transport|small GTPase mediated signal transduction
miR-10b	NM_014781	RB1CC1	RB1-inducible coiled-coil 1	P+T	kinase activity
miR-10b	NM_012234	RYBP	RING1 and YY1 binding protein	P+T	development|negative regulation of transcription from RNA polymerase II promoter|nucleus|transcription corepressor activity
miR-10b	NM_005506	SCARB2	scavenger receptor class B, member 2	P+T	cell adhesion|integral to plasma membrane|lysosomal membrane|membrane fraction|receptor activity
miR-10b	AF225986	SCN3A	sodium channel, voltage-gated, type III, alpha polypeptide	P+T	cation channel activity|cation transport|integral to membrane|membrane|sodium ion transport|voltage-gated sodium channel activity|voltage-gated sodium channel complex
miR-10b	NM_002997	SDC1	syndecan 1	P+T	cytoskeletal protein binding|integral to plasma membrane|membrane
miR-10b	NM_006924	SFRS1	splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor)	P+T	RNA binding|mRNA splice site selection|nuclear mRNA splicing, via spliceosome|nucleotide binding|nucleus

miR-10b	AI809967	SHC1	SHC (Src homology 2 domain containing) transforming protein 1	P+T	activation of MAPK|activation of MAPK|intracellular signaling cascade|phospholipid binding|phospholipid binding|plasma membrane|plasma membrane|positive regulation of cell proliferation|positive regulation of cell proliferation|positive regulation of mitosis|positive regulation of mitosis|regulation of cell growth|regulation of epidermal growth factor receptor activity|transmembrane receptor protein tyrosine kinase adaptor protein activity|transmembrane receptor protein tyrosine kinase adaptor protein activity
miR-10b	NM_018976	SLC38A2	solute carrier family 38, member 2	P+T	amino acid transport|amino acid-polyamine transporter activity|integral to membrane|membrane|oxygen transport|oxygen transporter activity|transport
miR-10b	NM_003794	SNX4	sorting nexin 4	P+T	endocytosis|intracellular signaling cascade|protein transport
miR-10b	NM_003103	SON	SON DNA binding protein	P+T	DNA binding|DNA binding|anti-apoptosis|double-stranded RNA binding|intracellular|nucleic acid binding|nucleus
miR-10b	Z48199	syndecan-1		P+T	
miR-10b	NM_003222	TFAP2C	transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma)	P+T	cell-cell signaling|nucleus|regulation of transcription from RNA polymerase II promoter|transcription|transcription factor activity
miR-10b	NM_003275	TMOD1	tropomodulin	P+T	actin binding|cytoskeleton|cytoskeleton organization and biogenesis|tropomyosin binding
miR-10b	NM_003367	USF2	upstream transcription factor 2, c-fos interacting	P+T	RNA polymerase II transcription factor activity|nucleus|regulation of transcription, DNA-dependent|transcription|transcription factor activity
miR-10b	N62196	ZNF367	zinc finger protein 367	P+T	nucleic acid binding|nucleus|zinc ion binding
miR-125b	AI948503	ABCC4	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	P+T	15-hydroxyprostaglandin dehydrogenase (NAD+) activity|ATP binding|ATPase activity|ATPase activity, coupled to transmembrane movement of substances|chloride channel activity|integral to membrane|ion transport|membrane
miR-125b	AL534702	ABHD3	abhydrolase domain containing 3	M+P+T	
miR-125b	AL527773	ABR	active BCR-related gene	P+T	GTPase activator activity|guanyl-nucleotide exchange factor activity|small GTPase mediated signal transduction
miR-125b	NM_020039	ACCN2	amiloride-sensitive cation channel 2, neuronal	P+T	amiloride-sensitive sodium channel activity|integral to plasma membrane|ion channel activity|ion transport|membrane|response to pH|signal transduction|sodium ion transport
miR-125b	NM_003816	ADAM9	a disintegrin and metalloproteinase domain 9 (meltrin gamma)	P+T	SH3 domain binding|integral to plasma membrane|integrin binding|metalloendopeptidase activity|protein binding|protein kinase binding|protein kinase cascade|proteolysis and peptidolysis|zinc ion binding
miR-125b	L05500	ADCY1	adenylate cyclase 1 (brain)	P+T	cAMP biosynthesis|calcium- and calmodulin-responsive adenylate cyclase activity|calmodulin binding|integral to membrane|intracellular signaling cascade|magnesium ion binding
miR-125b	NM_017488	ADD2	adducin 2 (beta)	P+T	actin binding|actin cytoskeleton|calmodulin binding|membrane
miR-125b	NM_003488	AKAP1	A kinase (PRKA) anchor protein 1	P+T	RNA binding|integral to membrane|mitochondrion|outer membrane
miR-125b	NM_005465	AKT3	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	P+T	ATP binding|protein amino acid phosphorylation|protein serine/threonine kinase activity|signal transduction|transferase activity

miR-125b	NM_001150	ANPEP	alanyl (membrane) aminopeptidase (aminopeptidase N, aminopeptidase M, microsomal aminopeptidase, CD13, p150)	P+T	aminopeptidase activity|angiogenesis|cell differentiation|integral to plasma membrane|membrane alanyl aminopeptidase activity|metallopeptidase activity|proteolysis and peptidolysis|receptor activity|zinc ion binding
miR-125b	AF193759	APBA2BP	amyloid beta (A4) precursor protein-binding, family A, member 2 binding protein	M+P+T	Golgi cis cisterna|Golgi cis cisterna|antibiotic biosynthesis|calcium ion binding|cytoplasm|cytoplasm|endoplasmic reticulum membrane|endoplasmic reticulum membrane|nucleus|oxidoreductase activity|protein binding|protein binding|protein binding|protein metabolism|protein metabolism|protein secretion|protein secretion|regulation of amyloid precursor protein biosynthesis
miR-125b	NM_000038	APC	adenomatosis polyposis coli	P+T	Wnt receptor signaling pathway|beta-catenin binding|cell adhesion|microtubule binding|negative regulation of cell cycle|protein complex assembly|signal transduction
miR-125b	NM_001655	ARCN1	archain 1	P+T	COPI vesicle coat|Golgi apparatus|clathrin vesicle coat|intra-Golgi transport|intracellular protein transport|intracellular protein transport|membrane|retrograde transport, Golgi to ER|transport
miR-125b	BC001719	ASB6	ankyrin repeat and SOCS box-containing 6	M+P	intracellular signaling cascade
miR-125b	AI478147	ATP10D	ATPase, Class V, type 10D	P+T	ATP binding|ATPase activity|cation transport|hydrolase activity|integral to membrane|magnesium ion binding|membrane|phospholipid-translocating ATPase activity
miR-125b	NM_012069	ATP1B4	ATPase, (Na+)/K+ transporting, beta 4 polypeptide	P+T	hydrogen ion transporter activity|integral to plasma membrane|ion transport|membrane|potassium ion transport|proton transport|sodium ion transport|sodium:potassium-exchanging ATPase activity
miR-125b	NM_005176	ATP5G2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2	M+P+T	ATP synthesis coupled proton transport|hydrogen-transporting ATP synthase activity, rotational mechanism|hydrogen-transporting ATPase activity, rotational mechanism|ion transport|lipid binding|membrane|membrane fraction|mitochondrion|proton transport|proton-transporting ATP synthase complex (sensu Eukaryota)|proton-transporting two-sector ATPase complex|transporter activity
miR-125b	NM_001702	BAI1	brain-specific angiogenesis inhibitor 1	M+P+T	G-protein coupled receptor activity|axonogenesis|brain-specific angiogenesis inhibitor activity|cell adhesion|integral to plasma membrane|intercellular junction|negative regulation of cell proliferation|neuropeptide signaling pathway|peripheral nervous system development|plasma membrane|protein binding|receptor activity|signal transduction
miR-125b	NM_001188	BAK1	BCL2-antagonist/killer 1	M+T	apoptotic mitochondrial changes|induction of apoptosis|integral to membrane|protein heterodimerization activity|regulation of apoptosis
miR-125b	NM_013449	BAZ2A	bromodomain adjacent to zinc finger domain, 2A	P+T	DNA binding|chromatin remodeling|nucleolus organizer complex|nucleus|regulation of transcription, DNA-dependent|transcription|transcription regulator activity
miR-125b	NM_004634	BRPF1	bromodomain and PHD finger containing, 1	M+P+T	DNA binding|nucleus|nucleus|regulation of transcription, DNA-dependent|transcription|zinc ion binding
miR-125b	NM_003458	BSN	bassoon (presynaptic cytomatrix protein)	P+T	cytoskeleton|metal ion binding|nucleus|structural constituent of cytoskeleton|synapse|synaptic transmission|synaptosome
miR-125b	NM_018108	C14orf130	hypothetical protein FLJ10483	P+T	ubiquitin cycle|ubiquitin-protein ligase activity
miR-125b	AA025877	C20orf136	chromosome 20 open reading frame 136	P+T	

miR-125b	AB054985	CACNB1	calcium channel, voltage-dependent, beta 1 subunit	M+P+T	calcium ion transport|ion transport|membrane fraction|muscle contraction|voltage-gated calcium channel activity|voltage-gated calcium channel complex
miR-125b	NM_001224	CASP2	caspase 2, apoptosis-related cysteine protease (neural precursor cell expressed, developmentally down-regulated 2)	P+T	anti-apoptosis|apoptotic program|caspase activity|caspase activity|caspase activity|cysteine-type peptidase activity|enzyme binding|intracellular|protein binding|proteolysis and peptidolysis|proteolysis and peptidolysis|regulation of apoptosis
miR-125b	NM_001755	CBFB	core-binding factor, beta subunit	M+P+T	RNA polymerase II transcription factor activity|nucleus|transcription coactivator activity|transcription factor activity|transcription from RNA polymerase II promoter
miR-125b	AV648364	CBX7	ESTs, Highly similar to potassium voltage-gated channel, Isk-related subfamily, gene 4; potassium voltage-gated channel-like protein, Isk-related subfamily [Homo sapiens] [H.sapiens]	P+T	chromatin|chromatin assembly or disassembly|chromatin binding|chromatin modification|nucleus|regulation of transcription, DNA-dependent|transcription
miR-125b	NM_001408	CELSR2	cadherin, EGF LAG seven-pass G-type receptor 2 (flamingo homolog, Drosophila)	M+P+T	G-protein coupled receptor activity|calcium ion binding|cell adhesion|development|homophilic cell adhesion|integral to membrane|membrane|neuropeptide signaling pathway|receptor activity|signal transduction|structural molecule activity
miR-125b	NM_015955	CGI-27	C21orf19-like protein	P+T	
miR-125b	AF263462	CGN	cingulin	P+T	actin binding|biological_process unknown|motor activity|myosin|protein binding|tight junction
miR-125b	AF064491	CLIM2	LIM domain binding 1	P+T	LIM domain binding|development|development|negative regulation of transcription, DNA-dependent|nucleus|transcription cofactor activity|transcriptional repressor activity
miR-125b	AU152178	CMG2	capillary morphogenesis protein 2	P+T	integral to membrane|receptor activity
miR-125b	NM_004073	CNK	cytokine-inducible kinase	P+T	ATP binding|protein amino acid phosphorylation|protein binding|protein serine/threonine kinase activity|regulation of cell cycle|transferase activity
miR-125b	NM_020348	CNNM1	cyclin M1	M+P+T	fatty acid biosynthesis
miR-125b	NM_022730	COPS7B	COP9 constitutive photomorphogenic homolog subunit 7B (Arabidopsis)	M+P+T	signalosome complex
miR-125b	NM_003389	CORO2A	coronin, actin binding protein, 2A	P+T	actin binding|glutamate-ammonia ligase activity|glutamine biosynthesis|intracellular signaling cascade|nitrogen compound metabolism|protein binding
miR-125b	BF939649	CORO2B	coronin, actin binding protein, 2B	P+T	actin binding|actin cytoskeleton|actin cytoskeleton organization and biogenesis|membrane
miR-125b	NM_007007	CPSF6	cleavage and polyadenylation specific factor 6, 68kDa	P+T	RNA binding|mRNA processing|nucleic acid binding|nucleotide binding|nucleus
miR-125b	NM_004386	CSPG3	chondroitin sulfate proteoglycan 3 (neurocan)	P+T	calcium ion binding|cell adhesion|cell motility|hyaluronic acid binding|sugar binding
miR-125b	NM_004393	DAG1	dystroglycan 1 (dystrophin-associated glycoprotein 1)	M+P+T	actin cytoskeleton|calcium ion binding|extracellular matrix (sensu Metazoa)|integral to plasma membrane|laminin receptor activity|membrane fraction|muscle contraction|plasma membrane|protein binding|protein complex assembly
miR-125b	NM_014764	DAZAP2	DAZ associated protein 2	P+T	
miR-125b	NM_030927	DC-TM4F2	tetraspanin similar to TM4SF9	P+T	integral to membrane
miR-125b	NM_004082	DCTN1	dynactin 1 (p150, glued homolog, Drosophila)	M+P+T	cytoplasm|cytoskeleton|dynein complex|mitosis|motor activity|neurogenesis

miR-125b	NM_030621	DICER1	Dicer1, Dcr-1 homolog (Drosophila)	P+T	ATP binding|ATP-dependent helicase activity|RNA interference, targeting of mRNA for destruction|RNA processing|double-stranded RNA binding|endonuclease activity|hydrolase activity|intracellular|ribonuclease III activity
miR-125b	U53506	DIO2	deiodinase, iodothyronine, type II	P+T	integral to membrane|membrane|selenium binding|selenocysteine incorporation|thyroid hormone generation|thyroxine 5'-deiodinase activity|thyroxine 5'-deiodinase activity
miR-125b	AL136139	dJ761I2.1		P+T	
miR-125b	AL357503	dJ899C14.1	Q9H4T4 like	P+T	
miR-125b	AL117482	DKFZP434C131	DKFZP434C131 protein	P+T	ATP binding|protein amino acid phosphorylation|protein serine/threonine kinase activity|protein-tyrosine kinase activity|transferase activity
miR-125b	AK023580	DKFZP434H0820	hypothetical protein DKFZp434H0820	P+T	
miR-125b	T16388	DKFZp564A176	hypothetical protein DKFZp564A176	P+T	development|integral to membrane|membrane|receptor activity|semaphorin receptor activity
miR-125b	AL137517	DKFZp564O1278	hypothetical protein DKFZp564O1278	P+T	integral to membrane
miR-125b	BE781961	DKFZp762A2013	hypothetical protein DKFZp762A2013	P+T	electron transport|electron transporter activity
miR-125b	AB036931	DLL4	delta-like 4 (Drosophila)	M+P+T	Notch binding|Notch signaling pathway|cell differentiation|circulation|integral to membrane|membrane|signal transduction
miR-125b	NM_012266	DNAJB5	DnaJ (Hsp40) homolog, subfamily B, member 5	P+T	heat shock protein binding|protein folding|response to unfolded protein|unfolded protein binding
miR-125b	NM_005740	DNAL4	dynein, axonemal, light polypeptide 4	P+T	ATPase activity, coupled|axonemal dynein complex|microtubule motor activity|microtubule-based movement
miR-125b	BF593175	DOCK3	dedicator of cyto-kinesis 3	P+T	GTP binding|GTPase binding|guanyl-nucleotide exchange factor activity
miR-125b	NM_006426	DPYSL4	dihydropyrimidinase-like 4	P+T	hydrolase activity|neurogenesis
miR-125b	NM_006465	DRIL2	dead ringer (Drosophila)-like 2 (bright and dead ringer)	P+T	DNA binding|biological_process unknown|nucleus
miR-125b	BC005047	DUSP6	dual specificity phosphatase 6	P+T	MAP kinase phosphatase activity|cytoplasm|hydrolase activity|inactivation of MAPK|protein amino acid dephosphorylation|protein serine/threonine phosphatase activity|protein tyrosine phosphatase activity|regulation of cell cycle|soluble fraction
miR-125b	NM_004423	DVL3	dishevelled, dsh homolog 3 (Drosophila)	P+T	development|frizzled signaling pathway|heart development|intracellular|intracellular signaling cascade|kinase activity|neurogenesis|protein binding|signal transducer activity
miR-125b	NM_001949	E2F3	E2F transcription factor 3	P+T	nucleus|protein binding|regulation of cell cycle|regulation of transcription, DNA-dependent|transcription|transcription factor activity|transcription factor complex|transcription initiation from RNA polymerase II promoter
miR-125b	AU149385	EAF1	Homo sapiens cDNA FLJ13155 fis, clone NT2RP3003433, mRNA sequence	P+T	
miR-125b	NM_014674	EDEM	KIAA0212 gene product	P+T	ER-associated protein catabolism|GTP binding|N-linked glycosylation|calcium ion binding|endoplasmic reticulum|integral to endoplasmic reticulum membrane|integral to membrane|mannosyl-oligosaccharide 1,2-alpha-mannosidase activity|membrane|protein binding|response to unfolded protein

miR-125b NM_001955	EDN1	endothelin 1	M+P+T	cell-cell signaling|extracellular space|hormone activity|pathogenesis|positive regulation of cell proliferation|regulation of blood pressure|regulation of vasoconstriction|signal transduction|soluble fraction
miR-125b AI832074	EIF2C2	eukaryotic translation initiation factor 2C, 2	M+P	cellular_component unknown|protein biosynthesis|translation initiation factor activity
miR-125b AB044548	EIF4EBP1	eukaryotic translation initiation factor 4E binding protein 1	P+T	eukaryotic initiation factor 4E binding|negative regulation of protein biosynthesis|negative regulation of translational initiation|regulation of translation
miR-125b NM_020390	EIF5A2	eukaryotic translation initiation factor 5A2	P+T	DNA binding|protein biosynthesis|translation initiation factor activity|translational initiation
miR-125b NM_004438	EPHA4	EphA4	P+T	ATP binding|ephrin receptor activity|integral to plasma membrane|membrane|protein amino acid phosphorylation|receptor activity|signal transduction|transferase activity|transmembrane receptor protein tyrosine kinase signaling pathway
miR-125b NM_004451	ESRRA	estrogen-related receptor alpha	P+T	nucleus|regulation of transcription, DNA-dependent|steroid binding|steroid hormone receptor activity|transcription|transcription factor activity
miR-125b NM_004907	ETR101	immediate early protein	P+T	
miR-125b NM_005238	ETS1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	P+T	RNA polymerase II transcription factor activity|immune response|negative regulation of cell proliferation|nucleus|regulation of transcription, DNA-dependent|transcription|transcription factor activity|transcription from RNA polymerase II promoter
miR-125b NM_001987	ETV6	ets variant gene 6 (TEL oncogene)	P+T	nucleus|regulation of transcription, DNA-dependent|transcription|transcription factor activity
miR-125b NM_022753	FAD104	FAD104	P+T	
miR-125b AF308300	FAPP2	phosphoinositol 4-phosphate adaptor protein-2	P+T	
miR-125b NM_022976	FGFR2	fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer syndrome, Jackson-Weiss syndrome)	M+P+T	ATP binding|cell growth|fibroblast growth factor receptor activity|heparin binding|integral to membrane|membrane|protein amino acid phosphorylation|protein amino acid phosphorylation|protein serine/threonine kinase activity|protein-tyrosine kinase activity|protein-tyrosine kinase activity|receptor activity|transferase activity
miR-125b NM_004470	FKBP2	FK506 binding protein 2, 13kDa	P+T	FK506 binding|endoplasmic reticulum|isomerase activity|peptidyl-prolyl cis-trans isomerase activity|protein folding
miR-125b AL160175	FKHL18	forkhead-like 18 (Drosophila)	P+T	
miR-125b BF515132	FLJ00024	hypothetical protein FLJ00024	P+T	
miR-125b BC002945	FLJ10101	hypothetical protein FLJ10101	M+P	GTP binding|protein transport|small GTPase mediated signal transduction
miR-125b NM_018243	FLJ10849	hypothetical protein FLJ10849	P+T	GTP binding|cell cycle|cytokinesis
miR-125b NM_019084	FLJ10895	hypothetical protein FLJ10895	P+T	nucleus|regulation of cell cycle
miR-125b NM_018320	FLJ11099	hypothetical protein FLJ11099	P+T	protein ubiquitination|ubiquitin ligase complex|ubiquitin-protein ligase activity|zinc ion binding
miR-125b NM_018375	FLJ11274	hypothetical protein FLJ11274	M+P+T	membrane|metal ion transport|metal ion transporter activity
miR-125b NM_024954	FLJ11807	hypothetical protein FLJ11807	P+T	protein modification
miR-125b BF434995	FLJ14708	hypothetical protein FLJ14708	P+T	
miR-125b NM_018992	FLJ20040	hypothetical protein FLJ20040	P+T	membrane|potassium ion transport|protein binding|voltage-gated potassium channel activity|voltage-gated potassium channel complex
miR-125b NM_017911	FLJ20635	hypothetical protein FLJ20635	P+T	

miR-125b NM_017936	FLJ20707	hypothetical protein FLJ20707	M+P+T	ATP synthesis coupled proton transport|cytoplasm|hydrogen-transporting ATP synthase activity, rotational mechanism|hydrogen-transporting ATPase activity, rotational mechanism|membrane|phosphate transport|proton-transporting two-sector ATPase complex
miR-125b NM_024789	FLJ22529	hypothetical protein FLJ22529	P+T	
miR-125b AA721230	FLJ25604	hypothetical protein FLJ25604	P+T	guanyl-nucleotide exchange factor activity|small GTPase mediated signal transduction
miR-125b AI677701	FLJ30829	hypothetical protein FLJ30829	P+T	nucleic acid binding|nucleotide binding
miR-125b NM_004475	FLOT2	flotillin 2	M+P+T	cell adhesion|epidermis development|flotillin complex|integral to membrane|plasma membrane|protein binding
miR-125b AA830884	FMR1	fragile X mental retardation 1	M+T	mRNA binding|mRNA processing|mRNA-nucleus export|nucleoplasm|polysome|ribosome|soluble fraction|transport
miR-125b AF305083	FUT4	fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)	P+T	Golgi apparatus|L-fucose catabolism|alpha(1,3)-fucosyltransferase activity|carbohydrate metabolism|integral to membrane|membrane|membrane fraction|protein amino acid glycosylation|transferase activity, transferring glycosyl groups
miR-125b X92762	G4.5	tafazzin (cardiomyopathy, dilated 3A (X-linked); endocardial fibroelastosis 2; Barth syndrome)	M+P+T	acyltransferase activity|heart development|integral to membrane|metabolism|muscle contraction|muscle development
miR-125b NM_012296	GAB2	GRB2-associated binding protein 2	P+T	
miR-125b NM_015044	GGA2	golgi associated, gamma adaptin ear containing, ARF binding protein 2	M+T	ADP-ribosylation factor binding|Golgi stack|Golgi trans face|clathrin coat of trans-Golgi network vesicle|intra-Golgi transport|intracellular protein transport|intracellular protein transport|membrane|protein complex assembly|protein transporter activity
miR-125b AL049709	GGTL3	gamma-glutamyltransferase-like 3	M+P+T	
miR-125b NM_000165	GJA1	gap junction protein, alpha 1, 43kDa (connexin 43)	P+T	cell-cell signaling|connexon channel activity|connexon complex|gap junction assembly|heart development|integral to plasma membrane|ion transporter activity|muscle contraction|perception of sound|positive regulation of I-kappaB kinase/NF-kappaB cascade|protein binding|signal transducer activity|transport
miR-125b NM_014905	GLS	glutaminase	P+T	glutaminase activity|glutamine catabolism|hydrolase activity|mitochondrion
miR-125b NM_005113	GOLGA5	golgi autoantigen, golgin subfamily a, 5	P+T	ATP binding|Golgi membrane|cell surface receptor linked signal transduction|integral to plasma membrane|protein amino acid phosphorylation|protein-tyrosine kinase activity
miR-125b NM_001448	GPC4	glypican 4	M+P+T	cell proliferation|extracellular matrix (sensu Metazoa)|integral to plasma membrane|membrane|morphogenesis
miR-125b NM_005296	GPR23	G protein-coupled receptor 23	M+T	G-protein coupled receptor protein signaling pathway|integral to plasma membrane|purinergic nucleotide receptor activity, G-protein coupled|receptor activity|rhodopsin-like receptor activity|signal transduction
miR-125b U66065	GRB10	growth factor receptor-bound protein 10	M+T	SH3/SH2 adaptor activity|cell-cell signaling|cytoplasm|insulin receptor signaling pathway|intracellular signaling cascade|plasma membrane
miR-125b NM_021643	GS3955	GS3955 protein	P+T	ATP binding|protein amino acid phosphorylation|protein kinase activity|transferase activity
miR-125b NM_019096	GTPBP2	GTP binding protein 2	M+T	GTP binding|GTPase activity|protein biosynthesis|small GTPase mediated signal transduction

miR-125b U78181	hBNaC2	amiloride-sensitive cation channel 2, neuronal	P+T	amiloride-sensitive sodium channel activity|integral to plasma membrane|ion channel activity|ion transport|membrane|response to pH|signal transduction|sodium ion transport
miR-125b NM_005477	HCN4	hyperpolarization activated cyclic nucleotide-gated potassium channel 4	P+T	3',5'-cAMP binding|cation channel activity|cation transport|circulation|integral to plasma membrane|membrane|membrane fraction|muscle contraction|nucleotide binding|potassium ion transport|sodium ion transport|voltage-gated potassium channel activity
miR-125b NM_002112	HDC	histidine decarboxylase	P+T	amino acid metabolism|catecholamine biosynthesis|histidine decarboxylase activity|histidine metabolism|lyase activity
miR-125b U64317	HEF1	enhancer of filamentation 1 (cas-like docking; Crk-associated substrate related)	P+T	actin filament bundle formation|cell adhesion|cytokinesis|cytoplasm|cytoskeleton|cytoskeleton organization and biogenesis|integrin-mediated signaling pathway|mitosis|nucleus|protein binding|regulation of cell cycle|regulation of cell growth|signal transduction|spindle
miR-125b L38487	hERRa	estrogen-related receptor alpha	P+T	nucleus|regulation of transcription, DNA-dependent|steroid binding|steroid hormone receptor activity|transcription|transcription factor activity
miR-125b AB028943	HIC2	hypermethylated in cancer 2	P+T	DNA binding|negative regulation of transcription, DNA-dependent|nucleus|protein C-terminus binding|transcription|zinc ion binding
miR-125b AL023584	HIVEP2	human immunodeficiency virus type I enhancer binding protein 2	P+T	
miR-125b AL023584	HIVEP2	human immunodeficiency virus type I enhancer binding protein 2	P+T	
miR-125b NM_005342	HMGB3	high-mobility group box 3	P+T	DNA bending activity|DNA binding|chromatin|development|nucleus|regulation of transcription, DNA-dependent
miR-125b AL031295	HMGCL; HL	lysophospholipase II	M+P+T	
miR-125b NM_004503	HOXC6	homeo box C6	P+T	development|development|nucleus|regulation of transcription from RNA polymerase II promoter|regulation of transcription, DNA-dependent|transcription corepressor activity|transcription factor activity
miR-125b AA844682	HRD1	HRD1 protein	P+T	protein ubiquitination|ubiquitin ligase complex|ubiquitin-protein ligase activity|zinc ion binding
miR-125b AL136667	HSPC039	HSPC039 protein	P+T	integral to membrane
miR-125b AF245044	HT023	hypothetical protein HT023	P+T	
miR-125b U13022	Ich-1	caspase 2, apoptosis-related cysteine protease (neural precursor cell expressed, developmentally down-regulated 2)	P+T	anti-apoptosis|apoptotic program|caspase activity|caspase activity|caspase activity|cysteine-type peptidase activity|enzyme binding|intracellular|protein binding|proteolysis and peptidolysis|proteolysis and peptidolysis|regulation of apoptosis
miR-125b NM_004513	IL16	interleukin 16 (lymphocyte chemoattractant factor)	M+P+T	chemotaxis|cytokine activity|extracellular space|immune response|protein binding|sensory perception

miR-125b NM_002460	IRF4	interferon regulatory factor 4	P+T	RNA polymerase II transcription factor activity|T-cell activation|T-cell activation|nucleus|nucleus|nucleus|positive regulation of interleukin-10 biosynthesis|positive regulation of interleukin-10 biosynthesis|positive regulation of interleukin-13 biosynthesis|positive regulation of interleukin-13 biosynthesis|positive regulation of interleukin-2 biosynthesis|positive regulation of interleukin-2 biosynthesis|positive regulation of interleukin-4 biosynthesis|positive regulation of interleukin-4 biosynthesis|positive regulation of transcription|positive regulation of transcription|regulation of T-helper cell differentiation|regulation of T-helper cell differentiation|regulation of transcription, DNA-dependent|regulation of transcription, DNA-dependent|transcription|transcription factor activity|transcription factor activity|transcription factor binding|transcription factor binding|transcriptional activator activity|transcriptional activator activity
miR-125b NM_002207	ITGA9	integrin, alpha 9	P+T	cell-matrix adhesion|integral to membrane|integrin complex|integrin-mediated signaling pathway|protein binding|receptor activity
miR-125b NM_000212	ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	P+T	blood coagulation|cell-matrix adhesion|integrin complex|integrin-mediated signaling pathway|protein binding|receptor activity
miR-125b NM_021991	JUP	junction plakoglobin	P+T	cell adhesion|cell adhesion|cytoplasm|cytoskeletal protein binding|cytoskeleton|cytoskeleton|membrane fraction|mitotic chromosome condensation|protein binding|soluble fraction|structural molecule activity
miR-125b AF032897	KCNH7	potassium voltage-gated channel, subfamily H (eag-related), member 7	P+T	cation transport|integral to membrane|membrane|potassium ion transport|regulation of transcription, DNA-dependent|signal transducer activity|signal transduction|voltage-gated potassium channel activity
miR-125b NM_002252	KCNS3	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3	M+P+T	cation transport|delayed rectifier potassium channel activity|membrane|membrane fraction|potassium channel regulator activity|potassium ion transport|protein binding|voltage-gated potassium channel complex
miR-125b NM_014735	KIAA0215	KIAA0215 gene product	P+T	DNA binding|regulation of transcription, DNA-dependent
miR-125b NM_015288	KIAA0239	KIAA0239 protein	P+T	DNA binding|regulation of transcription, DNA-dependent
miR-125b D87469	KIAA0279	cadherin, EGF LAG seven-pass G-type receptor 2 (flamingo homolog, Drosophila)	M+P+T	G-protein coupled receptor activity|calcium ion binding|cell adhesion|development|homophilic cell adhesion|integral to membrane|membrane|neuropeptide signaling pathway|receptor activity|signal transduction|structural molecule activity
miR-125b AB002356	KIAA0358	MAP-kinase activating death domain	P+T	cell surface receptor linked signal transduction|cytoplasm|death receptor binding|kinase activity|plasma membrane|protein kinase activator activity
miR-125b NM_014871	KIAA0710	KIAA0710 gene product	P+T	cysteine-type endopeptidase activity|exonuclease activity|nucleus|ubiquitin cycle|ubiquitin thiolesterase activity|ubiquitin-dependent protein catabolism
miR-125b AB018333	KIAA0790	KIAA0790 protein	P+T	cell cycle|negative regulation of cell cycle
miR-125b NM_014912	KIAA0940	KIAA0940 protein	P+T	nucleic acid binding
miR-125b AB028957	KIAA1034	KIAA1034 protein	P+T	DNA binding|nucleus|regulation of transcription, DNA-dependent|transcription factor activity
miR-125b NM_014901	KIAA1100	KIAA1100 protein	M+P+T	protein ubiquitination|ubiquitin ligase complex|ubiquitin-protein ligase activity|zinc ion binding
miR-125b AB033016	KIAA1190	hypothetical protein KIAA1190	P+T	DNA binding|nucleic acid binding|nucleus|protein binding|regulation of transcription, DNA-dependent|zinc ion binding

miR-125b AA056548	KIAA1268	KIAA1268 protein	P+T	NAD+ ADP-ribosyltransferase activity|nucleus|protein amino acid ADP-ribosylation
miR-125b BE670098	KIAA1594	KIAA1594 protein	M+P+T	cysteine-type endopeptidase activity|ubiquitin cycle|ubiquitin thiolesterase activity|ubiquitin-dependent protein catabolism
miR-125b AU157109	KIAA1598	KIAA1598 protein	P+T	
miR-125b AA772278	KIAA1673	KIAA1673	P+T	
miR-125b NM_015995	KLF13	Kruppel-like factor 13	P+T	DNA binding|RNA polymerase II transcription factor activity|nucleus|regulation of transcription, DNA-dependent|transcription|transcription from RNA polymerase II promoter|zinc ion binding
miR-125b NM_016531	KLF3	Kruppel-like factor 3 (basic)	P+T	development|negative regulation of transcription from RNA polymerase II promoter|nucleus|regulation of transcription, DNA-dependent|transcription|transcription factor activity|zinc ion binding
miR-125b BE892574	LACTB	lactamase, beta	P+T	hydrolase activity|integral to membrane|response to antibiotic
miR-125b BE566136	LBP-32	LBP protein 32	P+T	
miR-125b NM_024090	LCE	long-chain fatty-acyl elongase	P+T	integral to membrane
miR-125b NM_003893	LDB1	LIM domain binding 1	P+T	LIM domain binding|development|development|negative regulation of transcription, DNA-dependent|nucleus|transcription cofactor activity|transcriptional repressor activity
miR-125b U94354	LFNG	lunatic fringe homolog (Drosophila)	M+T	Golgi apparatus|development|extracellular region|integral to membrane|membrane|organogenesis|transferase activity, transferring glycosyl groups
miR-125b NM_002310	LIFR	leukemia inhibitory factor receptor	M+P+T	cell surface receptor linked signal transduction|integral to plasma membrane|leukemia inhibitory factor receptor activity|membrane|receptor activity
miR-125b NM_016339	Link-GEFII	Link guanine nucleotide exchange factor II	P+T	G-protein coupled receptor protein signaling pathway|guanyl-nucleotide exchange factor activity|membrane fraction|neurogenesis|small GTPase mediated signal transduction
miR-125b NM_005575	LNPEP	leucyl/cystinyl aminopeptidase	P+T	aminopeptidase activity|cell-cell signaling|integral to plasma membrane|membrane alanyl aminopeptidase activity|metallopeptidase activity|plasma membrane|pregnancy|proteolysis and peptidolysis|zinc ion binding
miR-125b AL031186	LOC129080	putative emu1	P+T	
miR-125b AI884701	LOC221002	CG4853 gene product	M+P	guanyl-nucleotide exchange factor activity|small GTPase mediated signal transduction
miR-125b AI953847	LOC255488	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 186647, mRNA sequence	P+T	electron transport|electron transporter activity|integral to membrane|iron ion binding|ligase activity|protein binding|protein ubiquitination during ubiquitin-dependent protein catabolism|ubiquitin ligase complex|ubiquitin-protein ligase activity|zinc ion binding
miR-125b NM_015899	LOC51054	putative glycolipid transfer protein	P+T	
miR-125b AA209239	LOC57406	lipase protein	P+T	aromatic compound metabolism|hydrolase activity|response to toxin|xenobiotic metabolism
miR-125b NM_005576	LOXL1	lysyl oxidase-like 1	M+P+T	copper ion binding|electron transporter activity|extracellular region|oxidoreductase activity|protein modification|protein-lysine 6-oxidase activity
miR-125b AA584297	LRP4	low density lipoprotein receptor-related protein 4	M+T	calcium ion binding|endocytosis|integral to membrane|membrane|receptor activity
miR-125b NM_007260	LYPLA2	lysophospholipase II	M+P+T	fatty acid metabolism|hydrolase activity|lipid metabolism

miR-125b	NM_004901	LYSAL1	lysosomal apyrase-like 1	P+T	Golgi apparatus|UDP catabolism|apyrase activity|hydrolase activity|integral to Golgi membrane|integral to membrane|lysosome|magnesium ion binding|nucleobase, nucleoside, nucleotide and nucleic acid metabolism|uridine-diphosphatase activity|vacuolar membrane
miR-125b	NM_002355	M6PR	mannose-6-phosphate receptor (cation dependent)	M+P+T	endosome to lysosome transport|integral to plasma membrane|lysosome|receptor mediated endocytosis|transmembrane receptor activity|transport|transporter activity
miR-125b	AB002356	MADD	MAP-kinase activating death domain	P+T	cell surface receptor linked signal transduction|cytoplasm|death receptor binding|kinase activity|plasma membrane|protein kinase activator activity
miR-125b	NM_016219	MAN1B1	mannosidase, alpha, class 1B, member 1	P+T	N-linked glycosylation|N-linked glycosylation|calcium ion binding|calcium ion binding|carbohydrate metabolism|endoplasmic reticulum|hydrolase activity, acting on glycosyl bonds|integral to membrane|mannosyl-oligosaccharide 1,2-alpha-mannosidase activity|mannosyl-oligosaccharide 1,2-alpha-mannosidase activity|membrane|membrane fraction|oligosaccharide metabolism
miR-125b	NM_002446	MAP3K10	mitogen-activated protein kinase kinase kinase 10	P+T	ATP binding|JUN kinase kinase kinase activity|activation of JNK|autophosphorylation|induction of apoptosis|protein homodimerization activity|protein serine/threonine kinase activity|protein-tyrosine kinase activity|signal transduction|transferase activity
miR-125b	NM_002419	MAP3K11	mitogen-activated protein kinase kinase kinase 11	M+P+T	ATP binding|G1 phase of mitotic cell cycle|JUN kinase kinase kinase activity|activation of JNK|autophosphorylation|cell proliferation|centrosome|microtubule|microtubule-based process|protein homodimerization activity|protein oligomerization|protein serine/threonine kinase activity|protein-tyrosine kinase activity|transferase activity
miR-125b	Z25432	MAPK14	mitogen-activated protein kinase 14	P+T	ATP binding|MAP kinase activity|MAP kinase kinase activity|MP kinase activity|antimicrobial humoral response (sensu Vertebrata)|cell motility|cell surface receptor linked signal transduction|chemotaxis|cytoplasm|nucleus|protein amino acid phosphorylation|protein kinase cascade|protein serine/threonine kinase activity|protein-tyrosine kinase activity|response to stress|transferase activity
miR-125b	NM_018650	MARK1	MAP/microtubule affinity-regulating kinase 1	P+T	ATP binding|cytoplasm|cytoskeleton|cytoskeleton organization and biogenesis|magnesium ion binding|microtubule cytoskeleton|protein amino acid phosphorylation|protein amino acid phosphorylation|protein kinase cascade|protein serine/threonine kinase activity|protein serine/threonine kinase activity|transferase activity
miR-125b	NM_001879	MASP1	mannan-binding lectin serine protease 1 (C4/C2 activating component of Ra-reactive factor)	P+T	calcium ion binding|chymotrypsin activity|complement activation|complement activation, classical pathway|extracellular region|immune response|peptidase activity|proteolysis and peptidolysis|trypsin activity
miR-125b	NM_005911	MAT2A	methionine adenosyltransferase II, alpha	P+T	ATP binding|magnesium ion binding|methionine adenosyltransferase activity|one-carbon compound metabolism|transferase activity
miR-125b	NM_005920	MEF2D	MADS box transcription enhancer factor 2, polypeptide D (myocyte enhancer factor 2D)	P+T	muscle development|nucleus|regulation of transcription, DNA-dependent|transcription|transcription coactivator activity|transcription factor activity|transcription from RNA polymerase II promoter

miR-125b NM_020149	MEIS2	Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse)	M+P	negative regulation of transcription from RNA polymerase II promoter|nucleus|regulation of transcription, DNA-dependent|specific RNA polymerase II transcription factor activity|transcription corepressor activity|transcription factor activity|transcription factor activity
miR-125b NM_017927	MFN1	mitofusin 1	P+T	GTP binding|GTPase activity|hydrolase activity|integral to membrane|mitochondrial fusion|mitochondrial outer membrane|mitochondrion
miR-125b AI139252	MGC16063	ribosomal protein L35a	P+T	JAK-STAT cascade|acute-phase response|calcium ion binding|cell motility|cytoplasm|hematopoietin/interferon-class (D200-domain) cytokine receptor signal transducer activity|intracellular signaling cascade|negative regulation of transcription from RNA polymerase II promoter|neurogenesis|nucleus|nucleus|regulation of transcription, DNA-dependent|signal transducer activity|transcription|transcription factor activity|transcription factor activity
miR-125b AI862120	MGC21981	hypothetical protein MGC21981	P+T	membrane
miR-125b AL515061	MGC24302	hypothetical protein MGC24302	P+T	
miR-125b BE618656	MGC2541	similar to RIKEN cDNA 2610030J16 gene	M+P+T	
miR-125b BC005842	MGC2705	hypothetical protein MGC2705	P+T	
miR-125b NM_024293	MGC3035	hypothetical protein MGC3035	M+P	
miR-125b NM_017572	MKNK2	MAP kinase-interacting serine/threonine kinase 2	P+T	ATP binding|ATP binding|cell surface receptor linked signal transduction|protein amino acid phosphorylation|protein amino acid phosphorylation|protein kinase cascade|protein serine/threonine kinase activity|protein serine/threonine kinase activity|protein-tyrosine kinase activity|regulation of translation|response to stress|transferase activity
miR-125b NM_005439	MLF2	myeloid leukemia factor 2	P+T	defense response|nucleus
miR-125b NM_007359	MLN51	MLN51 protein	P+T	mRNA processing|mRNA-nucleus export|molecular_function unknown|nucleus|transport
miR-125b NM_002442	MSI1	musashi homolog 1 (Drosophila)	M+P+T	RNA binding|neurogenesis|nucleotide binding|nucleus
miR-125b NM_021090	MTMR3	myotubularin related protein 3	M+P+T	cytoplasm|hydrolase activity|inositol or phosphatidylinositol phosphatase activity|membrane|membrane fraction|phospholipid dephosphorylation|protein amino acid dephosphorylation|protein serine/threonine phosphatase activity|protein tyrosine phosphatase activity|protein tyrosine/serine/threonine phosphatase activity|zinc ion binding
miR-125b AK024501	MXD4	MAX dimerization protein 4	M+P+T	DNA binding|negative regulation of cell proliferation|negative regulation of transcription from RNA polymerase II promoter|nucleus|protein binding|regulation of transcription, DNA-dependent|transcription|transcription corepressor activity
miR-125b AB020642	MYT1	myelin transcription factor 1	M+P+T	nucleus|regulation of transcription, DNA-dependent|transcription|transcription factor activity|zinc ion binding
miR-125b NM_004540	NCAM2	neural cell adhesion molecule 2	P+T	cell adhesion|integral to membrane|membrane|neuron adhesion|plasma membrane|protein binding
miR-125b NM_012338	NET-2	transmembrane 4 superfamily member tetraspan NET-2	P+T	integral to membrane|membrane fraction
miR-125b U84246	NEU1	sialidase 1 (lysosomal sialidase)	P+T	carbohydrate metabolism|exo-alpha-sialidase activity|hydrolase activity, acting on glycosyl bonds|lysosome
miR-125b AI824012	NRIP1	nuclear receptor interacting protein 1	P+T	nucleus|regulation of transcription, DNA-dependent|transcription|transcription coactivator activity
miR-125b D81048	NRM	nurim (nuclear envelope membrane protein)	P+T	

miR-125b BC001794	NUMBL	numb homolog (Drosophila)-like	P+T	neurogenesis
miR-125b AB020713	NUP210	nucleoporin 210	P+T	development|nucleus
miR-125b NM_002537	OAZ2	ornithine decarboxylase antizyme 2	M+P+T	ornithine decarboxylase inhibitor activity|polyamine metabolism
miR-125b NM_024586	OSBPL9	oxysterol binding protein-like 9	P+T	lipid transport|steroid metabolism
miR-125b U64661	PABP	ESTs, Highly similar to PAB1_HUMAN Polyadenylate-binding protein 1 (Poly(A)-binding protein 1) (PABP 1) (PABP1) [H.sapiens]	P+T	
miR-125b AK000003	PCQAP	PC2 (positive cofactor 2, multiprotein complex) glutamine/Q-rich-associated protein	P+T	
miR-125b NM_004716	PCSK7	proprotein convertase subtilisin/kexin type 7	M+P+T	integral to Golgi membrane|integral to membrane|peptidase activity|peptidase activity|peptide hormone processing|proteolysis and peptidolysis|subtilase activity
miR-125b NM_006201	PCTK1	PCTAIRE protein kinase 1	M+P+T	ATP binding|protein amino acid phosphorylation|protein amino acid phosphorylation|protein serine/threonine kinase activity|protein serine/threonine kinase activity|regulation of cell cycle|transferase activity
miR-125b NM_021213	PCTP	phosphatidylcholine transfer protein	M+P+T	cytosol|lipid binding|lipid transport|phosphatidylcholine transporter activity
miR-125b NM_021255	PELI2	pellino homolog 2 (Drosophila)	M+P+T	
miR-125b NM_002646	PIK3C2B	phosphoinositide-3-kinase, class 2, beta polypeptide	P+T	inositol or phosphatidylinositol kinase activity|intracellular signaling cascade|microsome|phosphatidylinositol 3-kinase activity|phosphatidylinositol-4-phosphate 3-kinase activity|phosphoinositide 3-kinase complex|plasma membrane|transferase activity
miR-125b NM_003628	PKP4	plakophilin 4	P+T	cell adhesion|cytoskeleton|intercellular junction|protein binding|structural molecule activity
miR-125b NM_006718	PLAGL1	pleiomorphic adenoma gene-like 1	P+T	DNA binding|cell cycle arrest|induction of apoptosis|nucleic acid binding|nucleus|regulation of transcription, DNA-dependent|transcription|zinc ion binding
miR-125b AI457120	PPAT	phosphoribosyl pyrophosphate amidotransferase	P+T	amidophosphoribosyltransferase activity|glutamine metabolism|magnesium ion binding|metabolism|nucleoside metabolism|purine base biosynthesis|purine nucleotide biosynthesis|transferase activity, transferring glycosyl groups
miR-125b NM_002719	PPP2R5C	protein phosphatase 2, regulatory subunit B (B56), gamma isoform	P+T	hydrolase activity|nucleus|phosphoprotein phosphatase activity|protein phosphatase type 2A complex|protein phosphatase type 2A complex|protein phosphatase type 2A regulator activity|protein phosphatase type 2A regulator activity|signal transduction|signal transduction
miR-125b AL022067	PRDM1	PR domain containing 1, with ZNF domain	P+T	
miR-125b U23736	PRDM2	PR domain containing 2, with ZNF domain	P+T	DNA binding|metal ion binding|nucleus|nucleus|regulation of transcription|regulation of transcription, DNA-dependent|transcription factor activity|transcription regulator activity|zinc ion binding|zinc ion binding
miR-125b AF083033	PRKRA	protein kinase, interferon-inducible double stranded RNA dependent activator	P+T	double-stranded RNA binding|enzyme activator activity|immune response|intracellular|kinase activity|negative regulation of cell proliferation|response to virus|signal transducer activity|signal transduction

miR-125b NM_014369	PTPN18	protein tyrosine phosphatase, non-receptor type 18 (brain-derived)	P+T	hydrolase activity|non-membrane spanning protein tyrosine phosphatase activity|protein amino acid dephosphorylation|protein amino acid dephosphorylation|protein tyrosine phosphatase activity
miR-125b AI762627	PTPRF	protein tyrosine phosphatase, receptor type, F	P+T	cell adhesion|hydrolase activity|integral to membrane|integral to plasma membrane|protein amino acid dephosphorylation|protein binding|protein tyrosine phosphatase activity|receptor activity|transmembrane receptor protein tyrosine phosphatase activity|transmembrane receptor protein tyrosine phosphatase signaling pathway
miR-125b NM_002840	PTPRF	protein tyrosine phosphatase, receptor type, F	P+T	cell adhesion|hydrolase activity|integral to membrane|integral to plasma membrane|protein amino acid dephosphorylation|protein binding|protein tyrosine phosphatase activity|receptor activity|transmembrane receptor protein tyrosine phosphatase activity|transmembrane receptor protein tyrosine phosphatase signaling pathway
miR-125b AF142419	QKI	homolog of mouse quaking QKI (KH domain RNA binding protein)	P+T	
miR-125b NM_004283	RAB3D	RAB3D, member RAS oncogene family	P+T	GTP binding|GTPase activity|exocytosis|hemocyte development|protein transport|small GTPase mediated signal transduction
miR-125b BC002510	RAB6B	RAB6B, member RAS oncogene family	P+T	GTP binding|GTPase activity|Golgi apparatus|intracellular protein transport|retrograde transport, Golgi to ER|small GTPase mediated signal transduction
miR-125b AK022662	RASAL2	RAS protein activator like 2	P+T	GTPase activator activity|Ras GTPase activator activity|signal transduction
miR-125b NM_004841	RASAL2	RAS protein activator like 2	P+T	GTPase activator activity|Ras GTPase activator activity|signal transduction
miR-125b NM_016090	RBM7	RNA binding motif protein 7	P+T	RNA binding|meiosis|nucleic acid binding|nucleotide binding
miR-125b NM_006268	REQ	requiem, apoptosis response zinc finger gene	M+P+T	DNA binding|apoptosis|induction of apoptosis by extracellular signals|nucleus|protein ubiquitination|regulation of transcription, DNA-dependent|transcription|ubiquitin ligase complex|ubiquitin-protein ligase activity|zinc ion binding
miR-125b NM_000449	RFX5	regulatory factor X, 5 (influences HLA class II expression)	P+T	nucleus|regulation of transcription, DNA-dependent|transcription|transcription coactivator activity|transcription factor activity|transcription from RNA polymerase II promoter
miR-125b NM_003721	RFXANK	regulatory factor X-associated ankyrin-containing protein	P+T	humoral immune response|nucleus|regulation of transcription, DNA-dependent|transcription|transcription coactivator activity|transcription factor activity|transcription from RNA polymerase II promoter
miR-125b NM_014746	RNF144	likely ortholog of mouse ubiquitin conjugating enzyme 7 interacting protein 4	P+T	nucleus|protein ubiquitination|ubiquitin ligase complex|ubiquitin-protein ligase activity|zinc ion binding
miR-125b NM_014771	RNF40	ring finger protein 40	M+P+T	protein ubiquitination|ubiquitin ligase complex|ubiquitin-protein ligase activity|zinc ion binding
miR-125b AL109955	RNPC1	RNA-binding region (RNP1, RRM) containing 1	P+T	
miR-125b AF116627	RPL29	ribosomal protein L29	M+T	
miR-125b NM_002953	RPS6KA1	ribosomal protein S6 kinase, 90kDa, polypeptide 1	M+P+T	ATP binding|protein amino acid phosphorylation|protein serine/threonine kinase activity|protein serine/threonine kinase activity|protein-tyrosine kinase activity|signal transduction|transferase activity

miR-125b	NM_000332	SCA1	spinocerebellar ataxia 1 (olivopontocerebellar ataxia 1, autosomal dominant, ataxin 1)	P+T	RNA binding|cytoplasm|nucleus
miR-125b	NM_012429	SEC14L2	SEC14-like 2 (S. cerevisiae)	P+T	cytoplasm|intracellular protein transport|membrane|nucleus|phospholipid binding|positive regulation of transcription, DNA-dependent|protein carrier activity|regulation of cholesterol biosynthesis|transcription|transcriptional activator activity|transport|vitamin E binding
miR-125b	NM_005065	SEL1L	sel-1 suppressor of lin-12-like (C. elegans)	P+T	catalytic activity|integral to membrane
miR-125b	NM_017789	SEMA4C	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4C	M+P+T	cell differentiation|integral to membrane|membrane|neurogenesis|receptor activity
miR-125b	NM_006378	SEMA4D	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D	P+T	anti-apoptosis|cell adhesion|cell differentiation|immune response|integral to membrane|membrane|neurogenesis|receptor activity
miR-125b	BE622841	SENP2	sentrin-specific protease	M+P	
miR-125b	NM_003011	SET	SET translocation (myeloid leukemia-associated)	M+T	DNA replication|endoplasmic reticulum|histone binding|negative regulation of histone acetylation|nucleocytoplasmic transport|nucleosome assembly|nucleosome disassembly|nucleus|perinuclear region|protein phosphatase inhibitor activity|protein phosphatase type 2A regulator activity
miR-125b	NM_006275	SFRS6	splicing factor, arginine/serine-rich 6	P+T	RNA binding|mRNA splice site selection|nuclear mRNA splicing, via spliceosome|nucleotide binding|nucleus
miR-125b	AF015043	SH3BP4	SH3-domain binding protein 4	P+T	cell cycle|endocytosis|nucleus|signal transducer activity
miR-125b	NM_016538	SIRT7	sirtuin silent mating type information regulation 2 homolog 7 (S. cerevisiae)	P+T	DNA binding|chromatin silencing|chromatin silencing complex|hydrolase activity|regulation of transcription, DNA-dependent
miR-125b	NM_020309	SLC17A7	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7	P+T	integral to membrane|phosphate transport|sodium-dependent phosphate transporter activity|transport|transporter activity
miR-125b	NM_013272	SLC21A11	solute carrier family 21 (organic anion transporter), member 11	P+T	integral to membrane|ion transport|membrane|transporter activity
miR-125b	AK000722	SLC27A4	solute carrier family 27 (fatty acid transporter), member 4	P+T	catalytic activity|fatty acid transport|fatty acid transporter activity|ligase activity|lipid metabolism|lipid transport|metabolism
miR-125b	NM_003759	SLC4A4	solute carrier family 4, sodium bicarbonate cotransporter, member 4	P+T	anion transport|inorganic anion exchanger activity|integral to membrane|integral to plasma membrane|membrane|sodium:bicarbonate symporter activity|transport
miR-125b	NM_003045	SLC7A1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	P+T	amino acid metabolism|amino acid permease activity|amino acid transport|basic amino acid transporter activity|integral to plasma membrane|membrane|receptor activity|transport
miR-125b	NM_003983	SLC7A6	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	P+T	amino acid metabolism|amino acid transport|amino acid-polyamine transporter activity|integral to plasma membrane|plasma membrane|protein complex assembly|transport
miR-125b	AF113019	SMARCD2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2	M+P+T	chromatin remodeling|nucleoplasm|regulation of transcription from RNA polymerase II promoter|transcription|transcription coactivator activity
miR-125b	NM_005985	SNAI1	snail homolog 1 (Drosophila)	P+T	DNA binding|cartilage condensation|development|neurogenesis|nucleus|zinc ion

				binding
miR-125b AB037750	SORCS2	VPS10 domain receptor protein	P+T	integral to membrane|intracellular protein transport|membrane|membrane|neuropeptide receptor activity|neuropeptide signaling pathway|protein binding|protein transporter activity|sugar binding
miR-125b BE742268	SORT1	sortilin 1	P+T	endocytosis|endosome|integral to membrane|integral to membrane|intracellular protein transport|membrane|neurotensin receptor activity, G-protein coupled|protein transporter activity|receptor activity
miR-125b AI360875	SOX11	SRY (sex determining region Y)-box 11	M+T	DNA binding|neurogenesis|nucleus|regulation of transcription, DNA-dependent|transcription
miR-125b AU121035	SP1	Sp1 transcription factor	P+T	DNA binding|RNA polymerase II transcription factor activity|nucleus|regulation of transcription, DNA-dependent|transcription|transcriptional activator activity|zinc ion binding
miR-125b NM_003131	SRF	serum response factor (c-fos serum response element-binding transcription factor)	M+T	RNA polymerase II transcription factor activity|nucleus|regulation of transcription from RNA polymerase II promoter|signal transduction|transcription|transcription factor activity
miR-125b NM_005637	SS18	synovial sarcoma translocation, chromosome 18	P+T	nucleus
miR-125b AF343880	SSX2	synovial sarcoma, X breakpoint 2	P+T	nucleus
miR-125b NM_014682	ST18	suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein)	P+T	nucleus|regulation of transcription, DNA-dependent|transcription factor activity
miR-125b AA128023	STARD13	START domain containing 13	P+T	
miR-125b BC000627	STAT3	signal transducer and activator of transcription 3 (acute-phase response factor)	P+T	JAK-STAT cascade|acute-phase response|calcium ion binding|cell motility|cytoplasm|hematopoietin/interferon-class (D200-domain) cytokine receptor signal transducer activity|intracellular signaling cascade|negative regulation of transcription from RNA polymerase II promoter|neurogenesis|nucleus|nucleus|regulation of transcription, DNA-dependent|signal transducer activity|transcription|transcription factor activity|transcription factor activity
miR-125b NM_003155	STC1	stanniocalcin 1	P+T	calcium ion homeostasis|cell surface receptor linked signal transduction|cell-cell signaling|extracellular region|hormone activity|response to nutrients
miR-125b NM_003173	SUV39H1	suppressor of variegation 3-9 homolog 1 (Drosophila)	P+T	DNA replication and chromosome cycle|S-adenosylmethionine-dependent methyltransferase activity|chromatin|chromatin assembly or disassembly|chromatin binding|chromatin modification|condensed nuclear chromosome|histone lysine N-methyltransferase activity (H3-K9 specific)|histone-lysine N-methyltransferase activity|methyltransferase activity|nucleus|nucleus|protein binding|transferase activity|zinc ion binding
miR-125b AW139618	SYN2	synapsin II	P+T	neurotransmitter secretion|synapse|synaptic transmission|synaptic vesicle
miR-125b R60550	TAF5L	TAF5-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor, 65kDa	M+P+T	nucleus|regulation of transcription, DNA-dependent|transcription factor activity|transcription from RNA polymerase II promoter
miR-125b AF220509	TAF9L	TAF9-like RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa	P+T	DNA binding|nucleus|regulation of transcription, DNA-dependent|transcription factor TFIID complex|transcription initiation

miR-125b	NM_000116	TAZ	tafazzin (cardiomyopathy, dilated 3A (X-linked); endocardial fibroelastosis 2; Barth syndrome)	M+P+T	acyltransferase activity|heart development|integral to membrane|metabolism|muscle contraction|muscle development
miR-125b	NM_018488	TBX4	T-box 4	P+T	development|nucleus|regulation of transcription, DNA-dependent|transcription|transcription factor activity
miR-125b	NM_012249	TC10	ras-like protein TC10	M+T	GTP binding|GTPase activity|plasma membrane|small GTPase mediated signal transduction
miR-125b	BG387172	TEAD2	TEA domain family member 2	P+T	nucleus|nucleus|regulation of transcription, DNA-dependent|regulation of transcription, DNA-dependent|transcription|transcription factor activity|transcription factor activity
miR-125b	U06935	TEF	thyrotrophic embryonic factor	P+T	RNA polymerase II transcription factor activity|nucleus|regulation of transcription from RNA polymerase II promoter|rhythmic process|transcription|transcription factor activity
miR-125b	NM_006464	TGOLN2	trans-golgi network protein 2	P+T	Golgi trans face|integral to membrane|transport vesicle
miR-125b	BE219311	TIMM22	translocase of inner mitochondrial membrane 22 homolog (yeast)	P+T	integral to membrane|mitochondrial inner membrane|mitochondrion|protein transport|protein transporter activity
miR-125b	NM_003326	TNFSF4	tumor necrosis factor (ligand) superfamily, member 4 (tax-transcriptionally activated glycoprotein 1, 34kDa)	P+T	cell-cell signaling|immune response|integral to plasma membrane|membrane|positive regulation of cell proliferation|signal transduction|tumor necrosis factor receptor binding
miR-125b	AA873275	TOR2A	torsin family 2, member A	P+T	ATP binding|GTP cyclohydrolase I activity|biosynthesis|chaperone cofactor dependent protein folding|endoplasmic reticulum|nucleoside-triphosphatase activity|nucleotide binding
miR-125b	AW341649	TP53INP1	tumor protein p53 inducible nuclear protein 1	M+P+T	apoptosis|nucleus
miR-125b	NM_014112	TRPS1	trichorhinophalangeal syndrome I	P+T	NLS-bearing substrate-nucleus import|nucleus|regulation of transcription, DNA-dependent|skeletal development|transcription|transcription factor activity|transcription from RNA polymerase II promoter|zinc ion binding
miR-125b	NM_001070	TUBG1	tubulin, gamma 1	P+T	GTP binding|GTPase activity|centrosome|condensed nuclear chromosome|gamma-tubulin complex|meiotic spindle organization and biogenesis|microtubule|microtubule nucleation|microtubule-based movement|mitotic spindle organization and biogenesis|polar microtubule|protein binding|protein polymerization|spindle pole body|structural constituent of cytoskeleton
miR-125b	NM_003330	TXNRD1	thioredoxin reductase 1	P+T	FAD binding|cell redox homeostasis|cytoplasm|disulfide oxidoreductase activity|electron transport|electron transporter activity|oxidoreductase activity, acting on NADH or NADPH, disulfide as acceptor|signal transduction|thioredoxin-disulfide reductase activity
miR-125b	BC004862	UBE2R2	ubiquitin-conjugating enzyme E2R 2	P+T	ligase activity|ubiquitin conjugating enzyme activity|ubiquitin cycle|ubiquitin-protein ligase activity
miR-125b	NM_003728	UNC5C	unc-5 homolog B (C. elegans)	P+T	apoptosis|axon guidance|brain development|development|integral to membrane|netrin receptor activity|protein binding|receptor activity|signal transduction
miR-125b	NM_003369	UVRAG	UV radiation resistance associated gene	P+T	DNA repair|cytoplasm

miR-125b	AF195514	VPS4B	vacuolar protein sorting 4B (yeast)	M+P+T	ATP binding|ATPase activity, coupled|membrane|membrane fusion|nucleoside-triphosphatase activity|nucleotide binding|peroxisome organization and biogenesis|protein binding|regulation of transcription, DNA-dependent
miR-125b	R51061	VTS58635	mitogen-activated protein kinase kinase kinase 1	P+T	GTP binding|small GTPase mediated signal transduction
miR-125b	NM_004184	WARS	tryptophanyl-tRNA synthetase	M+T	ATP binding|cytoplasm|ligase activity|negative regulation of cell proliferation|protein biosynthesis|soluble fraction|tryptophan-tRNA ligase activity|tryptophanyl-tRNA aminoacylation|tryptophanyl-tRNA aminoacylation
miR-125b	NM_005433	YES1	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	P+T	ATP binding|intracellular signaling cascade|protein amino acid phosphorylation|protein-tyrosine kinase activity|transferase activity
miR-125b	NM_017740	ZDHHC7	zinc finger, DHHC domain containing 7	P+T	integral to membrane|metal ion binding
miR-125b	BF525395	ZFP385	likely ortholog of mouse zinc finger protein 385	M+P+T	DNA binding|nucleic acid binding|nucleus|regulation of transcription, DNA-dependent|transcription|zinc ion binding
miR-125b	NM_007345	ZNF236	zinc finger protein 236	P+T	nucleus|regulation of transcription, DNA-dependent|transcription|transcription factor activity|zinc ion binding
miR-125b	NM_012482	ZNF281	zinc finger protein 281	M+P+T	DNA binding|DNA-directed RNA polymerase II, core complex|negative regulation of transcription from RNA polymerase II promoter|nucleus|regulation of transcription, DNA-dependent|specific RNA polymerase II transcription factor activity|transcription|zinc ion binding
miR-125b	NM_003427	ZNF76	zinc finger protein 76 (expressed in testis)	P+T	DNA binding|nucleus|regulation of transcription from RNA polymerase II promoter|regulation of transcription from RNA polymerase III promoter|transcription|zinc ion binding
miR-125b	NM_022465	ZNFN1A4	zinc finger protein, subfamily 1A, 4 (Eos)	M+P+T	nucleic acid binding|nucleus|transcription factor activity|transcriptional repressor activity|zinc ion binding
miR-145	NM_005502	ABCA1	ATP-binding cassette, sub-family A (ABC1), member 1	P+T	ATP binding|ATP binding|ATPase activity|anion transporter activity|cholesterol metabolism|integral to plasma membrane|lipid metabolism|membrane fraction|nucleotide binding|steroid metabolism|sterol transporter activity|transport|transport
miR-145	AL527773	ABR	active BCR-related gene	M+P+T	GTPase activator activity|guanyl-nucleotide exchange factor activity|small GTPase mediated signal transduction
miR-145	NM_001616	ACVR2	activin A receptor, type II	M+P+T	ATP binding|integral to plasma membrane|membrane|protein amino acid phosphorylation|receptor activity|transferase activity|transforming growth factor beta receptor activity|transmembrane receptor protein serine/threonine kinase signaling pathway
miR-145	NM_003183	ADAM17	a disintegrin and metalloproteinase domain 17 (tumor necrosis factor, alpha, converting enzyme)	P+T	cell-cell signaling|integral to plasma membrane|metalloendopeptidase activity|proteolysis and peptidolysis|zinc ion binding
miR-145	NM_019903	ADD3	adducin 3 (gamma)	M+P+T	calmodulin binding|cytoskeleton|membrane|structural constituent of cytoskeleton
miR-145	AB003476	AKAP12	A kinase (PRKA) anchor protein (gravin) 12	P+T	G-protein coupled receptor protein signaling pathway|cytoplasm|protein binding|protein kinase A binding|protein targeting|signal transduction
miR-145	NM_016201	AMOTL2	angiomotin like 2	M+P+T	
miR-145	NM_001128	AP1G1	adaptor-related protein complex 1, gamma 1 subunit	M+P+T	Golgi apparatus|binding|clathrin coat of trans-Golgi network vesicle|coated pit|endocytosis|intracellular protein transport|intracellular protein transport|membrane coat adaptor complex|protein complex assembly|transporter activity

miR-145	NM_001284	AP3S1	adaptor-related protein complex 3, sigma 1 subunit	M+P+T	Golgi apparatus|clathrin vesicle coat|insulin receptor signaling pathway|intracellular protein transport|membrane coat adaptor complex|transport|transport vesicle|transporter activity
miR-145	NM_006380	APPBP2	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	M+P+T	binding|cytoplasm|intracellular protein transport|membrane|microtubule associated complex|microtubule motor activity|nucleus
miR-145	AB037845	ARHGAP10	Rho-GTPase activating protein 10	M+T	protein binding
miR-145	AL516350	ARPC5	actin related protein 2/3 complex, subunit 5, 16kDa	P+T	Arp2/3 protein complex|actin cytoskeleton organization and biogenesis|cell motility|cytoplasm|cytoskeleton|regulation of actin filament polymerization|structural constituent of cytoskeleton
miR-145	U72937	ATRX	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)	M+T	ATP binding|DNA binding|DNA helicase activity|DNA methylation|DNA recombination|DNA repair|chromosome organization and biogenesis (sensu Eukaryota)|helicase activity|hydrolase activity|nuclear heterochromatin|nucleus|perception of sound|regulation of transcription, DNA-dependent|transcription factor activity
miR-145	NM_021813	BACH2	BTB and CNC homology 1, basic leucine zipper transcription factor 2	P+T	DNA binding|nucleus|protein binding|regulation of transcription, DNA-dependent|transcription
miR-145	NM_013449	BAZ2A	bromodomain adjacent to zinc finger domain, 2A	P+T	DNA binding|chromatin remodeling|nucleolus organizer complex|nucleus|regulation of transcription, DNA-dependent|transcription|transcription regulator activity
miR-145	NM_007005	BCE-1	BCE-1 protein	M+P	frizzled signaling pathway|molecular_function unknown|nucleus|nucleus|regulation of transcription|regulation of transcription, DNA-dependent
miR-145	NM_003458	BSN	bassoon (presynaptic cytomatrix protein)	P+T	cytoskeleton|metal ion binding|nucleus|structural constituent of cytoskeleton|synapse|synaptic transmission|synaptosome
miR-145	NM_013279	C11orf9	chromosome 11 open reading frame 9	M+P+T	
miR-145	NM_024643	C14orf140	hypothetical protein FLJ23093	P+T	
miR-145	NM_018270	C20orf20	chromosome 20 open reading frame 20	P+T	chromatin modification|nucleus|regulation of cell growth|regulation of transcription, DNA-dependent|transcription
miR-145	NM_004276	CABP1	calcium binding protein 1 (calbrain)	P+T	calcium ion binding|calcium ion binding|enzyme inhibitor activity
miR-145	NM_001755	CBFB	core-binding factor, beta subunit	M+P+T	RNA polymerase II transcription factor activity|nucleus|transcription coactivator activity|transcription factor activity|transcription from RNA polymerase II promoter
miR-145	NM_001759	CCND2	cyclin D2	P+T	cytokinesis|nucleus|regulation of cell cycle
miR-145	NM_020307	CCNL1	cyclin L ania-6a	M+P+T	cell cycle|regulation of cell cycle
miR-145	AL118798	CD47	CD47 antigen (Rh-related antigen, integrin-associated signal transducer)	P+T	cell-matrix adhesion|integral to plasma membrane|integrin-mediated signaling pathway|plasma membrane|protein binding
miR-145	BF576053	CFL2	cofilin 2 (muscle)	M+P+T	actin binding|cytoskeleton|nucleus
miR-145	AA835485	CKLiK	CamKI-like protein kinase	P+T	ATP binding|calcium- and calmodulin-dependent protein kinase activity|calmodulin binding|nucleus|protein amino acid phosphorylation|protein serine/threonine kinase activity|transferase activity
miR-145	NM_004921	CLCA3	chloride channel, calcium activated, family member 3	P+T	extracellular space|transport|transporter activity
miR-145	NM_001326	CSTF3	cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kDa	M+P+T	RNA binding|binding|mRNA cleavage|mRNA polyadenylylation|nucleus

miR-145	NM_020248	CTNNBIP1	catenin, beta interacting protein 1	P+T	Wnt receptor signaling pathway|beta-catenin binding|cell proliferation|development|nucleus|regulation of transcription, DNA-dependent|signal transduction
miR-145	AW772082	DACH	dachshund homolog (Drosophila)	P+T	DNA binding|development|eye morphogenesis (sensu Endopterygota)|nucleus|regulation of transcription, DNA-dependent|transcription
miR-145	NM_004393	DAG1	dystroglycan 1 (dystrophin-associated glycoprotein 1)	M+P+T	actin cytoskeleton|calcium ion binding|extracellular matrix (sensu Metazoa)|integral to plasma membrane|laminin receptor activity|membrane fraction|muscle contraction|plasma membrane|protein binding|protein complex assembly
miR-145	NM_003887	DDEF2	development and differentiation enhancing factor 2	P+T	GTPase activator activity|Golgi apparatus|regulation of GTPase activity
miR-145	AL080239	DKFZp547M2010	hypothetical protein DKFZp547M2010	M+P+T	
miR-145	AL137517	DKFZp564O1278	hypothetical protein DKFZp564O1278	P+T	integral to membrane
miR-145	NM_001386	DPYSL2	dihydropyrimidinase-like 2	P+T	dihydropyrimidinase activity|hydrolase activity|neurogenesis|nucleobase, nucleoside, nucleotide and nucleic acid metabolism|signal transduction
miR-145	BC003143	DUSP6	dual specificity phosphatase 6	P+T	MAP kinase phosphatase activity|cytoplasm|hydrolase activity|inactivation of MAPK|protein amino acid dephosphorylation|protein serine/threonine phosphatase activity|protein tyrosine phosphatase activity|regulation of cell cycle|soluble fraction
miR-145	D86550	DYRK1A	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A	P+T	ATP binding|neurogenesis|nucleus|protein amino acid phosphorylation|protein serine/threonine kinase activity|protein-tyrosine kinase activity|transferase activity
miR-145	NM_001967	EIF4A2	eukaryotic translation initiation factor 4A, isoform 2	M+P+T	ATP binding|ATP-dependent helicase activity|DNA binding|RNA binding|eukaryotic translation initiation factor 4F complex|hydrolase activity|protein biosynthesis|regulation of translational initiation|translation initiation factor activity
miR-145	NM_001417	EIF4B	eukaryotic translation initiation factor 4B	M+T	RNA binding|eukaryotic translation initiation factor 4F complex|nucleic acid binding|nucleotide binding|protein biosynthesis|regulation of translational initiation|translation initiation factor activity|translation initiation factor activity
miR-145	BC005057	EIF4EBP2	eukaryotic translation initiation factor 4E binding protein 2	P+T	eukaryotic initiation factor 4E binding|negative regulation of protein biosynthesis|negative regulation of translational initiation|regulation of translation
miR-145	NM_020909	EPB41L5	erythrocyte membrane protein band 4.1 like 5	P+T	binding|cytoplasm|cytoskeletal protein binding|cytoskeleton|membrane
miR-145	NM_005797	EVA1	epithelial V-like antigen 1	P+T	cell adhesion|cytoskeleton|homophilic cell adhesion|integral to membrane|membrane|morphogenesis|protein binding
miR-145	NM_022977	FACL4	fatty-acid-Coenzyme A ligase, long-chain 4	M+P+T	fatty acid metabolism|integral to membrane|learning and/or memory|ligase activity|lipid metabolism|long-chain-fatty-acid-CoA ligase activity|magnesium ion binding|metabolism
miR-145	AL042120	FHOD2	formin homology 2 domain containing 2	M+P	Rho GTPase binding|actin binding|actin cytoskeleton organization and biogenesis|cell organization and biogenesis|nucleus|regulation of transcription, DNA-dependent|transcription factor activity|translation initiation factor activity|translational initiation
miR-145	NM_002013	FKBP3	FK506 binding protein 3, 25kDa	P+T	FK506 binding|isomerase activity|nucleus|peptidyl-prolyl cis-trans isomerase activity|protein folding|receptor activity
miR-145	NM_002017	FLI1	Friend leukemia virus integration 1	M+P+T	hemostasis|nucleus|organogenesis|regulation of transcription, DNA-dependent|transcription|transcription factor activity
miR-145	NM_023071	FLJ13117	hypothetical protein FLJ13117	P+T	

miR-145	AL561281	FLJ20373	hypothetical protein FLJ20373	M+P+T	ATP binding|cellular_component unknown|protein amino acid phosphorylation|protein kinase cascade|protein serine/threonine kinase activity|response to stress|signal transduction|small GTPase regulator activity|transferase activity
miR-145	AK025444	FLJ21791	hypothetical protein FLJ21791	M+T	
miR-145	NM_024713	FLJ22557	hypothetical protein FLJ22557	P+T	
miR-145	AA872588	FLJ36155	likely ortholog of mouse Gli-similar 1 Kruppel-like zinc finger (Glis1)	P+T	DNA binding|negative regulation of transcription from RNA polymerase II promoter|nucleus|positive regulation of transcription from RNA polymerase II promoter|regulation of transcription, DNA-dependent|specific RNA polymerase II transcription factor activity|transcription|zinc ion binding
miR-145	AI434509	FLJ38499	Unnamed protein product [Homo sapiens], mRNA sequence	P+T	nucleic acid binding
miR-145	M62994	FLNB	filamin B, beta (actin binding protein 278)	P+T	actin binding|actin binding|actin cytoskeleton|actin cytoskeleton organization and biogenesis|cell differentiation|cytoskeletal anchoring|integral to plasma membrane|myogenesis|signal transduction
miR-145	NM_002025	FMR2	fragile X mental retardation 2	M+T	brain development|learning and/or memory
miR-145	N29672	FOS	v-fos FBJ murine osteosarcoma viral oncogene homolog	M+T	proto-oncogene
miR-145	NM_002015	FOXO1A	forkhead box O1A (rhabdomyosarcoma)	M+P+T	anti-apoptosis|nucleus|regulation of transcription from RNA polymerase II promoter|transcription|transcription factor activity
miR-145	NM_003507	FZD7	frizzled homolog 7 (Drosophila)	M+P+T	G-protein coupled receptor activity|G-protein coupled receptor protein signaling pathway|Wnt receptor activity|development|frizzled signaling pathway|integral to membrane|plasma membrane
miR-145	AL049709	GGTL3	gamma-glutamyltransferase-like 3	M+P+T	
miR-145	NM_022735	GOCAP1	golgi complex associated protein 1, 60kDa	M+P+T	Golgi apparatus|acyl-CoA binding|catalytic activity|intracellular protein transport|membrane|mitochondrion|protein carrier activity|steroid biosynthesis
miR-145	NM_020806	GPHN	gephyrin	P+T	Mo-molybdopterin cofactor biosynthesis|catalytic activity|cytoskeleton
miR-145	NM_015071	GRAF	GTPase regulator associated with focal adhesion kinase pp125(FAK)	P+T	Rho GTPase activator activity|actin cytoskeleton organization and biogenesis|cellular_component unknown|neurogenesis
miR-145	NM_017913	HARC	Hsp90-associating relative of Cdc37	P+T	cytokinesis|regulation of cell cycle
miR-145	BC006237	HECTD1	HECT domain containing 1	M+T	intracellular|ligase activity|receptor activity|ubiquitin cycle|ubiquitin-protein ligase activity
miR-145	U64317	HEF1	enhancer of filamentation 1 (cas-like docking; Crk-associated substrate related)	P+T	actin filament bundle formation|cell adhesion|cytokinesis|cytoplasm|cytoskeleton|cytoskeleton organization and biogenesis|integrin-mediated signaling pathway|mitosis|nucleus|protein binding|regulation of cell cycle|regulation of cell growth|signal transduction|spindle
miR-145	NM_016258	HGRG8	high-glucose-regulated protein 8	P+T	
miR-145	AL162003	HIC2	hypermethylated in cancer 2	P+T	DNA binding|negative regulation of transcription, DNA-dependent|nucleus|protein C-terminus binding|transcription|zinc ion binding
miR-145	NM_014212	HOXC11	homeo box C11	M+P+T	RNA polymerase II transcription factor activity|development|endoderm development|nucleus|regulation of transcription, DNA-dependent|transcription factor activity

miR-145	NM_002193	INHBB	inhibin, beta B (activin AB beta polypeptide)	M+P+T	cell differentiation|cytokine activity|defense response|extracellular region|growth|growth factor activity|hormone activity|host cell surface receptor binding|negative regulation of follicle-stimulating hormone secretion|negative regulation of hepatocyte growth factor biosynthesis|ovarian follicle development|positive regulation of follicle-stimulating hormone secretion|protein binding|protein homodimerization activity|response to external stimulus
miR-145	NM_005544	IRS1	insulin receptor substrate 1	M+P+T	cytoplasm|insulin receptor binding|protein binding|signal transducer activity|signal transduction|transmembrane receptor protein tyrosine kinase docking protein activity
miR-145	NM_006459	KEO4	similar to Caenorhabditis elegans protein C42C1.9	P+T	catalytic activity
miR-145	NM_014686	KIAA0355	KIAA0355 gene product	P+T	
miR-145	NM_015176	KIAA0483	KIAA0483 protein	P+T	ubiquitin cycle
miR-145	NM_014871	KIAA0710	KIAA0710 gene product	M+P+T	cysteine-type endopeptidase activity|exonuclease activity|nucleus|ubiquitin cycle|ubiquitin thiolesterase activity|ubiquitin-dependent protein catabolism
miR-145	AA772278	KIAA1673	KIAA1673	M+P+T	
miR-145	AB051495	KIAA1708	KIAA1708 protein	P+T	ATP binding|microtubule associated complex|microtubule motor activity|microtubule-based movement
miR-145	AI814587	KIAA1715	KIAA1715 protein	M+T	
miR-145	AI187364	KIAA1894	KIAA1894 protein	P+T	integral to membrane
miR-145	AF155117	KIF21A	kinesin family member 21A	P+T	ATP binding|microtubule associated complex|microtubule motor activity|microtubule-based movement
miR-145	NM_004235	KLF4	Kruppel-like factor 4 (gut)	M+T	mesodermal cell fate determination|negative regulation of cell proliferation|negative regulation of transcription, DNA-dependent|negative regulation of transcription, DNA-dependent|nucleic acid binding|nucleus|transcription|transcription factor activity|transcription factor activity|transcriptional activator activity|transcriptional activator activity|transcriptional repressor activity|transcriptional repressor activity|zinc ion binding|zinc ion binding
miR-145	T68150	LL5beta	hypothetical protein FLJ21791	M+T	
miR-145	AI797833	LOC285148	a disintegrin and metalloproteinase domain 17 (tumor necrosis factor, alpha, converting enzyme)	P+T	catalytic activity
miR-145	NM_025146	MAK3P	likely ortholog of mouse Mak3p homolog (S. cerevisiae)	P+T	N-acetyltransferase activity
miR-145	BF971923	MAP3K3	mitogen-activated protein kinase kinase kinase 3	M+P	ATP binding|MAP kinase kinase kinase activity|MAPKKK cascade|magnesium ion binding|positive regulation of I-kappaB kinase/NF-kappaB cascade|protein amino acid phosphorylation|protein kinase activity|protein serine/threonine kinase activity|signal transducer activity|transferase activity
miR-145	NM_004834	MAP4K4	mitogen-activated protein kinase kinase kinase kinase 4	M+P+T	ATP binding|cellular_component unknown|protein amino acid phosphorylation|protein kinase cascade|protein serine/threonine kinase activity|response to stress|signal transduction|small GTPase regulator activity|transferase activity
miR-145	BF382281	MGC10120	Homo sapiens cDNA FLJ30135 fis, clone BRACE2000061, mRNA sequence	P+T	

miR-145	BG231756	MGC10986	hypothetical protein MGC10986	M+P	ATP binding|MAP kinase kinase kinase activity|MAPKKK cascade|magnesium ion binding|positive regulation of I-kappaB kinase/NF-kappaB cascade|protein amino acid phosphorylation|protein kinase activity|protein serine/threonine kinase activity|signal transducer activity|transferase activity
miR-145	BC004869	MGC2817	hypothetical protein MGC2817	P+T	outer membrane|protein transport
miR-145	BC002712	MYCN	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	M+T	chromatin|nucleus|protein binding|regulation of transcription from RNA polymerase II promoter|transcription factor activity
miR-145	AB007899	NEDD4L	neural precursor cell expressed, developmentally down-regulated 4-like	P+T	excretion|intracellular|intracellular|ligase activity|positive regulation of endocytosis|protein binding|protein ubiquitination|regulation of protein catabolism|response to metal ion|sodium channel regulator activity|sodium ion homeostasis|sodium ion transport|ubiquitin cycle|ubiquitin-protein ligase activity|ubiquitin-protein ligase activity|water homeostasis
miR-145	NM_005863	NET1	neuroepithelial cell transforming gene 1	P+T	guanyl-nucleotide exchange factor activity|nucleus|regulation of cell growth|signal transduction
miR-145	NM_003204	NFE2L1	nuclear factor (erythroid-derived 2)-like 1	P+T	DNA binding|heme biosynthesis|inflammatory response|morphogenesis|nucleus|nucleus|regulation of transcription, DNA-dependent|transcription|transcription cofactor activity|transcription factor activity|transcription from RNA polymerase II promoter
miR-145	NM_006469	NS1-BP	NS1-binding protein	M+P+T	RNA splicing|protein binding|response to virus|spliceosome complex|transcription factor complex|transcription from RNA polymerase III promoter
miR-145	NM_019094	NUDT4	nudix (nucleoside diphosphate linked moiety X)-type motif 4	P+T	calcium-mediated signaling|cyclic nucleotide metabolism|cyclic-nucleotide-mediated signaling|diphosphoinositol-polyphosphate diphosphatase activity|hydrolase activity|intracellular|intracellular signaling cascade|intracellular transport|magnesium ion binding|regulation of RNA-nucleus export
miR-145	AW149417	OAZ	OLF-1/EBF associated zinc finger gene	P+T	nucleic acid binding|nucleus|zinc ion binding
miR-145	NM_024586	OSBPL9	oxysterol binding protein-like 9	M+P	lipid transport|steroid metabolism
miR-145	AB040812	PAK7	p21(CDKN1A)-activated kinase 7	M+T	ATP binding|protein amino acid phosphorylation|protein serine/threonine kinase activity|transferase activity
miR-145	NM_014456	PDCD4	programmed cell death 4 (neoplastic transformation inhibitor)	M+P+T	apoptosis
miR-145	NM_002657	PLAGL2	pleiomorphic adenoma gene-like 2	M+P+T	nucleus|regulation of transcription, DNA-dependent|transcription|transcription factor activity|zinc ion binding
miR-145	AK023546	PLCL2	phospholipase C-like 2	P+T	calcium ion binding|intracellular signaling cascade|lipid metabolism|phosphoinositide phospholipase C activity
miR-145	AI274352	PLN	phospholamban	P+T	
miR-145	NM_000944	PPP3CA	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha)	P+T	calcineurin complex|calcium ion binding|calmodulin binding|hydrolase activity|protein amino acid dephosphorylation|protein serine/threonine phosphatase activity
miR-145	BF247371	PRO1843	hypothetical protein PRO1843	M+T	
miR-145	NM_000959	PTGFR	prostaglandin F receptor (FP)	P+T	G-protein coupled receptor protein signaling pathway|G-protein coupled receptor protein signaling pathway|integral to membrane|integral to plasma membrane|parturition|prostaglandin F receptor activity|prostaglandin F receptor activity|receptor activity|rhodopsin-like receptor activity|signal transduction|thromboxane receptor activity

miR-145	NM_002890	RASA1	RAS p21 protein activator (GTPase activating protein) 1	P+T	Ras GTPase activator activity|intracellular signaling cascade
miR-145	NM_006506	RASA2	RAS p21 protein activator 2	P+T	Ras GTPase activator activity|intracellular signaling cascade
miR-145	NM_002912	REV3L	REV3-like, catalytic subunit of DNA polymerase zeta (yeast)	M+P+T	3'-5' exonuclease activity|DNA binding|DNA repair|DNA replication|DNA-dependent DNA replication|DNA-directed DNA polymerase activity|nucleotide binding|nucleus|transferase activity|zeta DNA polymerase activity|zeta DNA polymerase complex
miR-145	NM_002924	RGS7	regulator of G-protein signalling 7	P+T	heterotrimeric G-protein complex|intracellular signaling cascade|regulation of G-protein coupled receptor protein signaling pathway|regulator of G-protein signaling activity|signal transducer activity
miR-145	AL136924	RIN2	Ras and Rab interactor 2	P+T	GTPase activator activity|Rab guanyl-nucleotide exchange factor activity|cellular_component unknown|endocytosis|intracellular signaling cascade|small GTPase mediated signal transduction|small GTPase regulator activity
miR-145	BE463945	RTKN	rhotekin	P+T	intracellular|protein binding|signal transduction|signal transduction
miR-145	AF225986	SCN3A	sodium channel, voltage-gated, type III, alpha polypeptide	P+T	cation channel activity|cation transport|integral to membrane|membrane|sodium ion transport|voltage-gated sodium channel activity|voltage-gated sodium channel complex
miR-145	NM_006080	SEMA3A	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	P+T	cell differentiation|extracellular region|neurogenesis
miR-145	NM_020796	SEMA6A	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	P+T	apoptosis|axon|axon guidance|cell differentiation|cell surface receptor linked signal transduction|cytoskeleton organization and biogenesis|development|integral to membrane|membrane|neurogenesis|protein binding|receptor activity
miR-145	NM_004171	SLC1A2	solute carrier family 1 (glial high affinity glutamate transporter), member 2	P+T	L-glutamate transport|L-glutamate transporter activity|dicarboxylic acid transport|integral to membrane|membrane|membrane fraction|sodium:dicarboxylate symporter activity|symporter activity|synaptic transmission|transport
miR-145	NM_003759	SLC4A4	solute carrier family 4, sodium bicarbonate cotransporter, member 4	P+T	anion transport|inorganic anion exchanger activity|integral to membrane|integral to plasma membrane|membrane|sodium:bicarbonate symporter activity|transport
miR-145	NM_030918	SNX27	hypothetical protein My014	M+P+T	intracellular signaling cascade|protein binding|protein transport
miR-145	AI360875	SOX11	SRY (sex determining region Y)-box 11	M+T	DNA binding|neurogenesis|nucleus|regulation of transcription, DNA-dependent|transcription
miR-145	NM_000346	SOX9	SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal)	P+T	DNA binding|cartilage condensation|nucleus|regulation of transcription from RNA polymerase II promoter|skeletal development|specific RNA polymerase II transcription factor activity|transcription
miR-145	AK023899	SRGAP1	SLIT-ROBO Rho GTPase activating protein 1	P+T	GTPase activator activity
miR-145	NM_003155	STC1	stanniocalcin 1	M+T	calcium ion homeostasis|cell surface receptor linked signal transduction|cell-cell signaling|extracellular region|hormone activity|response to nutrients
miR-145	BE219311	TIMM22	translocase of inner mitochondrial membrane 22 homolog (yeast)	M+P+T	integral to membrane|mitochondrial inner membrane|mitochondrion|protein transport|protein transporter activity
miR-145	AA705845	TLE4	transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila)	M+P	frizzled signaling pathway|molecular_function unknown|nucleus|nucleus|regulation of transcription|regulation of transcription, DNA-dependent

miR-145	BC005016	TRIM2	tripartite motif-containing 2	P+T	cytoplasm|myosin binding|protein ubiquitination|ubiquitin ligase complex|ubiquitin-protein ligase activity|zinc ion binding
miR-145	NM_025076	UXS1	UDP-glucuronate decarboxylase 1	M+P+T	carbohydrate metabolism|isomerase activity|nucleotide-sugar metabolism
miR-145	NM_005433	YES1	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	P+T	ATP binding|intracellular signaling cascade|protein amino acid phosphorylation|protein-tyrosine kinase activity|transferase activity
miR-145	BC003128	ZDHHC9	zinc finger, DHHC domain containing 9	P+T	integral to membrane|metal ion binding
miR-155	NM_019903	ADD3	adducin 3 (gamma)	P+T	calmodulin binding|cytoskeleton|membrane|structural constituent of cytoskeleton
miR-155	NM_020661	AICDA	activation-induced cytidine deaminase	P+T	B-cell differentiation|cellular_component unknown|cytidine deaminase activity|hydrolase activity|mRNA processing|zinc ion binding
miR-155	NM_007202	AKAP10	A kinase (PRKA) anchor protein 10	P+T	kinase activity|mitochondrion|protein binding|protein localization|signal transducer activity|signal transduction
miR-155	AI806395	ALFY	ALFY	P+T	binding|zinc ion binding
miR-155	NM_000038	APC	adenomatosis polyposis coli	P+T	Wnt receptor signaling pathway|beta-catenin binding|cell adhesion|microtubule binding|negative regulation of cell cycle|protein complex assembly|signal transduction
miR-155	NM_017610	ARK	Arkadia	P+T	protein ubiquitination|ubiquitin ligase complex|ubiquitin-protein ligase activity|zinc ion binding
miR-155	BG032269	ARL8	ADP-ribosylation-like factor 8	M+P+T	GTP binding|small GTPase mediated signal transduction
miR-155	AB000815	ARNTL	aryl hydrocarbon receptor nuclear translocator-like	P+T	circadian rhythm|nucleus|regulation of transcription, DNA-dependent|signal transducer activity|signal transduction|transcription|transcription factor activity
miR-155	NM_001670	ARVCF	armadillo repeat gene deletes in velocardiofacial syndrome	P+T	cell adhesion|cytoskeleton|development|protein binding|structural molecule activity
miR-155	AK024064	ASTN2	astrotactin 2	P+T	integral to membrane
miR-155	M95541	ATP2B1	ATPase, Ca++ transporting, plasma membrane 1	M+P+T	ATP binding|calcium ion binding|calcium ion transport|calcium-transporting ATPase activity|calmodulin binding|cation transport|hydrolase activity|hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances|integral to plasma membrane|magnesium ion binding|membrane|metabolism
miR-155	NM_001186	BACH1	BTB and CNC homology 1, basic leucine zipper transcription factor 1	P+T	DNA binding|nucleus|protein binding|regulation of transcription, DNA-dependent|transcription|transcription factor activity
miR-155	NM_007005	BCE-1	BCE-1 protein	P+T	frizzled signaling pathway|molecular_function unknown|nucleus|nucleus|regulation of transcription|regulation of transcription, DNA-dependent
miR-155	NM_022893	BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein)	P+T	cytoplasm|hemopoiesis|nucleic acid binding|nucleus|nucleus|regulation of transcription, DNA-dependent|transcription|zinc ion binding
miR-155	NM_001709	BDNF	brain-derived neurotrophic factor	M+T	growth factor activity|growth factor activity|neurogenesis
miR-155	NM_014577	BRD1	bromodomain containing 1	P+T	DNA binding|cell cycle|nucleus|nucleus|regulation of transcription, DNA-dependent
miR-155	NM_024529	C1orf28	chromosome 1 open reading frame 28	M+P+T	
miR-155	NM_000719	CACNA1C	calcium channel, voltage-dependent, L type, alpha 1C subunit	P+T	calcium ion binding|calcium ion transport|cation transport|integral to membrane|ion channel activity|ion transport|membrane|regulation of heart contraction rate|voltage-gated calcium channel activity|voltage-gated calcium channel activity|voltage-gated calcium channel complex|voltage-gated calcium channel complex

miR-155	AL118798	CD47	CD47 antigen (Rh-related antigen, integrin-associated signal transducer)	P+T	cell-matrix adhesion|integral to plasma membrane|integrin-mediated signaling pathway|plasma membrane|protein binding
miR-155	AL564683	CEBPB	CCAAT/enhancer binding protein (C/EBP), beta	M+P+T	acute-phase response|inflammatory response|nucleus|regulation of transcription, DNA-dependent|transcription|transcription factor activity|transcription from RNA polymerase II promoter
miR-155	NM_007023	CGEF2	cAMP-regulated guanine nucleotide exchange factor II	M+P	3',5'-cAMP binding|G-protein coupled receptor protein signaling pathway|cAMP-dependent protein kinase complex|cAMP-dependent protein kinase regulator activity|exocytosis|guanyl-nucleotide exchange factor activity|membrane fraction|nucleotide binding|protein amino acid phosphorylation|small GTPase mediated signal transduction
miR-155	AU152178	CMG2	capillary morphogenesis protein 2	P+T	integral to membrane|receptor activity
miR-155	NM_005776	CNIH	cornichon homolog (Drosophila)	P+T	immune response|integral to membrane|intracellular signaling cascade|membrane
miR-155	AW241703	CNTN4	Homo sapiens cDNA FLJ32716 fis, clone TESTI2000808, highly similar to Rattus norvegicus neural cell adhesion protein BIG-2 precursor (BIG-2) mRNA, mRNA sequence	P+T	cell adhesion|membrane|protein binding
miR-155	NM_000094	COL7A1	collagen, type VII, alpha 1 (epidermolysis bullosa, dystrophic, dominant and recessive)	P+T	basement membrane|cell adhesion|collagen type VII|cytoplasm|epidermis development|phosphate transport|protein binding|serine-type endopeptidase inhibitor activity|structural molecule activity
miR-155	NM_003653	COPS3	COP9 constitutive photomorphogenic homolog subunit 3 (Arabidopsis)	P+T	signalosome complex
miR-155	NM_005211	CSF1R	colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog	M+P+T	ATP binding|antimicrobial humoral response (sensu Vertebrata)|cell proliferation|development|integral to plasma membrane|macrophage colony stimulating factor receptor activity|plasma membrane|protein amino acid phosphorylation|receptor activity|signal transduction|transferase activity|transmembrane receptor protein tyrosine kinase signaling pathway
miR-155	NM_001892	CSNK1A1	casein kinase 1, alpha 1	P+T	ATP binding|Wnt receptor signaling pathway|casein kinase I activity|protein amino acid phosphorylation|protein amino acid phosphorylation|protein serine/threonine kinase activity|protein-tyrosine kinase activity|transferase activity
miR-155	NM_005214	CTLA4	cytotoxic T-lymphocyte-associated protein 4	P+T	immune response|immune response|integral to plasma membrane|membrane
miR-155	U69546	CUGBP2	CUG triplet repeat, RNA binding protein 2	M+P+T	RNA binding|RNA binding|RNA processing|neuromuscular junction development|nucleotide binding|regulation of heart contraction rate
miR-155	NM_030927	DC-TM4F2	tetraspanin similar to TM4SF9	P+T	integral to membrane
miR-155	NM_015652	DKFZP564P1916	DKFZP564P1916 protein	P+T	
miR-155	AF151831	DKFZP566C134	DKFZP566C134 protein	P+T	protein binding
miR-155	NM_004411	DNCI1	dynein, cytoplasmic, intermediate polypeptide 1	P+T	cytoplasmic dynein complex|motor activity
miR-155	NM_001400	EDG1	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1	P+T	G-protein coupled receptor protein signaling pathway|cell adhesion|integral to plasma membrane|lysosphingolipid and lysophosphatidic acid receptor activity|plasma membrane|receptor activity|signal transduction

miR-155	NM_006795	EHD1	EH-domain containing 1	P+T	ATP binding|GTP binding|GTPase activity|biological_process unknown|calcium ion binding|cellular_component unknown
miR-155	NM_012081	ELL2	ELL-related RNA polymerase II, elongation factor	M+P+T	RNA elongation from RNA polymerase II promoter|RNA polymerase II transcription factor activity|nucleus|regulation of transcription, DNA-dependent|transcription|transcription elongation factor complex
miR-155	NM_005238	ETS1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	P+T	RNA polymerase II transcription factor activity|immune response|negative regulation of cell proliferation|nucleus|regulation of transcription, DNA-dependent|transcription|transcription factor activity|transcription from RNA polymerase II promoter
miR-155	NM_002009	FGF7	fibroblast growth factor 7 (keratinocyte growth factor)	P+T	cell proliferation|cell-cell signaling|epidermis development|extracellular region|growth factor activity|positive regulation of cell proliferation|regulation of cell cycle|response to wounding|signal transduction
miR-155	NM_018208	FLJ10761	hypothetical protein FLJ10761	P+T	biological_process unknown|cellular_component unknown|choline kinase activity|transferase activity
miR-155	NM_018243	FLJ10849	hypothetical protein FLJ10849	P+T	GTP binding|cell cycle|cytokinesis
miR-155	NM_022064	FLJ12565	hypothetical protein FLJ12565	P+T	ligase activity|protein ubiquitination|ubiquitin ligase complex|ubiquitin-protein ligase activity|zinc ion binding
miR-155	NM_018391	FLJ23277	FLJ23277 protein	P+T	
miR-155	NM_021078	GCN5L2	GCN5 general control of amino-acid synthesis 5-like 2 (yeast)	M+P+T	N-acetyltransferase activity|chromatin remodeling|histone acetyltransferase activity|histone deacetylase binding|nucleus|protein amino acid acetylation|regulation of transcription from RNA polymerase II promoter|transcription|transcription coactivator activity|transferase activity
miR-155	NM_018178	GPP34R	hypothetical protein FLJ10687	P+T	
miR-155	AF019214	HBP1	HMG-box containing protein 1	M+P	DNA binding|nucleus|regulation of transcription, DNA-dependent
miR-155	NM_006037	HDAC4	histone deacetylase 4	P+T	B-cell differentiation|cell cycle|chromatin modification|cytoplasm|development|histone deacetylase activity|histone deacetylase complex|hydrolase activity|inflammatory response|negative regulation of myogenesis|neurogenesis|nucleus|regulation of transcription, DNA-dependent|transcription|transcription factor binding|transcriptional repressor activity
miR-155	NM_001530	HIF1A	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	P+T	RNA polymerase II transcription factor activity, enhancer binding|electron transport|histone acetyltransferase binding|homeostasis|nucleus|nucleus|protein heterodimerization activity|protein heterodimerization activity|regulation of transcription, DNA-dependent|response to hypoxia|signal transducer activity|signal transduction|signal transduction|transcription factor activity
miR-155	AL023584	HIVEP2	human immunodeficiency virus type I enhancer binding protein 2	P+T	
miR-155	AI682088	HLCS	holocarboxylase synthetase (biotin-[propriony]-Coenzyme A-carboxylase (ATP-hydrolysing)] ligase)	P+T	biotin-[acetyl-CoA-carboxylase] ligase activity|biotin-[methylcrotonoyl-CoA-carboxylase] ligase activity|biotin-[methylmalonyl-CoA-carboxytransferase] ligase activity|biotin-[propionyl-CoA-carboxylase (ATP-hydrolyzing)] ligase activity|ligase activity|protein modification
miR-155	NM_020190	HNOEL-iso	HNOEL-iso protein	P+T	
miR-155	NM_014002	IKBKE	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon	P+T	ATP binding|NF-kappaB-inducing kinase activity|cytoplasm|immune response|positive regulation of I-kappaB kinase/NF-kappaB cascade|protein amino acid phosphorylation|protein serine/threonine kinase activity|signal transducer activity|transferase activity

miR-155	D13720	ITK	IL2-inducible T-cell kinase	P+T	ATP binding|cellular defense response|intracellular signaling cascade|non-membrane spanning protein tyrosine kinase activity|protein amino acid phosphorylation|transferase activity
miR-155	NM_002249	KCNN3	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 3	P+T	calcium-activated potassium channel activity|calcium-activated potassium channel activity|calmodulin binding|integral to membrane|ion channel activity|ion transport|membrane|membrane fraction|neurogenesis|potassium ion transport|potassium ion transport|small conductance calcium-activated potassium channel activity|synaptic transmission|voltage-gated potassium channel complex
miR-155	AB033100	KIAA1274	KIAA protein (similar to mouse paladin)	P+T	protein tyrosine phosphatase activity
miR-155	NM_017780	KIAA1416	KIAA1416 protein	P+T	ATP binding|chromatin|chromatin assembly or disassembly|chromatin binding|helicase activity|nucleus
miR-155	NM_002264	KPNA1	karyopherin alpha 1 (importin alpha 5)	P+T	NLS-bearing substrate-nucleus import|cytoplasm|intracellular protein transport|nuclear localization sequence binding|nuclear pore|nucleus|protein binding|protein transporter activity|regulation of DNA recombination
miR-155	AK021602	KPNA4	karyopherin alpha 4 (importin alpha 3)	P+T	NLS-bearing substrate-nucleus import|binding|intracellular protein transport|nucleus|protein transporter activity
miR-155	NM_020354	LALP1	lysosomal apyrase-like protein 1	M+P+T	hydrolase activity
miR-155	AW242408	LOC151531	Similar to uridine phosphorylase [Homo sapiens], mRNA sequence	M+P+T	cytosol|nucleoside metabolism|nucleotide catabolism|protein binding|transferase activity, transferring glycosyl groups|type III intermediate filament|uridine metabolism|uridine phosphorylase activity
miR-155	NM_016210	LOC51161	g20 protein	P+T	
miR-155	NM_018557	LRP1B	low density lipoprotein-related protein 1B (deleted in tumors)	P+T	calcium ion binding|integral to membrane|low-density lipoprotein receptor activity|membrane|protein transport|receptor activity|receptor mediated endocytosis
miR-155	NM_002446	MAP3K10	mitogen-activated protein kinase kinase kinase 10	M+P+T	ATP binding|JUN kinase kinase kinase activity|activation of JNK|autophosphorylation|induction of apoptosis|protein homodimerization activity|protein serine/threonine kinase activity|protein-tyrosine kinase activity|signal transduction|transferase activity
miR-155	NM_003954	MAP3K14	mitogen-activated protein kinase kinase kinase 14	P+T	ATP binding|protein amino acid phosphorylation|protein serine/threonine kinase activity|transferase activity
miR-155	AL117407	MAP3K7IP2	mitogen-activated protein kinase kinase kinase 7 interacting protein 2	P+T	kinase activity|positive regulation of I-kappaB kinase/NF-kappaB cascade|positive regulation of I-kappaB kinase/NF-kappaB cascade|signal transducer activity|signal transducer activity
miR-155	NM_004992	MECP2	methyl CpG binding protein 2 (Rett syndrome)	M+P+T	DNA binding|negative regulation of transcription from RNA polymerase II promoter|nucleus|regulation of transcription, DNA-dependent|transcription|transcription corepressor activity
miR-155	NM_002398	MEIS1	Meis1, myeloid ecotropic viral integration site 1 homolog (mouse)	M+P+T	RNA polymerase II transcription factor activity|nucleus|regulation of transcription, DNA-dependent|transcription factor activity
miR-155	NM_016289	MO25	MO25 protein	P+T	
miR-155	AA621962	MYO1D	myosin ID	M+P+T	ATP binding|actin binding|calmodulin binding|motor activity|myosin
miR-155	NM_030571	N4WBP5	likely ortholog of mouse Nedd4 WW binding protein 5	P+T	positive regulation of I-kappaB kinase/NF-kappaB cascade|signal transducer activity
miR-155	NM_014903	NAV3	neuron navigator 3	P+T	ATP binding|mitochondrion|nucleoside-triphosphatase activity|nucleotide binding
miR-155	NM_030571	NDFIP1	likely ortholog of mouse Nedd4 WW binding protein 5	P+T	positive regulation of I-kappaB kinase/NF-kappaB cascade|signal transducer activity

miR-155	NM_006599	NFAT5	nuclear factor of activated T-cells 5, tonicity-responsive	M+P+T	RNA polymerase II transcription factor activity|excretion|nucleus|regulation of transcription, DNA-dependent|signal transduction|transcription factor activity|transcription from RNA polymerase II promoter
miR-155	NM_002515	NOVA1	neuro-oncological ventral antigen 1	M+P+T	RNA binding|RNA binding|RNA splicing|RNA splicing|locomotory behavior|locomotory behavior|nucleus|synaptic transmission|synaptic transmission
miR-155	AI373299	PANK1	pantothenate kinase 1	P+T	ATP binding|coenzyme A biosynthesis|pantothenate kinase activity|transferase activity
miR-155	BG110231	PAPOLA	poly(A) polymerase alpha	P+T	RNA binding|cytoplasm|mRNA polyadenylylation|mRNA processing|nucleus|polynucleotide adenylyltransferase activity|transcription|transferase activity
miR-155	NM_020403	PCDH9	protocadherin 9	M+P+T	calcium ion binding|cell adhesion|homophilic cell adhesion|integral to membrane|membrane|protein binding
miR-155	NM_002655	PLAG1	pleiomorphic adenoma gene 1	P+T	nucleic acid binding|nucleus|transcription factor activity|zinc ion binding
miR-155	AJ272212	PSKH1	protein serine kinase H1	P+T	ATP binding|Golgi apparatus|nucleus|protein amino acid phosphorylation|protein serine/threonine kinase activity|transferase activity
miR-155	NM_014904	Rab11-FIP2	KIAA0941 protein	P+T	
miR-155	AF322067	RAB34	RAB34, member RAS oncogene family	P+T	GTP binding|Golgi apparatus|protein transport|small GTPase mediated signal transduction
miR-155	NM_002869	RAB6A	RAB6A, member RAS oncogene family	M+P+T	GTP binding|GTPase activity|Golgi apparatus|protein transport|small GTPase mediated signal transduction
miR-155	AL136727	RAB6C	RAB6C, member RAS oncogene family	M+P+T	GTP binding|GTPase activity|intracellular|protein transport|response to drug|small GTPase mediated signal transduction
miR-155	NM_002902	RCN2	reticulocalbin 2, EF-hand calcium binding domain	P+T	calcium ion binding|endoplasmic reticulum|protein binding
miR-155	AJ223321	RP58	zinc finger protein 238	M+P+T	
miR-155	NM_002968	SALL1	sal-like 1 (Drosophila)	P+T	morphogenesis|nucleus|regulation of transcription, DNA-dependent|transcription|transcription factor activity|zinc ion binding
miR-155	NM_002971	SATB1	special AT-rich sequence binding protein 1 (binds to nuclear matrix/scaffold-associating DNA's)	P+T	double-stranded DNA binding|establishment and/or maintenance of chromatin architecture|nucleus|regulation of transcription, DNA-dependent|transcription factor activity
miR-155	NM_003469	SCG2	secretogranin II (chromogranin C)	P+T	calcium ion binding|protein secretion
miR-155	NM_005625	SDCBP	syndecan binding protein (syntenin)	P+T	actin cytoskeleton organization and biogenesis|adherens junction|cytoskeletal adaptor activity|cytoskeleton|endoplasmic reticulum|interleukin-5 receptor binding|interleukin-5 receptor complex|intracellular signaling cascade|metabolism|neurexin binding|nucleus|oxidoreductase activity|plasma membrane|protein binding|protein heterodimerization activity|protein-membrane targeting|substrate-bound cell migration, cell extension|synaptic transmission|syndecan binding
miR-155	NM_000232	SGCB	sarcoglycan, beta (43kDa dystrophin-associated glycoprotein)	P+T	cytoskeleton|cytoskeleton organization and biogenesis|integral to plasma membrane|muscle development|sarcoglycan complex
miR-155	NM_013257	SGKL	serum/glucocorticoid regulated kinase-like	P+T	ATP binding|intracellular signaling cascade|protein amino acid phosphorylation|protein amino acid phosphorylation|protein serine/threonine kinase activity|protein serine/threonine kinase activity|protein-tyrosine kinase activity|response to stress|transferase activity

miR-155	NM_005069	SIM2	single-minded homolog 2 (Drosophila)	P+T	cell differentiation|neurogenesis|nucleus|regulation of transcription, DNA-dependent|signal transducer activity|signal transduction|transcription|transcription factor activity
miR-155	AA927480	SKI	v-ski sarcoma viral oncogene homolog (avian)	P+T	
miR-155	NM_006748	SLA	Src-like-adaptor	P+T	SH3/SH2 adaptor activity|intracellular signaling cascade
miR-155	AI684141	SMARCA4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	P+T	ATP binding|DNA binding|helicase activity|helicase activity|hydrolase activity|nucleoplasm|nucleus|regulation of transcription from RNA polymerase II promoter|transcription|transcription coactivator activity|transcription factor activity
miR-155	AB005043	SOCS1	suppressor of cytokine signaling 1	M+P+T	JAK-STAT cascade|cytoplasm|insulin-like growth factor receptor binding|intracellular signaling cascade|negative regulation of JAK-STAT cascade|protein kinase binding|protein kinase inhibitor activity|regulation of cell growth|ubiquitin cycle
miR-155	NM_004232	SOCS4	suppressor of cytokine signaling 4	M+P	JAK-STAT cascade|cytoplasm|defense response|intracellular signaling cascade|regulation of cell growth
miR-155	NM_005986	SOX1	SRY (sex determining region Y)-box 1	P+T	DNA binding|establishment and/or maintenance of chromatin architecture|nucleus|regulation of transcription, DNA-dependent|regulation of transcription, DNA-dependent|transcription factor activity
miR-155	AI360875	SOX11	SRY (sex determining region Y)-box 11	M+T	DNA binding|neurogenesis|nucleus|regulation of transcription, DNA-dependent|transcription
miR-155	AL136780	SOX6	SRY (sex determining region Y)-box 6	P+T	establishment and/or maintenance of chromatin architecture|heart development|muscle development|nucleus|regulation of transcription, DNA-dependent|transcription|transcription factor activity
miR-155	AW470841	SP3	Sp3 transcription factor	P+T	DNA binding|nucleus|regulation of transcription, DNA-dependent|transcription|transcriptional activator activity|transcriptional repressor activity|zinc ion binding
miR-155	BF224259	SPF30	splicing factor 30, survival of motor neuron-related	P+T	RNA splicing|RNA splicing factor activity, transesterification mechanism|apoptosis|cytoplasm|induction of apoptosis|spliceosome assembly|spliceosome complex
miR-155	NM_003120	SPI1	spleen focus forming virus (SFFV) proviral integration oncogene spi1	M+T	negative regulation of transcription from RNA polymerase II promoter|nucleus|regulation of transcription, DNA-dependent|transcription|transcription factor activity
miR-155	BE676214	SSH2	slingshot 2	P+T	protein amino acid dephosphorylation|protein tyrosine/serine/threonine phosphatase activity
miR-155	AF159447	SUFU	suppressor of fused homolog (Drosophila)	P+T	cell cycle|cytoplasm|development|negative regulation of cell cycle|nucleus|proteolysis and peptidolysis|signal transducer activity|signal transduction|skeletal development|transcription corepressor activity
miR-155	NM_006754	SYPL	synaptophysin-like protein	M+P+T	integral to plasma membrane|membrane|synaptic transmission|synaptic vesicle|transport|transporter activity
miR-155	NM_006286	TFDP2	transcription factor Dp-2 (E2F dimerization partner 2)	P+T	DNA metabolism|nucleus|regulation of cell cycle|regulation of transcription from RNA polymerase II promoter|transcription|transcription cofactor activity|transcription factor activity|transcription factor complex
miR-155	AA705845	TLE4	transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila)	P+T	frizzled signaling pathway|molecular_function unknown|nucleus|nucleus|regulation of transcription|regulation of transcription, DNA-dependent
miR-155	NM_014765	TOMM20	translocase of outer mitochondrial membrane 20 (yeast) homolog	P+T	integral to membrane|mitochondrial outer membrane translocase complex|mitochondrion|outer membrane|protein translocase activity|protein-mitochondrial targeting

miR-155	AW341649	TP53INP1	tumor protein p53 inducible nuclear protein 1	P+T	apoptosis|nucleus
miR-155	BC005016	TRIM2	tripartite motif-containing 2	P+T	cytoplasm|myosin binding|protein ubiquitination|ubiquitin ligase complex|ubiquitin-protein ligase activity|zinc ion binding
miR-155	AA524505	TSGA	zinc finger protein	P+T	nucleus
miR-155	AW157525	TSGA14	testis specific, 14	M+P+T	centrosome
miR-155	X62048	WEE1	WEE1 homolog (S. pombe)	P+T	ATP binding|cytokinesis|mitosis|nucleus|protein amino acid phosphorylation|protein serine/threonine kinase activity|protein-tyrosine kinase activity|regulation of cell cycle|transferase activity
miR-155	AC005539	WUGSC:H_NH0335J18.1	Similar to uridine phosphorylase [Homo sapiens], mRNA sequence	M+P+T	
miR-155	NM_003413	ZIC3	Zic family member 3 heterotaxy 1 (odd-paired homolog, Drosophila)	P+T	DNA binding|determination of left/right symmetry|nucleus|regulation of transcription, DNA-dependent|transcription|zinc ion binding
miR-155	NM_007345	ZNF236	zinc finger protein 236	P+T	nucleus|regulation of transcription, DNA-dependent|transcription|transcription factor activity|zinc ion binding
miR-155	NM_006352	ZNF238	zinc finger protein 238	M+P+T	chromosome organization and biogenesis (sensu Eukaryota)|negative regulation of transcription from RNA polymerase II promoter|nuclear chromosome|nucleic acid binding|nucleus|protein binding|protein binding|regulation of transcription, DNA-dependent|specific RNA polymerase II transcription factor activity|transcription|transcription factor activity|transport|zinc ion binding
miR-21	NM_005164	ABCD2	ATP-binding cassette, sub-family D (ALD), member 2	M+P	ATP binding|ATP-binding cassette (ABC) transporter complex|ATPase activity|ATPase activity, coupled to transmembrane movement of substances|fatty acid metabolism|integral to plasma membrane|membrane|peroxisome|transport
miR-21	NM_001616	ACVR2	activin A receptor, type II	P+T	ATP binding|integral to plasma membrane|membrane|protein amino acid phosphorylation|receptor activity|transferase activity|transforming growth factor beta receptor activity|transmembrane receptor protein serine/threonine kinase signaling pathway
miR-21	NM_015339	ADNP	activity-dependent neuroprotector	P+T	nucleus|regulation of transcription, DNA-dependent|transcription factor activity|zinc ion binding
miR-21	AI990366	ARHGEF7	Rho guanine nucleotide exchange factor (GEF) 7	P+T	guanyl-nucleotide exchange factor activity|signal transduction
miR-21	NM_017610	ARK	Arkadia	P+T	protein ubiquitination|ubiquitin ligase complex|ubiquitin-protein ligase activity|zinc ion binding
miR-21	NM_014034	ASF1A	DKFZP547E2110 protein	P+T	chromatin binding|loss of chromatin silencing|nucleus
miR-21	NM_017680	ASPN	asporin (LRR class 1)	P+T	
miR-21	NM_000657	BCL2	B-cell CLL/lymphoma 2	P+T	anti-apoptosis|endoplasmic reticulum|humoral immune response|integral to membrane|membrane|mitochondrial outer membrane|mitochondrial outer membrane|mitochondrion|negative regulation of cell proliferation|nucleus|protein binding|regulation of apoptosis|regulation of cell cycle|release of cytochrome c from mitochondria
miR-21	NM_014577	BRD1	bromodomain containing 1	P+T	DNA binding|cell cycle|nucleus|nucleus|regulation of transcription, DNA-dependent
miR-21	AA902767	BRD2	bromodomain containing 2	P+T	nucleus|protein serine/threonine kinase activity|spermatogenesis
miR-21	NM_014962	BTBD3	BTB (POZ) domain containing 3	P+T	protein binding

miR-21	NM_006763	BTG2	BTG family, member 2	P+T	DNA repair|negative regulation of cell proliferation|regulation of transcription, DNA-dependent|transcription|transcription factor activity
miR-21	AK025768	C20orf99	chromosome 20 open reading frame 99	P+T	nucleic acid binding
miR-21	AI671238	CAPN3	Homo sapiens cDNA FLJ23750 fis, clone HEP16527, mRNA sequence	P+T	calcium ion binding|calpain activity|calpain activity|intracellular|intracellular|muscle development|proteolysis and peptidolysis|proteolysis and peptidolysis|signal transducer activity
miR-21	NM_002981	CCL1	chemokine (C-C motif) ligand 1	P+T	calcium ion homeostasis|cell-cell signaling|chemokine activity|chemotaxis|extracellular space|inflammatory response|sensory perception|signal transduction|viral life cycle
miR-21	BF939071	CCM1	cerebral cavernous malformations 1	M+P	binding|catalytic activity|cytoskeleton|small GTPase mediated signal transduction|small GTPase regulator activity
miR-21	NM_001789	CDC25A	cell division cycle 25A	P+T	cell proliferation|cytokinesis|hydrolase activity|intracellular|mitosis|protein amino acid dephosphorylation|protein tyrosine phosphatase activity|regulation of cyclin dependent protein kinase activity
miR-21	NM_001842	CNTFR	ciliary neurotrophic factor receptor	M+P+T	ciliary neurotrophic factor receptor activity|cytokine binding|extrinsic to membrane|neurogenesis|receptor activity|signal transduction
miR-21	NM_001310	CREBL2	cAMP responsive element binding protein-like 2	P+T	nucleus|regulation of transcription, DNA-dependent|signal transduction|transcription|transcription factor activity
miR-21	NM_016441	CRIM1	cysteine-rich motor neuron 1	M+P+T	insulin-like growth factor receptor activity|integral to membrane|membrane fraction|neurogenesis|serine-type endopeptidase inhibitor activity
miR-21	NM_015396	DKFZP434A043	DKFZP434A043 protein	P+T	cell adhesion|cytoskeleton|mitotic chromosome condensation|protein binding|structural molecule activity
miR-21	AL047650	DKFZp434A2417	endozepine-related protein precursor	P+T	acyl-CoA binding
miR-21	AB028628	DKFZP547E2110	DKFZP547E2110 protein	P+T	chromatin binding|loss of chromatin silencing|nucleus
miR-21	NM_031305	DKFZP564B1162	hypothetical protein DKFZp564B1162	P+T	GTPase activator activity
miR-21	NM_004405	DLX2	distal-less homeo box 2	P+T	brain development|development|nucleus|regulation of transcription, DNA-dependent|transcription factor activity
miR-21	NM_001949	E2F3	E2F transcription factor 3	M+P+T	nucleus|protein binding|regulation of cell cycle|regulation of transcription, DNA-dependent|transcription|transcription factor activity|transcription factor complex|transcription initiation from RNA polymerase II promoter
miR-21	NM_006795	EHD1	EH-domain containing 1	P+T	ATP binding|GTP binding|GTPase activity|biological_process unknown|calcium ion binding|cellular_component unknown
miR-21	NM_001412	EIF1A	eukaryotic translation initiation factor 1A	P+T	RNA binding|eukaryotic translation initiation factor 4F complex|protein biosynthesis|translation initiation factor activity|translational initiation|translational initiation
miR-21	AI832074	EIF2C2	eukaryotic translation initiation factor 2C, 2	P+T	cellular_component unknown|protein biosynthesis|translation initiation factor activity
miR-21	NM_006874	ELF2	E74-like factor 2 (ets domain transcription factor)	P+T	nucleus|nucleus|protein binding|protein binding|regulation of transcription from RNA polymerase II promoter|regulation of transcription, DNA-dependent|transcription factor activity|transcriptional activator activity|transcriptional activator activity

miR-21	NM_004438	EPHA4	EphA4	P+T	ATP binding|ephrin receptor activity|integral to plasma membrane|membrane|protein amino acid phosphorylation|receptor activity|signal transduction|transferase activity|transmembrane receptor protein tyrosine kinase signaling pathway
miR-21	BE888593	FLJ11220	hypothetical protein FLJ11220	P+T	
miR-21	NM_017637	FLJ20043	hypothetical protein FLJ20043	P+T	nucleic acid binding|nucleus|zinc ion binding
miR-21	AF019214	HBP1	HMG-box containing protein 1	M+P+T	DNA binding|nucleus|regulation of transcription, DNA-dependent
miR-21	NM_000214	JAG1	jagged 1 (Alagille syndrome)	M+P+T	Notch binding|Notch signaling pathway|angiogenesis|calcium ion binding|calcium ion binding|cell communication|cell fate determination|development|endothelial cell differentiation|extracellular region|growth factor activity|hemopoiesis|integral to plasma membrane|keratinocyte differentiation|membrane|myoblast differentiation|neurogenesis|regulation of cell migration|regulation of cell proliferation|structural molecule activity
miR-21	NM_002232	KCNA3	potassium voltage-gated channel, shaker-related subfamily, member 3	M+P+T	cation transport|delayed rectifier potassium channel activity|integral to membrane|membrane|membrane fraction|potassium ion transport|voltage-gated potassium channel complex
miR-21	NM_014766	KIAA0193	KIAA0193 gene product	P+T	cellular_component unknown|dipeptidase activity|exocytosis|proteolysis and peptidolysis
miR-21	NM_014912	KIAA0940	KIAA0940 protein	M+P+T	nucleic acid binding
miR-21	NM_014952	KIAA0945	KIAA0945 protein	P+T	DNA binding
miR-21	NM_017780	KIAA1416	KIAA1416 protein	P+T	ATP binding|chromatin|chromatin assembly or disassembly|chromatin binding|helicase activity|nucleus
miR-21	AB040901	KIAA1468	KIAA1468 protein	P+T	binding|mitotic chromosome condensation
miR-21	U90268	Krit1	cerebral cavernous malformations 1	M+P	binding|catalytic activity|cytoskeleton|small GTPase mediated signal transduction|small GTPase regulator activity
miR-21	BF591611	LOC147632	hypothetical protein BC010734	P+T	oxidoreductase activity|zinc ion binding
miR-21	NM_005904	MADH7	MAD, mothers against decapentaplegic homolog 7 (Drosophila)	P+T	intracellular|protein binding|receptor signaling protein serine/threonine kinase signaling protein activity|regulation of transcription, DNA-dependent|response to stress|transcription|transforming growth factor beta receptor signaling pathway|transforming growth factor beta receptor, inhibitory cytoplasmic mediator activity
miR-21	NM_025146	MAK3P	likely ortholog of mouse Mak3p homolog (S. cerevisiae)	P+T	N-acetyltransferase activity
miR-21	NM_014319	MAN1	integral inner nuclear membrane protein	P+T	integral to membrane|integral to nuclear inner membrane|membrane fraction|nuclear membrane|nucleotide binding
miR-21	AW025150	MAP3K12	mitogen-activated protein kinase kinase kinase 12	M+T	ATP binding|JNK cascade|cytoplasm|magnesium ion binding|plasma membrane|protein amino acid phosphorylation|protein kinase cascade|protein serine/threonine kinase activity|protein-tyrosine kinase activity|transferase activity
miR-21	NM_012325	MAPRE1	microtubule-associated protein, RP/EB family, member 1	P+T	cell proliferation|cytokinesis|microtubule binding|mitosis|protein C-terminus binding|regulation of cell cycle
miR-21	NM_002380	MATN2	matrilin 2	P+T	biological_process unknown|calcium ion binding|extracellular matrix (sensu Metazoa)
miR-21	NM_018834	MATR3	matrin 3	M+P+T	RNA binding|nuclear inner membrane|nucleotide binding|nucleus|structural molecule activity|zinc ion binding
miR-21	NM_021038	MBNL1	muscleblind-like (Drosophila)	M+P+T	cytoplasm|double-stranded RNA binding|embryonic development (sensu Mammalia)|embryonic limb morphogenesis|muscle development|myoblast differentiation|neurogenesis|nucleic acid binding|nucleus|nucleus

miR-21	AI139252	MGC16063	ribosomal protein L35a	P+T	JAK-STAT cascade|acute-phase response|calcium ion binding|cell motility|cytoplasm|hematopoietin/interferon-class (D200-domain) cytokine receptor signal transducer activity|intracellular signaling cascade|negative regulation of transcription from RNA polymerase II promoter|neurogenesis|nucleus|nucleus|regulation of transcription, DNA-dependent|signal transducer activity|transcription|transcription factor activity|transcription factor activity
miR-21	BC004162	MGC2452	hypothetical protein MGC2452	P+T	fatty acid metabolism|generation of precursor metabolites and energy|ligand-dependent nuclear receptor activity|lipid metabolism|nucleus|nucleus|regulation of transcription, DNA-dependent|steroid hormone receptor activity|transcription|transcription factor activity|transcription factor activity|transcription from RNA polymerase II promoter
miR-21	NM_024052	MGC3048	hypothetical protein MGC3048	P+T	
miR-21	AB049636	MRPL9	mitochondrial ribosomal protein L9	P+T	mitochondrion|protein biosynthesis|ribosome|structural constituent of ribosome
miR-21	NM_015678	NBEA	neurobeachin	P+T	Golgi trans face|cytosol|endomembrane system|plasma membrane|post-Golgi transport|postsynaptic membrane|protein kinase A binding
miR-21	AI700518	NFIB	nuclear factor I/B	M+T	DNA replication|nucleus|nucleus|regulation of transcription, DNA-dependent|transcription|transcription factor activity|transcription factor activity
miR-21	NM_002527	NTF3	neurotrophin 3	M+P	anti-apoptosis|cell motility|cell-cell signaling|growth factor activity|neurogenesis|signal transduction
miR-21	U24223	PCBP1	poly(rC) binding protein 1	M+P+T	RNA binding|catalytic activity|cytoplasm|mRNA metabolism|nucleus|ribonucleoprotein complex|single-stranded DNA binding
miR-21	NM_005016	PCBP2	poly(rC) binding protein 2	M+T	DNA binding|RNA binding|cytoplasm|mRNA metabolism|nucleic acid binding|nucleus|ribonucleoprotein complex
miR-21	NM_014456	PDCD4	programmed cell death 4 (neoplastic transformation inhibitor)	P+T	apoptosis
miR-21	AF338650	PDZD2	PDZ domain containing 2	P+T	
miR-21	NM_000325	PITX2	paired-like homeodomain transcription factor 2	M+P+T	determination of left/right symmetry|development|nucleus|organogenesis|regulation of transcription, DNA-dependent|transcription factor activity
miR-21	NM_002655	PLAG1	pleiomorphic adenoma gene 1	P+T	nucleic acid binding|nucleus|transcription factor activity|zinc ion binding
miR-21	NM_005036	PPARA	peroxisome proliferative activated receptor, alpha	P+T	fatty acid metabolism|generation of precursor metabolites and energy|ligand-dependent nuclear receptor activity|lipid metabolism|nucleus|nucleus|regulation of transcription, DNA-dependent|steroid hormone receptor activity|transcription|transcription factor activity|transcription factor activity|transcription from RNA polymerase II promoter
miR-21	NM_002711	PPP1R3A	protein phosphatase 1, regulatory (inhibitor) subunit 3A (glycogen and sarcoplasmic reticulum binding subunit, skeletal muscle)	P+T	carbohydrate metabolism|glycogen metabolism|hydrolase activity|integral to membrane|phosphoprotein phosphatase activity|type 1 serine/threonine specific protein phosphatase inhibitor activity
miR-21	NM_000944	PPP3CA	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha)	P+T	calcineurin complex|calcium ion binding|calmodulin binding|hydrolase activity|protein amino acid dephosphorylation|protein serine/threonine phosphatase activity
miR-21	NM_018569	PRO0971	hypothetical protein PRO0971	P+T	

miR-21	AA156948	PRPF4B	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	M+T	ATP binding|RNA splicing|nuclear mRNA splicing, via spliceosome|nucleus|protein amino acid phosphorylation|protein serine/threonine kinase activity|transferase activity
miR-21	BF337790	PURB	purine-rich element binding protein B	M+P+T	
miR-21	NM_002869	RAB6A	RAB6A, member RAS oncogene family	P+T	GTP binding|GTPase activity|Golgi apparatus|protein transport|small GTPase mediated signal transduction
miR-21	AL136727	RAB6C	RAB6C, member RAS oncogene family	P+T	GTP binding|GTPase activity|intracellular|protein transport|response to drug|small GTPase mediated signal transduction
miR-21	NM_002890	RASA1	RAS p21 protein activator (GTPase activating protein) 1	P+T	Ras GTPase activator activity|intracellular signaling cascade
miR-21	NM_005739	RASGRP1	RAS guanyl releasing protein 1 (calcium and DAG-regulated)	P+T	Ras guanyl-nucleotide exchange factor activity|Ras protein signal transduction|calcium ion binding|calcium ion binding|diacylglycerol binding|guanyl-nucleotide exchange factor activity|membrane fraction|small GTPase mediated signal transduction
miR-21	NM_021111	RECK	reversion-inducing-cysteine-rich protein with kazal motifs	M+P+T	cell cycle|membrane|membrane fraction|metalloendopeptidase inhibitor activity|negative regulation of cell cycle|serine-type endopeptidase inhibitor activity
miR-21	NM_006915	RP2	retinitis pigmentosa 2 (X-linked recessive)	P+T	beta-tubulin folding|membrane|sensory perception|unfolded protein binding|visual perception
miR-21	AA906056	RPS6KA3	ribosomal protein S6 kinase, 90kDa, polypeptide 3	M+T	ATP binding|central nervous system development|protein amino acid phosphorylation|protein serine/threonine kinase activity|signal transduction|skeletal development|transferase activity
miR-21	NM_002971	SATB1	special AT-rich sequence binding protein 1 (binds to nuclear matrix/scaffold-associating DNA's)	M+P+T	double-stranded DNA binding|establishment and/or maintenance of chromatin architecture|nucleus|regulation of transcription, DNA-dependent|transcription factor activity
miR-21	NM_014191	SCN8A	sodium channel, voltage gated, type VIII, alpha polypeptide	M+P+T	ATP binding|cation channel activity|cation transport|integral to membrane|membrane|neurogenesis|sodium ion transport|voltage-gated sodium channel activity|voltage-gated sodium channel complex
miR-21	AA927480	SKI	v-ski sarcoma viral oncogene homolog (avian)	M+P+T	
miR-21	NM_003983	SLC7A6	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	P+T	amino acid metabolism|amino acid transport|amino acid-polyamine transporter activity|integral to plasma membrane|plasma membrane|protein complex assembly|transport
miR-21	NM_006359	SLC9A6	solute carrier family 9 (sodium/hydrogen exchanger), isoform 6	P+T	antiporter activity|endoplasmic reticulum membrane|integral to membrane|integral to membrane|ion transport|microsome|mitochondrion|regulation of pH|sodium ion transport|sodium:hydrogen antiporter activity|solute:hydrogen antiporter activity
miR-21	NM_003076	SMARCD1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 1	P+T	chromatin remodeling|chromatin remodeling complex|regulation of transcription from RNA polymerase II promoter|transcription coactivator activity
miR-21	AI669815	SOX2	SRY (sex determining region Y)-box 2	P+T	establishment and/or maintenance of chromatin architecture|nucleus|regulation of transcription, DNA-dependent|transcription|transcription factor activity
miR-21	NM_006940	SOX5	SRY (sex determining region Y)-box 5	P+T	nucleus|regulation of transcription, DNA-dependent|transcription|transcription factor activity|transcription from RNA polymerase II promoter
miR-21	AI808807	SOX7	SRY (sex determining region Y)-box 7	P+T	DNA binding|nucleus|regulation of transcription, DNA-dependent|transcription
miR-21	NM_006717	SPIN	Spindling	P+T	gametogenesis|ribonucleoprotein complex

miR-21	NM_005842	SPRY2	sprouty homolog 2 (Drosophila)	P+T	cell-cell signaling|development|membrane|organogenesis|regulation of signal transduction
miR-21	NM_006751	SSFA2	sperm specific antigen 2	P+T	plasma membrane
miR-21	NM_006603	STAG2	stromal antigen 2	P+T	cell cycle|chromosome segregation|cytokinesis|meiosis|mitosis|molecular_function unknown|nucleus
miR-21	BC000627	STAT3	signal transducer and activator of transcription 3 (acute-phase response factor)	P+T	JAK-STAT cascade|acute-phase response|calcium ion binding|cell motility|cytoplasm|hematopoietin/interferon-class (D200-domain) cytokine receptor signal transducer activity|intracellular signaling cascade|negative regulation of transcription from RNA polymerase II promoter|neurogenesis|nucleus|nucleus|regulation of transcription, DNA-dependent|signal transducer activity|transcription|transcription factor activity|transcription factor activity
miR-21	AW138827	TAF5	TAF5 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 100kDa	P+T	nucleus|regulation of transcription, DNA-dependent|transcription factor TFIID complex|transcription factor activity
miR-21	BF591040	TAGAP	T-cell activation GTPase activating protein	P+T	GTPase activator activity
miR-21	NM_000358	TGFBI	transforming growth factor, beta-induced, 68kDa	M+P+T	cell adhesion|cell proliferation|extracellular matrix (sensu Metazoa)|extracellular space|integrin binding|negative regulation of cell adhesion|protein binding|sensory perception|visual perception
miR-21	NM_000362	TIMP3	tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory)	P+T	enzyme inhibitor activity|extracellular matrix (sensu Metazoa)|extracellular matrix (sensu Metazoa)|induction of apoptosis by extracellular signals|metalloendopeptidase inhibitor activity|sensory perception|visual perception
miR-21	AA149745	TRIM2	tripartite motif-containing 2	M+P+T	cytoplasm|myosin binding|protein ubiquitination|ubiquitin ligase complex|ubiquitin-protein ligase activity|zinc ion binding
miR-21	AF346629	TRPM7	transient receptor potential cation channel, subfamily M, member 7	P+T	ATP binding|calcium channel activity|calcium ion transport|cation transport|integral to membrane|membrane|protein amino acid phosphorylation|protein serine/threonine kinase activity|transferase activity
miR-21	AI745185	YAP1	Yes-associated protein 1, 65kDa	P+T	
miR-21	NM_005667	ZFP103	zinc finger protein 103 homolog (mouse)	P+T	central nervous system development|integral to membrane|protein ubiquitination|ubiquitin ligase complex|ubiquitin-protein ligase activity|zinc ion binding
miR-21	N62196	ZNF367	zinc finger protein 367	M+P+T	nucleic acid binding|nucleus|zinc ion binding

M=MiRanda P=PicTar T=TargetScan

Example 3: *Bio-pathological features and microRNA expression*

Materials and Methods

Immunohistochemical analysis of breast cancer samples.

Staining procedures were performed as described (Querzoli, P., *et al., Anal. Quant. Cytol. Histol. 21*:151-160 (1999)). Hormonal receptors were evaluated with

6F11 antibody for estrogen receptor α (ER) and PGR-1A6 antibody for progesterone receptor (PR) (Ventana, Tucson, AZ, U.S.A.). The proliferation index was assessed with MIB1 antibody (DAKO, Copenhagen). ERBB2 was detected with CB11 antibody (Ventana, Tucson, AZ, U.S.A.) and p53 protein expression was examined with DO7 antibody (Ventana, Tucson, AZ, U.S.A.). Only tumor cells with distinct nuclear immunostaining for ER, PR, Mib1 and p53 were recorded as positive. Tumor cells were considered positive for ERBB2 when they showed distinct membrane immunoreactivity.

To perform a quantitative analysis of the expression of these various biological markers, the Eureka Menarini computerized image analysis system was used. For each tumor section, at least 20 microscopic fields of invasive carcinoma were measured using a 40x objective. The following cut-off values were employed: 10% of positive nuclear area for ER, PR, c-erbB2 and p53, 13% of nuclei expressing Mib1 was introduced to discriminate cases with high and low proliferative activity.

Results

To evaluate whether a correlation exists between various bio-pathological features associated with breast cancer and the expression of particular miRNAs, we generated and compared miRNA expression profiles for various cancer samples associated with the presence or absence of a particular breast cancer feature. In particular, we analyzed breast cancers with lobular or ductal histotypes, breast cancers with differential expression of either estrogen receptor alpha (ER) or progesterone receptor, and breast cancers with differences in lymph node metastasis, vascular invasion, proliferation index, and expression of ERBB2 and p53.

Expression profiles of lobular or ductal and +/- ERBB2 expression classes did not reveal any microRNAs that were differentially-expressed, while all other comparisons revealed a small number of differentially-expressed microRNAs ($P<0.05$). Tumor grade was not analyzed. The results of this analysis are shown in FIG. 4.

Differentially-expressed miRNA families were identified for various bio-pathological features that are associated with human breast cancer. For example, all miR-30 miRNAs are down-regulated in both ER- and PR- tumors, suggesting that

expression of miR-30 miRNAs is regulated by these hormones. In addition, the expression of various *let-7* miRNAs was down-regulated in breast cancer samples with either lymph node metastasis or a high proliferation index, suggesting that reduced *let-7* expression could be associated with a poor prognosis, a result that is consistent with previous findings (Takamizawa, J., *et al.*, *Cancer Res. 39*: 167-169 (2004)). The discovery that the *let-7* family of miRNAs regulates the expression of members of the *RAS* oncogene family provides a potential explanation for the role of *let-7* miRNAs in human cancer (Johnson, S.M., *et al.*, *Cell 120*:635-647 (2005)).

miR-145 and *miR-21*, two miRNAs whose expression could differentiate cancer or normal tissues, were also differentially-expressed in cancers with a different proliferation index or different tumor stage. In particular, *miR-145* is progressively down-regulated from normal breast to cancers with a high proliferation index. Similarly, *miR-21* is progressively up-regulated from normal breast to cancers with high tumor stage. These findings suggest that deregulation of these two miRNAs may affect critical molecular events involved in tumor progression.

Another miRNA potentially involved in cancer progression is *miR-9-3*. *miR-9-3* was downregulated in breast cancers with either high vascular invasion or lymph node metastasis, suggesting that its down-regulation was acquired during the course of tumor progression and, in particular, during the acquisition of metastatic potential.

The relevant teachings of all publications cited herein that have not explicitly been incorporated by reference, are incorporated herein by reference in their entirety. 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.

CLAIMS

What is claimed is:

1. A method of diagnosing whether a subject has, or is at risk for developing, breast cancer, comprising measuring the level of at least one miR gene product in a test sample from said subject, wherein an alteration in the level of the miR gene product in the test sample, relative to the level of a corresponding miR gene product in a control sample, is indicative of the subject either having, or being at risk for developing, breast cancer.

2. The method of Claim 1, wherein the at least one miR gene product is miR-125b-1 or miR125b-2.

3. The method of Claim 1, wherein the at least one miR gene product is miR-145.

4. The method of Claim 1, wherein the at least one miR gene product is miR-21.

5. The method of Claim 1, wherein the at least one miR gene product is miR-155.

6. The method of Claim 1, wherein the at least one miR gene product is miR-10b.

7. The method of Claim 1, wherein the at least one miR gene product is selected from the group consisting of miR-125b, miR-145, miR-21, miR-155, miR-10b, miR-009-1 (miR131-1), miR-34 (miR-170), miR-102 (miR-29b), miR-123 (miR-126), miR-140-as, miR-125a, miR-125b-1, miR-125b-2, miR-194, miR-204, miR-213, let-7a-2, let-7a-3, let-7d (let-7d-v1), let-7f-2, let-7i (let-7d-v2), miR-101-1, miR-122a, miR-128b, miR-136, miR-143, miR-149, miR-191, miR-196-1, miR-196-2, miR-202, miR-203, miR-206, miR-210 and combinations thereof.

8. The method of Claim 1, wherein the level of the at least one miR gene product is measured using Northern blot analysis.

9. The method of Claim 1, wherein the level of the at least one miR gene product in the test sample is less than the level of the corresponding miR gene product in the control sample.

10. The method of Claim 1, wherein the level of the at least one miR gene product in the test sample is greater than the level of the corresponding miR gene product in the control sample.

11. A method of diagnosing a breast cancer associated with one or more prognostic markers in a subject, comprising measuring the level of at least one miR gene product in a breast cancer sample from said subject, wherein an alteration in the level of the at least one miR gene product in the test sample, relative to the level of a corresponding miR gene product in a control sample, is indicative of the subject having a breast cancer associated with the one or more prognostic markers.

12. The method of Claim 11, wherein the one or more prognostic markers is selected from the group consisting of estrogen receptor expression, progesterone receptor expression, positive lymph node metastasis, a high proliferative index, detectable p53 expression, advanced tumor stage and high vascular invasion.

13. The method of Claim 11, wherein the breast cancer associated with one or more prognostic markers and the at least one miR gene product are selected from the group consisting of:

(i) the breast cancer is a breast cancer associated with estrogen receptor expression and the miR gene product is selected from the group consisting of miR-26a, miR-26b, miR-102 (miR-29b), miR-30a-5p, miR-30b, miR-30c, miR-30d, miR-185, miR-191, miR-206, miR-212, and combinations thereof;

(ii) the breast cancer is a breast cancer associated with progesterone receptor expression and the miR gene product is selected from the group consisting of

let-7c, miR-26a, miR-29b, miR-30a-5p, miR-30b, miR-30c, miR-30d, and combinations thereof;

(iii) the breast cancer is a breast cancer associated with positive lymph node metastasis and the miR gene product is selected from the group consisting of let-7f-1, let-7a-3, let-7a-2, miR-9-3, and combinations thereof;

(iv) the breast cancer is a breast cancer associated with a high proliferative index and the miR gene product is selected from the group consisting of let-7c, let-7d, miR-26a, miR-26b, miR-30a-5p, miR-102, miR-145, and combinations thereof;

(v) the breast cancer is a breast cancer associated with detectable p53 expression and the miR gene product is selected from the group consisting of miR-16a, miR-128b and a combination thereof;

(vi) the breast cancer is a breast cancer associated with high vascular invasion and the miR gene product is selected from the group consisting of miR-9-3, miR-10b, miR-27a, miR-29a, miR-123, miR-205 and combinations thereof; and

(vii) the breast cancer is a breast cancer associated with an advanced tumor stage and the miR gene product is selected from the group consisting of miR-9-2, miR-15-a, miR-21, miR-30a-s, miR-133a-1, miR-137, miR-153-2, miR-154, miR-181a, miR-203, miR-213, and combinations thereof.

14. A method of diagnosing whether a subject has, or is at risk for developing, breast cancer, comprising:

(1) reverse transcribing RNA from a test sample obtained from the subject to provide a set of target oligodeoxynucleotides;

(2) hybridizing the target oligodeoxynucleotides to a microarray comprising miRNA-specific probe oligonucleotides to provide a hybridization profile for the test sample; and

(3) comparing the test sample hybridization profile to a hybridization profile generated from a control sample,

wherein an alteration in the signal of at least one miRNA is indicative of the subject either having, or being at risk for developing, breast cancer.

15. The method of Claim 14 wherein the signal of at least one miRNA, relative to the signal generated from the control sample, is down-regulated.

16. The method of Claim 14 wherein the signal of at least one miRNA, relative to the signal generated from the control sample is up-regulated.

17. The method of Claim 14 wherein the microarray comprises miRNA-specific probe oligonucleotides for one or more miRNAs selected from the group consisting of miR-145, miR-21, miR-155, miR-10b, miR-009-1 (miR131-1), miR-34 (miR-170), miR-102 (miR-29b), miR-123 (miR-126), miR-140-as, miR-125a, miR-125b-1, miR-125b-2, miR-194, miR-204, miR-213, let-7a-2, let-7a-3, let-7d (let-7d-v1), let-7f-2, let-7i (let-7d-v2), miR-101-1, miR-122a, miR-128b, miR-136, miR-143, miR-149, miR-191, miR-196-1, miR-196-2, miR-202, miR-203, miR-206, miR-210 and combinations thereof.

18. A method of diagnosing whether a subject has, or is at risk for developing, a breast cancer associated with one or more adverse prognostic markers in a subject, comprising:

(1) reverse transcribing RNA from a test sample obtained from the subject to provide a set of target oligodeoxynucleotides;

(2) hybridizing the target oligodeoxynucleotides to a microarray comprising miRNA-specific probe oligonucleotides to provide a hybridization profile for said test sample; and

(3) comparing the test sample hybridization profile to a hybridization profile generated from a control sample,

wherein an alteration in the signal is indicative of the subject either having, or being at risk for developing, the cancer.

19. The method of Claim 18, wherein the one or more adverse prognostic markers is selected from the group consisting of estrogen receptor expression, progesterone receptor expression, positive lymph node metastasis, high proliferative index, detectable p53 expression, advanced tumor stage and high vascular invasion.

20. The method of Claim 18, wherein the microarray comprises at least one miRNA-specific probe oligonucleotide for a miRNA selected from the group consisting of miR-26a, miR-26b, miR-102 (miR-29b), miR-30a-5p, miR-30b, miR-30c, miR-30d, miR-185, miR-191, miR-206, miR-212, let-7c, miR-9-2, miR-15-a, miR-21, miR-30a-s, miR-133a-1, miR-137, miR-153-2, miR-154, miR-181a, miR-203, miR-213, let-7f-1, let-7a-3, let-7a-2, miR-9-3, miR-10b, miR-27a, miR-29a, miR-123, miR-205, let-7d, miR-145, miR-16a, miR-128b and combinations thereof.

21. A method of treating breast cancer in a subject who has a breast cancer in which at least one miR gene product is down-regulated or up-regulated in the cancer cells of the subject relative to control cells, comprising:

(1) when the at least one miR gene product is down-regulated in the cancer cells, administering to the subject an effective amount of at least one isolated miR gene product, provided that the miR gene product is not miR-15a or miR-16-1, such that proliferation of cancer cells in the subject is inhibited; or

(2) when the at least one miR gene product is up-regulated in the cancer cells, administering to the subject an effective amount of at least one compound for inhibiting expression of the at least one miR gene product, such that proliferation of cancer cells in the subject is inhibited.

22. The method of Claim 21, wherein the at least one isolated miR gene product in step (1) is selected from the group consisting of miR-145, miR-10b, miR-123 (miR-126), miR-140-as, miR-125a, miR-125b-1, miR-125b-2, miR-194, miR-204, let-7a-2, let-7a-3, let-7d (let-7d-v1), let-7f-2, miR-101-1, miR-143 and combinations thereof.

23. The method of Claim 21, wherein the at least one miR gene product in step (2) is selected from the group consisting of: miR-21, miR-155, miR-009-1 (miR131-1), miR-34 (miR-170), miR-102 (miR-29b), miR-213, let-7i (let-7d-v2), miR-122a, miR-128b, miR-136, miR-149, miR-191, miR-196-1, miR-196-2, miR-202, miR-203, miR-206, miR-210, miR-213 and combinations thereof.

24. A method of treating breast cancer in a subject, comprising:

(1) determining the amount of at least one miR gene product in breast cancer cells, relative to control cells; and

(2) altering the amount of miR gene product expressed in the breast cancer cells by:

(i) administering to the subject an effective amount of at least one isolated miR gene product, provided that the miR gene product is not miR-15a or miR-16-1, if the amount of the miR gene product expressed in the cancer cells is less than the amount of the miR gene product expressed in control cells; or

(ii) administering to the subject an effective amount of at least one compound for inhibiting expression of the at least one miR gene product, if the amount of the miR gene product expressed in the cancer cells is greater than the amount of the miR gene product expressed in control cells,

such that proliferation of cancer cells in the subject is inhibited.

25. The method of Claim 24, wherein the at least one isolated miR gene product in step (i) is selected from the group consisting of miR-145, miR-10b, miR-123 (miR-126), miR-140-as, miR-125a, miR-125b-1, miR-125b-2, miR-194, miR-204, let-7a-2, let-7a-3, let-7d (let-7d-v1), let-7f-2, miR-101-1, miR-143 and combinations thereof.

26. The method of Claim 24, wherein the at least one miR gene product in step (ii) is selected from the group consisting of miR-21, miR-155, miR-009-1 (miR131-1), miR-34 (miR-170), miR-102 (miR-29b), miR-213, let-7i (let-7d-v2), miR-122a, miR-128b, miR-136, miR-149, miR-191, miR-196-1, miR-196-2, miR-202, miR-203, miR-206, miR-210, miR-213 and combinations thereof.

27. A pharmaceutical composition for treating breast cancer, comprising at least one isolated miR gene product and a pharmaceutically-acceptable carrier.

28. The pharmaceutical composition of Claim 27, wherein the at least one isolated miR gene product corresponds to a miR gene product that is down-regulated in breast cancer cells relative to suitable control cells.

29. The pharmaceutical composition of Claim 27, wherein the isolated miR gene product is selected from the group consisting of miR-145, miR-10b, miR-123 (miR-126), miR-140-as, miR-125a, miR-125b-1, miR-125b-2, miR-194, miR-204, let-7a-2, let-7a-3, let-7d (let-7d-v1), let-7f-2, miR-101-1, miR-143 and combinations thereof.

30. A pharmaceutical composition for treating breast cancer, comprising at least one miR expression inhibitor compound and a pharmaceutically-acceptable carrier.

31. The pharmaceutical composition of Claim 30, wherein the at least one miR expression inhibitor compound is specific for a miR gene product that is up-regulated in breast cancer cells relative to suitable control cells.

32. The pharmaceutical composition of Claim 30, wherein the at least one miR expression inhibitor compound is specific for a miR gene product selected from the group consisting of miR-21, miR-155, miR-009-1 (miR131-1), miR-34 (miR-170), miR-102 (miR-29b), miR-213, let-7i (let-7d-v2), miR-122a, miR-128b, miR-136, miR-149, miR-191, miR-196-1, miR-196-2, miR-202, miR-203, miR-206, miR-210, miR-213 and combinations thereof.

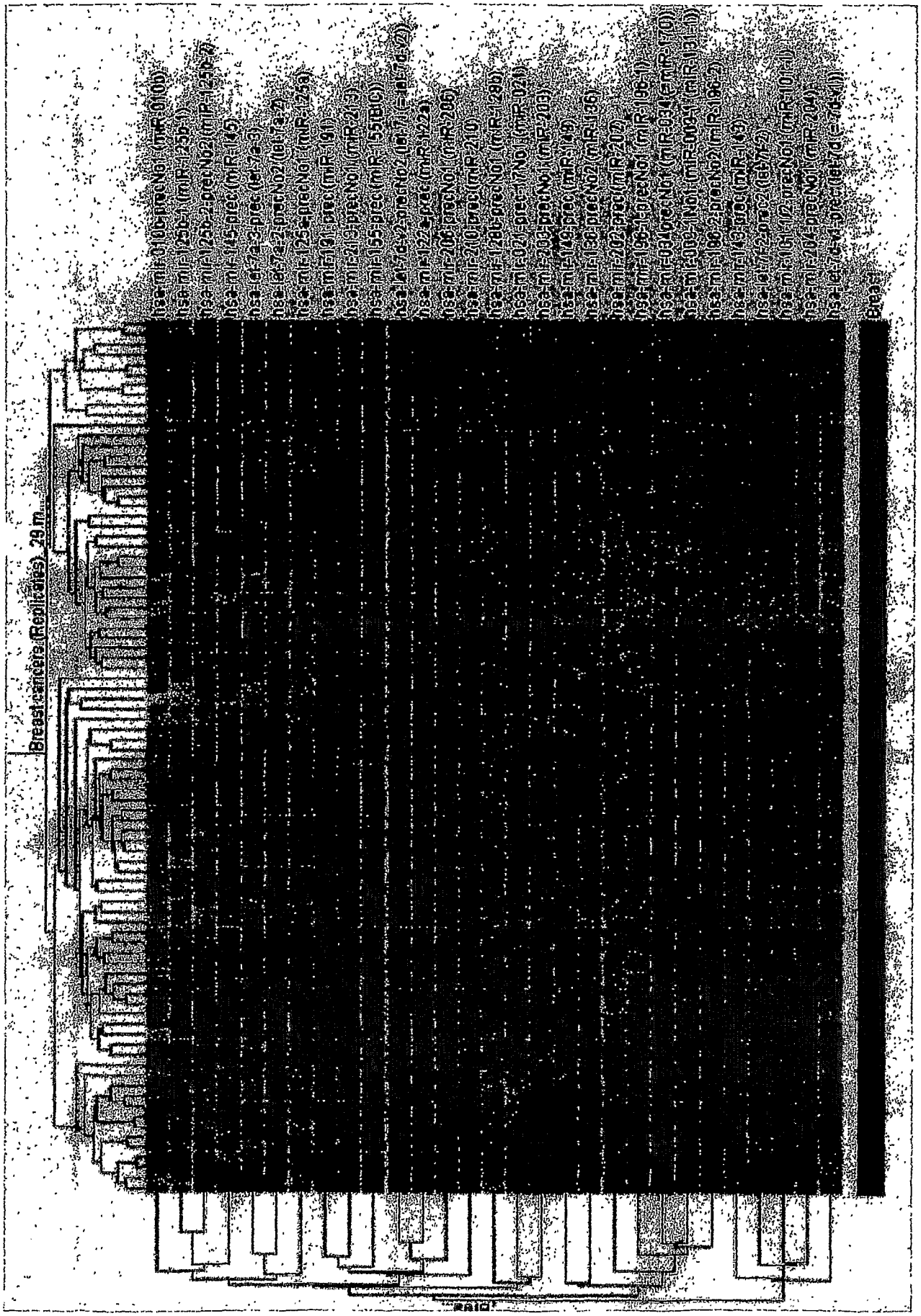
33. A method of identifying an anti-breast cancer agent, comprising providing a test agent to a cell and measuring the level of at least one miR gene product associated with decreased expression levels in breast cancer cells, wherein an increase in the level of the miR gene product in the cell, relative to a suitable control cell, is indicative of the test agent being an anti-breast cancer agent.

34. The method of Claim 33, wherein the miR gene product is selected from the group consisting of miR-145, miR-10b, miR-123 (miR-126), miR-140-as, miR-125a, miR-125b-1, miR-125b-2, miR-194, miR-204, let-7a-2, let-7a-3, let-7d (let-7d-v1), let-7f-2, miR-101-1, miR-143 and combinations thereof.

35. A method of identifying an anti-breast cancer agent, comprising providing a test agent to a cell and measuring the level of at least one miR gene product associated with

increased expression levels in breast cancer cells, wherein an decrease in the level of the miR gene product in the cell, relative to a suitable control cell, is indicative of the test agent being an anti-breast cancer agent.

36. The method of Claim 35, wherein the miR gene product is selected from the group consisting of miR-21, miR-155, miR-009-1 (miR131-1), miR-34 (miR-170), miR-102 (miR-29b), miR-213, let-7i (let-7d-v2), miR-122a, miR-128b, miR-136, miR-149, miR-191, miR-196-1, miR-196-2, miR-202, miR-203, miR-206, miR-210, miR-213 and combinations thereof.


Breast cancers (Replicates), 29 m
hsa-mir-210-prec-No1 (miR-210b)
hsa-mir-125b-1 (miR-125b-1)
hsa-mir-125a-2-prec-No2 (miR-125a-2)
hsa-mir-145-prec (miR-145)
hsa-let-7a-3-prec (let-7a-3)
hsa-let-7a-2-prec-No2 (let-7a-2)
hsa-mir-125a-prec-No1 (miR-125a)
hsa-mir-191 prec (miR-191)
hsa-mir-219-prec-No1 (miR-219-1)
hsa-mir-155-prec (miR-155BIC)
hsa-let-7c-2-prec-No2 (let-7i=let-7c-2)
hsa-mir-122a-prec (miR-122a)
hsa-mir-205-prec-No1 (miR-205)
hsa-mir-210-prec (miR-210)
hsa-mir-128b-prec-No1 (miR-128b)
hsa-let-7d-prec-1 (let-7d)
hsa-mir-203-prec-No1 (miR-203)
hsa-mir-149-prec (miR-149)
hsa-mir-130-prec-No2 (miR-130)
hsa-mir-20-prec (miR-20)
hsa-mir-196-1-prec-No1 (miR-196-1)
hsa-mir-034-prec-No1 (miR-034 miR-170)
hsa-mir-009-1-No1 (miR-009-1 miR-191-1)
hsa-mir-196-2-prec-No2 (miR-196-2)
hsa-mir-143-prec (miR-143)
hsa-let-7f-2-prec-2 (let-7f-2)
hsa-mir-101-1/2-prec-No1 (miR-101-1)
hsa-mir-204-prec-No1 (miR-204)
hsa-let-7d-4-prec (let-7d=let-7d-4)
Breast

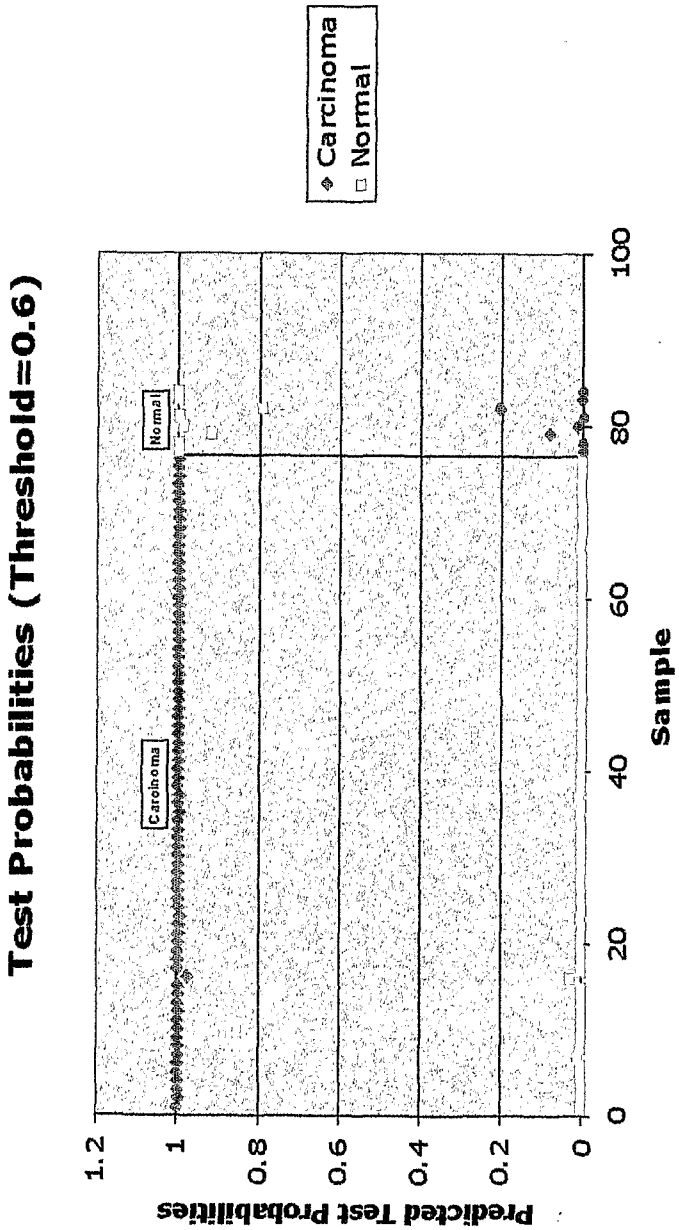

Test Probabilities (Threshold=0.6)
Carcinoma
Normal
Carcinoma
Normal
Predicted Test Probabilities
1.2
1
0.8
0.6
0.4
0.2
0
0
20
40
60
80
100
Sample

FIG. 2

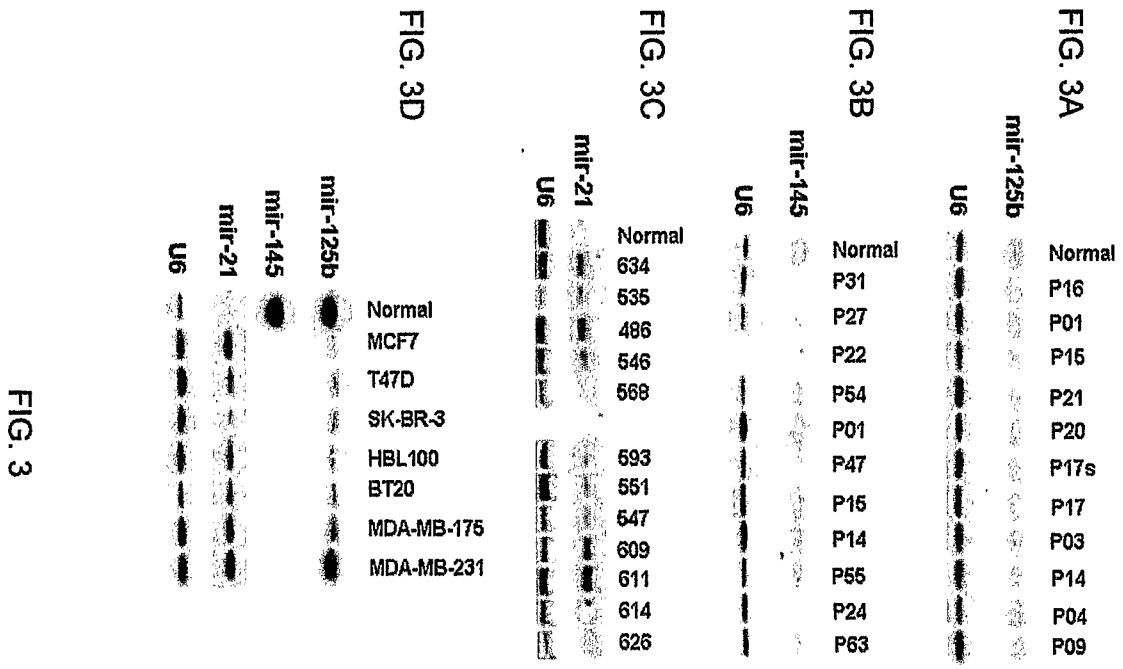


FIG. 3A
mir-125b
U6
Normal
P16
P01
P15
P21
P20
P17s
P17
P03
P14
P04
P09
FIG. 3B
mir-145
U6
Normal
P31
P27
P22
P54
P01
P47
P15
P14
P55
P24
P63
FIG. 3C
mir-21
U6
Normal
634
535
486
546
568
693
551
547
609
611
614
626
FIG. 3D
mir-125b
mir-145
mir-21
U6
Normal
MCF7
T47D
SK-BR-3
HBL100
BT20
MDA-MB-175
MDA-MB-231
FIG. 3

4A

N. samples	20	13	
feature	ER+	ER-	Probability
mir-26a	2.473	1.483	0.0273
mir-26b	3.751	1.932	0.0273
mir-29b	1.280	0.935	0.0188
mir-30a-5p	1.779	1.202	0.0191
mir-30b	1.810	1.184	0.0250
mir-30c	1.587	1.040	0.0191
mir-30d	2.986	1.736	0.0273
mir-185	1.568	2.296	0.0399
mir-191	6.354	2.908	0.0273
mir-206	1.811	2.373	0.0273
mir-212	2.811	3.905	0.0403

4B

N. samples	18	14	
feature	PR+	PR-	Probability
let-7c	1.445	1.129	0.0130
mir-26a	2.451	1.673	0.0474
mir-29b	1.283	0.997	0.0194
mir-30a-5p	1.879	1.219	0.0012
mir-30b	1.898	1.220	0.0044
mir-30c	1.643	1.089	0.0047
mir-30d	3.211	1.777	0.0055

4C

N. samples	9	22	
feature	pT1	pT2-3	Probability
mir-9-2	0.894	0.840	0.0078
mir-15-a	0.905	0.830	0.0024
mir-21	1.080	1.348	0.0040
mir-30a-s	0.944	0.875	0.0065
mir-133a-1	0.928	0.843	0.0025
mir-137	0.894	0.818	0.0100
mir-153-2	0.896	0.833	0.0096
mir-154	0.924	0.852	0.0062
mir-181a	1.024	1.225	0.0045
mir-203	0.905	1.102	0.0011
mir-213	1.915	3.197	0.0003

FIG. 4D

N. samples	16	6	
feature	pN0	pN10+	Probability
let-7f-1	1.195	1.053	0.0378
let-7a-3	1.191	1.039	0.0303
let-7a-2	1.470	1.213	0.0300
mir-9-3	1.634	1.344	0.0152

FIG. 4E

N. samples	21	11	
feature	Vascular invasion absent	Vascular invasion present	Probability
mir-9-3	1.059	0.988	0.0451
mir-10b	1.048	0.972	0.0210
mir-27a	1.104	0.992	0.0317
mir-29a	1.101	0.970	0.0346
mir-123	1.125	0.852	0.0161
mir-205	1.299	0.762	0.0451

FIG. 4F

N. samples	26	23	
feature	Low PI	High PI	Probability
let-7c	1.817	1.361	0.0071
let-7d	1.594	1.310	0.0073
mir-26a	2.602	1.928	0.0492
mir-26b	4.039	2.695	0.0297
mir-30a-5p	1.783	1.394	0.0257
mir-102	1.389	1.037	0.0017
mir-145	1.557	1.281	0.0136

FIG. 4G

N. samples	39	14	
feature	p53 +	p53 -	Probability
mir-16a	0.895	1.030	0.0026
mir-128b	0.964	1.059	0.0096

FIG. 4