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(54) **COLORECTAL CANCER DETECTION KIT OR DEVICE, AND DETECTION METHOD**

(57) It is intended to provide a kit or a device for the detection of colorectal cancer and a method for detecting colorectal cancer. The present invention provides a kit or a device for the detection of colorectal cancer, comprising a nucleic acid capable of specifically binding to a miRNA in a sample from a subject, and a method for detecting colorectal cancer, comprising measuring the miRNA *in vitro*.

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Description

Technical Field

[0001] The present invention relates to a kit or a device for the detection of colorectal cancer, comprising a nucleic acid capable of specifically binding to a particular miRNA, which is used for examining the presence or absence of colorectal cancer in a subject, and a method for detecting colorectal cancer, comprising measuring an expression level of the miRNA using the nucleic acid.

Background Art

[0002] The large intestine is an organ that stores residual bowel contents after digestion and absorption, and produces feces while absorbing water. The large intestine begins with the cecum, which is then connected to the ascending colon, the transverse colon, the descending colon, the sigmoid colon, the rectum, and the anal canal. According to the 2011 type-specific cancer statistics in Japan disclosed by the Center for Cancer Control and Information Services, National Cancer Center, the number of individuals affected by colorectal cancer was 112,772 people. Namely, it is estimated that one in approximately 14 Japanese people experience colorectal cancer. The number of incidences of this cancer takes the 2nd place by cancer site. The number of colorectal cancer deaths in men and women together climbs to 45,744 people and takes the 3rd place by cancer site. It is estimated that one in approximately 20 Americans develop colorectal cancer. The estimated number of American individuals affected by colorectal cancer climbed to 96,830 people in 2014, among which approximately 40,000 people reportedly died (Non Patent Literature 1).

[0003] The progression stages of colorectal cancer are specified in Non Patent Literature 2 and classified into stage 0 (Tis/N0/M0), stage I (T1 to T2/N0/M0), stage II (T3 to T4/N0/M0), stage IIA (T3/N0/M0), stage IIB (T4a/N0/M0), stage IIC (T4b/N0/M0), stage III (N1 to N2/M0), stage IIIA (T1 to T2/N1/M0 and T1/N2a/M0) stage IIIB (T3 to T4a/N1M0 and T2 to T3/N2a/M0 and T1 to T2/N2b/M0), stage IIIC (T4a/N2a/M0 and T3 to T4a/N2b/M0 and T4b/N1 to N2/M0), stage IVA (M1a), and stage IVB (M1b) according to the degrees of tumor spread (Tis and T1 to T4), lymph node metastasis (N0, N1a to N1c, and N2a to N2b), and distant metastasis (M0 and M1a to M1b).

[0004] The survival rate of colorectal cancer differs depending on the stages of progression. Non Patent Literature 1 has reported the following respective statistic values of colon cancer and rectal cancer. The 5-year relative survival rate of colon cancer is reportedly 74% for stage I, 67% for stage IIA, 59% for stage IIB, 37% for stage IIC, 73% for stage IIIA, 46% for stage IIIB, 28% for stage IIIC, and 6% for stage IV. Also, the 5-year relative survival rate of rectal cancer is reportedly 74% for stage I, 65% for stage IIA, 52% for stage IIB, 32% for stage IIC, 74% for stage IIIA, 45% for stage IIIB, 33% for stage IIIC, and 6% for stage IV. Evidently, colorectal cancer at an early stage of progression leads to a high survival rate. Thus, the early detection and treatment of colorectal cancer makes a significant contribution to improvement in survival rate.

[0005] The treatment of colorectal cancer is mainly laparotomy or laparoscopic surgery, which is often used in combination with postoperative anticancer drug treatment or radiotherapy (Non Patent Literature 1). Particularly, early colorectal cancer may be adaptable to endoscopic surgery which permits treatment without abdominal resection.

[0006] As described in Non Patent Literature 1, fecal occult blood test and endoscopy are widely prevalent as tests of colorectal cancer. Particularly, the fecal occult blood test is inexpensive and noninvasive and is also carried out at home. Therefore, the American Cancer Society recommends taking the fecal occult blood test every year. In order to further examine a tumor site and spread of the cancer, an imaging test such as barium enema, CT, or MRI is also carried out in addition to the colonoscopy. Alternatively, tests on blood tumor markers such as CEA and CA19-9 may be carried out for the purpose of observing the prognosis or the therapeutic effects on patients already diagnosed with colorectal cancer (Non Patent Literature 1).

[0007] As shown in Patent Literatures 1 to 4, there are reports, albeit at a research stage, on the detection of colorectal cancer using the expression levels of microRNAs (miRNAs) or combinations of the expression levels of miRNAs and the expression levels of additional protein markers in biological samples including blood.

[0008] Patent Literature 1 discloses a method for detecting colorectal cancer or other cancers using hsa-miR-92a-2-5p, hsa-miR-128-2-5p, and hsa-miR-24-3p in colorectal cancer tissues.

[0009] Patent Literature 2 discloses a method for detecting colorectal cancer using hsa-miR-1233-5p and hsa-miR-1225-3p in plasma.

[0010] Patent Literature 3 discloses a method for detecting colorectal cancer using multiple miRNAs such as hsa-miR-1231, hsa-miR-423-5p, and hsa-miR-1268a in large intestine tissues or feces.

[0011] Patent Literature 4 discloses a method for detecting colorectal cancer using hsa-miR-150-3p, miR-92a-2-5p, and the like in tissues.

Citation List

Patent Literature

[0012]

Patent Literature 1: International Publication No. WO 2007/081740
Patent Literature 2: U.S. Patent Application Publication No. 2013/102487
Patent Literature 3: U.S. Patent Application Publication No. 2012/088687
Patent Literature 4: JP Patent Publication (Kohyo) No. 2009-531019 A (2009)

Non Patent Literature

[0013]

Non Patent Literature 1: American Cancer Society, "Colorectal Cancer", 2013, p. 5 to 6, 17 to 28, 33 to, 45 to 54, and 67 to 71
Non Patent Literature 2: Sobin, L. et al., "TNM Classification of Malignant Tumours, the 7th edition", 2010, p. 94-99
Non Patent Literature 3: Allison, JE. et al., 1996, The New England Journal of Medicine, Vol. 334 (3), p. 155-9
Non Patent Literature 4: Palmqvist, R. et al., 2007, Diseases of colon and rectum, Vol. 46 (11), p. 1538-44

Summary of Invention

Technical Problem

[0014] An object of the present invention is to find a novel tumor marker for colorectal cancer and to provide a method that can effectively detect colorectal cancer using a nucleic acid capable of specifically binding to the marker. The fecal occult blood test, which is widely used at present as a first test of colorectal cancer, produces positive results even for non-cancerous reasons such as hemorrhoid, whereas this test fails to detect early colorectal cancer without bleeding and overlooks 90% or more of abnormalities in the large intestine (including cancer) according to the report (Non Patent Literature 1). The specific sensitivity of the fecal occult blood test differs largely from 37% to 79.4% depending on a testing kit used, and its specificity is reportedly 86.7% to 97.7% (Non Patent Literature 3). Although the colonoscopy is known to have high examination accuracy, this examination is difficult to apply as a primary screening because of the necessity of pretreatment or sedatives on patients, relatively high cost, etc. (Non Patent Literature 1). The tumor markers such as CEA and CA19-9 in blood may elevate in cancers other than colorectal cancer and therefore allegedly fail to determine the presence or absence of colorectal cancer. The false diagnosis of other cancers as colorectal cancer wastes appropriate therapeutic opportunity or places unnecessary economical and physical burdens on patients due to the application of wrong medicine. Therefore, use of CEA or CA19-9 is often limited to the observation of the prognosis and of therapeutic effects on patients already diagnosed with colorectal cancer (Non Patent Literature 1). The report states that the CEA test has specificity of 99%, but sensitivity of only 12%, suggesting that the significance of tumor marker measurement as a colorectal cancer screening test is poor (Non Patent Literature 4).

[0015] As described below, there are reports, albeit at a research stage, on the determination of colorectal cancer using the expression levels of microRNAs (miRNAs) in biological samples including blood, none of which, however, have yet been brought into practical use.

[0016] Patent Literature 1 discloses a method for detecting colorectal cancer or other cancers using hsa-miR-92a-2-5p, hsa-miR-128-2-5p, and hsa-miR-24-3p in colorectal cancer tissues. This detection method, however, requires obtaining colorectal cancer tissue samples by surgical operation, and this step places a heavy physical burden on patients. Therefore, this method is not favorable as an examination method. In addition, this detection method does not describe specific colorectal cancer detection performance such as accuracy, sensitivity, or specificity and is thus industrially less practical.

[0017] Patent Literature 3 discloses a method for detecting colorectal cancer using multiple miRNAs such as hsa-miR-1231, hsa-miR-423-5p, and hsa-miR-1268a in large intestine tissues or feces. Since surgical operation for obtaining colorectal cancer tissues places a heavy physical burden on patients, this method is not favorable as an examination method. In addition, although the collection of fecal samples is noninvasive, test substances may exist unevenly in feces. This tends to cause unfavorable variations in testing results.

[0018] Patent Literature 4 discloses a method for detecting colorectal cancer using hsa-miR-150-3p, miR-92a-2-5p, and the like in tissues. This literature, however, neither describes detection performance such as accuracy, sensitivity, or specificity nor describes a specific method for determining colorectal cancer using blood. Therefore, this method is

industrially less practical. In addition, these miRNA markers were not validated in an independent sample group and are thus less reliable.

[0019] As mentioned above, the existing tumor markers exhibit low performance in the detection of colorectal cancer, or neither performance nor detection methods are specifically shown as to the markers at a research stage. Therefore, use of these markers might lead to imposing needless extra examination due to the false detection of healthy subjects as being colorectal cancer patients, or might waste therapeutic opportunity because of overlooking colorectal cancer patients. In addition, the measurement of several dozens to several hundreds of miRNAs increases examination cost and is therefore difficult to use in large-scale screening such as medical checkup. Furthermore, the collection of colorectal tissues for measuring the tumor markers is highly invasive to patients and is not favorable. Hence, there is a demand for a highly accurate colorectal cancer marker that is detectable from blood, which can be collected in a less invasive manner, and is capable of correctly determining a colorectal cancer patient as a colorectal cancer patient and a healthy subject as a healthy subject. The early detection and treatment of colorectal cancer can drastically improve survival rates. Furthermore, the early detection of colorectal cancer leads to the applicability of endoscopic surgery which permits treatment without abdominal resection. Therefore, a highly sensitive colorectal cancer marker that can detect colorectal cancer even at an early stage of progression is desired.

Solution to Problem

[0020] The present inventors have conducted diligent studies to attain the object and consequently completed the present invention by finding multiple genes usable as markers for the detection of colorectal cancer from blood, which can be collected with limited invasiveness, and finding that colorectal cancer can be significantly detected by using a nucleic acid capable of specifically binding to any of these markers.

<Summary of Invention>

[0021] Specifically, the present invention has the following features:

(1) A kit for the detection of colorectal cancer, comprising a nucleic acid capable of specifically binding to at least one or more polynucleotide(s) selected from the group consisting of colorectal cancer markers miR-6726-5p, miR-4257, miR-6787-5p, miR-6780b-5p, miR-3131, miR-7108-5p, miR-1343-3p, miR-1247-3p, miR-4651, miR-6757-5p, miR-3679-5p, miR-7641, miR-6746-5p, miR-8072, miR-6741-5p, miR-1908-5p, miR-6857-5p, miR-4746-3p, miR-744-5p, miR-4792, miR-564, miR-6791-5p, miR-6825-5p, miR-6826-5p, miR-4665-3p, miR-4467, miR-3188, miR-6125, miR-6756-5p, miR-1228-3p, miR-8063, miR-8069, miR-6875-5p, miR-3185, miR-4433b-3p, miR-6887-5p, miR-128-1-5p, miR-6724-5p, miR-1914-3p, miR-1225-5p, miR-4419b, miR-7110-5p, miR-187-5p, miR-3184-5p, miR-204-3p, miR-5572, miR-6729-5p, miR-615-5p, miR-6749-5p, miR-6515-3p, miR-3937, miR-6840-3p, miR-6893-5p, miR-4728-5p, miR-6717-5p, miR-7113-3p, miR-4665-5p, miR-642b-3p, miR-7109-5p, miR-6842-5p, miR-4442, miR-4433-3p, miR-4707-5p, miR-6126, miR-4449, miR-4706, miR-1913, miR-602, miR-939-5p, miR-4695-5p, miR-711, miR-6816-5p, miR-4632-5p, miR-6721-5p, miR-7847-3p, miR-6132, miR-887-3p, miR-3679-3p, miR-6784-5p, miR-1249, miR-937-5p, miR-5195-3p, miR-6732-5p, miR-4417, miR-4281, miR-4734, miR-6766-3p, miR-663a, miR-4513, miR-6781-5p, miR-1227-5p, miR-6845-5p, miR-6798-5p, miR-3620-5p, miR-1915-5p, miR-4294, miR-642a-3p, miR-371a-5p, miR-940, miR-4450, miR-4723-5p, miR-1469, miR-6861-5p, miR-7975, miR-6879-5p, miR-6802-5p, miR-1268b, miR-663b, miR-125a-3p, miR-2861, miR-6088, miR-4758-5p, miR-296-3p, miR-6738-5p, miR-671-5p, miR-4454, miR-4516, miR-7845-5p, miR-4741, miR-92b-5p, miR-6795-5p, miR-6805-3p, miR-4725-3p, miR-6782-5p, miR-4688, miR-6850-5p, miR-6777-5p, miR-6785-5p, miR-7106-5p, miR-3663-3p, miR-6131, miR-1915-3p, miR-4532, miR-6820-5p, miR-4689, miR-4638-5p, miR-3656, miR-3621, miR-6769b-5p, miR-149-3p, miR-23b-3p, miR-3135b, miR-6848-5p, miR-6769a-5p, miR-4327, miR-6765-3p, miR-6716-5p, miR-6877-5p, miR-6727-5p, miR-4534, miR-614, miR-1202, miR-575, miR-6870-5p, miR-6722-3p, miR-7977, miR-4649-5p, miR-4675, miR-6075, miR-6779-5p, miR-4271, miR-3196, miR-6803-5p, miR-6789-5p, miR-4648, miR-4508, miR-4749-5p, miR-4505, miR-5698, miR-1199-5p, miR-4763-3p, miR-6836-3p, miR-3195, miR-718, miR-3178, miR-638, miR-4497, miR-6085, miR-6752-5p andmiR-135a-3p.

(2) The kit according to (1), wherein miR-6726-5p is hsa-miR-6726-5p, miR-4257 is hsa-miR-4257, miR-6787-5p is hsa-miR-6787-5p, miR-6780b-5p is hsa-miR-6780b-5p, miR-3131 is hsa-miR-3131, miR-7108-5p is hsa-miR-7108-5p, miR-1343-3p is hsa-miR-1343-3p, miR-1247-3p is hsa-miR-1247-3p, miR-4651 is hsa-miR-4651, miR-6757-5p is hsa-miR-6757-5p, miR-3679-5p is hsa-miR-3679-5p, miR-7641 is hsa-miR-7641, miR-6746-5p is hsa-miR-6746-5p, miR-8072 is hsa-miR-8072, miR-6741-5p is hsa-miR-6741-5p, miR-1908-5p is hsa-miR-1908-5p, miR-6857-5p is hsa-miR-6857-5p, miR-4746-3p is hsa-miR-4746-3p, miR-744-5p is hsa-miR-744-5p, miR-4792 is hsa-miR-4792, miR-564 is hsa-miR-564, miR-6791-5p is hsa-miR-6791-5p, miR-6825-5p is hsa-miR-6825-5p, miR-6826-5p is hsa-miR-6826-5p, miR-4665-3p is hsa-miR-4665-3p, miR-4467 is hsa-miR-4467, miR-3188 is hsa-miR-

3188, miR-6125 is hsa-miR-6125, miR-6756-5p is hsa-miR-6756-5p, miR-1228-3p is hsa-miR-1228-3p, miR-8063 is hsa-miR-8063, miR-8069 is hsa-miR-8069, miR-6875-5p is hsa-miR-6875-5p, miR-3185 is hsa-miR-3185, miR-4433b-3p is hsa-miR-4433b-3p, miR-6887-5p is hsa-miR-6887-5p, miR-128-1-5p is hsa-miR-128-1-5p, miR-6724-5p is hsa-miR-6724-5p, miR-1914-3p is hsa-miR-1914-3p, miR-1225-5p is hsa-miR-1225-5p, miR-4419b is hsa-miR-4419b, miR-7110-5p is hsa-miR-7110-5p, miR-187-5p is hsa-miR-187-5p, miR-3184-5p is hsa-miR-3184-5p, miR-204-3p is hsa-miR-204-3p, miR-5572 is hsa-miR-5572, miR-6729-5p is hsa-miR-6729-5p, miR-615-5p is hsa-miR-615-5p, miR-6749-5p is hsa-miR-6749-5p, miR-6515-3p is hsa-miR-6515-3p, miR-3937 is hsa-miR-3937, miR-6840-3p is hsa-miR-6840-3p, miR-6893-5p is hsa-miR-6893-5p, miR-4728-5p is hsa-miR-4728-5p, miR-6717-5p is hsa-miR-6717-5p, miR-7113-3p is hsa-miR-7113-3p, miR-4665-5p is hsa-miR-4665-5p, miR-642b-3p is hsa-miR-642b-3p, miR-7109-5p is hsa-miR-7109-5p, miR-6842-5p is hsa-miR-6842-5p, miR-4442 is hsa-miR-4442, miR-4433-3p is hsa-miR-4433-3p, miR-4707-5p is hsa-miR-4707-5p, miR-6126 is hsa-miR-6126, miR-4449 is hsa-miR-4449, miR-4706 is hsa-miR-4706, miR-1913 is hsa-miR-1913, miR-602 is hsa-miR-602, miR-939-5p is hsa-miR-939-5p, miR-4695-5p is hsa-miR-4695-5p, miR-711 is hsa-miR-711, miR-6816-5p is hsa-miR-6816-5p, miR-4632-5p is hsa-miR-4632-5p, miR-6721-5p is hsa-miR-6721-5p, miR-7847-3p is hsa-miR-7847-3p, miR-6132 is hsa-miR-6132, miR-887-3p is hsa-miR-887-3p, miR-3679-3p is hsa-miR-3679-3p, miR-6784-5p is hsa-miR-6784-5p, miR-1249 is hsa-miR-1249, miR-937-5p is hsa-miR-937-5p, miR-5195-3p is hsa-miR-5195-3p, miR-6732-5p is hsa-miR-6732-5p, miR-4417 is hsa-miR-4417, miR-4281 is hsa-miR-4281, miR-4734 is hsa-miR-4734, miR-6766-3p is hsa-miR-6766-3p, miR-663a is hsa-miR-663a, miR-4513 is hsa-miR-4513, miR-6781-5p is hsa-miR-6781-5p, miR-1227-5p is hsa-miR-1227-5p, miR-6845-5p is hsa-miR-6845-5p, miR-6798-5p is hsa-miR-6798-5p, miR-3620-5p is hsa-miR-3620-5p, miR-1915-5p is hsa-miR-1915-5p, miR-4294 is hsa-miR-4294, miR-642a-3p is hsa-miR-642a-3p, miR-371a-5p is hsa-miR-371a-5p, miR-940 is hsa-miR-940, miR-4450 is hsa-miR-4450, miR-4723-5p is hsa-miR-4723-5p, miR-1469 is hsa-miR-1469, miR-6861-5p is hsa-miR-6861-5p, miR-7975 is hsa-miR-7975, miR-6879-5p is hsa-miR-6879-5p, miR-6802-5p is hsa-miR-6802-5p, miR-1268b is hsa-miR-1268b, miR-663b is hsa-miR-663b, miR-125a-3p is hsa-miR-125a-3p, miR-2861 is hsa-miR-2861, miR-6088 is hsa-miR-6088, miR-4758-5p is hsa-miR-4758-5p, miR-296-3p is hsa-miR-296-3p, miR-6738-5p is hsa-miR-6738-5p, miR-671-5p is hsa-miR-671-5p, miR-4454 is hsa-miR-4454, miR-4516 is hsa-miR-4516, miR-7845-5p is hsa-miR-7845-5p, miR-4741 is hsa-miR-4741, miR-92b-5p is hsa-miR-92b-5p, miR-6795-5p is hsa-miR-6795-5p, miR-6805-3p is hsa-miR-6805-3p, miR-4725-3p is hsa-miR-4725-3p, miR-6782-5p is hsa-miR-6782-5p, miR-4688 is hsa-miR-4688, miR-6850-5p is hsa-miR-6850-5p, miR-6777-5p is hsa-miR-6777-5p, miR-6785-5p is hsa-miR-6785-5p, miR-7106-5p is hsa-miR-7106-5p, miR-3663-3p is hsa-miR-3663-3p, miR-6131 is hsa-miR-6131, miR-1915-3p is hsa-miR-1915-3p, miR-4532 is hsa-miR-4532, miR-6820-5p is hsa-miR-6820-5p, miR-4689 is hsa-miR-4689, miR-4638-5p is hsa-miR-4638-5p, miR-3656 is hsa-miR-3656, miR-3621 is hsa-miR-3621, miR-6769b-5p is hsa-miR-6769b-5p, miR-149-3p is hsa-miR-149-3p, miR-23b-3p is hsa-miR-23b-3p, miR-3135b is hsa-miR-3135b, miR-6848-5p is hsa-miR-6848-5p, miR-6769a-5p is hsa-miR-6769a-5p, miR-4327 is hsa-miR-4327, miR-6765-3p is hsa-miR-6765-3p, miR-6716-5p is hsa-miR-6716-5p, miR-6877-5p is hsa-miR-6877-5p, miR-6727-5p is hsa-miR-6727-5p, miR-4534 is hsa-miR-4534, miR-614 is hsa-miR-614, miR-1202 is hsa-miR-1202, miR-575 is hsa-miR-575, miR-6870-5p is hsa-miR-6870-5p, miR-6722-3p is hsa-miR-6722-3p, miR-7977 is hsa-miR-7977, miR-4649-5p is hsa-miR-4649-5p, miR-4675 is hsa-miR-4675, miR-6075 is hsa-miR-6075, miR-6779-5p is hsa-miR-6779-5p, miR-4271 is hsa-miR-4271, miR-3196 is hsa-miR-3196, miR-6803-5p is hsa-miR-6803-5p, miR-6789-5p is hsa-miR-6789-5p, miR-4648 is hsa-miR-4648, miR-4508 is hsa-miR-4508, miR-4749-5p is hsa-miR-4749-5p, miR-4505 is hsa-miR-4505, miR-5698 is hsa-miR-5698, miR-1199-5p is hsa-miR-1199-5p, miR-4763-3p is hsa-miR-4763-3p, miR-6836-3p is hsa-miR-6836-3p, miR-3195 is hsa-miR-3195, miR-718 is hsa-miR-718, miR-3178 is hsa-miR-3178, miR-638 is hsa-miR-638, miR-4497 is hsa-miR-4497, miR-6085 is hsa-miR-6085, miR-6752-5p is hsa-miR-6752-5p, and miR-135a-3p is hsa-miR-135a-3p.

(3) The kit according to (1) or (2), wherein the nucleic acid is a polynucleotide selected from the group consisting of the following polynucleotides (a) to (e):

(a) a polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 1 to 171 and 606 to 614 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,

(b) a polynucleotide comprising a nucleotide sequence represented by any of SEQ ID NOs: 1 to 171 and 606 to 614,

(c) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 1 to 171 and 606 to 614 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,

(d) a polynucleotide comprising a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 1 to 171 and 606 to 614 or a nucleotide sequence derived from the nucleotide sequence

by the replacement of u with t, and
(e) a polynucleotide hybridizing under stringent conditions to any of the polynucleotides (a) to (d).

(4) The kit according to any of (1) to (3), wherein the kit further comprises a nucleic acid capable of specifically binding to at least one or more polynucleotide(s) selected from the group consisting of other colorectal cancer markers miR-1231-5p, miR-1233-5p, miR-150-3p, miR-1225-3p, miR-92a-2-5p, miR-423-5p, miR-1268a, miR-128-2-5p and miR-24-3p.
(5) The kit according to (4), wherein miR-1231 is hsa-miR-1231, miR-1233-5p is hsa-miR-1233-5p, miR-150-3p is hsa-miR-150-3p, miR-1225-3p is hsa-miR-1225-3p, miR-92a-2-5p is hsa-miR-92a-2-5p, miR-423-5p is hsa-miR-423-5p, miR-1268a is hsa-miR-1268a, miR-128-2-5p is hsa-miR-128-2-5p, and miR-24-3p is hsa-miR-24-3p.
(6) The kit according to (4) or (5), wherein the nucleic acid is a polynucleotide selected from the group consisting of the following polynucleotides (f) to (j):

(f) a polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 172 to 180 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,
(g) a polynucleotide comprising a nucleotide sequence represented by any of SEQ ID NOs: 172 to 180,
(h) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 172 to 180 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,
(i) a polynucleotide comprising a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 172 to 180 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, and
(j) a polynucleotide hybridizing under stringent conditions to any of the polynucleotides (f) to (i).

(7) The kit according to any (6), wherein the kit further comprises a nucleic acid capable of specifically binding to at least one or more polynucleotide(s) selected from the group consisting of other colorectal cancer markers miR-4697-5p, miR-3197, miR-675-5p, miR-4486, miR-7107-5p, miR-23a-3p, miR-4667-5p, miR-451a, miR-3940-5p, miR-8059, miR-6813-5p, miR-4492, miR-4476 and miR-6090.
(8) The kit according to (7), wherein miR-4697-5p is hsa-miR-4697-5p, miR-3197 is hsa-miR-3197, miR-675-5p is hsa-miR-675-5p, miR-4486 is hsa-miR-4486, miR-7107-5p is hsa-miR-7107-5p, miR-23a-3p is hsa-miR-23a-3p, miR-4667-5p is hsa-miR-4667-5p, miR-451a is hsa-miR-451a, miR-3940-5p is hsa-miR-3940-5p, miR-8059 is hsa-miR-8059, miR-6813-5p is hsa-miR-6813-5p, miR-4492 is hsa-miR-4492, miR-4476 is hsa-miR-4476, and miR-6090 is hsa-miR-6090.
(9) The kit according to (7) or (8), wherein the nucleic acid is a polynucleotide selected from the group consisting of the following polynucleotides (k) to (o):

(k) a polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 181 to 194 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,
(l) a polynucleotide comprising a nucleotide sequence represented by any of SEQ ID NOs: 181 to 194,
(m) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 181 to 194 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,
(n) a polynucleotide comprising a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 181 to 194 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, and
(o) a polynucleotide hybridizing under stringent conditions to any of the polynucleotides (k) to (n).

(10) The kit according to any one (9), wherein the kit comprises at least two or more nucleic acids capable of specifically binding to at least two or more polynucleotides, respectively, selected from the group consisting of all of the colorectal cancer markers according to (1) or (2).
(11) A device for the detection of colorectal cancer, comprising a nucleic acid capable of specifically binding to at least one or more polynucleotide(s) selected from the group consisting of colorectal cancer markers miR-6726-5p, miR-4257, miR-6787-5p, miR-6780b-5p, miR-3131, miR-7108-5p, miR-1343-3p, miR-1247-3p, miR-4651, miR-6757-5p, miR-3679-5p, miR-7641, miR-6746-5p, miR-8072, miR-6741-5p, miR-1908-5p, miR-6857-5p, miR-

4746-3p, miR-744-5p, miR-4792, miR-564, miR-6791-5p, miR-6825-5p, miR-6826-5p, miR-4665-3p, miR-4467, miR-3188, miR-6125, miR-6756-5p, miR-1228-3p, miR-8063, miR-8069, miR-6875-5p, miR-3185, miR-4433b-3p, miR-6887-5p, miR-128-1-5p, miR-6724-5p, miR-1914-3p, miR-1225-5p, miR-4419b, miR-7110-5p, miR-187-5p, miR-3184-5p, miR-204-3p, miR-5572, miR-6729-5p, miR-615-5p, miR-6749-5p, miR-6515-3p, miR-3937, miR-6840-3p, miR-6893-5p, miR-4728-5p, miR-6717-5p, miR-7113-3p, miR-4665-5p, miR-642b-3p, miR-7109-5p, miR-6842-5p, miR-4442, miR-4433-3p, miR-4707-5p, miR-6126, miR-4449, miR-4706, miR-1913, miR-602, miR-939-5p, miR-4695-5p, miR-711, miR-6816-5p, miR-4632-5p, miR-6721-5p, miR-7847-3p, miR-6132, miR-887-3p, miR-3679-3p, miR-6784-5p, miR-1249, miR-937-5p, miR-5195-3p, miR-6732-5p, miR-4417, miR-4281, miR-4734, miR-6766-3p, miR-663a, miR-4513, miR-6781-5p, miR-1227-5p, miR-6845-5p, miR-6798-5p, miR-3620-5p, miR-1915-5p, miR-4294, miR-642a-3p, miR-371a-5p, miR-940, miR-4450, miR-4723-5p, miR-1469, miR-6861-5p, miR-7975, miR-6879-5p, miR-6802-5p, miR-1268b, miR-663b, miR-125a-3p, miR-2861, miR-6088, miR-4758-5p, miR-296-3p, miR-6738-5p, miR-671-5p, miR-4454, miR-4516, miR-7845-5p, miR-4741, miR-92b-5p, miR-6795-5p, miR-6805-3p, miR-4725-3p, miR-6782-5p, miR-4688, miR-6850-5p, miR-6777-5p, miR-6785-5p, miR-7106-5p, miR-3663-3p, miR-6131, miR-1915-3p, miR-4532, miR-6820-5p, miR-4689, miR-4638-5p, miR-3656, miR-3621, miR-6769b-5p, miR-149-3p, miR-23b-3p, miR-3135b, miR-6848-5p, miR-6769a-5p, miR-4327, miR-6765-3p, miR-6716-5p, miR-6877-5p, miR-6727-5p, miR-4534, miR-614, miR-1202, miR-575, miR-6870-5p, miR-6722-3p, miR-7977, miR-4649-5p, miR-4675, miR-6075, miR-6779-5p, miR-4271, miR-3196, miR-6803-5p, miR-6789-5p, miR-4648, miR-4508, miR-4749-5p, miR-4505, miR-5698, miR-1199-5p, miR-4763-3p, miR-6836-3p, miR-3195, miR-718, miR-3178, miR-638, miR-4497, miR-6085, miR-6752-5p and miR-135a-3p.

(12) The device according to (11), wherein miR-6726-5p is hsa-miR-6726-5p, miR-4257 is hsa-miR-4257, miR-6787-5p is hsa-miR-6787-5p, miR-6780b-5p is hsa-miR-6780b-5p, miR-3131 is hsa-miR-3131, miR-7108-5p is hsa-miR-7108-5p, miR-1343-3p is hsa-miR-1343-3p, miR-1247-3p is hsa-miR-1247-3p, miR-4651 is hsa-miR-4651, miR-6757-5p is hsa-miR-6757-5p, miR-3679-5p is hsa-miR-3679-5p, miR-7641 is hsa-miR-7641, miR-6746-5p is hsa-miR-6746-5p, miR-8072 is hsa-miR-8072, miR-6741-5p is hsa-miR-6741-5p, miR-1908-5p is hsa-miR-1908-5p, miR-6857-5p is hsa-miR-6857-5p, miR-4746-3p is hsa-miR-4746-3p, miR-744-5p is hsa-miR-744-5p, miR-4792 is hsa-miR-4792, miR-564 is hsa-miR-564, miR-6791-5p is hsa-miR-6791-5p, miR-6825-5p is hsa-miR-6825-5p, miR-6826-5p is hsa-miR-6826-5p, miR-4665-3p is hsa-miR-4665-3p, miR-4467 is hsa-miR-4467, miR-3188 is hsa-miR-3188, miR-6125 is hsa-miR-6125, miR-6756-5p is hsa-miR-6756-5p, miR-1228-3p is hsa-miR-1228-3p, miR-8063 is hsa-miR-8063, miR-8069 is hsa-miR-8069, miR-6875-5p is hsa-miR-6875-5p, miR-3185 is hsa-miR-3185, miR-4433b-3p is hsa-miR-4433b-3p, miR-6887-5p is hsa-miR-6887-5p, miR-128-1-5p is hsa-miR-128-1-5p, miR-6724-5p is hsa-miR-6724-5p, miR-1914-3p is hsa-miR-1914-3p, miR-1225-5p is hsa-miR-1225-5p, miR-4419b is hsa-miR-4419b, miR-7110-5p is hsa-miR-7110-5p, miR-187-5p is hsa-miR-187-5p, miR-3184-5p is hsa-miR-3184-5p, miR-204-3p is hsa-miR-204-3p, miR-5572 is hsa-miR-5572, miR-6729-5p is hsa-miR-6729-5p, miR-615-5p is hsa-miR-615-5p, miR-6749-5p is hsa-miR-6749-5p, miR-6515-3p is hsa-miR-6515-3p, miR-3937 is hsa-miR-3937, miR-6840-3p is hsa-miR-6840-3p, miR-6893-5p is hsa-miR-6893-5p, miR-4728-5p is hsa-miR-4728-5p, miR-6717-5p is hsa-miR-6717-5p, miR-7113-3p is hsa-miR-7113-3p, miR-4665-5p is hsa-miR-4665-5p, miR-642b-3p is hsa-miR-642b-3p, miR-7109-5p is hsa-miR-7109-5p, miR-6842-5p is hsa-miR-6842-5p, miR-4442 is hsa-miR-4442, miR-4433-3p is hsa-miR-4433-3p, miR-4707-5p is hsa-miR-4707-5p, miR-6126 is hsa-miR-6126, miR-4449 is hsa-miR-4449, miR-4706 is hsa-miR-4706, miR-1913 is hsa-miR-1913, miR-602 is hsa-miR-602, miR-939-5p is hsa-miR-939-5p, miR-4695-5p is hsa-miR-4695-5p, miR-711 is hsa-miR-711, miR-6816-5p is hsa-miR-6816-5p, miR-4632-5p is hsa-miR-4632-5p, miR-6721-5p is hsa-miR-6721-5p, miR-7847-3p is hsa-miR-7847-3p, miR-6132 is hsa-miR-6132, miR-887-3p is hsa-miR-887-3p, miR-3679-3p is hsa-miR-3679-3p, miR-6784-5p is hsa-miR-6784-5p, miR-1249 is hsa-miR-1249, miR-937-5p is hsa-miR-937-5p, miR-5195-3p is hsa-miR-5195-3p, miR-6732-5p is hsa-miR-6732-5p, miR-4417 is hsa-miR-4417, miR-4281 is hsa-miR-4281, miR-4734 is hsa-miR-4734, miR-6766-3p is hsa-miR-6766-3p, miR-663a is hsa-miR-663a, miR-4513 is hsa-miR-4513, miR-6781-5p is hsa-miR-6781-5p, miR-1227-5p is hsa-miR-1227-5p, miR-6845-5p is hsa-miR-6845-5p, miR-6798-5p is hsa-miR-6798-5p, miR-3620-5p is hsa-miR-3620-5p, miR-1915-5p is hsa-miR-1915-5p, miR-4294 is hsa-miR-4294, miR-642a-3p is hsa-miR-642a-3p, miR-371a-5p is hsa-miR-371a-5p, miR-940 is hsa-miR-940, miR-4450 is hsa-miR-4450, miR-4723-5p is hsa-miR-4723-5p, miR-1469 is hsa-miR-1469, miR-6861-5p is hsa-miR-6861-5p, miR-7975 is hsa-miR-7975, miR-6879-5p is hsa-miR-6879-5p, miR-6802-5p is hsa-miR-6802-5p, miR-1268b is hsa-miR-1268b, miR-663b is hsa-miR-663b, miR-125a-3p is hsa-miR-125a-3p, miR-2861 is hsa-miR-2861, miR-6088 is hsa-miR-6088, miR-4758-5p is hsa-miR-4758-5p, miR-296-3p is hsa-miR-296-3p, miR-6738-5p is hsa-miR-6738-5p, miR-671-5p is hsa-miR-671-5p, miR-4454 is hsa-miR-4454, miR-4516 is hsa-miR-4516, miR-7845-5p is hsa-miR-7845-5p, miR-4741 is hsa-miR-4741, miR-92b-5p is hsa-miR-92b-5p, miR-6795-5p is hsa-miR-6795-5p, miR-6805-3p is hsa-miR-6805-3p, miR-4725-3p is hsa-miR-4725-3p, miR-6782-5p is hsa-miR-6782-5p, miR-4688 is hsa-miR-4688, miR-6850-5p is hsa-miR-6850-5p, miR-6777-5p is hsa-miR-6777-5p, miR-6785-5p is hsa-miR-6785-5p, miR-7106-5p is hsa-miR-7106-5p, miR-3663-3p is hsa-miR-3663-3p, miR-6131 is hsa-miR-6131, miR-1915-3p is hsa-miR-1915-3p, miR-4532 is hsa-miR-4532, miR-6820-5p is hsa-miR-6820-5p, miR-4689 is hsa-miR-

4689, miR-4638-5p is hsa-miR-4638-5p, miR-3656 is hsa-miR-3656, miR-3621 is hsa-miR-3621, miR-6769b-5p is hsa-miR-6769b-5p, miR-149-3p is hsa-miR-149-3p, miR-23b-3p is hsa-miR-23b-3p, miR-3135b is hsa-miR-3135b, miR-6848-5p is hsa-miR-6848-5p, miR-6769a-5p is hsa-miR-6769a-5p, miR-4327 is hsa-miR-4327, miR-6765-3p is hsa-miR-6765-3p, miR-6716-5p is hsa-miR-6716-5p, miR-6877-5p is hsa-miR-6877-5p, miR-6727-5p is hsa-miR-6727-5p, miR-4534 is hsa-miR-4534, miR-614 is hsa-miR-614, miR-1202 is hsa-miR-1202, miR-575 is hsa-miR-575, miR-6870-5p is hsa-miR-6870-5p, miR-6722-3p is hsa-miR-6722-3p, miR-7977 is hsa-miR-7977, miR-4649-5p is hsa-miR-4649-5p, miR-4675 is hsa-miR-4675, miR-6075 is hsa-miR-6075, miR-6779-5p is hsa-miR-6779-5p, miR-4271 is hsa-miR-4271, miR-3196 is hsa-miR-3196, miR-6803-5p is hsa-miR-6803-5p, miR-6789-5p is hsa-miR-6789-5p, miR-4648 is hsa-miR-4648, miR-4508 is hsa-miR-4508, miR-4749-5p is hsa-miR-4749-5p, miR-4505 is hsa-miR-4505, miR-5698 is hsa-miR-5698, miR-1199-5p is hsa-miR-1199-5p, miR-4763-3p is hsa-miR-4763-3p, miR-6836-3p is hsa-miR-6836-3p, miR-3195 is hsa-miR-3195, miR-718 is hsa-miR-718, miR-3178 is hsa-miR-3178, miR-638 is hsa-miR-638, miR-4497 is hsa-miR-4497, miR-6085 is hsa-miR-6085, miR-6752-5p is hsa-miR-6752-5p, and miR-135a-3p is hsa-miR-135a-3p.

(13) The device according to (11) or (12), wherein the nucleic acid is a polynucleotide selected from the group consisting of the following polynucleotides (a) to (e):

(a) a polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 1 to 171 and 606 to 614 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,
(b) a polynucleotide comprising a nucleotide sequence represented by any of SEQ ID NOs: 1 to 171 and 606 to 614,
(c) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 1 to 171 and 606 to 614 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,
(d) a polynucleotide comprising a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 1 to 171 and 606 to 614 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, and
(e) a polynucleotide hybridizing under stringent conditions to any of the polynucleotides (a) to (d).

(14) The device according to any of (11) to (13), wherein the device further comprises a nucleic acid capable of specifically binding to at least one or more polynucleotide(s) selected from the group consisting of other colorectal cancer markers miR-1231, miR-1233-5p, miR-150-3p, miR-1225-3p, miR-92a-2-5p, miR-423-5p, miR-1268a, miR-128-2-5p and miR-24-3p.

(15) The device according to (14), wherein miR-1231 is hsa-miR-1231, miR-1233-5p is hsa-miR-1233-5p, miR-150-3p is hsa-miR-150-3p, miR-1225-3p is hsa-miR-1225-3p, miR-92a-2-5p is hsa-miR-92a-2-5p, miR-423-5p is hsa-miR-423-5p, miR-1268a is hsa-miR-1268a, miR-128-2-5p is hsa-miR-128-2-5p, and miR-24-3p is hsa-miR-24-3p.

(16) The device according to (14) or (15), wherein the nucleic acid is a polynucleotide selected from the group consisting of the following polynucleotides (f) to (j):

(f) a polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 172 to 180 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,
(g) a polynucleotide comprising a nucleotide sequence represented by any of SEQ ID NOs: 172 to 180,
(h) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 172 to 180 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,
(i) a polynucleotide comprising a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 172 to 180 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, and
(j) a polynucleotide hybridizing under stringent conditions to any of the polynucleotides (f) to (i).

(17) The device according to any of (11) to (16), wherein the device further comprises a nucleic acid capable of specifically binding to at least one or more polynucleotide(s) selected from the group consisting of other colorectal cancer markers miR-4697-5p, miR-3197, miR-675-5p, miR-4486, miR-7107-5p, miR-23a-3p, miR-4667-5p, miR-451a, miR-3940-5p, miR-8059, miR-6813-5p, miR-4492, miR-4476, and miR-6090.

(18) The device according to (17), wherein miR-4697-5p is hsa-miR-4697-5p, miR-3197 is hsa-miR-3197, miR-675-5p is hsa-miR-675-5p, miR-4486 is hsa-miR-4486, miR-7107-5p is hsa-miR-7107-5p, miR-23a-3p is hsa-miR-23a-3p, miR-4667-5p is hsa-miR-4667-5p, miR-451a is hsa-miR-451a, miR-3940-5p is hsa-miR-3940-5p, miR-8059 is hsa-miR-8059, miR-6813-5p is hsa-miR-6813-5p, miR-4492 is hsa-miR-4492, miR-4476 is hsa-miR-4476, and miR-6090 is hsa-miR-6090.

(19) The device according to (17) or (18), wherein the nucleic acid is a polynucleotide selected from the group consisting of the following polynucleotides (k) to (o):

(k) a polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 181 to 194 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,

(l) a polynucleotide comprising a nucleotide sequence represented by any of SEQ ID NOs: 181 to 194,

(m) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 181 to 194 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,

(n) a polynucleotide comprising a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 181 to 194 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, and

(o) a polynucleotide hybridizing under stringent conditions to any of the polynucleotides (k) to (n).

(20) The device according to any one of (11) to (19), wherein the device is a device for measurement by a hybridization technique.

(21) The device according to (20), wherein the hybridization technique is a nucleic acid array technique.

(22) The device according to any one of (11) to (21), wherein the device comprises at least two or more nucleic acids capable of specifically binding to at least two or more polynucleotides, respectively, selected from all of the colorectal cancer markers according to (11) or (12).

(23) A method for detecting colorectal cancer, comprising measuring an expression level of a target nucleic acid in a sample from a subject using a kit according to any one of (1) to (10) or a device according to any one of (11) to (22), and evaluating *in vitro* whether or not the subject has colorectal cancer using both of the measured expression level and a control expression level in a sample from a healthy subject measured in the same way.

(24) The method according to (23), wherein the subject is a human.

(25) The method according to (23) or (24), wherein the sample is blood, serum, or plasma.

<Definition of Term>

[0022] The terms used herein are defined as follows.

[0023] Abbreviations or terms such as nucleotide, polynucleotide, DNA, and RNA abide by "Guidelines for the preparation of specification which contain nucleotide and/or amino acid sequences" (edited by Japan Patent Office) and common use in the art.

[0024] The term "polynucleotide" used herein is used for a nucleic acid including any of RNA, DNA, and RNA/DNA (chimera). The DNA includes any of cDNA, genomic DNA, and synthetic DNA. The RNA includes any of total RNA, mRNA, rRNA, miRNA, siRNA, snoRNA, snRNA, non-coding RNA and synthetic RNA. Here, the "synthetic DNA" and the "synthetic RNA" refer to DNA and RNA artificially prepared using, for example, an automatic nucleic acid synthesizer, on the basis of predetermined nucleotide sequences (which may be any of natural and non-natural sequences). The "non-natural sequence" is intended to be used in a broad sense and includes, for example, a sequence comprising substitution, deletion, insertion, and/or addition of one or more nucleotide(s) (i.e., a variant sequence) and a sequence comprising one or more modified nucleotide(s) (i.e., a modified sequence), which are different from the natural sequence. Here, the term "polynucleotide" is used interchangeably with the term "nucleic acid".

[0025] The term "fragment" used herein is a polynucleotide having a nucleotide sequence that consists of a consecutive portion of a polynucleotide and desirably has a length of 15 or more nucleotides, preferably 17 or more nucleotides, more preferably 19 or more nucleotides.

[0026] The term "gene" used herein is intended to include not only RNA and double-stranded DNA but each single-stranded DNA such as a plus strand (or a sense strand) or a complementary strand (or an antisense strand) that constitutes a duplex. The gene is not particularly limited by its length.

[0027] Thus, the "gene" used herein includes any of double-stranded DNA including human genomic DNA, single-stranded DNA (plus strand) including cDNA, single-stranded DNA having a sequence complementary to the plus strand (complementary strand), microRNA (miRNA), and their fragments, and transcripts, unless otherwise specified. The

"gene" includes not only a "gene" represented by a particular nucleotide sequence (or SEQ ID NO) but "nucleic acids" encoding RNAs having biological functions equivalent to RNA encoded by the gene, for example, a congener (i.e., a homolog or an ortholog), a variant (e.g., a genetic polymorph), and a derivative. Specific examples of such a "nucleic acid" encoding a congener, a variant, or a derivative can include a "nucleic acid" having a nucleotide sequence hybridizing under stringent conditions described later to a complementary sequence of a nucleotide sequence represented by any of SEQ ID NOs: 1 to 635 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t. The "gene" is not particularly limited by its functional region and can contain, for example, an expression control region, a coding region, an exon, or an intron. The "gene" may be contained in a cell or may exist alone after being released into the outside of a cell. Alternatively, the "gene" may be in a state enclosed in a vesicle called exosome.

[0028] The term "exosome" used herein is a vesicle that is encapsulated by a lipid bilayer and secreted from a cell. The exosome is derived from a multivesicular endosome and may incorporate a biomaterial such as a "gene" (e.g., RNA or DNA) or a protein when released into an extracellular environment. The exosome is known to be contained in a body fluid such as blood, serum, plasma, or lymph.

[0029] The term "transcript" used herein refers to RNA synthesized with the DNA sequence of a gene as a template. RNA polymerase binds to a site called promoter which is located upstream of the gene and adds ribonucleotides complementary to the nucleotide sequence of the DNA to the 3' end to synthesize RNA. This RNA contains not only the gene itself but the whole sequence from a transcription initiation site to the end of a polyA sequence, including an expression regulatory region, a coding region, an exon, or an intron.

[0030] The term "microRNA (miRNA)" used herein is intended to mean a 15- to 25-nucleotide non-coding RNA that is transcribed as an RNA precursor having a hairpin-like structure, cleaved by a dsRNA-cleaving enzyme having RNase III cleavage activity, and integrated into a protein complex called RISC, and is involved in the suppression of translation of mRNA, unless otherwise specified. The term "miRNA" used herein includes not only a "miRNA" represented by a particular nucleotide sequence (or SEQ ID NO) but a precursor of the "miRNA" (pre-miRNA or pri-miRNA), and miRNAs having biological functions equivalent thereto, for example, a congener (i.e., a homolog or an ortholog), a variant (e.g., a genetic polymorph), and a derivative. Such a precursor, a congener, a variant, or a derivative can be specifically identified using miRBase Release 20 (http://www.mirbase.org/), and examples thereof can include a "miRNA" having a nucleotide sequence hybridizing under stringent conditions described later to a complementary sequence of any particular nucleotide sequence represented by any of SEQ ID NOs: 1 to 635. The term "miRNA" used herein may be a gene product of a miR gene. Such a gene product includes a mature miRNA (e.g., a 15- to 25-nucleotide or 19- to 25-nucleotide non-coding RNA involved in the suppression of translation of mRNA as described above) or a miRNA precursor (e.g., pre-miRNA or pri-miRNA as described above).

[0031] The term "probe" used herein includes a polynucleotide that is used for specifically detecting RNA resulting from the expression of a gene or a polynucleotide derived from the RNA, and/or a polynucleotide complementary thereto.

[0032] The term "primer" used herein includes a polynucleotide that specifically recognizes and amplifies RNA resulting from the expression of a gene or a polynucleotide derived from the RNA, and/or a polynucleotide complementary thereto.

[0033] In this context, the complementary polynucleotide (complementary strand or reverse strand) means a polynucleotide in a complementary base relationship of A:T (U) and G:C base pairs with the full-length sequence of a polynucleotide consisting of a nucleotide sequence defined by any of SEQ ID NOs: 1 to 635 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, or a partial sequence thereof (here, this full-length or partial sequence is referred to as a plus strand for the sake of convenience). However, such a complementary strand is not limited to a sequence completely complementary to the nucleotide sequence of the target plus strand and may have a complementary relationship to an extent that permits hybridization under stringent conditions to the target plus strand.

[0034] The term "stringent conditions" used herein refers to conditions under which a nucleic acid probe hybridizes to its target sequence to a larger extent (e.g., a measurement value equal to or larger than a mean of background measurement values + a standard deviation of the background measurement values x 2) than that for other sequences. The stringent conditions are dependent on a sequence and differ depending on an environment where hybridization is performed. A target sequence complementary 100% to the nucleic acid probe can be identified by controlling the stringency of hybridization and/or washing conditions. Specific examples of the "stringent conditions" will be mentioned later.

[0035] The term "Tm value" used herein means a temperature at which the double-stranded moiety of a polynucleotide is denatured into single strands so that the double strands and the single strands exist at a ratio of 1:1.

[0036] The term "variant" used herein means, in the case of a nucleic acid, a natural variant attributed to polymorphism, mutation, or the like; a variant that contains the deletion, substitution, addition, or insertion of 1 or 2 or more nucleotides in a nucleotide sequence represented by any of SEQ ID NOs: 1 to 194 and 606 to 614 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, or a partial sequence thereof; a variant that exhibits % identity of approximately 90% or higher, approximately 95% or higher, approximately 97% or higher, approximately 98% or higher, approximately 99% or higher to each of these nucleotide sequences or the partial sequence thereof; or a nucleic acid hybridizing under the stringent conditions defined above to a polynucleotide or an oligonucleotide comprising each of these nucleotide sequences or the partial sequence thereof.

[0037] The term "several" used herein means an integer of approximately 10, 9, 8, 7, 6, 5, 4, 3, or 2.

[0038] The variant used herein can be prepared by use of a well-known technique such as site-directed mutagenesis or PCR-based mutagenesis.

[0039] The term "percent (%) identity" used herein can be determined with or without an introduced gap, using a protein or gene search system based on BLAST or FASTA described above (Zheng Zhang et al., 2000, J. Comput. Biol., Vol. 7, p. 203-214; Altschul, S.F. et al., 1990, Journal of Molecular Biology, Vol. 215, p. 403-410; and Pearson, W.R. et al., 1988, Proc. Natl. Acad. Sci. U. S. A., Vol. 85, p. 2444-2448).

[0040] The term "derivative" used herein is meant to include a modified nucleic acid, for example, a derivative that is labeled with a fluorophore or the like, a derivative containing a modified nucleotide (e.g., a nucleotide containing a group such as halogen, alkyl such as methyl, alkoxy such as methoxy, thio, or carboxymethyl, and a nucleotide that has undergone base rearrangement, double bond saturation, deamination, replacement of an oxygen molecule with a sulfur atom, etc.), PNA (peptide nucleic acid; Nielsen, P.E. et al., 1991, Science, Vol. 254, p. 1497-500), and LNA (locked nucleic acid; Obika, S. et al., 1998, Tetrahedron Lett., Vol. 39, p. 5401-5404) without any limitation.

[0041] As used herein, the "nucleic acid" capable of specifically binding to a polynucleotide selected from the colorectal cancer marker miRNAs described above is a synthesized or prepared nucleic acid and specifically includes a "nucleic acid probe" or a "primer". The "nucleic acid" is utilized directly or indirectly for detecting the presence or absence of colorectal cancer in a subject, for diagnosing the presence or absence of colorectal cancer, for diagnosing the severity of colorectal cancer, the presence or absence of amelioration or the degree of amelioration of colorectal cancer, or the sensitivity to treatment for colorectal cancer, or for screening for a candidate substance useful in the prevention, amelioration, or treatment of colorectal cancer. The "nucleic acid" includes a nucleotide, an oligonucleotide, and a polynucleotide capable of specifically recognizing and binding to a transcript represented by any of SEQ ID NOs: 1 to 635 or a synthetic cDNA nucleic acid thereof *in vivo*, particularly, in a sample such as a body fluid (e.g., blood or urine), in relation to the development of colorectal cancer. The nucleotide, the oligonucleotide, and the polynucleotide can be effectively used as probes for detecting the aforementioned gene expressed *in vivo*, in tissues, in cells, or the like on the basis of the properties described above, or as primers for amplifying the aforementioned gene expressed *in vivo.*

[0042] The term "capable of specifically binding" used herein means that the nucleic acid probe or the primer used in the present invention binds to a particular target nucleic acid and cannot substantially bind to other nucleic acids.

[0043] The term "detection" used herein is interchangeable with the term "examination", "measurement", "detection", or "decision support". As used herein, the term "evaluation" is meant to include diagnosing or evaluation-supporting on the basis of examination results or measurement results.

[0044] The term "subject" used herein means a mammal such as a primate including a human and a chimpanzee, a pet animal including a dog and a cat, a livestock animal including cattle, a horse, sheep, and a goat, and a rodent including a mouse and a rat. The term "healthy subject" also means such a mammal without the cancer to be detected.

[0045] The term "P" or "P value" used herein refers to a probability at which a more extreme statistic than that is actually calculated from data under null hypothesis is observed in a statistical test. Thus, smaller "P" or "P value" means more significant difference between subjects to be compared.

[0046] The term "sensitivity" used herein means a value of (the number of true positives) / (the number of true positives + the number of false negatives). High sensitivity allows colorectal cancer to be detected early, leading to the complete resection of cancer sites and reduction in the rate of recurrence.

[0047] The term "specificity" used herein means a value of (the number of true negatives) / (the number of true negatives + the number of false positives). High specificity prevents needless extra examination for healthy subjects misjudged as being colorectal cancer patients, leading to reduction in burden on patients and reduction in medical expense.

[0048] The term "accuracy" used herein means a value of (the number of true positives + the number of true negatives) / (the total number of cases). The accuracy indicates the ratio of samples that correctly identified in discriminant results to all samples, and serves as a primary index for evaluating detection performance.

[0049] As used herein, the "sample" that is subject to determination, detection, or diagnosis refers to a tissue and a biological material in which the expression of the gene of the present invention varies as colorectal cancer develops, colorectal cancer progresses, and therapeutic effects on colorectal cancer are exerted. Specifically, the "sample" refers to a large intestine tissue, a vascular channel around the large intestine, lymph node, and organ, an organ suspected of having metastasis, the skin, a body fluid such as blood, urine, saliva, sweat, or tissue exudates, serum or plasma prepared from blood, feces, hair, and the like. The "sample" further refers to a biological sample extracted therefrom, specifically, a gene such as RNA or miRNA.

[0050] The term "hsa-miR-6726-5p gene" or "hsa-miR-6726-5p" used herein includes the hsa-miR-6726-5p gene (miRBase Accession No. MIMAT0027353) described in SEQ ID NO: 1, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6726-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6726" (miRBase Accession No. MI0022571, SEQ ID NO: 195) having a hairpin-like structure is known as a precursor of "hsa-miR-6726-5p".

[0051] The term "hsa-miR-4257 gene" or "hsa-miR-4257" used herein includes the hsa-miR-4257 gene (miRBase

Accession No. MIMAT0016878) described in SEQ ID NO: 2, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4257 gene can be obtained by a method described in Goff LA et al., 2009, PLoS One, Vol. 4, e7192. Also, "hsa-mir-4257" (miRBase Accession No. MI0015856, SEQ ID NO: 196) having a hairpin-like structure is known as a precursor of "hsa-miR-4257".

[0052] The term "hsa-miR-6787-5p gene" or "hsa-miR-6787-5p" used herein includes the hsa-miR-6787-5p gene (miRBase Accession No. MIMAT0027474) described in SEQ ID NO: 3, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6787-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6787" (miRBase Accession No. MI0022632, SEQ ID NO: 197) having a hairpin-like structure is known as a precursor of "hsa-miR-6787-5p".

[0053] The term "hsa-miR-6780b-5p gene" or "hsa-miR-6780b-5p" used herein includes the hsa-miR-6780b-5p gene (miRBase Accession No. MIMAT0027572) described in SEQ ID NO: 4, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6780b-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6780b" (miRBase Accession No. MI0022681, SEQ ID NO: 198) having a hairpin-like structure is known as a precursor of "hsa-miR-6780b-5p".

[0054] The term "hsa-miR-3131 gene" or "hsa-miR-3131" used herein includes the hsa-miR-3131 gene (miRBase Accession No. MIMAT0014996) described in SEQ ID NO: 5, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3131 gene can be obtained by a method described in Stark MS et al., 2010, PLoS One, Vol. 5, e9685. Also, "hsa-mir-3131" (miRBase Accession No. MI0014151, SEQ ID NO: 199) having a hairpin-like structure is known as a precursor of "hsa-miR-3131".

[0055] The term "hsa-miR-7108-5p gene" or "hsa-miR-7108-5p" used herein includes the hsa-miR-7108-5p gene (miRBase Accession No. MIMAT0028113) described in SEQ ID NO: 6, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-7108-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-7108" (miRBase Accession No. MI0022959, SEQ ID NO: 200) having a hairpin-like structure is known as a precursor of "hsa-miR-7108-5p".

[0056] The term "hsa-miR-1343-3p gene" or "hsa-miR-1343-3p" used herein includes the hsa-miR-1343-3p gene (miRBase Accession No. MIMAT0019776) described in SEQ ID NO: 7, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1343-3p gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-1343" (miRBase Accession No. MI0017320, SEQ ID NO: 201) having a hairpin-like structure is known as a precursor of "hsa-miR-1343-3p".

[0057] The term "hsa-miR-1247-3p gene" or "hsa-miR-1247-3p" used herein includes the hsa-miR-1247-3p gene (miRBase Accession No. MIMAT0022721) described in SEQ ID NO: 8, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1247-3p gene can be obtained by a method described in Morin RD et al., 2008, Genome Res, Vol. 18, p. 610-621. Also, "hsa-mir-1247" (miRBase Accession No. MI0006382, SEQ ID NO: 202) having a hairpin-like structure is known as a precursor of "hsa-miR-1247-3p".

[0058] The term "hsa-miR-4651 gene" or "hsa-miR-4651" used herein includes the hsa-miR-4651 gene (miRBase Accession No. MIMAT0019715) described in SEQ ID NO: 9, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4651 gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4651" (miRBase Accession No. MI0017279, SEQ ID NO: 203) having a hairpin-like structure is known as a precursor of "hsa-miR-4651".

[0059] The term "hsa-miR-6757-5p gene" or "hsa-miR-6757-5p" used herein includes the hsa-miR-6757-5p gene (miRBase Accession No. MIMAT0027414) described in SEQ ID NO: 10, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6757-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6757" (miRBase Accession No. MI0022602, SEQ ID NO: 204) having a hairpin-like structure is known as a precursor of "hsa-miR-6757-5p".

[0060] The term "hsa-miR-3679-5p gene" or "hsa-miR-3679-5p" used herein includes the hsa-miR-3679-5p gene (miRBase Accession No. MIMAT0018104) described in SEQ ID NO: 11, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3679-5p gene can be obtained by a method described in Creighton CJ et al., 2010, PLoS One, Vol. 5, e9637. Also, "hsa-mir-3679" (miRBase Accession No. MI0016080, SEQ ID NO: 205) having a hairpin-like structure is known as a precursor of "hsa-miR-3679-Sp".

[0061] The term "hsa-miR-7641 gene" or "hsa-miR-7641" used herein includes the hsa-miR-7641 gene (miRBase Accession No. MIMAT0029782) described in SEQ ID NO: 12, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-7641 gene can be obtained by a method described in Yoo JK et al., 2013, Arch Pharm Res, Vol. 36, p. 353-358. Also, "hsa-mir-7641-1" and "hsa-mir-7641-2" (miRBase Accession Nos. MI0024975 and MI0024976, SEQ ID NOs: 206 and 207) having a hairpin-like structure are known as precursors of "hsa-miR-7641".

[0062] The term "hsa-miR-6746-5p gene" or "hsa-miR-6746-5p" used herein includes the hsa-miR-6746-5p gene (miRBase Accession No. MIMAT0027392) described in SEQ ID NO: 13, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6746-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6746" (miRBase Accession No. MI0022591, SEQ ID NO: 208)

having a hairpin-like structure is known as a precursor of "hsa-miR-6746-5p".

[0063] The term "hsa-miR-8072 gene" or "hsa-miR-8072" used herein includes the hsa-miR-8072 gene (miRBase Accession No. MIMAT0030999) described in SEQ ID NO: 14, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-8072 gene can be obtained by a method described in Wang HJ et al., 2013, Shock, Vol. 39, p. 480-487. Also, "hsa-mir-8072" (miRBase Accession No. MI0025908, SEQ ID NO: 209) having a hairpin-like structure is known as a precursor of "hsa-miR-8072".

[0064] The term "hsa-miR-6741-5p gene" or "hsa-miR-6741-5p" used herein includes the hsa-miR-6741-5p gene (miRBase Accession No. MIMAT0027383) described in SEQ ID NO: 15, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6741-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6741" (miRBase Accession No. MI0022586, SEQ ID NO: 210) having a hairpin-like structure is known as a precursor of "hsa-miR-6741-5p".

[0065] The term "hsa-miR-1908-5p gene" or "hsa-miR-1908-5p" used herein includes the hsa-miR-1908-5p gene (miRBase Accession No. MIMAT0007881) described in SEQ ID NO: 16, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1908-5p gene can be obtained by a method described in Bar M et al., 2008, Stem Cells, Vol. 26, p. 2496-2505. Also, "hsa-mir-1908" (miRBase Accession No. MI0008329, SEQ ID NO: 211) having a hairpin-like structure is known as a precursor of "hsa-miR-1908-5p".

[0066] The term "hsa-miR-6857-5p gene" or "hsa-miR-6857-5p" used herein includes the hsa-miR-6857-5p gene (miRBase Accession No. MIMAT0027614) described in SEQ ID NO: 17, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6857-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6857" (miRBase Accession No. MI0022703, SEQ ID NO: 212) having a hairpin-like structure is known as a precursor of "hsa-miR-6857-5p".

[0067] The term "hsa-miR-4746-3p gene" or "hsa-miR-4746-3p" used herein includes the hsa-miR-4746-3p gene (miRBase Accession No. MIMAT0019881) described in SEQ ID NO: 18, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4746-3p gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4746" (miRBase Accession No. MI0017385, SEQ ID NO: 213) having a hairpin-like structure is known as a precursor of "hsa-miR-4746-3p".

[0068] The term "hsa-miR-744-5p gene" or "hsa-miR-744-5p" used herein includes the hsa-miR-744-5p gene (miRBase Accession No. MIMAT0004945) described in SEQ ID NO: 19, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-744-5p gene can be obtained by a method described in Berezikov E et al., 2006, Genome Res, Vol. 16, p. 1289-1298. Also, "hsa-mir-744" (miRBase Accession No. MI0005559, SEQ ID NO: 214) having a hairpin-like structure is known as a precursor of "hsa-miR-744-5p".

[0069] The term "hsa-miR-4792 gene" or "hsa-miR-4792" used herein includes the hsa-miR-4792 gene (miRBase Accession No. MIMAT0019964) described in SEQ ID NO: 20, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4792 gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4792" (miRBase Accession No. MI0017439, SEQ ID NO: 215) having a hairpin-like structure is known as a precursor of "hsa-miR-4792".

[0070] The term "hsa-miR-564 gene" or "hsa-miR-564" used herein includes the hsa-miR-564 gene (miRBase Accession No. MIMAT0003228) described in SEQ ID NO: 21, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-564 gene can be obtained by a method described in Cummins JM et al., 2006, Proc Natl Acad Sci USA, Vol. 103, p. 3687-3692. Also, "hsa-mir-564" (miRBase Accession No. MI0003570, SEQ ID NO: 216) having a hairpin-like structure is known as a precursor of "hsa-miR-564".

[0071] The term "hsa-miR-6791-5p gene" or "hsa-miR-6791-5p" used herein includes the hsa-miR-6791-5p gene (miRBase Accession No. MIMAT0027482) described in SEQ ID NO: 22, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6791-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6791" (miRBase Accession No. MI0022636, SEQ ID NO: 217) having a hairpin-like structure is known as a precursor of "hsa-miR-6791-5p".

[0072] The term "hsa-miR-6825-5p gene" or "hsa-miR-6825-5p" used herein includes the hsa-miR-6825-5p gene (miRBase Accession No. MIMAT0027550) described in SEQ ID NO: 23, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6825-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6825" (miRBase Accession No. MI0022670, SEQ ID NO: 218) having a hairpin-like structure is known as a precursor of "hsa-miR-6825-5p".

[0073] The term "hsa-miR-6826-5p gene" or "hsa-miR-6826-5p" used herein includes the hsa-miR-6826-5p gene (miRBase Accession No. MIMAT0027552) described in SEQ ID NO: 24, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6826-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6826" (miRBase Accession No. MI0022671, SEQ ID NO: 219) having a hairpin-like structure is known as a precursor of "hsa-miR-6826-5p".

[0074] The term "hsa-miR-4665-3p gene" or "hsa-miR-4665-3p" used herein includes the hsa-miR-4665-3p gene (miRBase Accession No. MIMAT0019740) described in SEQ ID NO: 25, a homolog or an ortholog of a different organism

species, and the like. The hsa-miR-4665-3p gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4665" (miRBase Accession No. MI0017295, SEQ ID NO: 220) having a hairpin-like structure is known as a precursor of "hsa-miR-4665-3p".

[0075] The term "hsa-miR-4467 gene" or "hsa-miR-4467" used herein includes the hsa-miR-4467 gene (miRBase Accession No. MIMAT0018994) described in SEQ ID NO: 26, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4467 gene can be obtained by a method described in Jima DD et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4467" (miRBase Accession No. MI0016818, SEQ ID NO: 221) having a hairpin-like structure is known as a precursor of "hsa-miR-4467".

[0076] The term "hsa-miR-3188 gene" or "hsa-miR-3188" used herein includes the hsa-miR-3188 gene (miRBase Accession No. MIMAT0015070) described in SEQ ID NO: 27, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3188 gene can be obtained by a method described in Stark MS et al., 2010, PLoS One, Vol. 5, e9685. Also, "hsa-mir-3188" (miRBase Accession No. MI0014232, SEQ ID NO: 222) having a hairpin-like structure is known as a precursor of "hsa-miR-3188".

[0077] The term "hsa-miR-6125 gene" or "hsa-miR-6125" used herein includes the hsa-miR-6125 gene (miRBase Accession No. MIMAT0024598) described in SEQ ID NO: 28, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6125 gene can be obtained by a method described in Smith JL et al., 2012, J Virol, Vol. 86, p. 5278-5287. Also, "hsa-mir-6125" (miRBase Accession No. MI0021259, SEQ ID NO: 223) having a hairpin-like structure is known as a precursor of "hsa-miR-6125".

[0078] The term "hsa-miR-6756-5p gene" or "hsa-miR-6756-5p" used herein includes the hsa-miR-6756-5p gene (miRBase Accession No. MIMAT0027412) described in SEQ ID NO: 29, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6756-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6756" (miRBase Accession No. MI0022601, SEQ ID NO: 224) having a hairpin-like structure is known as a precursor of "hsa-miR-6756-5p".

[0079] The term "hsa-miR-1228-3p gene" or "hsa-miR-1228-3p" used herein includes the hsa-miR-1228-3p gene (miRBase Accession No. MIMAT0005583) described in SEQ ID NO: 30, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1228-3p gene can be obtained by a method described in Berezikov E et al., 2007, Mol Cell, Vol. 28, p. 328-336. Also, "hsa-mir-1228" (miRBase Accession No. MI0006318, SEQ ID NO: 225) having a hairpin-like structure is known as a precursor of "hsa-miR-1228-3p".

[0080] The term "hsa-miR-8063 gene" or "hsa-miR-8063" used herein includes the hsa-miR-8063 gene (miRBase Accession No. MIMAT0030990) described in SEQ ID NO: 31, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-8063 gene can be obtained by a method described in Wang HJ et al., 2013, Shock, Vol. 39, p. 480-487. Also, "hsa-mir-8063" (miRBase Accession No. MI0025899, SEQ ID NO: 226) having a hairpin-like structure is known as a precursor of "hsa-miR-8063".

[0081] The term "hsa-miR-8069 gene" or "hsa-miR-8069" used herein includes the hsa-miR-8069 gene (miRBase Accession No. MIMAT0030996) described in SEQ ID NO: 32, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-8069 gene can be obtained by a method described in Wang HJ et al., 2013, Shock, Vol. 39, p. 480-487. Also, "hsa-mir-8069" (miRBase Accession No. MI0025905, SEQ ID NO: 227) having a hairpin-like structure is known as a precursor of "hsa-miR-8069".

[0082] The term "hsa-miR-6875-5p gene" or "hsa-miR-6875-5p" used herein includes the hsa-miR-6875-5p gene (miRBase Accession No. MIMAT0027650) described in SEQ ID NO: 33, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6875-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6875" (miRBase Accession No. MI0022722, SEQ ID NO: 228) having a hairpin-like structure is known as a precursor of "hsa-miR-6875-5p".

[0083] The term "hsa-miR-3185 gene" or "hsa-miR-3185" used herein includes the hsa-miR-3185 gene (miRBase Accession No. MIMAT0015065) described in SEQ ID NO: 34, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3185 gene can be obtained by a method described in Stark MS et al., 2010, PLoS One, Vol. 5, e9685. Also, "hsa-mir-3185" (miRBase Accession No. MI0014227, SEQ ID NO: 229) having a hairpin-like structure is known as a precursor of "hsa-miR-3185".

[0084] The term "hsa-miR-4433b-3p gene" or "hsa-miR-4433b-3p" used herein includes the hsa-miR-4433b-3p gene (miRBase Accession No. MIMAT0030414) described in SEQ ID NO: 35, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4433b-3p gene can be obtained by a method described in Ple H et al., 2012, PLoS One, Vol. 7, e50746. Also, "hsa-mir-4433b" (miRBase Accession No. MI0025511, SEQ ID NO: 230) having a hairpin-like structure is known as a precursor of "hsa-miR-4433b-3p".

[0085] The term "hsa-miR-6887-5p gene" or "hsa-miR-6887-5p" used herein includes the hsa-miR-6887-5p gene (miRBase Accession No. MIMAT0027674) described in SEQ ID NO: 36, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6887-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6887" (miRBase Accession No. MI0022734, SEQ ID NO: 231) having a hairpin-like structure is known as a precursor of "hsa-miR-6887-5p".

[0086] The term "hsa-miR-128-1-5p gene" or "hsa-miR-128-1-5p" used herein includes the hsa-miR-128-1-5p gene (miRBase Accession No. MIMAT0026477) described in SEQ ID NO: 37, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-128-1-5p gene can be obtained by a method described in Lagos-Quintana M et al., 2002, Curr Biol, Vol. 12, p. 735-739. Also, "hsa-mir-128-1" (miRBase Accession No. MI0000447, SEQ ID NO: 232) having a hairpin-like structure is known as a precursor of "hsa-miR-128-1-5p".

[0087] The term "hsa-miR-6724-5p gene" or "hsa-miR-6724-5p" used herein includes the hsa-miR-6724-5p gene (miRBase Accession No. MIMAT0025856) described in SEQ ID NO: 38, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6724-5p gene can be obtained by a method described in Li Y et al., 2012, Gene, Vol. 497, p. 330-335. Also, "hsa-mir-6724" (miRBase Accession No. MI0022559, SEQ ID NO: 233) having a hairpin-like structure is known as a precursor of "hsa-miR-6724-5p".

[0088] The term "hsa-miR-1914-3p gene" or "hsa-miR-1914-3p" used herein includes the hsa-miR-1914-3p gene (miRBase Accession No. MIMAT0007890) described in SEQ ID NO: 39, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1914-3p gene can be obtained by a method described in Bar M et al., 2008, Stem Cells, Vol. 26, p. 2496-2505. Also, "hsa-mir-1914" (miRBase Accession No. MI0008335, SEQ ID NO: 234) having a hairpin-like structure is known as a precursor of "hsa-miR-1914-3p".

[0089] The term "hsa-miR-1225-5p gene" or "hsa-miR-1225-5p" used herein includes the hsa-miR-1225-5p gene (miRBase Accession No. MIMAT0005572) described in SEQ ID NO: 40, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1225-5p gene can be obtained by a method described in Berezikov E et al., 2007, Mol Cell, Vol. 28, p. 328-336. Also, "hsa-mir-1225" (miRBase Accession No. MI0006311, SEQ ID NO: 235) having a hairpin-like structure is known as a precursor of "hsa-miR-1225-5p".

[0090] The term "hsa-miR-4419b gene" or "hsa-miR-4419b" used herein includes the hsa-miR-4419b gene (miRBase Accession No. MIMAT0019034) described in SEQ ID NO: 41, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4419b gene can be obtained by a method described in Jima DD et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4419b" (miRBase Accession No. MI0016861, SEQ ID NO: 236) having a hairpin-like structure is known as a precursor of "hsa-miR-4419b".

[0091] The term "hsa-miR-7110-5p gene" or "hsa-miR-7110-5p" used herein includes the hsa-miR-7110-5p gene (miRBase Accession No. MIMAT0028117) described in SEQ ID NO: 42, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-7110-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-7110" (miRBase Accession No. MI0022961, SEQ ID NO: 237) having a hairpin-like structure is known as a precursor of "hsa-miR-7110-5p".

[0092] The term "hsa-miR-187-5p gene" or "hsa-miR-187-5p" used herein includes the hsa-miR-187-5p gene (miRBase Accession No. MIMAT0004561) described in SEQ ID NO: 43, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-187-5p gene can be obtained by a method described in Lim LP et al., 2003, Science, Vol. 299, p. 1540. Also, "hsa-mir-187" (miRBase Accession No. MI0000274, SEQ ID NO: 238) having a hairpin-like structure is known as a precursor of "hsa-miR-187-5p".

[0093] The term "hsa-miR-3184-5p gene" or "hsa-miR-3184-5p" used herein includes the hsa-miR-3184-5p gene (miRBase Accession No. MIMAT0015064) described in SEQ ID NO: 44, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3184-5p gene can be obtained by a method described in Stark MS et al., 2010, PLoS One, Vol. 5, e9685. Also, "hsa-mir-3184" (miRBase Accession No. MI0014226, SEQ ID NO: 239) having a hairpin-like structure is known as a precursor of "hsa-miR-3184-5p".

[0094] The term "hsa-miR-204-3p gene" or "hsa-miR-204-3p" used herein includes the hsa-miR-204-3p gene (miRBase Accession No. MIMAT0022693) described in SEQ ID NO: 45, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-204-3p gene can be obtained by a method described in Lim LP et al., 2003, Science, Vol. 299, p. 1540. Also, "hsa-mir-204" (miRBase Accession No. MI0000284, SEQ ID NO: 240) having a hairpin-like structure is known as a precursor of "hsa-miR-204-3p".

[0095] The term "hsa-miR-5572 gene" or "hsa-miR-5572" used herein includes the hsa-miR-5572 gene (miRBase Accession No. MIMAT0022260) described in SEQ ID NO: 46, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-5572 gene can be obtained by a method described in Tandon M et al., 2012, Oral Dis, Vol. 18, p. 127-131. Also, "hsa-mir-5572" (miRBase Accession No. MI0019117, SEQ ID NO: 241) having a hairpin-like structure is known as a precursor of "hsa-miR-5572".

[0096] The term "hsa-miR-6729-5p gene" or "hsa-miR-6729-5p" used herein includes the hsa-miR-6729-5p gene (miRBase Accession No. MIMAT0027359) described in SEQ ID NO: 47, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6729-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6729" (miRBase Accession No. MI0022574, SEQ ID NO: 242) having a hairpin-like structure is known as a precursor of "hsa-miR-6729-5p".

[0097] The term "hsa-miR-615-5p gene" or "hsa-miR-615-5p" used herein includes the hsa-miR-615-5p gene (miRBase Accession No. MIMAT0004804) described in SEQ ID NO: 48, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-615-5p gene can be obtained by a method described in Cummins JM et al., 2006,

Proc Natl Acad Sci USA, Vol. 103, p. 3687-3692. Also, "hsa-mir-615" (miRBase Accession No. MI0003628, SEQ ID NO: 243) having a hairpin-like structure is known as a precursor of "hsa-miR-615-5p".

[0098] The term "hsa-miR-6749-5p gene" or "hsa-miR-6749-5p" used herein includes the hsa-miR-6749-5p gene (miRBase Accession No. MIMAT0027398) described in SEQ ID NO: 49, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6749-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6749" (miRBase Accession No. MI0022594, SEQ ID NO: 244) having a hairpin-like structure is known as a precursor of "hsa-miR-6749-5p".

[0099] The term "hsa-miR-6515-3p gene" or "hsa-miR-6515-3p" used herein includes the hsa-miR-6515-3p gene (miRBase Accession No. MIMAT0025487) described in SEQ ID NO: 50, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6515-3p gene can be obtained by a method described in Joyce CE et al., 2011, Hum Mol Genet, Vol. 20, p. 4025-4040. Also, "hsa-mir-6515" (miRBase Accession No. MI0022227, SEQ ID NO: 245) having a hairpin-like structure is known as a precursor of "hsa-miR-6515-3p".

[0100] The term "hsa-miR-3937 gene" or "hsa-miR-3937" used herein includes the hsa-miR-3937 gene (miRBase Accession No. MIMAT0018352) described in SEQ ID NO: 51, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3937 gene can be obtained by a method described in Liao JY et al., 2010, PLoS One, Vol. 5, e10563. Also, "hsa-mir-3937" (miRBase Accession No. MI0016593, SEQ ID NO: 246) having a hairpin-like structure is known as a precursor of "hsa-miR-3937".

[0101] The term "hsa-miR-6840-3p gene" or "hsa-miR-6840-3p" used herein includes the hsa-miR-6840-3p gene (miRBase Accession No. MIMAT0027583) described in SEQ ID NO: 52, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6840-3p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6840" (miRBase Accession No. MI0022686, SEQ ID NO: 247) having a hairpin-like structure is known as a precursor of "hsa-miR-6840-3p".

[0102] The term "hsa-miR-6893-5p gene" or "hsa-miR-6893-5p" used herein includes the hsa-miR-6893-5p gene (miRBase Accession No. MIMAT0027686) described in SEQ ID NO: 53, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6893-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6893" (miRBase Accession No. MI0022740, SEQ ID NO: 248) having a hairpin-like structure is known as a precursor of "hsa-miR-6893-5p".

[0103] The term "hsa-miR-4728-5p gene" or "hsa-miR-4728-5p" used herein includes the hsa-miR-4728-5p gene (miRBase Accession No. MIMAT0019849) described in SEQ ID NO: 54, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4728-5p gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4728" (miRBase Accession No. MI0017365, SEQ ID NO: 249) having a hairpin-like structure is known as a precursor of "hsa-miR-4728-5p".

[0104] The term "hsa-miR-6717-5p gene" or "hsa-miR-6717-5p" used herein includes the hsa-miR-6717-5p gene (miRBase Accession No. MIMAT0025846) described in SEQ ID NO: 55, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6717-5p gene can be obtained by a method described in Li Y et al., 2012, Gene, Vol. 497, p. 330-335. Also, "hsa-mir-6717" (miRBase Accession No. MI0022551, SEQ ID NO: 250) having a hairpin-like structure is known as a precursor of "hsa-miR-6717-5p".

[0105] The term "hsa-miR-7113-3p gene" or "hsa-miR-7113-3p" used herein includes the hsa-miR-7113-3p gene (miRBase Accession No. MIMAT0028124) described in SEQ ID NO: 56, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-7113-3p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-7113" (miRBase Accession No. MI0022964, SEQ ID NO: 251) having a hairpin-like structure is known as a precursor of "hsa-miR-7113-3p".

[0106] The term "hsa-miR-4665-5p gene" or "hsa-miR-4665-5p" used herein includes the hsa-miR-4665-5p gene (miRBase Accession No. MIMAT0019739) described in SEQ ID NO: 57, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4665-5p gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4665" (miRBase Accession No. MI0017295, SEQ ID NO: 220) having a hairpin-like structure is known as a precursor of "hsa-miR-4665-5p".

[0107] The term "hsa-miR-642b-3p gene" or "hsa-miR-642b-3p" used herein includes the hsa-miR-642b-3p gene (miRBase Accession No. MIMAT0018444) described in SEQ ID NO: 58, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-642b-3p gene can be obtained by a method described in Witten D et al., 2010, BMC Biol, Vol. 8, p. 58. Also, "hsa-mir-642b" (miRBase Accession No. MI0016685, SEQ ID NO: 252) having a hairpin-like structure is known as a precursor of "hsa-miR-642b-3p".

[0108] The term "hsa-miR-7109-5p gene" or "hsa-miR-7109-5p" used herein includes the hsa-miR-7109-5p gene (miRBase Accession No. MIMAT0028115) described in SEQ ID NO: 59, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-7109-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-7109" (miRBase Accession No. MI0022960, SEQ ID NO: 253) having a hairpin-like structure is known as a precursor of "hsa-miR-7109-5p".

[0109] The term "hsa-miR-6842-5p gene" or "hsa-miR-6842-5p" used herein includes the hsa-miR-6842-5p gene

(miRBase Accession No. MIMAT0027586) described in SEQ ID NO: 60, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6842-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6842" (miRBase Accession No. MI0022688, SEQ ID NO: 254) having a hairpin-like structure is known as a precursor of "hsa-miR-6842-5p".

[0110] The term "hsa-miR-4442 gene" or "hsa-miR-4442" used herein includes the hsa-miR-4442 gene (miRBase Accession No. MIMAT0018960) described in SEQ ID NO: 61, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4442 gene can be obtained by a method described in Jima DD et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4442" (miRBase Accession No. MI0016785, SEQ ID NO: 255) having a hairpin-like structure is known as a precursor of "hsa-miR-4442".

[0111] The term "hsa-miR-4433-3p gene" or "hsa-miR-4433-3p" used herein includes the hsa-miR-4433-3p gene (miRBase Accession No. MIMAT0018949) described in SEQ ID NO: 62, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4433-3p gene can be obtained by a method described in Jima DD et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4433" (miRBase Accession No. MI0016773, SEQ ID NO: 256) having a hairpin-like structure is known as a precursor of "hsa-miR-4433-3p".

[0112] The term "hsa-miR-4707-5p gene" or "hsa-miR-4707-5p" used herein includes the hsa-miR-4707-5p gene (miRBase Accession No. MIMAT0019807) described in SEQ ID NO: 63, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4707-5p gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4707" (miRBase Accession No. MI0017340, SEQ ID NO: 257) having a hairpin-like structure is known as a precursor of "hsa-miR-4707-5p".

[0113] The term "hsa-miR-6126 gene" or "hsa-miR-6126" used herein includes the hsa-miR-6126 gene (miRBase Accession No. MIMAT0024599) described in SEQ ID NO: 64, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6126 gene can be obtained by a method described in Smith JL et al., 2012, J Virol, Vol. 86, p. 5278-5287. Also, "hsa-mir-6126" (miRBase Accession No. MI0021260, SEQ ID NO: 258) having a hairpin-like structure is known as a precursor of "hsa-miR-6126".

[0114] The term "hsa-miR-4449 gene" or "hsa-miR-4449" used herein includes the hsa-miR-4449 gene (miRBase Accession No. MIMAT0018968) described in SEQ ID NO: 65, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4449 gene can be obtained by a method described in Jima DD et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4449" (miRBase Accession No. MI0016792, SEQ ID NO: 259) having a hairpin-like structure is known as a precursor of "hsa-miR-4449".

[0115] The term "hsa-miR-4706 gene" or "hsa-miR-4706" used herein includes the hsa-miR-4706 gene (miRBase Accession No. MIMAT0019806) described in SEQ ID NO: 66, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4706 gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4706" (miRBase Accession No. MI0017339, SEQ ID NO: 260) having a hairpin-like structure is known as a precursor of "hsa-miR-4706".

[0116] The term "hsa-miR-1913 gene" or "hsa-miR-1913" used herein includes the hsa-miR-1913 gene (miRBase Accession No. MIMAT0007888) described in SEQ ID NO: 67, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1913 gene can be obtained by a method described in Bar M et al., 2008, Stem Cells, Vol. 26, p. 2496-2505. Also, "hsa-mir-1913" (miRBase Accession No. MI0008334, SEQ ID NO: 261) having a hairpin-like structure is known as a precursor of "hsa-miR-1913".

[0117] The term "hsa-miR-602 gene" or "hsa-miR-602" used herein includes the hsa-miR-602 gene (miRBase Accession No. MIMAT0003270) described in SEQ ID NO: 68, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-602 gene can be obtained by a method described in Cummins JM et al., 2006, Proc Natl Acad Sci USA, Vol. 103, p. 3687-3692. Also, "hsa-mir-602" (miRBase Accession No. MI0003615, SEQ ID NO: 262) having a hairpin-like structure is known as a precursor of "hsa-miR-602".

[0118] The term "hsa-miR-939-5p gene" or "hsa-miR-939-5p" used herein includes the hsa-miR-939-5p gene (miRBase Accession No. MIMAT0004982) described in SEQ ID NO: 69, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-939-5p gene can be obtained by a method described in Lui WO et al., 2007, Cancer Res, Vol. 67, p. 6031-6043. Also, "hsa-mir-939" (miRBase Accession No. MI0005761, SEQ ID NO: 263) having a hairpin-like structure is known as a precursor of "hsa-miR-939-5p".

[0119] The term "hsa-miR-4695-5p gene" or "hsa-miR-4695-5p" used herein includes the hsa-miR-4695-5p gene (miRBase Accession No. MIMAT0019788) described in SEQ ID NO: 70, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4695-5p gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4695" (miRBase Accession No. MI0017328, SEQ ID NO: 264) having a hairpin-like structure is known as a precursor of "hsa-miR-4695-5p".

[0120] The term "hsa-miR-711 gene" or "hsa-miR-711" used herein includes the hsa-miR-711 gene (miRBase Accession No. MIMAT0012734) described in SEQ ID NO: 71, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-711 gene can be obtained by a method described in Artzi S et al., 2008, BMC Bioinformatics, Vol. 9, p. 39. Also, "hsa-mir-711" (miRBase Accession No. MI0012488, SEQ ID NO: 265) having a hairpin-like structure is

known as a precursor of "hsa-miR-711".

[0121] The term "hsa-miR-6816-5p gene" or "hsa-miR-6816-5p" used herein includes the hsa-miR-6816-5p gene (miRBase Accession No. MIMAT0027532) described in SEQ ID NO: 72, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6816-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6816" (miRBase Accession No. MI0022661, SEQ ID NO: 266) having a hairpin-like structure is known as a precursor of "hsa-miR-6816-5p".

[0122] The term "hsa-miR-4632-5p gene" or "hsa-miR-4632-5p" used herein includes the hsa-miR-4632-5p gene (miRBase Accession No. MIMAT0022977) described in SEQ ID NO: 73, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4632-5p gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4632" (miRBase Accession No. MI0017259, SEQ ID NO: 267) having a hairpin-like structure is known as a precursor of "hsa-miR-4632-5p".

[0123] The term "hsa-miR-6721-5p gene" or "hsa-miR-6721-5p" used herein includes the hsa-miR-6721-5p gene (miRBase Accession No. MIMAT0025852) described in SEQ ID NO: 74, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6721-5p gene can be obtained by a method described in Li Y et al., 2012, Gene, Vol. 497, p. 330-335. Also, "hsa-mir-6721" (miRBase Accession No. MI0022556, SEQ ID NO: 268) having a hairpin-like structure is known as a precursor of "hsa-miR-6721-5p".

[0124] The term "hsa-miR-7847-3p gene" or "hsa-miR-7847-3p" used herein includes the hsa-miR-7847-3p gene (miRBase Accession No. MIMAT0030422) described in SEQ ID NO: 75, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-7847-3p gene can be obtained by a method described in Ple H et al., 2012, PLoS One, Vol. 7, e50746. Also, "hsa-mir-7847" (miRBase Accession No. MI0025517, SEQ ID NO: 269) having a hairpin-like structure is known as a precursor of "hsa-miR-7847-3p".

[0125] The term "hsa-miR-6132 gene" or "hsa-miR-6132" used herein includes the hsa-miR-6132 gene (miRBase Accession No. MIMAT0024616) described in SEQ ID NO: 76, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6132 gene can be obtained by a method described in Dannemann M et al., 2012, Genome Biol Evol, Vol. 4, p. 552-564. Also, "hsa-mir-6132" (miRBase Accession No. MI0021277, SEQ ID NO: 270) having a hairpin-like structure is known as a precursor of "hsa-miR-6132".

[0126] The term "hsa-miR-887-3p gene" or "hsa-miR-887-3p" used herein includes the hsa-miR-887-3p gene (miRBase Accession No. MIMAT0004951) described in SEQ ID NO: 77, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-887-3p gene can be obtained by a method described in Berezikov E et al., 2006, Genome Res, Vol. 16, p. 1289-1298. Also, "hsa-mir-887" (miRBase Accession No. MI0005562, SEQ ID NO: 271) having a hairpin-like structure is known as a precursor of "hsa-miR-887-3p".

[0127] The term "hsa-miR-3679-3p gene" or "hsa-miR-3679-3p" used herein includes the hsa-miR-3679-3p gene (miRBase Accession No. MIMAT0018105) described in SEQ ID NO: 78, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3679-3p gene can be obtained by a method described in Creighton CJ et al., 2010, PLoS One, Vol. 5, e9637. Also, "hsa-mir-3679" (miRBase Accession No. MI0016080, SEQ ID NO: 205) having a hairpin-like structure is known as a precursor of "hsa-miR-3679-3p".

[0128] The term "hsa-miR-6784-5p gene" or "hsa-miR-6784-5p" used herein includes the hsa-miR-6784-5p gene (miRBase Accession No. MIMAT0027468) described in SEQ ID NO: 79, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6784-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6784" (miRBase Accession No. MI0022629, SEQ ID NO: 272) having a hairpin-like structure is known as a precursor of "hsa-miR-6784-5p".

[0129] The term "hsa-miR-1249 gene" or "hsa-miR-1249" used herein includes the hsa-miR-1249 gene (miRBase Accession No. MIMAT0005901) described in SEQ ID NO: 80, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1249 gene can be obtained by a method described in Morin RD et al., 2008, Genome Res, Vol. 18, p. 610-621. Also, "hsa-mir-1249" (miRBase Accession No. MI0006384, SEQ ID NO: 273) having a hairpin-like structure is known as a precursor of "hsa-miR-1249".

[0130] The term "hsa-miR-937-5p gene" or "hsa-miR-937-5p" used herein includes the hsa-miR-937-5p gene (miRBase Accession No. MIMAT0022938) described in SEQ ID NO: 81, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-937-5p gene can be obtained by a method described in Lui WO et al., 2007, Cancer Res, Vol. 67, p. 6031-6043. Also, "hsa-mir-937" (miRBase Accession No. MI0005759, SEQ ID NO: 274) having a hairpin-like structure is known as a precursor of "hsa-miR-937-5p".

[0131] The term "hsa-miR-5195-3p gene" or "hsa-miR-5195-3p" used herein includes the hsa-miR-5195-3p gene (miRBase Accession No. MIMAT0021127) described in SEQ ID NO: 82, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-5195-3p gene can be obtained by a method described in Schotte D et al., 2011, Leukemia, Vol. 25, p. 1389-1399. Also, "hsa-mir-5195" (miRBase Accession No. MI0018174, SEQ ID NO: 275) having a hairpin-like structure is known as a precursor of "hsa-miR-5195-3p".

[0132] The term "hsa-miR-6732-5p gene" or "hsa-miR-6732-5p" used herein includes the hsa-miR-6732-5p gene (miRBase Accession No. MIMAT0027365) described in SEQ ID NO: 83, a homolog or an ortholog of a different organism

species, and the like. The hsa-miR-6732-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6732" (miRBase Accession No. MI0022577, SEQ ID NO: 276) having a hairpin-like structure is known as a precursor of "hsa-miR-6732-5p".

[0133] The term "hsa-miR-4417 gene" or "hsa-miR-4417" used herein includes the hsa-miR-4417 gene (miRBase Accession No. MIMAT0018929) described in SEQ ID NO: 84, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4417 gene can be obtained by a method described in Jima DD et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4417" (miRBase Accession No. MI0016753, SEQ ID NO: 277) having a hairpin-like structure is known as a precursor of "hsa-miR-4417".

[0134] The term "hsa-miR-4281 gene" or "hsa-miR-4281" used herein includes the hsa-miR-4281 gene (miRBase Accession No. MIMAT0016907) described in SEQ ID NO: 85, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4281 gene can be obtained by a method described in Goff LA et al., 2009, PLoS One, Vol. 4, e7192. Also, "hsa-mir-4281" (miRBase Accession No. MI0015885, SEQ ID NO: 278) having a hairpin-like structure is known as a precursor of "hsa-miR-4281".

[0135] The term "hsa-miR-4734 gene" or "hsa-miR-4734" used herein includes the hsa-miR-4734 gene (miRBase Accession No. MIMAT0019859) described in SEQ ID NO: 86, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4734 gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4734" (miRBase Accession No. MI0017371, SEQ ID NO: 279) having a hairpin-like structure is known as a precursor of "hsa-miR-4734".

[0136] The term "hsa-miR-6766-3p gene" or "hsa-miR-6766-3p" used herein includes the hsa-miR-6766-3p gene (miRBase Accession No. MIMAT0027433) described in SEQ ID NO: 87, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6766-3p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6766" (miRBase Accession No. MI0022611, SEQ ID NO: 280) having a hairpin-like structure is known as a precursor of "hsa-miR-6766-3p".

[0137] The term "hsa-miR-663a gene" or "hsa-miR-663a" used herein includes the hsa-miR-663a gene (miRBase Accession No. MIMAT0003326) described in SEQ ID NO: 88, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-663a gene can be obtained by a method described in Cummins JM et al., 2006, Proc Natl Acad Sci USA, Vol. 103, p. 3687-3692. Also, "hsa-mir-663a" (miRBase Accession No. MI0003672, SEQ ID NO: 281) having a hairpin-like structure is known as a precursor of "hsa-miR-663a".

[0138] The term "hsa-miR-4513 gene" or "hsa-miR-4513" used herein includes the hsa-miR-4513 gene (miRBase Accession No. MIMAT0019050) described in SEQ ID NO: 89, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4513 gene can be obtained by a method described in Jima DD et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4513" (miRBase Accession No. MI0016879, SEQ ID NO: 282) having a hairpin-like structure is known as a precursor of "hsa-miR-4513".

[0139] The term "hsa-miR-6781-5p gene" or "hsa-miR-6781-5p" used herein includes the hsa-miR-6781-5p gene (miRBase Accession No. MIMAT0027462) described in SEQ ID NO: 90, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6781-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6781" (miRBase Accession No. MI0022626, SEQ ID NO: 283) having a hairpin-like structure is known as a precursor of "hsa-miR-6781-5p".

[0140] The term "hsa-miR-1227-5p gene" or "hsa-miR-1227-5p" used herein includes the hsa-miR-1227-5p gene (miRBase Accession No. MIMAT0022941) described in SEQ ID NO: 91, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1227-5p gene can be obtained by a method described in Berezikov E et al., 2007, Mol Cell, Vol. 28, p. 328-336. Also, "hsa-mir-1227" (miRBase Accession No. MI0006316, SEQ ID NO: 284) having a hairpin-like structure is known as a precursor of "hsa-miR-1227-5p".

[0141] The term "hsa-miR-6845-5p gene" or "hsa-miR-6845-5p" used herein includes the hsa-miR-6845-5p gene (miRBase Accession No. MIMAT0027590) described in SEQ ID NO: 92, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6845-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6845" (miRBase Accession No. MI0022691, SEQ ID NO: 285) having a hairpin-like structure is known as a precursor of "hsa-miR-6845-5p".

[0142] The term "hsa-miR-6798-5p gene" or "hsa-miR-6798-5p" used herein includes the hsa-miR-6798-5p gene (miRBase Accession No. MIMAT0027496) described in SEQ ID NO: 93, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6798-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6798" (miRBase Accession No. MI0022643, SEQ ID NO: 286) having a hairpin-like structure is known as a precursor of "hsa-miR-6798-5p".

[0143] The term "hsa-miR-3620-5p gene" or "hsa-miR-3620-5p" used herein includes the hsa-miR-3620-5p gene (miRBase Accession No. MIMAT0022967) described in SEQ ID NO: 94, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3620-5p gene can be obtained by a method described in Witten D et al., 2010, BMC Biol, Vol. 8, p. 58. Also, "hsa-mir-3620" (miRBase Accession No. MI0016011, SEQ ID NO: 287) having a hairpin-like structure is known as a precursor of "hsa-miR-3620-5p".

[0144] The term "hsa-miR-1915-5p gene" or "hsa-miR-1915-5p" used herein includes the hsa-miR-1915-5p gene (miRBase Accession No. MIMAT0007891) described in SEQ ID NO: 95, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1915-5p gene can be obtained by a method described in Bar M et al., 2008, Stem Cells, Vol. 26, p. 2496-2505. Also, "hsa-mir-1915" (miRBase Accession No. MI0008336, SEQ ID NO: 288) having a hairpin-like structure is known as a precursor of "hsa-miR-1915-5p".

[0145] The term "hsa-miR-4294 gene" or "hsa-miR-4294" used herein includes the hsa-miR-4294 gene (miRBase Accession No. MIMAT0016849) described in SEQ ID NO: 96, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4294 gene can be obtained by a method described in Goff LA et al., 2009, PLoS One, Vol. 4, e7192. Also, "hsa-mir-4294" (miRBase Accession No. MI0015827, SEQ ID NO: 289) having a hairpin-like structure is known as a precursor of "hsa-miR-4294".

[0146] The term "hsa-miR-642a-3p gene" or "hsa-miR-642a-3p" used herein includes the hsa-miR-642a-3p gene (miRBase Accession No. MIMAT0020924) described in SEQ ID NO: 97, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-642a-3p gene can be obtained by a method described in Cummins JM et al., 2006, Proc Natl Acad Sci USA, Vol. 103, p. 3687-3692. Also, "hsa-mir-642a" (miRBase Accession No. MI0003657, SEQ ID NO: 290) having a hairpin-like structure is known as a precursor of "hsa-miR-642a-3p".

[0147] The term "hsa-miR-371a-5p gene" or "hsa-miR-371a-5p" used herein includes the hsa-miR-371a-5p gene (miRBase Accession No. MIMAT0004687) described in SEQ ID NO: 98, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-371a-5p gene can be obtained by a method described in Suh MR et al., 2004, Dev Biol, Vol. 270, p. 488-498. Also, "hsa-mir-371a" (miRBase Accession No. MI0000779, SEQ ID NO: 291) having a hairpin-like structure is known as a precursor of "hsa-miR-371a-5p".

[0148] The term "hsa-miR-940 gene" or "hsa-miR-940" used herein includes the hsa-miR-940 gene (miRBase Accession No. MIMAT0004983) described in SEQ ID NO: 99, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-940 gene can be obtained by a method described in Lui WO et al., 2007, Cancer Res, Vol. 67, p. 6031-6043. Also, "hsa-mir-940" (miRBase Accession No. MI0005762, SEQ ID NO: 292) having a hairpin-like structure is known as a precursor of "hsa-miR-940".

[0149] The term "hsa-miR-4450 gene" or "hsa-miR-4450" used herein includes the hsa-miR-4450 gene (miRBase Accession No. MIMAT0018971) described in SEQ ID NO: 100, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4450 gene can be obtained by a method described in Jima DD et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4450" (miRBase Accession No. MI0016795, SEQ ID NO: 293) having a hairpin-like structure is known as a precursor of "hsa-miR-4450".

[0150] The term "hsa-miR-4723-5p gene" or "hsa-miR-4723-5p" used herein includes the hsa-miR-4723-5p gene (miRBase Accession No. MIMAT0019838) described in SEQ ID NO: 101, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4723-5p gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4723" (miRBase Accession No. MI0017359, SEQ ID NO: 294) having a hairpin-like structure is known as a precursor of "hsa-miR-4723-5p".

[0151] The term "hsa-miR-1469 gene" or "hsa-miR-1469" used herein includes the hsa-miR-1469 gene (miRBase Accession No. MIMAT0007347) described in SEQ ID NO: 102, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1469 gene can be obtained by a method described in Kawaji H et al., 2008, BMC Genomics, Vol. 9, p. 157. Also, "hsa-mir-1469" (miRBase Accession No. MI0007074, SEQ ID NO: 295) having a hairpin-like structure is known as a precursor of "hsa-miR-1469".

[0152] The term "hsa-miR-6861-5p gene" or "hsa-miR-6861-5p" used herein includes the hsa-miR-6861-5p gene (miRBase Accession No. MIMAT0027623) described in SEQ ID NO: 103, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6861-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6861" (miRBase Accession No. MI0022708, SEQ ID NO: 296) having a hairpin-like structure is known as a precursor of "hsa-miR-6861-5p".

[0153] The term "hsa-miR-7975 gene" or "hsa-miR-7975" used herein includes the hsa-miR-7975 gene (miRBase Accession No. MIMAT0031178) described in SEQ ID NO: 104, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-7975 gene can be obtained by a method described in Velthut-Meikas A et al., 2013, Mol Endocrinol, online. Also, "hsa-mir-7975" (miRBase Accession No. MI0025751, SEQ ID NO: 297) having a hairpin-like structure is known as a precursor of "hsa-miR-7975".

[0154] The term "hsa-miR-6879-5p gene" or "hsa-miR-6879-5p" used herein includes the hsa-miR-6879-5p gene (miRBase Accession No. MIMAT0027658) described in SEQ ID NO: 105, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6879-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6879" (miRBase Accession No. MI0022726, SEQ ID NO: 298) having a hairpin-like structure is known as a precursor of "hsa-miR-6879-5p".

[0155] The term "hsa-miR-6802-5p gene" or "hsa-miR-6802-5p" used herein includes the hsa-miR-6802-5p gene (miRBase Accession No. MIMAT0027504) described in SEQ ID NO: 106, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6802-5p gene can be obtained by a method described in Ladewig E et al., 2012,

Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6802" (miRBase Accession No. MI0022647, SEQ ID NO: 299) having a hairpin-like structure is known as a precursor of "hsa-miR-6802-5p".

[0156] The term "hsa-miR-1268b gene" or "hsa-miR-1268b" used herein includes the hsa-miR-1268b gene (miRBase Accession No. MIMAT0018925) described in SEQ ID NO: 107, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1268b gene can be obtained by a method described in Jima DD et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-1268b" (miRBase Accession No. MI0016748, SEQ ID NO: 300) having a hairpin-like structure is known as a precursor of "hsa-miR-1268b".

[0157] The term "hsa-miR-663b gene" or "hsa-miR-663b" used herein includes the hsa-miR-663b gene (miRBase Accession No. MIMAT0005867) described in SEQ ID NO: 108, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-663b gene can be obtained by a method described in Takada S et al., 2008, Leukemia, Vol. 22, p. 1274-1278. Also, "hsa-mir-663b" (miRBase Accession No. MI0006336, SEQ ID NO: 301) having a hairpin-like structure is known as a precursor of "hsa-miR-663b".

[0158] The term "hsa-miR-125a-3p gene" or "hsa-miR-125a-3p" used herein includes the hsa-miR-125a-3p gene (miRBase Accession No. MIMAT0004602) described in SEQ ID NO: 109, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-125a-3p gene can be obtained by a method described in Lagos-Quintana M et al., 2002, Curr Biol, Vol. 12, p. 735-739. Also, "hsa-mir-125a" (miRBase Accession No. MI0000469, SEQ ID NO: 302) having a hairpin-like structure is known as a precursor of "hsa-miR-125a-3p".

[0159] The term "hsa-miR-2861 gene" or "hsa-miR-2861" used herein includes the hsa-miR-2861 gene (miRBase Accession No. MIMAT0013802) described in SEQ ID NO: 110, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-2861 gene can be obtained by a method described in Li H et al., 2009, J Clin Invest, Vol. 119, p. 3666-3677. Also, "hsa-mir-2861" (miRBase Accession No. MI0013006, SEQ ID NO: 303) having a hairpin-like structure is known as a precursor of "hsa-miR-2861".

[0160] The term "hsa-miR-6088 gene" or "hsa-miR-6088" used herein includes the hsa-miR-6088 gene (miRBase Accession No. MIMAT0023713) described in SEQ ID NO: 111, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6088 gene can be obtained by a method described in Yoo JK et al., 2012, Stem Cells Dev, Vol. 21, p. 2049-2057. Also, "hsa-mir-6088" (miRBase Accession No. MI0020365, SEQ ID NO: 304) having a hairpin-like structure is known as a precursor of "hsa-miR-6088".

[0161] The term "hsa-miR-4758-5p gene" or "hsa-miR-4758-5p" used herein includes the hsa-miR-4758-5p gene (miRBase Accession No. MIMAT0019903) described in SEQ ID NO: 112, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4758-5p gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4758" (miRBase Accession No. MI0017399, SEQ ID NO: 305) having a hairpin-like structure is known as a precursor of "hsa-miR-4758-5p".

[0162] The term "hsa-miR-296-3p gene" or "hsa-miR-296-3p" used herein includes the hsa-miR-296-3p gene (miRBase Accession No. MIMAT0004679) described in SEQ ID NO: 113, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-296-3p gene can be obtained by a method described in Houbaviy HB et al., 2003, Dev Cell, Vol. 5, p. 351-358. Also, "hsa-mir-296" (miRBase Accession No. MI0000747, SEQ ID NO: 306) having a hairpin-like structure is known as a precursor of "hsa-miR-296-3p".

[0163] The term "hsa-miR-6738-5p gene" or "hsa-miR-6738-5p" used herein includes the hsa-miR-6738-5p gene (miRBase Accession No. MIMAT0027377) described in SEQ ID NO: 114, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6738-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6738" (miRBase Accession No. MI0022583, SEQ ID NO: 307) having a hairpin-like structure is known as a precursor of "hsa-miR-6738-5p".

[0164] The term "hsa-miR-671-5p gene" or "hsa-miR-671-5p" used herein includes the hsa-miR-671-5p gene (miRBase Accession No. MIMAT0003880) described in SEQ ID NO: 115, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-671-5p gene can be obtained by a method described in Berezikov E et al., 2006, Genome Res, Vol. 16, p. 1289-1298. Also, "hsa-mir-671" (miRBase Accession No. MI0003760, SEQ ID NO: 308) having a hairpin-like structure is known as a precursor of "hsa-miR-671-5p".

[0165] The term "hsa-miR-4454 gene" or "hsa-miR-4454" used herein includes the hsa-miR-4454 gene (miRBase Accession No. MIMAT0018976) described in SEQ ID NO: 116, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4454 gene can be obtained by a method described in Jima DD et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4454" (miRBase Accession No. MI0016800, SEQ ID NO: 309) having a hairpin-like structure is known as a precursor of "hsa-miR-4454".

[0166] The term "hsa-miR-4516 gene" or "hsa-miR-4516" used herein includes the hsa-miR-4516 gene (miRBase Accession No. MIMAT0019053) described in SEQ ID NO: 117, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4516 gene can be obtained by a method described in Jima DD et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4516" (miRBase Accession No. MI0016882, SEQ ID NO: 310) having a hairpin-like structure is known as a precursor of "hsa-miR-4516".

[0167] The term "hsa-miR-7845-5p gene" or "hsa-miR-7845-5p" used herein includes the hsa-miR-7845-5p gene

(miRBase Accession No. MIMAT0030420) described in SEQ ID NO: 118, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-7845-5p gene can be obtained by a method described in Ple H et al., 2012, PLoS One, Vol. 7, e50746. Also, "hsa-mir-7845" (miRBase Accession No. MI0025515, SEQ ID NO: 311) having a hairpin-like structure is known as a precursor of "hsa-miR-7845-5p".

[0168] The term "hsa-miR-4741 gene" or "hsa-miR-4741" used herein includes the hsa-miR-4741 gene (miRBase Accession No. MIMAT0019871) described in SEQ ID NO: 119, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4741 gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4741" (miRBase Accession No. MI0017379, SEQ ID NO: 312) having a hairpin-like structure is known as a precursor of "hsa-miR-4741".

[0169] The term "hsa-miR-92b-5p gene" or "hsa-miR-92b-5p" used herein includes the hsa-miR-92b-5p gene (miRBase Accession No. MIMAT0004792) described in SEQ ID NO: 120, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-92b-5p gene can be obtained by a method described in Cummins JM et al., 2006, Proc Natl Acad Sci USA, Vol. 103, p. 3687-3692. Also, "hsa-mir-92b" (miRBase Accession No. MI0003560, SEQ ID NO: 313) having a hairpin-like structure is known as a precursor of "hsa-miR-92b-5p".

[0170] The term "hsa-miR-6795-5p gene" or "hsa-miR-6795-5p" used herein includes the hsa-miR-6795-5p gene (miRBase Accession No. MIMAT0027490) described in SEQ ID NO: 121, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6795-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6795" (miRBase Accession No. MI0022640, SEQ ID NO: 314) having a hairpin-like structure is known as a precursor of "hsa-miR-6795-5p".

[0171] The term "hsa-miR-6805-3p gene" or "hsa-miR-6805-3p" used herein includes the hsa-miR-6805-3p gene (miRBase Accession No. MIMAT0027511) described in SEQ ID NO: 122, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6805-3p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6805" (miRBase Accession No. MI0022650, SEQ ID NO: 315) having a hairpin-like structure is known as a precursor of "hsa-miR-6805-3p".

[0172] The term "hsa-miR-4725-3p gene" or "hsa-miR-4725-3p" used herein includes the hsa-miR-4725-3p gene (miRBase Accession No. MIMAT0019844) described in SEQ ID NO: 123, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4725-3p gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4725" (miRBase Accession No. MI0017362, SEQ ID NO: 316) having a hairpin-like structure is known as a precursor of "hsa-miR-4725-3p".

[0173] The term "hsa-miR-6782-5p gene" or "hsa-miR-6782-5p" used herein includes the hsa-miR-6782-5p gene (miRBase Accession No. MIMAT0027464) described in SEQ ID NO: 124, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6782-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6782" (miRBase Accession No. MI0022627, SEQ ID NO: 317) having a hairpin-like structure is known as a precursor of "hsa-miR-6782-5p".

[0174] The term "hsa-miR-4688 gene" or "hsa-miR-4688" used herein includes the hsa-miR-4688 gene (miRBase Accession No. MIMAT0019777) described in SEQ ID NO: 125, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4688 gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4688" (miRBase Accession No. MI0017321, SEQ ID NO: 318) having a hairpin-like structure is known as a precursor of "hsa-miR-4688".

[0175] The term "hsa-miR-6850-5p gene" or "hsa-miR-6850-5p" used herein includes the hsa-miR-6850-5p gene (miRBase Accession No. MIMAT0027600) described in SEQ ID NO: 126, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6850-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6850" (miRBase Accession No. MI0022696, SEQ ID NO: 319) having a hairpin-like structure is known as a precursor of "hsa-miR-6850-5p".

[0176] The term "hsa-miR-6777-5p gene" or "hsa-miR-6777-5p" used herein includes the hsa-miR-6777-5p gene (miRBase Accession No. MIMAT0027454) described in SEQ ID NO: 127, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6777-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6777" (miRBase Accession No. MI0022622, SEQ ID NO: 320) having a hairpin-like structure is known as a precursor of "hsa-miR-6777-5p".

[0177] The term "hsa-miR-6785-5p gene" or "hsa-miR-6785-5p" used herein includes the hsa-miR-6785-5p gene (miRBase Accession No. MIMAT0027470) described in SEQ ID NO: 128, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6785-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6785" (miRBase Accession No. MI0022630, SEQ ID NO: 321) having a hairpin-like structure is known as a precursor of "hsa-miR-6785-5p".

[0178] The term "hsa-miR-7106-5p gene" or "hsa-miR-7106-5p" used herein includes the hsa-miR-7106-5p gene (miRBase Accession No. MIMAT0028109) described in SEQ ID NO: 129, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-7106-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-7106" (miRBase Accession No. MI0022957, SEQ ID NO: 322)

having a hairpin-like structure is known as a precursor of "hsa-miR-7106-5p".

[0179] The term "hsa-miR-3663-3p gene" or "hsa-miR-3663-3p" used herein includes the hsa-miR-3663-3p gene (miRBase Accession No. MIMAT0018085) described in SEQ ID NO: 130, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3663-3p gene can be obtained by a method described in Liao JY et al., 2010, PLoS One, Vol. 5, e10563. Also, "hsa-mir-3663" (miRBase Accession No. MI0016064, SEQ ID NO: 323) having a hairpin-like structure is known as a precursor of "hsa-miR-3663-3p".

[0180] The term "hsa-miR-6131 gene" or "hsa-miR-6131" used herein includes the hsa-miR-6131 gene (miRBase Accession No. MIMAT0024615) described in SEQ ID NO: 131, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6131 gene can be obtained by a method described in Dannemann M et al., 2012, Genome Biol Evol, Vol. 4, p. 552-564. Also, "hsa-mir-6131" (miRBase Accession No. MI0021276, SEQ ID NO: 324) having a hairpin-like structure is known as a precursor of "hsa-miR-6131".

[0181] The term "hsa-miR-1915-3p gene" or "hsa-miR-1915-3p" used herein includes the hsa-miR-1915-3p gene (miRBase Accession No. MIMAT0007892) described in SEQ ID NO: 132, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1915-3p gene can be obtained by a method described in Bar M et al., 2008, Stem Cells, Vol. 26, p. 2496-2505. Also, "hsa-mir-1915" (miRBase Accession No. MI0008336, SEQ ID NO: 288) having a hairpin-like structure is known as a precursor of "hsa-miR-1915-3p".

[0182] The term "hsa-miR-4532 gene" or "hsa-miR-4532" used herein includes the hsa-miR-4532 gene (miRBase Accession No. MIMAT0019071) described in SEQ ID NO: 133, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4532 gene can be obtained by a method described in Jima DD et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4532" (miRBase Accession No. MI0016899, SEQ ID NO: 325) having a hairpin-like structure is known as a precursor of "hsa-miR-4532".

[0183] The term "hsa-miR-6820-5p gene" or "hsa-miR-6820-5p" used herein includes the hsa-miR-6820-5p gene (miRBase Accession No. MIMAT0027540) described in SEQ ID NO: 134, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6820-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6820" (miRBase Accession No. MI0022665, SEQ ID NO: 326) having a hairpin-like structure is known as a precursor of "hsa-miR-6820-5p".

[0184] The term "hsa-miR-4689 gene" or "hsa-miR-4689" used herein includes the hsa-miR-4689 gene (miRBase Accession No. MIMAT0019778) described in SEQ ID NO: 135, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4689 gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4689" (miRBase Accession No. MI0017322, SEQ ID NO: 327) having a hairpin-like structure is known as a precursor of "hsa-miR-4689".

[0185] The term "hsa-miR-4638-5p gene" or "hsa-miR-4638-5p" used herein includes the hsa-miR-4638-5p gene (miRBase Accession No. MIMAT0019695) described in SEQ ID NO: 136, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4638-5p gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4638" (miRBase Accession No. MI0017265, SEQ ID NO: 328) having a hairpin-like structure is known as a precursor of "hsa-miR-4638-5p".

[0186] The term "hsa-miR-3656 gene" or "hsa-miR-3656" used herein includes the hsa-miR-3656 gene (miRBase Accession No. MIMAT0018076) described in SEQ ID NO: 137, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3656 gene can be obtained by a method described in Meiri E et al., 2010, Nucleic Acids Res, Vol. 38, p. 6234-6246. Also, "hsa-mir-3656" (miRBase Accession No. MI0016056, SEQ ID NO: 329) having a hairpin-like structure is known as a precursor of "hsa-miR-3656".

[0187] The term "hsa-miR-3621 gene" or "hsa-miR-3621" used herein includes the hsa-miR-3621 gene (miRBase Accession No. MIMAT0018002) described in SEQ ID NO: 138, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3621 gene can be obtained by a method described in Witten D et al., 2010, BMC Biol, Vol. 8, p. 58. Also, "hsa-mir-3621" (miRBase Accession No. MI0016012, SEQ ID NO: 330) having a hairpin-like structure is known as a precursor of "hsa-miR-3621".

[0188] The term "hsa-miR-6769b-5p gene" or "hsa-miR-6769b-5p" used herein includes the hsa-miR-6769b-5p gene (miRBase Accession No. MIMAT0027620) described in SEQ ID NO: 139, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6769b-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6769b" (miRBase Accession No. MI0022706, SEQ ID NO: 331) having a hairpin-like structure is known as a precursor of "hsa-miR-6769b-5p".

[0189] The term "hsa-miR-149-3p gene" or "hsa-miR-149-3p" used herein includes the hsa-miR-149-3p gene (miRBase Accession No. MIMAT0004609) described in SEQ ID NO: 140, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-149-3p gene can be obtained by a method described in Lagos-Quintana M et al., 2002, Curr Biol, Vol. 12, p. 735-739. Also, "hsa-mir-149" (miRBase Accession No. MI0000478, SEQ ID NO: 332) having a hairpin-like structure is known as a precursor of "hsa-miR-149-3p".

[0190] The term "hsa-miR-23b-3p gene" or "hsa-miR-23b-3p" used herein includes the hsa-miR-23b-3p gene (miRBase Accession No. MIMAT0000418) described in SEQ ID NO: 141, a homolog or an ortholog of a different organism

species, and the like. The hsa-miR-23b-3p gene can be obtained by a method described in Lagos-Quintana M et al., 2002, Curr Biol, Vol. 12, p. 735-739. Also, "hsa-mir-23b" (miRBase Accession No. MI0000439, SEQ ID NO: 333) having a hairpin-like structure is known as a precursor of "hsa-miR-23b-3p".

[0191] The term "hsa-miR-3135b gene" or "hsa-miR-3135b" used herein includes the hsa-miR-3135b gene (miRBase Accession No. MIMAT0018985) described in SEQ ID NO: 142, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3135b gene can be obtained by a method described in Jima DD et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-3135b" (miRBase Accession No. MI0016809, SEQ ID NO: 334) having a hairpin-like structure is known as a precursor of "hsa-miR-3135b".

[0192] The term "hsa-miR-6848-5p gene" or "hsa-miR-6848-5p" used herein includes the hsa-miR-6848-5p gene (miRBase Accession No. MIMAT0027596) described in SEQ ID NO: 143, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6848-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6848" (miRBase Accession No. MI0022694, SEQ ID NO: 335) having a hairpin-like structure is known as a precursor of "hsa-miR-6848-5p".

[0193] The term "hsa-miR-6769a-5p gene" or "hsa-miR-6769a-5p" used herein includes the hsa-miR-6769a-5p gene (miRBase Accession No. MIMAT0027438) described in SEQ ID NO: 144, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6769a-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6769a" (miRBase Accession No. MI0022614, SEQ ID NO: 336) having a hairpin-like structure is known as a precursor of "hsa-miR-6769a-5p".

[0194] The term "hsa-miR-4327 gene" or "hsa-miR-4327" used herein includes the hsa-miR-4327 gene (miRBase Accession No. MIMAT0016889) described in SEQ ID NO: 145, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4327 gene can be obtained by a method described in Goff LA et al., 2009, PLoS One, Vol. 4, e7192. Also, "hsa-mir-4327" (miRBase Accession No. MI0015867, SEQ ID NO: 337) having a hairpin-like structure is known as a precursor of "hsa-miR-4327".

[0195] The term "hsa-miR-6765-3p gene" or "hsa-miR-6765-3p" used herein includes the hsa-miR-6765-3p gene (miRBase Accession No. MIMAT0027431) described in SEQ ID NO: 146, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6765-3p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6765" (miRBase Accession No. MI0022610, SEQ ID NO: 338) having a hairpin-like structure is known as a precursor of "hsa-miR-6765-3p".

[0196] The term "hsa-miR-6716-5p gene" or "hsa-miR-6716-5p" used herein includes the hsa-miR-6716-5p gene (miRBase Accession No. MIMAT0025844) described in SEQ ID NO: 147, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6716-5p gene can be obtained by a method described in Li Y et al., 2012, Gene, Vol. 497, p. 330-335. Also, "hsa-mir-6716" (miRBase Accession No. MI0022550, SEQ ID NO: 339) having a hairpin-like structure is known as a precursor of "hsa-miR-6716-5p".

[0197] The term "hsa-miR-6877-5p gene" or "hsa-miR-6877-5p" used herein includes the hsa-miR-6877-5p gene (miRBase Accession No. MIMAT0027654) described in SEQ ID NO: 148, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6877-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6877" (miRBase Accession No. MI0022724, SEQ ID NO: 340) having a hairpin-like structure is known as a precursor of "hsa-miR-6877-5p".

[0198] The term "hsa-miR-6727-5p gene" or "hsa-miR-6727-5p" used herein includes the hsa-miR-6727-5p gene (miRBase Accession No. MIMAT0027355) described in SEQ ID NO: 149, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6727-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6727" (miRBase Accession No. MI0022572, SEQ ID NO: 341) having a hairpin-like structure is known as a precursor of "hsa-miR-6727-5p".

[0199] The term "hsa-miR-4534 gene" or "hsa-miR-4534" used herein includes the hsa-miR-4534 gene (miRBase Accession No. MIMAT0019073) described in SEQ ID NO: 150, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4534 gene can be obtained by a method described in Jima DD et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4534" (miRBase Accession No. MI0016901, SEQ ID NO: 342) having a hairpin-like structure is known as a precursor of "hsa-miR-4534".

[0200] The term "hsa-miR-614 gene" or "hsa-miR-614" used herein includes the hsa-miR-614 gene (miRBase Accession No. MIMAT0003282) described in SEQ ID NO: 151, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-614 gene can be obtained by a method described in Cummins JM et al., 2006, Proc Natl Acad Sci USA, Vol. 103, p. 3687-3692. Also, "hsa-mir-614" (miRBase Accession No. MI0003627, SEQ ID NO: 343) having a hairpin-like structure is known as a precursor of "hsa-miR-614".

[0201] The term "hsa-miR-1202 gene" or "hsa-miR-1202" used herein includes the hsa-miR-1202 gene (miRBase Accession No. MIMAT0005865) described in SEQ ID NO: 152, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1202 gene can be obtained by a method described in Marton S et al., 2008, Leukemia, Vol. 22, p. 330-338. Also, "hsa-mir-1202" (miRBase Accession No. MI0006334, SEQ ID NO: 344) having a hairpin-like structure is known as a precursor of "hsa-miR-1202".

[0202] The term "hsa-miR-575 gene" or "hsa-miR-575" used herein includes the hsa-miR-575 gene (miRBase Accession No. MIMAT0003240) described in SEQ ID NO: 153, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-575 gene can be obtained by a method described in Cummins JM et al., 2006, Proc Natl Acad Sci USA, Vol. 103, p. 3687-3692. Also, "hsa-mir-575" (miRBase Accession No. MI0003582, SEQ ID NO: 345) having a hairpin-like structure is known as a precursor of "hsa-miR-575".

[0203] The term "hsa-miR-6870-5p gene" or "hsa-miR-6870-5p" used herein includes the hsa-miR-6870-5p gene (miRBase Accession No. MIMAT0027640) described in SEQ ID NO: 154, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6870-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6870" (miRBase Accession No. MI0022717, SEQ ID NO: 346) having a hairpin-like structure is known as a precursor of "hsa-miR-6870-5p".

[0204] The term "hsa-miR-6722-3p gene" or "hsa-miR-6722-3p" used herein includes the hsa-miR-6722-3p gene (miRBase Accession No. MIMAT0025854) described in SEQ ID NO: 155, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6722-3p gene can be obtained by a method described in Li Y et al., 2012, Gene, Vol. 497, p. 330-335. Also, "hsa-mir-6722" (miRBase Accession No. MI0022557, SEQ ID NO: 347) having a hairpin-like structure is known as a precursor of "hsa-miR-6722-3p".

[0205] The term "hsa-miR-7977 gene" or "hsa-miR-7977" used herein includes the hsa-miR-7977 gene (miRBase Accession No. MIMAT0031180) described in SEQ ID NO: 156, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-7977 gene can be obtained by a method described in Velthut-Meikas A et al., 2013, Mol Endocrinol, online. Also, "hsa-mir-7977" (miRBase Accession No. MI0025753, SEQ ID NO: 348) having a hairpin-like structure is known as a precursor of "hsa-miR-7977".

[0206] The term "hsa-miR-4649-5p gene" or "hsa-miR-4649-5p" used herein includes the hsa-miR-4649-5p gene (miRBase Accession No. MIMAT0019711) described in SEQ ID NO: 157, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4649-5p gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4649" (miRBase Accession No. MI0017276, SEQ ID NO: 349) having a hairpin-like structure is known as a precursor of "hsa-miR-4649-5p".

[0207] The term "hsa-miR-4675 gene" or "hsa-miR-4675" used herein includes the hsa-miR-4675 gene (miRBase Accession No. MIMAT0019757) described in SEQ ID NO: 158, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4675 gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4675" (miRBase Accession No. MI0017306, SEQ ID NO: 350) having a hairpin-like structure is known as a precursor of "hsa-miR-4675".

[0208] The term "hsa-miR-6075 gene" or "hsa-miR-6075" used herein includes the hsa-miR-6075 gene (miRBase Accession No. MIMAT0023700) described in SEQ ID NO: 159, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6075 gene can be obtained by a method described in Voellenkle C et al., 2012, RNA, Vol. 18, p. 472-484. Also, "hsa-mir-6075" (miRBase Accession No. MI0020352, SEQ ID NO: 351) having a hairpin-like structure is known as a precursor of "hsa-miR-6075".

[0209] The term "hsa-miR-6779-5p gene" or "hsa-miR-6779-5p" used herein includes the hsa-miR-6779-5p gene (miRBase Accession No. MIMAT0027458) described in SEQ ID NO: 160, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6779-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6779" (miRBase Accession No. MI0022624, SEQ ID NO: 352) having a hairpin-like structure is known as a precursor of "hsa-miR-6779-5p".

[0210] The term "hsa-miR-4271 gene" or "hsa-miR-4271" used herein includes the hsa-miR-4271 gene (miRBase Accession No. MIMAT0016901) described in SEQ ID NO: 161, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4271 gene can be obtained by a method described in Goff LA et al., 2009, PLoS One, Vol. 4, e7192. Also, "hsa-mir-4271" (miRBase Accession No. MI0015879, SEQ ID NO: 353) having a hairpin-like structure is known as a precursor of "hsa-miR-4271".

[0211] The term "hsa-miR-3196 gene" or "hsa-miR-3196" used herein includes the hsa-miR-3196 gene (miRBase Accession No. MIMAT0015080) described in SEQ ID NO: 162, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3196 gene can be obtained by a method described in Stark MS et al., 2010, PLoS One, Vol. 5, e9685. Also, "hsa-mir-3196" (miRBase Accession No. MI0014241, SEQ ID NO: 354) having a hairpin-like structure is known as a precursor of "hsa-miR-3196".

[0212] The term "hsa-miR-6803-5p gene" or "hsa-miR-6803-5p" used herein includes the hsa-miR-6803-5p gene (miRBase Accession No. MIMAT0027506) described in SEQ ID NO: 163, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6803-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6803" (miRBase Accession No. MI0022648, SEQ ID NO: 355) having a hairpin-like structure is known as a precursor of "hsa-miR-6803-5p".

[0213] The term "hsa-miR-6789-5p gene" or "hsa-miR-6789-5p" used herein includes the hsa-miR-6789-5p gene (miRBase Accession No. MIMAT0027478) described in SEQ ID NO: 164, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6789-5p gene can be obtained by a method described in Ladewig E et al., 2012,

Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6789" (miRBase Accession No. MI0022634, SEQ ID NO: 356) having a hairpin-like structure is known as a precursor of "hsa-miR-6789-5p".

[0214] The term "hsa-miR-4648 gene" or "hsa-miR-4648" used herein includes the hsa-miR-4648 gene (miRBase Accession No. MIMAT0019710) described in SEQ ID NO: 165, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4648 gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4648" (miRBase Accession No. MI0017275, SEQ ID NO: 357) having a hairpin-like structure is known as a precursor of "hsa-miR-4648".

[0215] The term "hsa-miR-4508 gene" or "hsa-miR-4508" used herein includes the hsa-miR-4508 gene (miRBase Accession No. MIMAT0019045) described in SEQ ID NO: 166, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4508 gene can be obtained by a method described in Jima DD et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4508" (miRBase Accession No. MI0016872, SEQ ID NO: 358) having a hairpin-like structure is known as a precursor of "hsa-miR-4508".

[0216] The term "hsa-miR-4749-5p gene" or "hsa-miR-4749-5p" used herein includes the hsa-miR-4749-5p gene (miRBase Accession No. MIMAT0019885) described in SEQ ID NO: 167, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4749-5p gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4749" (miRBase Accession No. MI0017388, SEQ ID NO: 359) having a hairpin-like structure is known as a precursor of "hsa-miR-4749-5p".

[0217] The term "hsa-miR-4505 gene" or "hsa-miR-4505" used herein includes the hsa-miR-4505 gene (miRBase Accession No. MIMAT0019041) described in SEQ ID NO: 168, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4505 gene can be obtained by a method described in Jima DD et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4505" (miRBase Accession No. MI0016868, SEQ ID NO: 360) having a hairpin-like structure is known as a precursor of "hsa-miR-4505".

[0218] The term "hsa-miR-5698 gene" or "hsa-miR-5698" used herein includes the hsa-miR-5698 gene (miRBase Accession No. MIMAT0022491) described in SEQ ID NO: 169, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-5698 gene can be obtained by a method described in Watahiki A et al., 2011, PLoS One, Vol. 6, e24950. Also, "hsa-mir-5698" (miRBase Accession No. MI0019305, SEQ ID NO: 361) having a hairpin-like structure is known as a precursor of "hsa-miR-5698".

[0219] The term "hsa-miR-1199-Sp gene" or "hsa-miR-1199-Sp" used herein includes the hsa-miR-1199-5p gene (miRBase Accession No. MIMAT0031119) described in SEQ ID NO: 170, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1199-5p gene can be obtained by a method described in Salvi A et al., 2013, Int J Oncol, Vol. 42, p. 391-402. Also, "hsa-mir-1199" (miRBase Accession No. MI0020340, SEQ ID NO: 362) having a hairpin-like structure is known as a precursor of "hsa-miR-1199-5p".

[0220] The term "hsa-miR-4763-3p gene" or "hsa-miR-4763-3p" used herein includes the hsa-miR-4763-3p gene (miRBase Accession No. MIMAT0019913) described in SEQ ID NO: 171, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4763-3p gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4763" (miRBase Accession No. MI0017404, SEQ ID NO: 363) having a hairpin-like structure is known as a precursor of "hsa-miR-4763-3p".

[0221] The term "hsa-miR-1231 gene" or "hsa-miR-1231" used herein includes the hsa-miR-1231 gene (miRBase Accession No. MIMAT0005586) described in SEQ ID NO: 172, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1231 gene can be obtained by a method described in Berezikov E et al., 2007, Mol Cell, Vol. 28, p. 328-336. Also, "hsa-mir-1231" (miRBase Accession No. MI0006321, SEQ ID NO: 364) having a hairpin-like structure is known as a precursor of "hsa-miR-1231".

[0222] The term "hsa-miR-1233-5p gene" or "hsa-miR-1233-5p" used herein includes the hsa-miR-1233-5p gene (miRBase Accession No. MIMAT0022943) described in SEQ ID NO: 173, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1233-5p gene can be obtained by a method described in Berezikov E et al., 2007, Mol Cell, Vol. 28, p. 328-336. Also, "hsa-mir-1233-1 and hsa-mir-1233-2" (miRBase Accession Nos. MI0006323 and MI0015973, SEQ ID NOs: 365 and 366) having a hairpin-like structure are known as precursors of "hsa-miR-1233-5p".

[0223] The term "hsa-miR-150-3p gene" or "hsa-miR-150-3p" used herein includes the hsa-miR-150-3p gene (miRBase Accession No. MIMAT0004610) described in SEQ ID NO: 174, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-150-3p gene can be obtained by a method described in Lagos-Quintana M et al., 2002, Curr Biol, Vol. 12, p. 735-739. Also, "hsa-mir-150" (miRBase Accession No. MI0000479, SEQ ID NO: 367) having a hairpin-like structure is known as a precursor of "hsa-miR-150-3p".

[0224] The term "hsa-miR-1225-3p gene" or "hsa-miR-1225-3p" used herein includes the hsa-miR-1225-3p gene (miRBase Accession No. MIMAT0005573) described in SEQ ID NO: 175, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1225-3p gene can be obtained by a method described in Berezikov E et al., 2007, Mol Cell, Vol. 28, p. 328-336. Also, "hsa-mir-1225" (miRBase Accession No. MI0006311, SEQ ID NO: 235) having a hairpin-like structure is known as a precursor of "hsa-miR-1225-3p".

[0225] The term "hsa-miR-92a-2-5p gene" or "hsa-miR-92a-2-5p" used herein includes the hsa-miR-92a-2-5p gene

(miRBase Accession No. MIMAT0004508) described in SEQ ID NO: 176, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-92a-2-5p gene can be obtained by a method described in Mourelatos Z et al., 2002, Genes Dev, Vol. 16, p. 720-728. Also, "hsa-mir-92a-2" (miRBase Accession No. MI0000094, SEQ ID NO: 368) having a hairpin-like structure is known as a precursor of "hsa-miR-92a-2-5p".

[0226] The term "hsa-miR-423-5p gene" or "hsa-miR-423-5p" used herein includes the hsa-miR-423-5p gene (miRBase Accession No. MIMAT0004748) described in SEQ ID NO: 177, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-423-5p gene can be obtained by a method described in Kasashima K et al., 2004, Biochem Biophys Res Commun, Vol. 322, p. 403-410. Also, "hsa-mir-423" (miRBase Accession No. MI0001445, SEQ ID NO: 369) having a hairpin-like structure is known as a precursor of "hsa-miR-423-5p".

[0227] The term "hsa-miR-1268a gene" or "hsa-miR-1268a" used herein includes the hsa-miR-1268a gene (miRBase Accession No. MIMAT0005922) described in SEQ ID NO: 178, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1268a gene can be obtained by a method described in Morin RD et al., 2008, Genome Res, Vol. 18, p. 610-621. Also, "hsa-mir-1268a" (miRBase Accession No. MI0006405, SEQ ID NO: 370) having a hairpin-like structure is known as a precursor of "hsa-miR-1268a".

[0228] The term "hsa-miR-128-2-5p gene" or "hsa-miR-128-2-5p" used herein includes the hsa-miR-128-2-5p gene (miRBase Accession No. MIMAT0031095) described in SEQ ID NO: 179, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-128-2-5p gene can be obtained by a method described in Lagos-Quintana M et al., 2002, Curr Biol, Vol. 12, p. 735-739. Also, "hsa-mir-128-2" (miRBase Accession No. MI0000727, SEQ ID NO: 371) having a hairpin-like structure is known as a precursor of "hsa-miR-128-2-5p".

[0229] The term "hsa-miR-24-3p gene" or "hsa-miR-24-3p" used herein includes the hsa-miR-24-3p gene (miRBase Accession No. MIMAT0000080) described in SEQ ID NO: 180, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-24-3p gene can be obtained by a method described in Lagos-Quintana M et al., 2001, Science, Vol. 294, p. 853-858. Also, "hsa-mir-24-1 and hsa-mir-24-2" (miRBase Accession Nos. MI0000080 and MI0000081, SEQ ID NOs: 372 and 373) having a hairpin-like structure are known as precursors of "hsa-miR-24-3p".

[0230] The term "hsa-miR-4697-5p gene" or "hsa-miR-4697-5p" used herein includes the hsa-miR-4697-5p gene (miRBase Accession No. MIMAT0019791) described in SEQ ID NO: 181, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4697-5p gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4697" (miRBase Accession No. MI0017330, SEQ ID NO: 374) having a hairpin-like structure is known as a precursor of "hsa-miR-4697-5p".

[0231] The term "hsa-miR-3197 gene" or "hsa-miR-3197" used herein includes the hsa-miR-3197 gene (miRBase Accession No. MIMAT0015082) described in SEQ ID NO: 182, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3197 gene can be obtained by a method described in Stark MS et al., 2010, PLoS One, Vol. 5, e9685. Also, "hsa-mir-3197" (miRBase Accession No. MI0014245, SEQ ID NO: 375) having a hairpin-like structure is known as a precursor of "hsa-miR-3197".

[0232] The term "hsa-miR-675-5p gene" or "hsa-miR-675-5p" used herein includes the hsa-miR-675-5p gene (miRBase Accession No. MIMAT0004284) described in SEQ ID NO: 183, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-675-5p gene can be obtained by a method described in Cai X et al., 2007, RNA, Vol. 13, p. 313-316. Also, "hsa-mir-675" (miRBase Accession No. MI0005416, SEQ ID NO: 376) having a hairpin-like structure is known as a precursor of "hsa-miR-675-5p".

[0233] The term "hsa-miR-4486 gene" or "hsa-miR-4486" used herein includes the hsa-miR-4486 gene (miRBase Accession No. MIMAT0019020) described in SEQ ID NO: 184, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4486 gene can be obtained by a method described in Jima DD et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4486" (miRBase Accession No. MI0016847, SEQ ID NO: 377) having a hairpin-like structure is known as a precursor of "hsa-miR-4486".

[0234] The term "hsa-miR-7107-5p gene" or "hsa-miR-7107-5p" used herein includes the hsa-miR-7107-5p gene (miRBase Accession No. MIMAT0028111) described in SEQ ID NO: 185, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-7107-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-7107" (miRBase Accession No. MI0022958, SEQ ID NO: 378) having a hairpin-like structure is known as a precursor of "hsa-miR-7107-5p".

[0235] The term "hsa-miR-23a-3p gene" or "hsa-miR-23a-3p" used herein includes the hsa-miR-23a-3p gene (miRBase Accession No. MIMAT0000078) described in SEQ ID NO: 186, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-23a-3p gene can be obtained by a method described in Lagos-Quintana M et al., 2001, Science, Vol. 294, p. 853-858. Also, "hsa-mir-23a" (miRBase Accession No. MI0000079, SEQ ID NO: 379) having a hairpin-like structure is known as a precursor of "hsa-miR-23a-3p".

[0236] The term "hsa-miR-4667-5p gene" or "hsa-miR-4667-5p" used herein includes the hsa-miR-4667-5p gene (miRBase Accession No. MIMAT0019743) described in SEQ ID NO: 187, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4667-5p gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4667" (miRBase Accession No. MI0017297, SEQ ID NO: 380) having a

hairpin-like structure is known as a precursor of "hsa-miR-4667-5p".

[0237] The term "hsa-miR-451a gene" or "hsa-miR-451a" used herein includes the hsa-miR-451a gene (miRBase Accession No. MIMAT0001631) described in SEQ ID NO: 188, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-451a gene can be obtained by a method described in Altuvia Y et al., 2005, Nucleic Acids Res, Vol. 33, p. 2697-2706. Also, "hsa-mir-451a" (miRBase Accession No. MI0001729, SEQ ID NO: 381) having a hairpin-like structure is known as a precursor of "hsa-miR-451a".

[0238] The term "hsa-miR-3940-5p gene" or "hsa-miR-3940-5p" used herein includes the hsa-miR-3940-5p gene (miRBase Accession No. MIMAT0019229) described in SEQ ID NO: 189, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3940-5p gene can be obtained by a method described in Liao JY et al., 2010, PLoS One, Vol. 5, e10563. Also, "hsa-mir-3940" (miRBase Accession No. MI0016597, SEQ ID NO: 382) having a hairpin-like structure is known as a precursor of "hsa-miR-3940-5p".

[0239] The term "hsa-miR-8059 gene" or "hsa-miR-8059" used herein includes the hsa-miR-8059 gene (miRBase Accession No. MIMAT0030986) described in SEQ ID NO: 190, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-8059 gene can be obtained by a method described in Wang HJ et al., 2013, Shock, Vol. 39, p. 480-487. Also, "hsa-mir-8059" (miRBase Accession No. MI0025895, SEQ ID NO: 383) having a hairpin-like structure is known as a precursor of "hsa-miR-8059".

[0240] The term "hsa-miR-6813-5p gene" or "hsa-miR-6813-5p" used herein includes the hsa-miR-6813-5p gene (miRBase Accession No. MIMAT0027526) described in SEQ ID NO: 191, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6813-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6813" (miRBase Accession No. MI0022658, SEQ ID NO: 384) having a hairpin-like structure is known as a precursor of "hsa-miR-6813-5p".

[0241] The term "hsa-miR-4492 gene" or "hsa-miR-4492" used herein includes the hsa-miR-4492 gene (miRBase Accession No. MIMAT0019027) described in SEQ ID NO: 192, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4492 gene can be obtained by a method described in Jima DD et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4492" (miRBase Accession No. MI0016854, SEQ ID NO: 385) having a hairpin-like structure is known as a precursor of "hsa-miR-4492".

[0242] The term "hsa-miR-4476 gene" or "hsa-miR-4476" used herein includes the hsa-miR-4476 gene (miRBase Accession No. MIMAT0019003) described in SEQ ID NO: 193, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4476 gene can be obtained by a method described in Jima DD et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4476" (miRBase Accession No. MI0016828, SEQ ID NO: 386) having a hairpin-like structure is known as a precursor of "hsa-miR-4476".

[0243] The term "hsa-miR-6090 gene" or "hsa-miR-6090" used herein includes the hsa-miR-6090 gene (miRBase Accession No. MIMAT0023715) described in SEQ ID NO: 194, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6090 gene can be obtained by a method described in Yoo JK et al., 2012, Stem Cells Dev, Vol. 21, p. 2049-2057. Also, "hsa-mir-6090" (miRBase Accession No. MI0020367, SEQ ID NO: 387) having a hairpin-like structure is known as a precursor of "hsa-miR-6090".

[0244] The term "hsa-miR-6836-3p gene" or "hsa-miR-6836-3p" used herein includes the hsa-miR-6836-3p gene (miRBase Accession No. MIMAT0027575) described in SEQ ID NO: 606, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6836-3p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6836" (miRBase Accession No. MI0022682, SEQ ID NO: 615) having a hairpin-like structure is known as a precursor of "hsa-miR-6836-3p".

[0245] The term "hsa-miR-3195 gene" or "hsa-miR-3195" used herein includes the hsa-miR-3195 gene (miRBase Accession No. MIMAT0015079) described in SEQ ID NO: 607, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3195 gene can be obtained by a method described in Stark MS et al., 2010, PLoS One, Vol. 5, e9685. Also, "hsa-mir-3195" (miRBase Accession No. MI0014240, SEQ ID NO: 616) having a hairpin-like structure is known as a precursor of "hsa-miR-3195".

[0246] The term "hsa-miR-718 gene" or "hsa-miR-718" used herein includes the hsa-miR-718 gene (miRBase Accession No. MIMAT0012735) described in SEQ ID NO: 608, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-718 gene can be obtained by a method described in Artzi S et al., 2008, BMC Bioinformatics, Vol. 9, p. 39. Also, "hsa-mir-718" (miRBase Accession No. MI0012489, SEQ ID NO: 617) having a hairpin-like structure is known as a precursor of "hsa-miR-718".

[0247] The term "hsa-miR-3178 gene" or "hsa-miR-3178" used herein includes the hsa-miR-3178 gene (miRBase Accession No. MIMAT0015055) described in SEQ ID NO: 609, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3178 gene can be obtained by a method described in Stark MS et al., 2010, PLoS One, Vol. 5, e9685. Also, "hsa-mir-3178" (miRBase Accession No. MI0014212, SEQ ID NO: 618) having a hairpin-like structure is known as a precursor of "hsa-miR-3178".

[0248] The term "hsa-miR-638 gene" or "hsa-miR-638" used herein includes the hsa-miR-638 gene (miRBase Accession No. MIMAT0003308) described in SEQ ID NO: 610, a homolog or an ortholog of a different organism species, and

the like. The hsa-miR-638 gene can be obtained by a method described in Cummins JM et al., 2006, Proc Natl Acad Sci USA, Vol. 103, p. 3687-3692. Also, "hsa-mir-638" (miRBase Accession No. MI0003653, SEQ ID NO: 619) having a hairpin-like structure is known as a precursor of "hsa-miR-638".

[0249] The term "hsa-miR-4497 gene" or "hsa-miR-4497" used herein includes the hsa-miR-4497 gene (miRBase Accession No. MIMAT0019032) described in SEQ ID NO: 611, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4497 gene can be obtained by a method described in Jima DD et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4497" (miRBase Accession No. MI0016859, SEQ ID NO: 620) having a hairpin-like structure is known as a precursor of "hsa-miR-4497".

[0250] The term "hsa-miR-6085 gene" or "hsa-miR-6085" used herein includes the hsa-miR-6085 gene (miRBase Accession No. MIMAT0023710) described in SEQ ID NO: 612, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6085 gene can be obtained by a method described in Voellenkle C et al., 2012, RNA, Vol. 18, p. 472-484. Also, "hsa-mir-6085" (miRBase Accession No. MI0020362, SEQ ID NO: 621) having a hairpin-like structure is known as a precursor of "hsa-miR-6085".

[0251] The term "hsa-miR-6752-5p gene" or "hsa-miR-6752-5p" used herein includes the hsa-miR-6752-5p gene (miRBase Accession No. MIMAT0027404) described in SEQ ID NO: 613, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6752-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6752" (miRBase Accession No. MI0022597, SEQ ID NO: 622) having a hairpin-like structure is known as a precursor of "hsa-miR-6752-5p".

[0252] The term "hsa-miR-135a-3p gene" or "hsa-miR-135a-3p" used herein includes the hsa-miR-135a-3p gene (miRBase Accession No. MIMAT0004595) described in SEQ ID NO: 614, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-135a-3p gene can be obtained by a method described in Lagos-Quintana M et al., 2002, Curr Biol, Vol. 12, p. 735-739. Also, "hsa-mir-135a" (miRBase Accession No. MI0000452, SEQ ID NO: 623) having a hairpin-like structure is known as a precursor of "hsa-miR-135a-3p".

[0253] A mature miRNA may become a variant due to the sequence that is cleaved shorter or longer by one to several upstream or downstream nucleotides or nucleotide substitution when cut out as the mature miRNA from its RNA precursor having a hairpin-like structure. This variant is called isomiR (Morin RD. et al., 2008, Genome Res., Vol. 18, p. 610-621). The miRBase Release 20 shows the nucleotide sequences represented by SEQ ID NOs: 1 to 194 and 606 to 614 as well as a large number of the nucleotide sequence variants and fragments represented by SEQ ID NOs: 388 to 605 and 624 to 635, which are called isomiRs. These variants can also be obtained as miRNAs having a nucleotide sequence represented by any of SEQ ID NOs: 1 to 194 and 606 to 614. Specifically, among the variants of polynucleotides consisting of the nucleotide sequence represented by any of SEQ ID NOs: 5, 7, 8, 9, 11, 16, 19, 20, 21, 26, 27, 28, 30, 34, 37, 38, 39, 41, 43, 45, 46, 48, 50, 54, 55, 57, 58, 61, 62, 63, 64, 65, 66, 67, 69, 70, 71, 73, 74, 76, 77, 78, 80, 81, 82, 84, 85, 86, 88, 89, 94, 95, 97, 98, 99, 100, 101, 104, 107, 108, 109, 110, 111, 112, 113, 115, 116, 117, 119, 120, 123, 125, 131, 132, 133, 135, 136, 137, 140, 141, 142, 147, 151, 152, 157, 161, 162, 165, 166, 167, 168, 169, 171, 173, 174, 176, 177, 178, 179, 180, 182, 183, 184, 186, 187, 188, 189, 192, 193, 607, 608, 609, 610, 611 and 614, or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t according to the present invention, examples of the longest variants registered in the miRBase Release 20 include polynucleotides represented by SEQ ID NOs:388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 624, 626, 628, 630, 632 and 634, respectively. Also, among the variants of polynucleotides consisting of a nucleotide sequence represented by any of SEQ ID NOs: 5, 7, 8, 9, 11, 16, 19, 20, 21, 26, 27, 28, 30, 34, 37, 38, 39, 41, 43, 45, 46, 48, 50, 54, 55, 57, 58, 61, 62, 63, 64, 65, 66, 67, 69, 70, 71, 73, 74, 76, 77, 78, 80, 81, 82, 84, 85, 86, 88, 89, 94, 95, 97, 98, 99, 100, 101, 104, 107, 108, 109, 110, 111, 112, 113, 115, 116, 117, 119, 120, 123, 125, 131, 132, 133, 135, 136, 137, 140, 141, 142, 147, 151, 152, 157, 161, 162, 165, 166, 167, 168, 169, 171, 173, 174, 176, 177, 178, 179, 180, 182, 183, 184, 186, 187, 188, 189, 192, 193, 607, 608, 609, 610, 611 and 614, or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t according to the present invention, examples of the shortest variants registered in the miRBase Release 20 include polynucleotides having sequences represented by SEQ ID NOs: 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 625, 627, 629, 631, 633 and 635, respectively. In addition to these variants and fragments, examples thereof include a large number of isomiR polynucleotides of SEQ ID NOs: 1 to 194 and 606 to 614 registered in miRBase. Examples of the polynucleotide comprising a nucleotide sequence represented by any of SEQ ID NOs: 1 to 194 and 606 to 614 to 494 include a polynucleotide represented by any of SEQ ID NOs: 195 to 387 and 615 to 623, which are

their respective precursors.

[0254] The names and miRBase Accession Nos. (registration numbers) of the genes represented by SEQ ID NOs: 1 to 635 are shown in Table 1.

[Table 1]

SEQ ID NO:	Gene name	miRBase registration No.
1	hsa-miR-6726-5p	MIMAT0027353
2	hsa-miR-4257	MIMAT0016878
3	hsa-miR-6787-5p	MIMAT0027474
4	hsa-miR-6780b-5p	MIMAT0027572
5	hsa-miR-3131	MIMAT0014996
6	hsa-miR-7108-5p	MIMAT0028113
7	hsa-miR-1343-3p	MIMAT0019776
8	hsa-miR-1247-3p	MIMAT0022721
9	hsa-miR-4651	MIMAT0019715
10	hsa-miR-6757-5p	MIMAT0027414
11	hsa-miR-3679-5p	MIMAT0018104
12	hsa-miR-7641	MIMAT0029782
13	hsa-miR-6746-5p	MIMAT0027392
14	hsa-miR-8072	MIMAT0030999
15	hsa-miR-6741-5p	MIMAT0027383
16	hsa-miR-1908-5p	MIMAT0007881
17	hsa-miR-6857-5p	MIMAT0027614
18	hsa-miR-4746-3p	MIMAT0019881
19	hsa-miR-744-5p	MIMAT0004945
20	hsa-miR-4792	MIMAT0019964
21	hsa-miR-564	MIMAT0003228
22	hsa-miR-6791-5p	MIMAT0027482
23	hsa-miR-6825-5p	MIMAT0027550
24	hsa-miR-6826-5p	MIMAT0027552
25	hsa-miR-4665-3p	MIMAT0019740
26	hsa-miR-4467	MIMAT0018994
27	hsa-miR-3188	MIMAT0015070
28	hsa-miR-6125	MIMAT0024598
29	hsa-miR-6756-5p	MIMAT0027412
30	hsa-miR-1228-3p	MIMAT0005583
31	hsa-miR-8063	MIMAT0030990
32	hsa-miR-8069	MIMAT0030996
33	hsa-miR-6875-5p	MIMAT0027650
34	hsa-miR-3185	MIMAT0015065
35	hsa-miR-4433b-3p	MIMAT0030414

(continued)

SEQ ID NO:	Gene name	miRBase registration No.
36	hsa-miR-6887-5p	MIMAT0027674
37	hsa-miR-128-1-5p	MIMAT0026477
38	hsa-miR-6724-5p	MIMAT0025856
39	hsa-miR-1914-3p	MIMAT0007890
40	hsa-miR-1225-5p	MIMAT0005572
41	hsa-miR-4419b	MIMAT0019034
42	hsa-miR-7110-5p	MIMAT0028117
43	hsa-miR-187-5p	MIMAT0004561
44	hsa-miR-3184-5p	MIMAT0015064
45	hsa-miR-204-3p	MIMAT0022693
46	hsa-miR-5572	MIMAT0022260
47	hsa-miR-6729-5p	MIMAT0027359
48	hsa-miR-615-5p	MIMAT0004804
49	hsa-miR-6749-5p	MIMAT0027398
50	hsa-miR-6515-3p	MIMAT0025487
51	hsa-miR-3937	MIMAT0018352
52	hsa-miR-6840-3p	MIMAT0027583
53	hsa-miR-6893-5p	MIMAT0027686
54	hsa-miR-4728-5p	MIMAT0019849
55	hsa-miR-6717-5p	MIMAT0025846
56	hsa-miR-7113-3p	MIMAT0028124
57	hsa-miR-4665-5p	MIMAT0019739
58	hsa-miR-642b-3p	MIMAT0018444
59	hsa-miR-7109-5p	MIMAT0028115
60	hsa-miR-6842-5p	MIMAT0027586
61	hsa-miR-4442	MIMAT0018960
62	hsa-miR-4433-3p	MIMAT0018949
63	hsa-miR-4707-5p	MIMAT0019807
64	hsa-miR-6126	MIMAT0024599
65	hsa-miR-4449	MIMAT0018968
66	hsa-miR-4706	MIMAT0019806
67	hsa-miR-1913	MIMAT0007888
68	hsa-miR-602	MIMAT0003270
69	hsa-miR-939-5p	MIMAT0004982
70	hsa-miR-4695-5p	MIMAT0019788
71	hsa-miR-711	MIMAT0012734
72	hsa-miR-6816-5p	MIMAT0027532
73	hsa-miR-4632-5p	MIMAT0022977

(continued)

SEQ ID NO:	Gene name	miRBase registration No.
74	hsa-miR-6721-5p	MIMAT0025852
75	hsa-miR-7847-3p	MIMAT0030422
76	hsa-miR-6132	MIMAT0024616
77	hsa-miR-887-3p	MIMAT0004951
78	hsa-miR-3679-3p	MIMAT0018105
79	hsa-miR-6784-5p	MIMAT0027468
80	hsa-miR-1249	MIMAT0005901
81	hsa-miR-937-5p	MIMAT0022938
82	hsa-miR-5195-3p	MIMAT0021127
83	hsa-miR-6732-5p	MIMAT0027365
84	hsa-miR-4417	MIMAT0018929
85	hsa-miR-4281	MIMAT0016907
86	hsa-miR-4734	MIMAT0019859
87	hsa-miR-6766-3p	MIMAT0027433
88	hsa-miR-663a	MIMAT0003326
89	hsa-miR-4513	MIMAT0019050
90	hsa-miR-6781-5p	MIMAT0027462
91	hsa-miR-1227-5p	MIMAT0022941
92	hsa-miR-6845-5p	MIMAT0027590
93	hsa-miR-6798-5p	MIMAT0027496
94	hsa-miR-3620-5p	MIMAT0022967
95	hsa-miR-1915-5p	MIMAT0007891
96	hsa-miR-4294	MIMAT0016849
97	hsa-miR-642a-3p	MIMAT0020924
98	hsa-miR-371a-5p	MIMAT0004687
99	hsa-miR-940	MIMAT0004983
100	hsa-miR-4450	MIMAT0018971
101	hsa-miR-4723-5p	MIMAT0019838
102	hsa-miR-1469	MIMAT0007347
103	hsa-miR-6861-5p	MIMAT0027623
104	hsa-miR-7975	MIMAT0031178
105	hsa-miR-6879-5p	MIMAT0027658
106	hsa-miR-6802-5p	MIMAT0027504
107	hsa-miR-1268b	MIMAT0018925
108	hsa-miR-663b	MIMAT0005867
109	hsa-miR-125a-3p	MIMAT0004602
110	hsa-miR-2861	MIMAT0013 802
111	hsa-miR-6088	MIMAT0023713

(continued)

SEQ ID NO:	Gene name	miRBase registration No.
112	hsa-miR-4758-5p	MIMAT0019903
113	hsa-miR-296-3p	MIMAT0004679
114	hsa-miR-6738-5p	MIMAT0027377
115	hsa-miR-671-5p	MIMAT0003880
116	hsa-miR-4454	MIMAT0018976
117	hsa-miR-4516	MIMAT0019053
118	hsa-miR-7845-5p	MIMAT0030420
119	hsa-miR-4741	MIMAT0019871
120	hsa-miR-92b-5p	MIMAT0004792
121	hsa-miR-6795-5p	MIMAT0027490
122	hsa-miR-6805-3p	MIMAT0027511
123	hsa-miR-4725-3p	MIMAT0019844
124	hsa-miR-6782-5p	MIMAT0027464
125	hsa-miR-4688	MIMAT0019777
126	hsa-miR-6850-5p	MIMAT0027600
127	hsa-miR-6777-5p	MIMAT0027454
128	hsa-miR-6785-5p	MIMAT0027470
129	hsa-miR-7106-5p	MIMAT0028109
130	hsa-miR-3663-3p	MIMAT0018085
131	hsa-miR-6131	MIMAT0024615
132	hsa-miR-1915-3p	MIMAT0007892
133	hsa-miR-4532	MIMAT0019071
134	hsa-miR-6820-5p	MIMAT0027540
135	hsa-miR-4689	MIMAT0019778
136	hsa-miR-4638-5p	MIMAT0019695
137	hsa-miR-3656	MIMAT0018076
138	hsa-miR-3621	MIMAT0018002
139	hsa-miR-6769b-5p	MIMAT0027620
140	hsa-miR-149-3p	MIMAT0004609
141	hsa-miR-23b-3p	MIMAT0000418
142	hsa-miR-3135b	MIMAT0018985
143	hsa-miR-6848-5p	MIMAT0027596
144	hsa-miR-6769a-5p	MIMAT0027438
145	hsa-miR-4327	MIMAT0016889
146	hsa-miR-6765-3p	MIMAT0027431
147	hsa-miR-6716-5p	MIMAT0025844
148	hsa-miR-6877-5p	MIMAT0027654
149	hsa-miR-6727-5p	MIMAT0027355

(continued)

SEQ ID NO:	Gene name	miRBase registration No.
150	hsa-miR-4534	MIMAT0019073
151	hsa-miR-614	MIMAT0003282
152	hsa-miR-1202	MIMAT0005865
153	hsa-miR-575	MIMAT0003240
154	hsa-miR-6870-5p	MIMAT0027640
155	hsa-miR-6722-3p	MIMAT0025854
156	hsa-miR-7977	MIMAT0031180
157	hsa-miR-4649-5p	MIMAT0019711
158	hsa-miR-4675	MIMAT0019757
159	hsa-miR-6075	MIMAT0023700
160	hsa-miR-6779-5p	MIMAT0027458
161	hsa-miR-4271	MIMAT0016901
162	hsa-miR-3196	MIMAT0015080
163	hsa-miR-6803-5p	MIMAT0027506
164	hsa-miR-6789-5p	MIMAT0027478
165	hsa-miR-4648	MIMAT0019710
166	hsa-miR-4508	MIMAT0019045
167	hsa-miR-4749-5p	MIMAT0019885
168	hsa-miR-4505	MIMAT0019041
169	hsa-miR-5698	MIMAT0022491
170	hsa-miR-1199-5p	MIMAT0031119
171	hsa-miR-4763-3p	MIMAT0019913
172	hsa-miR-1231	MIMAT0005586
173	hsa-miR-1233-5p	MIMAT0022943
174	hsa-miR-150-3p	MIMAT0004610
175	hsa-miR-1225-3p	MIMAT0005573
176	hsa-miR-92a-2-5p	MIMAT0004508
177	hsa-miR-423-5p	MIMAT0004748
178	hsa-miR-1268a	MIMAT0005922
179	hsa-miR-128-2-5p	MIMAT0031095
180	hsa-miR-24-3p	MIMAT0000080
181	hsa-miR-4697-5p	MIMAT0019791
182	hsa-miR-3197	MIMAT0015082
183	hsa-miR-675-5p	MIMAT0004284
184	hsa-miR-4486	MIMAT0019020
185	hsa-miR-7107-5p	MIMAT0028111
186	hsa-miR-23a-3p	MIMAT0000078
187	hsa-miR-4667-5p	MIMAT0019743

(continued)

SEQ ID NO:	Gene name	miRBase registration No.
188	hsa-miR-451a	MIMAT0001631
189	hsa-miR-3940-5p	MIMAT0019229
190	hsa-miR-8059	MIMAT0030986
191	hsa-miR-6813-5p	MIMAT0027526
192	hsa-miR-4492	MIMAT0019027
193	hsa-miR-4476	MIMAT0019003
194	hsa-miR-6090	MIMAT0023715
195	hsa-mir-6726	MI0022571
196	hsa-mir-4257	MI0015856
197	hsa-mir-6787	MI0022632
198	hsa-mir-6780b	MI0022681
199	hsa-mir-3131	MI0014151
200	hsa-mir-7108	MI0022959
201	hsa-mir-1343	MI0017320
202	hsa-mir-1247	MI0006382
203	hsa-mir-4651	MI0017279
204	hsa-mir-6757	MI0022602
205	hsa-mir-3679	MI0016080
206	hsa-mir-7641-1	MI0024975
207	hsa-mir-7641-2	MI0024976
208	hsa-mir-6746	MI0022591
209	hsa-mir-8072	MI0025908
210	hsa-mir-6741	MI0022586
211	hsa-mir-1908	MI0008329
212	hsa-mir-6857	MI0022703
213	hsa-mir-4746	MI0017385
214	hsa-mir-744	MI0005559
215	hsa-mir-4792	MI0017439
216	hsa-mir-564	MI0003570
217	hsa-mir-6791	MI0022636
218	hsa-mir-6825	MI0022670
219	hsa-mir-6826	MI0022671
220	hsa-mir-4665	MI0017295
221	hsa-mir-4467	MI0016818
222	hsa-mir-3188	MI0014232
223	hsa-mir-6125	MI0021259
224	hsa-mir-6756	MI0022601
225	hsa-mir-1228	MI0006318

(continued)

SEQ ID NO:	Gene name	miRBase registration No.
226	hsa-mir-8063	MI0025899
227	hsa-mir-8069	MI0025905
228	hsa-mir-6875	MI0022722
229	hsa-mir-3185	MI0014227
230	hsa-mir-4433b	MI0025511
231	hsa-mir-6887	MI0022734
232	hsa-mir-128-1	MI0000447
233	hsa-mir-6724	MI0022559
234	hsa-mir-1914	MI0008335
235	hsa-mir-1225	MI0006311
236	hsa-mir-4419b	MI0016861
237	hsa-mir-7110	MI0022961
238	hsa-mir-187	MI0000274
239	hsa-mir-3184	MI0014226
240	hsa-mir-204	MI0000284
241	hsa-mir-5572	MI0019117
242	hsa-mir-6729	MI0022574
243	hsa-mir-615	MI0003628
244	hsa-mir-6749	MI0022594
245	hsa-mir-6515	MI0022227
246	hsa-mir-3937	MI0016593
247	hsa-mir-6840	MI0022686
248	hsa-mir-6893	MI0022740
249	hsa-mir-4728	MI0017365
250	hsa-mir-6717	MI0022551
251	hsa-mir-7113	MI0022964
252	hsa-mir-642b	MI0016685
253	hsa-mir-7109	MI0022960
254	hsa-mir-6842	MI0022688
255	hsa-mir-4442	MI0016785
256	hsa-mir-4433	MI0016773
257	hsa-mir-4707	MI0017340
258	hsa-mir-6126	MI0021260
259	hsa-mir-4449	MI0016792
260	hsa-mir-4706	MI0017339
261	hsa-mir-1913	MI0008334
262	hsa-mir-602	MI0003615
263	hsa-mir-939	MI0005761

(continued)

SEQ ID NO:	Gene name	miRBase registration No.
264	hsa-mir-4695	MI0017328
265	hsa-mir-711	MI0012488
266	hsa-mir-6816	MI0022661
267	hsa-mir-4632	MI0017259
268	hsa-mir-6721	MI0022556
269	hsa-mir-7847	MI0025517
270	hsa-mir-6132	MI0021277
271	hsa-mir-887	MI0005562
272	hsa-mir-6784	MI0022629
273	hsa-mir-1249	MI0006384
274	hsa-mir-937	MI0005759
275	hsa-mir-5195	MI0018174
276	hsa-mir-6732	MI0022577
277	hsa-mir-4417	M10016753
278	hsa-mir-4281	MI0015885
279	hsa-mir-4734	MI0017371
280	hsa-mir-6766	MI0022611
281	hsa-mir-663a	MI0003672
282	hsa-mir-4513	MI0016879
283	hsa-mir-6781	MI0022626
284	hsa-mir-1227	MI0006316
285	hsa-mir-6845	MI0022691
286	hsa-mir-6798	MI0022643
287	hsa-mir-3620	MI0016011
288	hsa-mir-1915	MI0008336
289	hsa-mir-4294	MI0015827
290	hsa-mir-642a	MI0003657
291	hsa-mir-371a	MI0000779
292	hsa-mir-940	MI0005762
293	hsa-mir-4450	MI0016795
294	hsa-mir-4723	MI0017359
295	hsa-mir-1469	MI0007074
296	hsa-mir-6861	MI0022708
297	hsa-mir-7975	MI0025751
298	hsa-mir-6879	MI0022726
299	hsa-mir-6802	MI0022647
300	hsa-mir-1268b	MI0016748
301	hsa-mir-663b	MI0006336

(continued)

SEQ ID NO:	Gene name	miRBase registration No.
302	hsa-mir-125a	MI0000469
303	hsa-mir-2861	MI0013006
304	hsa-mir-6088	MI0020365
305	hsa-mir-4758	MI0017399
306	hsa-mir-296	MI0000747
307	hsa-mir-6738	MI0022583
308	hsa-mir-671	MI0003760
309	hsa-mir-4454	MI0016800
310	hsa-mir-4516	MI0016882
311	hsa-mir-7845	MI0025515
312	hsa-mir-4741	MI0017379
313	hsa-mir-92b	MI0003560
314	hsa-mir-6795	MI0022640
315	hsa-mir-6805	MI0022650
316	hsa-mir-4725	MI0017362
317	hsa-mir-6782	MI0022627
318	hsa-mir-4688	MI0017321
319	hsa-mir-6850	MI0022696
320	hsa-mir-6777	MI0022622
321	hsa-mir-6785	MI0022630
322	hsa-mir-7106	MI0022957
323	hsa-mir-3663	MI0016064
324	hsa-mir-6131	MI0021276
325	hsa-mir-4532	MI0016899
326	hsa-mir-6820	MI0022665
327	hsa-mir-4689	MI0017322
328	hsa-mir-4638	MI0017265
329	hsa-mir-3656	MI0016056
330	hsa-mir-3621	MI0016012
331	hsa-mir-6769b	MI0022706
332	hsa-mir-149	MI0000478
333	hsa-mir-23b	MI0000439
334	hsa-mir-3135b	MI0016809
335	hsa-mir-6848	MI0022694
336	hsa-mir-6769a	MI0022614
337	hsa-mir-4327	MI0015867
338	hsa-mir-6765	MI0022610
339	hsa-mir-6716	MI0022550

(continued)

SEQ ID NO:	Gene name	miRBase registration No.
340	hsa-mir-6877	MI0022724
341	hsa-mir-6727	MI0022572
342	hsa-mir-4534	MI0016901
343	hsa-mir-614	MI0003627
344	hsa-mir-1202	MI0006334
345	hsa-mir-575	MI0003582
346	hsa-mir-6870	MI0022717
347	hsa-mir-6722	MI0022557
348	hsa-mir-7977	MI0025753
349	hsa-mir-4649	MI0017276
350	hsa-mir-4675	MI0017306
351	hsa-mir-6075	MI0020352
352	hsa-mir-6779	MI0022624
353	hsa-mir-4271	MI0015879
354	hsa-mir-3196	MI0014241
355	hsa-mir-6803	MI0022648
356	hsa-mir-6789	MI0022634
357	hsa-mir-4648	MI0017275
358	hsa-mir-4508	MI0016872
359	hsa-mir-4749	MI0017388
360	hsa-mir-4505	MI0016868
361	hsa-mir-5698	MI0019305
362	hsa-mir-1199	MI0020340
363	hsa-mir-4763	MI0017404
364	hsa-mir-1231	MI0006321
365	hsa-mir-1233-1	MI0006323
366	hsa-mir-1233-2	MI0015973
367	hsa-mir-150	MI0000479
368	hsa-mir-92a-2	MI0000094
369	hsa-mir-423	MI0001445
370	hsa-mir-1268a	MI0006405
371	hsa-mir-128-2	MI0000727
372	hsa-mir-24-1	MI0000080
373	hsa-mir-24-2	MI0000081
374	hsa-mir-4697	MI0017330
375	hsa-mir-3197	MI0014245
376	hsa-mir-675	MI0005416
377	hsa-mir-4486	MI0016847

(continued)

SEQ ID NO:	Gene name	miRBase registration No.
378	hsa-mir-7107	MI0022958
379	hsa-mir-23a	MI0000079
380	hsa-mir-4667	MI0017297
381	hsa-mir-451a	MI0001729
382	hsa-mir-3940	MI0016597
383	hsa-mir-8059	MI0025895
384	hsa-mir-6813	MI0022658
385	hsa-mir-4492	MI0016854
386	hsa-mir-4476	MI0016828
387	hsa-mir-6090	MI0020367
388	isomiR example 1 of SEQ ID NO: 5	-
389	isomiR example 2 of SEQ ID NO: 5	-
390	isomiR example 1 of SEQ ID NO: 7	-
391	isomiR example 2 of SEQ ID NO: 7	-
392	isomiR example 1 of SEQ ID NO: 8	-
393	isomiR example 2 of SEQ ID NO: 8	-
394	isomiR example 1 of SEQ ID NO: 9	-
395	isomiR example 2 of SEQ ID NO: 9	-
396	isomiR example 1 of SEQ ID NO: 11	-
397	isomiR example 2 of SEQ ID NO: 11	-
398	isomiR example 1 of SEQ ID NO: 16	-
399	isomiR example 2 of SEQ ID NO: 16	-
400	isomiR example 1 of SEQ ID NO: 19	-
401	isomiR example 2 of SEQ ID NO: 19	-
402	isomiR example 1 of SEQ ID NO: 20	-
403	isomiR example 2 of SEQ ID NO: 20	-
404	isomiR example 1 of SEQ ID NO: 21	-
405	isomiR example 2 of SEQ ID NO: 21	-
406	isomiR example 1 of SEQ ID NO: 26	-
407	isomiR example 2 of SEQ ID NO: 26	-
408	isomiR example 1 of SEQ ID NO: 27	-
409	isomiR example 2 of SEQ ID NO: 27	-
410	isomiR example 1 of SEQ ID NO: 28	-
411	isomiR example 2 of SEQ ID NO: 28	-
412	isomiR example 1 of SEQ ID NO: 30	-
413	isomiR example 2 of SEQ ID NO: 30	-
414	isomiR example 1 of SEQ ID NO: 34	-
415	isomiR example 2 of SEQ ID NO: 34	-

(continued)

SEQ ID NO:	Gene name	miRBase registration No.
416	isomiR example 1 of SEQ ID NO: 37	-
417	isomiR example 2 of SEQ ID NO: 37	-
418	isomiR example 1 of SEQ ID NO: 38	-
419	isomiR example 2 of SEQ ID NO: 38	-
420	isomiR example 1 of SEQ ID NO: 39	-
421	isomiR example 2 of SEQ ID NO: 39	-
422	isomiR example 1 of SEQ ID NO: 41	-
423	isomiR example 2 of SEQ ID NO: 41	-
424	isomiR example 1 of SEQ ID NO: 43	-
425	isomiR example 2 of SEQ ID NO: 43	-
426	isomiR example 1 of SEQ ID NO: 45	-
427	isomiR example 2 of SEQ ID NO: 45	-
428	isomiR example 1 of SEQ ID NO: 46	-
429	isomiR example 2 of SEQ ID NO: 46	-
430	isomiR example 1 of SEQ ID NO: 48	-
431	isomiR example 2 of SEQ ID NO: 48	-
432	isomiR example 1 of SEQ ID NO: 50	-
433	isomiR example 2 of SEQ ID NO: 50	-
434	isomiR example 1 of SEQ ID NO: 54	-
435	isomiR example 2 of SEQ ID NO: 54	-
436	isomiR example 1 of SEQ ID NO: 55	-
437	isomiR example 2 of SEQ ID NO: 55	-
438	isomiR example 1 of SEQ ID NO: 57	-
439	isomiR example 2 of SEQ ID NO: 57	-
440	isomiR example 1 of SEQ ID NO: 58	-
441	isomiR example 2 of SEQ ID NO: 58	-
442	isomiR example 1 of SEQ ID NO: 61	-
443	isomiR example 2 of SEQ ID NO: 61	-
444	isomiR example 1 of SEQ ID NO: 62	-
445	isomiR example 2 of SEQ ID NO: 62	-
446	isomiR example 1 of SEQ ID NO: 63	-
447	isomiR example 2 of SEQ ID NO: 63	-
448	isomiR example 1 of SEQ ID NO: 64	-
449	isomiR example 2 of SEQ ID NO: 64	-
450	isomiR example 1 of SEQ ID NO: 65	-
451	isomiR example 2 of SEQ ID NO: 65	-
452	isomiR example 1 of SEQ ID NO: 66	-
453	isomiR example 2 of SEQ ID NO: 66	-

(continued)

SEQ ID NO:	Gene name	miRBase registration No.
454	isomiR example 1 of SEQ ID NO: 67	-
455	isomiR example 2 of SEQ ID NO: 67	-
456	isomiR example 1 of SEQ ID NO: 69	-
457	isomiR example 2 of SEQ ID NO: 69	-
458	isomiR example 1 of SEQ ID NO: 70	-
459	isomiR example 2 of SEQ ID NO: 70	-
460	isomiR example 1 of SEQ ID NO: 71	-
461	isomiR example 2 of SEQ ID NO: 71	-
462	isomiR example 1 of SEQ ID NO: 73	-
463	isomiR example 2 of SEQ ID NO: 73	-
464	isomiR example 1 of SEQ ID NO: 74	-
465	isomiR example 2 of SEQ ID NO: 74	-
466	isomiR example 1 of SEQ ID NO: 76	-
467	isomiR example 2 of SEQ ID NO: 76	-
468	isomiR example 1 of SEQ ID NO: 77	-
469	isomiR example 2 of SEQ ID NO: 77	-
470	isomiR example 1 of SEQ ID NO: 78	-
471	isomiR example 2 of SEQ ID NO: 78	-
472	isomiR example 1 of SEQ ID NO: 80	-
473	isomiR example 2 of SEQ ID NO: 80	-
474	isomiR example 1 of SEQ ID NO: 81	-
475	isomiR example 2 of SEQ ID NO: 81	-
476	isomiR example 1 of SEQ ID NO: 82	-
477	isomiR example 2 of SEQ ID NO: 82	-
478	isomiR example 1 of SEQ ID NO: 84	-
479	isomiR example 2 of SEQ ID NO: 84	-
480	isomiR example 1 of SEQ ID NO: 85	-
481	isomiR example 2 of SEQ ID NO: 85	-
482	isomiR example 1 of SEQ ID NO: 86	-
483	isomiR example 2 of SEQ ID NO: 86	-
484	isomiR example 1 of SEQ ID NO: 88	-
485	isomiR example 2 of SEQ ID NO: 88	-
486	isomiR example 1 of SEQ ID NO: 89	-
487	isomiR example 2 of SEQ ID NO: 89	-
488	isomiR example 1 of SEQ ID NO: 94	-
489	isomiR example 2 of SEQ ID NO: 94	-
490	isomiR example 1 of SEQ ID NO: 95	-
491	isomiR example 2 of SEQ ID NO: 95	-

(continued)

SEQ ID NO:	Gene name	miRBase registration No.
492	isomiR example 1 of SEQ ID NO: 97	-
493	isomiR example 2 of SEQ ID NO: 97	-
494	isomiR example 1 of SEQ ID NO: 98	-
495	isomiR example 2 of SEQ ID NO: 98	-
496	isomiR example 1 of SEQ ID NO: 99	-
497	isomiR example 2 of SEQ ID NO: 99	-
498	isomiR example 1 of SEQ ID NO: 100	-
499	isomiR example 2 of SEQ ID NO: 100	-
500	isomiR example 1 of SEQ ID NO: 101	-
501	isomiR example 2 of SEQ ID NO: 101	-
502	isomiR example 1 of SEQ ID NO: 104	-
503	isomiR example 2 of SEQ ID NO: 104	-
504	isomiR example 1 of SEQ ID NO: 107	-
505	isomiR example 2 of SEQ ID NO: 107	-
506	isomiR example 1 of SEQ ID NO: 108	-
507	isomiR example 2 of SEQ ID NO: 108	-
508	isomiR example 1 of SEQ ID NO: 109	-
509	isomiR example 2 of SEQ ID NO: 109	-
510	isomiR example 1 of SEQ ID NO: 110	-
511	isomiR example 2 of SEQ ID NO: 110	-
512	isomiR example 1 of SEQ ID NO: 111	-
513	isomiR example 2 of SEQ ID NO: 111	-
514	isomiR example 1 of SEQ ID NO: 112	-
515	isomiR example 2 of SEQ ID NO: 112	-
516	isomiR example 1 of SEQ ID NO: 113	-
517	isomiR example 2 of SEQ ID NO: 113	-
518	isomiR example 1 of SEQ ID NO: 115	-
519	isomiR example 2 of SEQ ID NO: 115	-
520	isomiR example 1 of SEQ ID NO: 116	-
521	isomiR example 2 of SEQ ID NO: 116	-
522	isomiR example 1 of SEQ ID NO: 117	-
523	isomiR example 2 of SEQ ID NO: 117	-
524	isomiR example 1 of SEQ ID NO: 119	-
525	isomiR example 2 of SEQ ID NO: 119	-
526	isomiR example 1 of SEQ ID NO: 120	-
527	isomiR example 2 of SEQ ID NO: 120	-
528	isomiR example 1 of SEQ ID NO: 123	-
529	isomiR example 2 of SEQ ID NO: 123	-

(continued)

SEQ ID NO:	Gene name	miRBase registration No.
530	isomiR example 1 of SEQ ID NO: 125	-
531	isomiR example 2 of SEQ ID NO: 125	-
532	isomiR example 1 of SEQ ID NO: 131	-
533	isomiR example 2 of SEQ ID NO: 131	-
534	isomiR example 1 of SEQ ID NO: 132	-
535	isomiR example 2 of SEQ ID NO: 132	-
536	isomiR example 1 of SEQ ID NO: 133	-
537	isomiR example 2 of SEQ ID NO: 133	-
538	isomiR example 1 of SEQ ID NO: 135	-
539	isomiR example 2 of SEQ ID NO: 135	-
540	isomiR example 1 of SEQ ID NO: 136	-
541	isomiR example 2 of SEQ ID NO: 136	-
542	isomiR example 1 of SEQ ID NO: 137	-
543	isomiR example 2 of SEQ ID NO: 137	-
544	isomiR example 1 of SEQ ID NO: 140	-
545	isomiR example 2 of SEQ ID NO: 140	-
546	isomiR example 1 of SEQ ID NO: 141	-
547	isomiR example 2 of SEQ ID NO: 141	-
548	isomiR example 1 of SEQ ID NO: 142	-
549	isomiR example 2 of SEQ ID NO: 142	-
550	isomiR example 1 of SEQ ID NO: 147	-
551	isomiR example 2 of SEQ ID NO: 147	-
552	isomiR example 1 of SEQ ID NO: 151	-
553	isomiR example 2 of SEQ ID NO: 151	-
554	isomiR example 1 of SEQ ID NO: 152	-
555	isomiR example 2 of SEQ ID NO: 152	-
556	isomiR example 1 of SEQ ID NO: 157	-
557	isomiR example 2 of SEQ ID NO: 157	-
558	isomiR example 1 of SEQ ID NO: 161	-
559	isomiR example 2 of SEQ ID NO: 161	-
560	isomiR example 1 of SEQ ID NO: 162	-
561	isomiR example 2 of SEQ ID NO: 162	-
562	isomiR example 1 of SEQ ID NO: 165	-
563	isomiR example 2 of SEQ ID NO: 165	-
564	isomiR example 1 of SEQ ID NO: 166	-
565	isomiR example 2 of SEQ ID NO: 166	-
566	isomiR example 1 of SEQ ID NO: 167	-
567	isomiR example 2 of SEQ ID NO: 167	-

(continued)

SEQ ID NO:	Gene name	miRBase registration No.
568	isomiR example 1 of SEQ ID NO: 168	-
569	isomiR example 2 of SEQ ID NO: 168	-
570	isomiR example 1 of SEQ ID NO: 169	-
571	isomiR example 2 of SEQ ID NO: 169	-
572	isomiR example 1 of SEQ ID NO: 171	-
573	isomiR example 2 of SEQ ID NO: 171	-
574	isomiR example 1 of SEQ ID NO: 173	-
575	isomiR example 2 of SEQ ID NO: 173	-
576	isomiR example 1 of SEQ ID NO: 174	-
577	isomiR example 2 of SEQ ID NO: 174	-
578	isomiR example 1 of SEQ ID NO: 176	-
579	isomiR example 2 of SEQ ID NO: 176	-
580	isomiR example 1 of SEQ ID NO: 177	-
581	isomiR example 2 of SEQ ID NO: 177	-
582	isomiR example 1 of SEQ ID NO: 178	-
583	isomiR example 2 of SEQ ID NO: 178	-
584	isomiR example 1 of SEQ ID NO: 179	-
585	isomiR example 2 of SEQ ID NO: 179	-
586	isomiR example 1 of SEQ ID NO: 180	-
587	isomiR example 2 of SEQ ID NO: 180	-
588	isomiR example 1 of SEQ ID NO: 182	-
589	isomiR example 2 of SEQ ID NO: 182	-
590	isomiR example 1 of SEQ ID NO: 183	-
591	isomiR example 2 of SEQ ID NO: 183	-
592	isomiR example 1 of SEQ ID NO: 184	-
593	isomiR example 2 of SEQ ID NO: 184	-
594	isomiR example 1 of SEQ ID NO: 186	-
595	isomiR example 2 of SEQ ID NO: 186	-
596	isomiR example 1 of SEQ ID NO: 187	-
597	isomiR example 2 of SEQ ID NO: 187	-
598	isomiR example 1 of SEQ ID NO: 188	-
599	isomiR example 2 of SEQ ID NO: 188	-
600	isomiR example 1 of SEQ ID NO: 189	-
601	isomiR example 2 of SEQ ID NO: 189	-
602	isomiR example 1 of SEQ ID NO: 192	-
603	isomiR example 2 of SEQ ID NO: 192	-
604	isomiR example 1 of SEQ ID NO: 193	-
605	isomiR example 2 of SEQ ID NO: 193	-

(continued)

SEQ ID NO:	Gene name	miRBase registration No.
606	hsa-miR-6836-3p	MIMAT0027575
607	hsa-miR-3195	MIMAT0015079
608	hsa-miR-718	MIMAT0012735
609	hsa-miR-3178	MIMAT0015055
610	hsa-miR-638	MIMAT0003308
611	hsa-miR-4497	MIMAT0019032
612	hsa-miR-6085	MIMAT0023710
613	hsa-miR-6752-5p	MIMAT0027404
614	hsa-miR-135a-3p	MIMAT0004595
615	hsa-mir-6836	MI0022682
616	hsa-mir-3195	M0014240
617	hsa-mir-718	M10012489
618	hsa-mir-3178	MI0014212
619	hsa-mir-638	MI0003653
620	hsa-mir-4497	MI0016859
621	hsa-mir-6085	MI0020362
622	hsa-mir-6752	MI0022597
623	hsa-mir-135a	MI0000452
624	isomiR example 1 of SEQ ID NO: 607	-
625	isomiR example 2 of SEQ ID NO: 607	-
626	isomiR example 1 of SEQ ID NO: 608	-
627	isomiR example 2 of SEQ ID NO: 608	-
628	isomiR example 1 of SEQ ID NO: 609	-
629	isomiR example 2 of SEQ ID NO: 609	-
630	isomiR example 1 of SEQ ID NO: 610	-
631	isomiR example 2 of SEQ ID NO: 610	-
632	isomiR example 1 of SEQ ID NO: 611	-
633	isomiR example 2 of SEQ ID NO: 611	-
634	isomiR example 1 of SEQ ID NO: 614	-
635	isomiR example 2 of SEQ ID NO: 614	-

[0255] The present specification encompasses the contents described in the specifications and/or drawings of Japanese Patent Application No. 2014-122686 and Japanese Patent Application No. 2015-070182 on which the priority of the present application is based.

Advantageous Effects of Invention

[0256] According to the present invention, colorectal cancer can be detected easily and highly accurately.

[0257] For example, the presence or absence of colorectal cancer in a patient can be easily detected by using, as an index, the expression level measurement values of several miRNAs in blood, serum, and/or plasma of the patient, which can be collected with limited invasiveness.

Brief Description of Drawings

[0258]

[Figure 1] This figure shows the relationship between the nucleotide sequences of hsa-miR-3679-5p represented by SEQ ID NO: 11 and hsa-miR-3679-3p represented by SEQ ID NO: 78, which are produced from a precursor hsa-mir-3679 represented by SEQ ID NO: 205.

[Figure 2] Left diagram: the expression level measurement values of hsa-miR-6726-5p (SEQ ID NO: 1) in healthy subjects (100 persons) and colorectal cancer patients (34 persons) selected as a training cohort were each plotted on the ordinate. The horizontal line in the diagram depicts a threshold (9.43) that was optimized by Fisher's discriminant analysis and discriminated between the two groups. Right diagram: the expression level measurement values of hsa-miR-6726-5p (SEQ ID NO: 1) in healthy subjects (50 persons) and colorectal cancer patients (16 persons) selected as validation cohort were each plotted on the ordinate. The horizontal line in the diagram depicts the threshold (9.43) that was set for the training cohort and discriminated between the two groups.

[Figure 3] Left diagram: the expression level measurement values of hsa-miR-6726-5p (SEQ ID NO: 1) in healthy subjects (100 persons, circles) and colorectal cancer patients (34 persons, triangles) selected as a training cohort were each plotted on the abscissa against their expression level measurement values of hsa-miR-4257 (SEQ ID NO: 2) on the ordinate. The line in the diagram depicts a discriminant function (0 = 1.26x + y - 18.06) that was optimized by Fisher's discriminant analysis and discriminated between the two groups. Right diagram: the expression level measurement values of hsa-miR-6726-5p (SEQ ID NO: 1) in healthy subjects (50 persons, circles) and colorectal cancer patients (16 persons, triangles) selected as a validation cohort were each plotted on the abscissa against their expression level measurement values of hsa-miR-4257 (SEQ ID NO: 2) on the ordinate. The line in the diagram depicts the threshold (0 = 1.26x + y - 18.06) that was set in the training cohort and discriminated between the two groups.

[Figure 4] Upper diagram: a discriminant (1.49 x hsa-miR-3131 - 0.23 x has-miR-7847-3p - 1.13 x hsa-miR-3196 + 1.11 x hsa-miR-3195 + 2.25 x hsa-miR-4665-5p - 1.00 x hsa-miR-204-3p - 11.16) was prepared by use of Fisher's discriminant analysis from the expression level measurement values of hsa-miR-3131 (SEQ ID NO: 5), hsa-miR-204-3p (SEQ ID NO: 45), hsa-miR-4665-5p (SEQ ID NO: 57), hsa-miR-7847-3p (SEQ ID NO: 75), hsa-miR-3196 (SEQ ID NO: 162), and hsa-miR-3195 (SEQ ID NO: 607) in 34 colorectal cancer patients, 103 healthy subjects, 69 pancreatic cancer patients, 66 bile duct cancer patients, 30 stomach cancer patients, 33 esophageal cancer patients, 32 liver cancer patients, and 15 benign pancreaticobiliary disease patients selected as a training cohort, and discriminant scores obtained from the discriminant were plotted on the ordinate against the sample groups on the abscissa. The dotted line in the diagram depicts a discriminant boundary that offered a discriminant score of 0 and discriminated between the groups. Lower diagram: discriminant scores obtained from the discriminant prepared in the training cohort as to the expression level measurement values of hsa-miR-3131 (SEQ ID NO: 5), hsa-miR-204-3p (SEQ ID NO: 45), hsa-miR-4665-5p (SEQ ID NO: 57), hsa-miR-7847-3p (SEQ ID NO: 75), hsa-miR-3196 (SEQ ID NO: 162), and hsa-miR-3195 (SEQ ID NO: 607) in 16 colorectal cancer patients, 47 healthy subjects, 30 pancreatic cancer patients, 33 bile duct cancer patients, 20 stomach cancer patients, 17 esophageal cancer patients, 20 liver cancer patients, and 6 benign pancreaticobiliary disease patients selected as a validation cohort were plotted on the ordinate against the sample groups on the abscissa. The dotted line in the diagram depicts the discriminant boundary that offered a discriminant score of 0 and discriminated between the two groups.

Description of Embodiments

[0259] Hereinafter, the present invention will be described further specifically.

1. Target nucleic acid for colorectal cancer

[0260] A primary target nucleic acid as a colorectal cancer marker for detecting the presence and/or absence of colorectal cancer or colorectal cancer cells using the nucleic acid probe or the primer for the detection of colorectal cancer defined above according to the present invention can use at least one or more miRNA(s) selected from the group consisting of hsa-miR-6726-5p, hsa-miR-4257, hsa-miR-6787-5p, hsa-miR-6780b-5p, hsa-miR-3131, hsa-miR-7108-5p, hsa-miR-1343-3p, hsa-miR-1247-3p, hsa-miR-4651, hsa-miR-6757-5p, hsa-miR-3679-5p, hsa-miR-7641, hsa-miR-6746-5p, hsa-miR-8072, hsa-miR-6741-5p, hsa-miR-1908-5p, hsa-miR-6857-5p, hsa-miR-4746-3p, hsa-miR-744-5p, hsa-miR-4792, hsa-miR-564, hsa-miR-6791-5p, hsa-miR-6825-5p, hsa-miR-6826-5p, hsa-miR-4665-3p, hsa-miR-4467, hsa-miR-3188, hsa-miR-6125, hsa-miR-6756-5p, hsa-miR-1228-3p, hsa-miR-8063, hsa-miR-8069, hsa-miR-6875-5p, hsa-miR-3185, hsa-miR-4433b-3p, hsa-miR-6887-5p, hsa-miR-128-1-5p, hsa-miR-6724-5p, hsa-miR-1914-3p, hsa-miR-1225-5p, hsa-miR-4419b, hsa-miR-7110-5p, hsa-miR-187-5p, hsa-miR-3184-5p, hsa-miR-204-3p, hsa-miR-5572,

hsa-miR-6729-5p, hsa-miR-615-5p, hsa-miR-6749-5p, hsa-miR-6515-3p, hsa-miR-3937, hsa-miR-6840-3p, hsa-miR-6893-5p, hsa-miR-4728-5p, hsa-miR-6717-5p, hsa-miR-7113-3p, hsa-miR-4665-5p, hsa-miR-642b-3p, hsa-miR-7109-5p, hsa-miR-6842-5p, hsa-miR-4442, hsa-miR-4433-3p, hsa-miR-4707-5p, hsa-miR-6126, hsa-miR-4449, hsa-miR-4706, hsa-miR-1913, hsa-miR-602, hsa-miR-939-5p, hsa-miR-4695-5p, hsa-miR-711, hsa-miR-6816-5p, hsa-miR-4632-5p, hsa-miR-6721-5p, hsa-miR-7847-3p, hsa-miR-6132, hsa-miR-887-3p, hsa-miR-3679-3p, hsa-miR-6784-5p, hsa-miR-1249, hsa-miR-937-5p, hsa-miR-5195-3p, hsa-miR-6732-5p, hsa-miR-4417, hsa-miR-4281, hsa-miR-4734, hsa-miR-6766-3p, hsa-miR-663a, hsa-miR-4513, hsa-miR-6781-5p, hsa-miR-1227-5p, hsa-miR-6845-5p, hsa-miR-6798-5p, hsa-miR-3620-5p, hsa-miR-1915-5p, hsa-miR-4294, hsa-miR-642a-3p, hsa-miR-371a-5p, hsa-miR-940, hsa-miR-4450, hsa-miR-4723-5p, hsa-miR-1469, hsa-miR-6861-5p, hsa-miR-7975, hsa-miR-6879-5p, hsa-miR-6802-5p, hsa-miR-1268b, hsa-miR-663b, hsa-miR-125a-3p, hsa-miR-2861, hsa-miR-6088, hsa-miR-4758-5p, hsa-miR-296-3p, hsa-miR-6738-5p, hsa-miR-671-5p, hsa-miR-4454, hsa-miR-4516, hsa-miR-7845-5p, hsa-miR-4741, hsa-miR-92b-5p, hsa-miR-6795-5p, hsa-miR-6805-3p, hsa-miR-4725-3p, hsa-miR-6782-5p, hsa-miR-4688, hsa-miR-6850-5p, hsa-miR-6777-5p, hsa-miR-6785-5p, hsa-miR-7106-5p, hsa-miR-3663-3p, hsa-miR-6131, hsa-miR-1915-3p, hsa-miR-4532, hsa-miR-6820-5p, hsa-miR-4689, hsa-miR-4638-5p, hsa-miR-3656, hsa-miR-3621, hsa-miR-6769b-5p, hsa-miR-149-3p, hsa-miR-23b-3p, hsa-miR-3135b, hsa-miR-6848-5p, hsa-miR-6769a-5p, hsa-miR-4327, hsa-miR-6765-3p, hsa-miR-6716-5p, hsa-miR-6877-5p, hsa-miR-6727-5p, hsa-miR-4534, hsa-miR-614, hsa-miR-1202, hsa-miR-575, hsa-miR-6870-5p, hsa-miR-6722-3p, hsa-miR-7977, hsa-miR-4649-5p, hsa-miR-4675, hsa-miR-6075, hsa-miR-6779-5p, hsa-miR-4271, hsa-miR-3196, hsa-miR-6803-5p, hsa-miR-6789-5p, hsa-miR-4648, hsa-miR-4508, hsa-miR-4749-5p, hsa-miR-4505, hsa-miR-5698, hsa-miR-1199-5p, hsa-miR-4763-3p, hsa-miR-6836-3p, hsa-miR-3195, hsa-miR-718, hsa-miR-3178, hsa-miR-638, hsa-miR-4497, hsa-miR-6085, hsa-miR-6752-5p and hsa-miR-135a-3p. Furthermore, at least one or more miRNA(s) selected from the group consisting of other colorectal cancer markers that can be combined with these miRNAs, i.e., hsa-miR-1231, hsa-miR-1233-5p, hsa-miR-150-3p, hsa-miR-1225-3p, hsa-miR-92a-2-5p, hsa-miR-423-5p, hsa-miR-1268a, hsa-miR-128-2-5p and hsa-miR-24-3p can also be preferably used as a target nucleic acid. Moreover, at least one or more miRNA(s) selected from the group consisting of other colorectal cancer markers that can be combined with these miRNAs, i.e., hsa-miR-4697-5p, hsa-miR-3197, hsa-miR-675-5p, hsa-miR-4486, hsa-miR-7107-5p, hsa-miR-23a-3p, hsa-miR-4667-5p, hsa-miR-451a, hsa-miR-3940-5p, hsa-miR-8059, hsa-miR-6813-5p, hsa-miR-4492, hsa-miR-4476 and hsa-miR-6090 can also be preferably used as a target nucleic acid.

[0261] These miRNAs include, for example, a human gene comprising a nucleotide sequence represented by any of SEQ ID NOs: 1 to 194 and 606 to 614 (i.e., hsa-miR-6726-5p, hsa-miR-4257, hsa-miR-6787-5p, hsa-miR-6780b-5p, hsa-miR-3131, hsa-miR-7108-5p, hsa-miR-1343-3p, hsa-miR-1247-3p, hsa-miR-4651, hsa-miR-6757-5p, hsa-miR-3679-5p, hsa-miR-7641, hsa-miR-6746-5p, hsa-miR-8072, hsa-miR-6741-5p, hsa-miR-1908-5p, hsa-miR-6857-5p, hsa-miR-4746-3p, hsa-miR-744-5p, hsa-miR-4792, hsa-miR-564, hsa-miR-6791-5p, hsa-miR-6825-5p, hsa-miR-6826-5p, hsa-miR-4665-3p, hsa-miR-4467, hsa-miR-3188, hsa-miR-6125, hsa-miR-6756-5p, hsa-miR-1228-3p, hsa-miR-8063, hsa-miR-8069, hsa-miR-6875-5p, hsa-miR-3185, hsa-miR-4433b-3p, hsa-miR-6887-5p, hsa-miR-128-1-5p, hsa-miR-6724-5p, hsa-miR-1914-3p, hsa-miR-1225-5p, hsa-miR-4419b, hsa-miR-7110-5p, hsa-miR-187-5p, hsa-miR-3184-5p, hsa-miR-204-3p, hsa-miR-5572, hsa-miR-6729-5p, hsa-miR-615-5p, hsa-miR-6749-5p, hsa-miR-6515-3p, hsa-miR-3937, hsa-miR-6840-3p, hsa-miR-6893-5p, hsa-miR-4728-5p, hsa-miR-6717-5p, hsa-miR-7113-3p, hsa-miR-4665-5p, hsa-miR-642b-3p, hsa-miR-7109-5p, hsa-miR-6842-5p, hsa-miR-4442, hsa-miR-4433-3p, hsa-miR-4707-5p, hsa-miR-6126, hsa-miR-4449, hsa-miR-4706, hsa-miR-1913, hsa-miR-602, hsa-miR-939-5p, hsa-miR-4695-5p, hsa-miR-711, hsa-miR-6816-5p, hsa-miR-4632-5p, hsa-miR-6721-5p, hsa-miR-7847-3p, hsa-miR-6132, hsa-miR-887-3p, hsa-miR-3679-3p, hsa-miR-6784-5p, hsa-miR-1249, hsa-miR-937-5p, hsa-miR-5195-3p, hsa-miR-6732-5p, hsa-miR-4417, hsa-miR-4281, hsa-miR-4734, hsa-miR-6766-3p, hsa-miR-663a, hsa-miR-4513, hsa-miR-6781-5p, hsa-miR-1227-5p, hsa-miR-6845-5p, hsa-miR-6798-5p, hsa-miR-3620-5p, hsa-miR-1915-5p, hsa-miR-4294, hsa-miR-642a-3p, hsa-miR-371a-5p, hsa-miR-940, hsa-miR-4450, hsa-miR-4723-5p, hsa-miR-1469, hsa-miR-6861-5p, hsa-miR-7975, hsa-miR-6879-5p, hsa-miR-6802-5p, hsa-miR-1268b, hsa-miR-663b, hsa-miR-125a-3p, hsa-miR-2861, hsa-miR-6088, hsa-miR-4758-5p, hsa-miR-296-3p, hsa-miR-6738-5p, hsa-miR-671-5p, hsa-miR-4454, hsa-miR-4516, hsa-miR-7845-5p, hsa-miR-4741, hsa-miR-92b-5p, hsa-miR-6795-5p, hsa-miR-6805-3p, hsa-miR-4725-3p, hsa-miR-6782-5p, hsa-miR-4688, hsa-miR-6850-5p, hsa-miR-6777-5p, hsa-miR-6785-5p, hsa-miR-7106-5p, hsa-miR-3663-3p, hsa-miR-6131, hsa-miR-1915-3p, hsa-miR-4532, hsa-miR-6820-5p, hsa-miR-4689, hsa-miR-4638-5p, hsa-miR-3656, hsa-miR-3621, hsa-miR-6769b-5p, hsa-miR-149-3p, hsa-miR-23b-3p, hsa-miR-3135b, hsa-miR-6848-5p, hsa-miR-6769a-5p, hsa-miR-4327, hsa-miR-6765-3p, hsa-miR-6716-5p, hsa-miR-6877-5p, hsa-miR-6727-5p, hsa-miR-4534, hsa-miR-614, hsa-miR-1202, hsa-miR-575, hsa-miR-6870-5p, hsa-miR-6722-3p, hsa-miR-7977, hsa-miR-4649-5p, hsa-miR-4675, hsa-miR-6075, hsa-miR-6779-5p, hsa-miR-4271, hsa-miR-3196, hsa-miR-6803-5p, hsa-miR-6789-5p, hsa-miR-4648, hsa-miR-4508, hsa-miR-4749-5p, hsa-miR-4505, hsa-miR-5698, hsa-miR-1199-5p, hsa-miR-4763-3p, hsa-miR-1231, hsa-miR-1233-5p, hsa-miR-150-3p, hsa-miR-1225-3p, hsa-miR-92a-2-5p, hsa-miR-423-5p, hsa-miR-1268a, hsa-miR-128-2-5p, hsa-miR-24-3p, hsa-miR-4697-5p, hsa-miR-3197, hsa-miR-675-5p, hsa-miR-4486, hsa-miR-7107-5p, hsa-miR-23a-3p, hsa-miR-4667-5p, hsa-miR-451a, hsa-miR-3940-5p, hsa-miR-8059, hsa-miR-6813-5p, hsa-miR-4492, hsa-miR-4476, hsa-miR-6090, hsa-miR-6836-3p, hsa-miR-3195, hsa-miR-718, hsa-miR-3178, hsa-miR-638, hsa-miR-4497, hsa-miR-

6085, hsa-miR-6752-5p and hsa-miR-135a-3p, respectively), a congener thereof, a transcript thereof, and a variant or a derivative thereof. In this context, the gene, the congener, the transcript, the variant, and the derivative are as defined above.

[0262] The target nucleic acid is preferably a human gene comprising a nucleotide sequence represented by any of SEQ ID NOs: 1 to 635 or a transcript thereof, more preferably the transcript, i.e., a miRNA or its precursor RNA (pri-miRNA or pre-miRNA).

[0263] The first target gene is the hsa-miR-6726-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0264] The second target gene is the hsa-miR-4257 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0265] The third target gene is the hsa-miR-6787-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0266] The fourth target gene is the hsa-miR-6780b-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0267] The fifth target gene is the hsa-miR-3131 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0268] The sixth target gene is the hsa-miR-7108-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0269] The seventh target gene is the hsa-miR-1343-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0270] The eighth target gene is the hsa-miR-1247-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0271] The ninth target gene is the hsa-miR-4651 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0272] The 10th target gene is the hsa-miR-6757-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0273] The 11th target gene is the hsa-miR-3679-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0274] The 12th target gene is the hsa-miR-7641 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0275] The 13th target gene is the hsa-miR-6746-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0276] The 14th target gene is the hsa-miR-8072 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0277] The 15th target gene is the hsa-miR-6741-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0278] The 16th target gene is the hsa-miR-1908-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0279] The 17th target gene is the hsa-miR-6857-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0280] The 18th target gene is the hsa-miR-4746-3p gene, a congener thereof, a transcript thereof, or a variant or a

derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0281] The 19th target gene is the hsa-miR-744-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0282] The 20th target gene is the hsa-miR-4792 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0283] The 21st target gene is the hsa-miR-564 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0284] The 22nd target gene is the hsa-miR-6791-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0285] The 23rd target gene is the hsa-miR-6825-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0286] The 24th target gene is the hsa-miR-6826-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0287] The 25th target gene is the hsa-miR-4665-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0288] The 26th target gene is the hsa-miR-4467 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0289] The 27th target gene is the hsa-miR-3188 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0290] The 28th target gene is the hsa-miR-6125 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0291] The 29th target gene is the hsa-miR-6756-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0292] The 30th target gene is the hsa-miR-1228-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0293] The 31st target gene is the hsa-miR-8063 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0294] The 32nd target gene is the hsa-miR-8069 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0295] The 33rd target gene is the hsa-miR-6875-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0296] The 34th target gene is the hsa-miR-3185 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0297] The 35th target gene is the hsa-miR-4433b-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0298] The 36th target gene is the hsa-miR-6887-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0299] The 37th target gene is the hsa-miR-128-1-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript

thereof can serve as a marker for colorectal cancer.

[0300] The 38th target gene is the hsa-miR-6724-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0301] The 39th target gene is the hsa-miR-1914-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0302] The 40th target gene is the hsa-miR-1225-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0303] The 41st target gene is the hsa-miR-4419b gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0304] The 42nd target gene is the hsa-miR-7110-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0305] The 43rd target gene is the hsa-miR-187-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0306] The 44th target gene is the hsa-miR-3184-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0307] The 45th target gene is the hsa-miR-204-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0308] The 46th target gene is the hsa-miR-5572 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0309] The 47th target gene is the hsa-miR-6729-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0310] The 48th target gene is the hsa-miR-615-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0311] The 49th target gene is the hsa-miR-6749-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0312] The 50th target gene is the hsa-miR-6515-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0313] The 51st target gene is the hsa-miR-3937 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0314] The 52nd target gene is the hsa-miR-6840-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0315] The 53rd target gene is the hsa-miR-6893-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0316] The 54th target gene is the hsa-miR-4728-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0317] The 55th target gene is the hsa-miR-6717-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0318] The 56th target gene is the hsa-miR-7113-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0319] The 57th target gene is the hsa-miR-4665-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0320] The 58th target gene is the hsa-miR-642b-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0321] The 59th target gene is the hsa-miR-7109-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0322] The 60th target gene is the hsa-miR-6842-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0323] The 61st target gene is the hsa-miR-4442 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0324] The 62nd target gene is the hsa-miR-4433-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0325] The 63rd target gene is the hsa-miR-4707-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0326] The 64th target gene is the hsa-miR-6126 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0327] The 65th target gene is the hsa-miR-4449 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0328] The 66th target gene is the hsa-miR-4706 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0329] The 67th target gene is the hsa-miR-1913 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0330] The 68th target gene is the hsa-miR-602 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0331] The 69th target gene is the hsa-miR-939-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0332] The 70th target gene is the hsa-miR-4695-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0333] The 71st target gene is the hsa-miR-711 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0334] The 72nd target gene is the hsa-miR-6816-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0335] The 73rd target gene is the hsa-miR-4632-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0336] The 74th target gene is the hsa-miR-6721-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0337] The 75th target gene is the hsa-miR-7847-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0338] The 76th target gene is the hsa-miR-6132 gene, a congener thereof, a transcript thereof, or a variant or a

derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0339] The 77th target gene is the hsa-miR-887-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0340] The 78th target gene is the hsa-miR-3679-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0341] The 79th target gene is the hsa-miR-6784-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0342] The 80th target gene is the hsa-miR-1249 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0343] The 81st target gene is the hsa-miR-937-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0344] The 82nd target gene is the hsa-miR-5195-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0345] The 83rd target gene is the hsa-miR-6732-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0346] The 84th target gene is the hsa-miR-4417 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0347] The 85th target gene is the hsa-miR-4281 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0348] The 86th target gene is the hsa-miR-4734 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0349] The 87th target gene is the hsa-miR-6766-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0350] The 88th target gene is the hsa-miR-663a gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0351] The 89th target gene is the hsa-miR-4513 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0352] The 90th target gene is the hsa-miR-6781-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0353] The 91st target gene is the hsa-miR-1227-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0354] The 92nd target gene is the hsa-miR-6845-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0355] The 93rd target gene is the hsa-miR-6798-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0356] The 94th target gene is the hsa-miR-3620-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0357] The 95th target gene is the hsa-miR-1915-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript

thereof can serve as a marker for colorectal cancer.

[0358] The 96th target gene is the hsa-miR-4294 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0359] The 97th target gene is the hsa-miR-642a-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0360] The 98th target gene is the hsa-miR-371a-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0361] The 99th target gene is the hsa-miR-940 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0362] The 100th target gene is the hsa-miR-4450 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0363] The 101st target gene is the hsa-miR-4723-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0364] The 102nd target gene is the hsa-miR-1469 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0365] The 103rd target gene is the hsa-miR-6861-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0366] The 104th target gene is the hsa-miR-7975 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0367] The 105th target gene is the hsa-miR-6879-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0368] The 106th target gene is the hsa-miR-6802-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0369] The 107th target gene is the hsa-miR-1268b gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0370] The 108th target gene is the hsa-miR-663b gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0371] The 109th target gene is the hsa-miR-125a-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0372] The 110th target gene is the hsa-miR-2861 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0373] The 111th target gene is the hsa-miR-6088 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0374] The 112th target gene is the hsa-miR-4758-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0375] The 113th target gene is the hsa-miR-296-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0376] The 114th target gene is the hsa-miR-6738-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0377] The 115th target gene is the hsa-miR-671-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0378] The 116th target gene is the hsa-miR-4454 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0379] The 117th target gene is the hsa-miR-4516 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0380] The 118th target gene is the hsa-miR-7845-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0381] The 119th target gene is the hsa-miR-4741 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0382] The 120th target gene is the hsa-miR-92b-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0383] The 121st target gene is the hsa-miR-6795-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0384] The 122nd target gene is the hsa-miR-6805-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0385] The 123rd target gene is the hsa-miR-4725-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0386] The 124th target gene is the hsa-miR-6782-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0387] The 125th target gene is the hsa-miR-4688 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0388] The 126th target gene is the hsa-miR-6850-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0389] The 127th target gene is the hsa-miR-6777-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0390] The 128th target gene is the hsa-miR-6785-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0391] The 129th target gene is the hsa-miR-7106-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0392] The 130th target gene is the hsa-miR-3663-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0393] The 131 st target gene is the hsa-miR-6131 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0394] The 132nd target gene is the hsa-miR-1915-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0395] The 133rd target gene is the hsa-miR-4532 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0396] The 134th target gene is the hsa-miR-6820-5p gene, a congener thereof, a transcript thereof, or a variant or a

derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0397] The 135th target gene is the hsa-miR-4689 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0398] The 136th target gene is the hsa-miR-4638-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0399] The 137th target gene is the hsa-miR-3656 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0400] The 138th target gene is the hsa-miR-3621 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0401] The 139th target gene is the hsa-miR-6769b-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0402] The 140th target gene is the hsa-miR-149-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0403] The 141st target gene is the hsa-miR-23b-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0404] The 142nd target gene is the hsa-miR-3135b gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0405] The 143rd target gene is the hsa-miR-6848-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0406] The 144th target gene is the hsa-miR-6769a-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0407] The 145th target gene is the hsa-miR-4327 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0408] The 146th target gene is the hsa-miR-6765-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0409] The 147th target gene is the hsa-miR-6716-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0410] The 148th target gene is the hsa-miR-6877-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0411] The 149th target gene is the hsa-miR-6727-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0412] The 150th target gene is the hsa-miR-4534 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0413] The 151st target gene is the hsa-miR-614 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0414] The 152nd target gene is the hsa-miR-1202 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0415] The 153rd target gene is the hsa-miR-575 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript

thereof can serve as a marker for colorectal cancer.

[0416] The 154th target gene is the hsa-miR-6870-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0417] The 155th target gene is the hsa-miR-6722-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0418] The 156th target gene is the hsa-miR-7977 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0419] The 157th target gene is the hsa-miR-4649-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0420] The 158th target gene is the hsa-miR-4675 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0421] The 159th target gene is the hsa-miR-6075 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0422] The 160th target gene is the hsa-miR-6779-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0423] The 161st target gene is the hsa-miR-4271 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0424] The 162nd target gene is the hsa-miR-3196 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0425] The 163rd target gene is the hsa-miR-6803-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0426] The 164th target gene is the hsa-miR-6789-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0427] The 165th target gene is the hsa-miR-4648 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0428] The 166th target gene is the hsa-miR-4508 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0429] The 167th target gene is the hsa-miR-4749-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0430] The 168th target gene is the hsa-miR-4505 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0431] The 169th target gene is the hsa-miR-5698 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0432] The 170th target gene is the hsa-miR-1199-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0433] The 171 st target gene is the hsa-miR-4763-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0434] The 172nd target gene is the hsa-miR-1231 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer (Patent Literature 3).

[0435] The 173rd target gene is the hsa-miR-1233-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer (Patent Literature 2).

[0436] The 174th target gene is the hsa-miR-150-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer (Patent Literature 4).

[0437] The 175th target gene is the hsa-miR-1225-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer (Patent Literature 2).

[0438] The 176th target gene is the hsa-miR-92a-2-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer (Patent Literatures 1 and 4).

[0439] The 177th target gene is the hsa-miR-423-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer (Patent Literature 3).

[0440] The 178th target gene is the hsa-miR-1268a gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer (Patent Literature 3).

[0441] The 179th target gene is the hsa-miR-128-2-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer (Patent Literature 1).

[0442] The 180th target gene is the hsa-miR-24-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer (Patent Literature 1).

[0443] The 181st target gene is the hsa-miR-4697-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0444] The 182nd target gene is the hsa-miR-3197 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0445] The 183rd target gene is the hsa-miR-675-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0446] The 184th target gene is the hsa-miR-4486 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0447] The 185th target gene is the hsa-miR-7107-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0448] The 186th target gene is the hsa-miR-23a-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer (Patent Literature 2).

[0449] The 187th target gene is the hsa-miR-4667-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0450] The 188th target gene is the hsa-miR-451a gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0451] The 189th target gene is the hsa-miR-3940-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0452] The 190th target gene is the hsa-miR-8059 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0453] The 191 st target gene is the hsa-miR-6813-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0454] The 192nd target gene is the hsa-miR-4492 gene, a congener thereof, a transcript thereof, or a variant or a

derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0455] The 193rd target gene is the hsa-miR-4476 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0456] The 194th target gene is the hsa-miR-6090 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0457] The 195th target gene is the hsa-miR-6836-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0458] The 196th target gene is the hsa-miR-3195 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0459] The 197th target gene is the hsa-miR-718 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0460] The 198th target gene is the hsa-miR-3178 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0461] The 199th target gene is the hsa-miR-638 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0462] The 200th target gene is the hsa-miR-4497 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0463] The 201st target gene is the hsa-miR-6085 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0464] The 202nd target gene is the hsa-miR-6752-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

[0465] The 203rd target gene is the hsa-miR-135a-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for colorectal cancer.

2. Nucleic acid probe or primer for detection of colorectal cancer

[0466] In the present invention, a nucleic acid capable of specifically binding to any of the target nucleic acids as the colorectal cancer markers described above can be used as a nucleic acid, for example, a nucleic acid probe or a primer, for the detection or diagnosis of colorectal cancer.

[0467] In the present invention, the nucleic acid probe or the primer that can be used for detecting colorectal cancer or for diagnosing colorectal cancer permits qualitative and/or quantitative measurement of the presence, expression level, or abundance of any of the target nucleic acids as the colorectal cancer markers described above, for example, human-derived hsa-miR-6726-5p, hsa-miR-4257, hsa-miR-6787-5p, hsa-miR-6780b-5p, hsa-miR-3131, hsa-miR-7108-5p, hsa-miR-1343-3p, hsa-miR-1247-3p, hsa-miR-4651, hsa-miR-6757-5p, hsa-miR-3679-5p, hsa-miR-7641, hsa-miR-6746-5p, hsa-miR-8072, hsa-miR-6741-5p, hsa-miR-1908-5p, hsa-miR-6857-5p, hsa-miR-4746-3p, hsa-miR-744-5p, hsa-miR-4792, hsa-miR-564, hsa-miR-6791-5p, hsa-miR-6825-5p, hsa-miR-6826-5p, hsa-miR-4665-3p, hsa-miR-4467, hsa-miR-3188, hsa-miR-6125, hsa-miR-6756-5p, hsa-miR-1228-3p, hsa-miR-8063, hsa-miR-8069, hsa-miR-6875-5p, hsa-miR-3185, hsa-miR-4433b-3p, hsa-miR-6887-5p, hsa-miR-128-1-5p, hsa-miR-6724-5p, hsa-miR-1914-3p, hsa-miR-1225-5p, hsa-miR-4419b, hsa-miR-7110-5p, hsa-miR-187-5p, hsa-miR-3184-5p, hsa-miR-204-3p, hsa-miR-5572, hsa-miR-6729-5p, hsa-miR-615-5p, hsa-miR-6749-5p, hsa-miR-6515-3p, hsa-miR-3937, hsa-miR-6840-3p, hsa-miR-6893-5p, hsa-miR-4728-5p, hsa-miR-6717-5p, hsa-miR-7113-3p, hsa-miR-4665-5p, hsa-miR-642b-3p, hsa-miR-7109-5p, hsa-miR-6842-5p, hsa-miR-4442, hsa-miR-4433-3p, hsa-miR-4707-5p, hsa-miR-6126, hsa-miR-4449, hsa-miR-4706, hsa-miR-1913, hsa-miR-602, hsa-miR-939-5p, hsa-miR-4695-5p, hsa-miR-711, hsa-miR-6816-5p, hsa-miR-4632-5p, hsa-miR-6721-5p, hsa-miR-7847-3p, hsa-miR-6132, hsa-miR-887-3p, hsa-miR-3679-3p, hsa-miR-6784-5p, hsa-miR-1249, hsa-miR-937-5p, hsa-miR-5195-3p, hsa-miR-6732-5p, hsa-miR-4417, hsa-miR-4281, hsa-miR-4734, hsa-miR-6766-3p, hsa-miR-663a, hsa-miR-4513, hsa-miR-6781-5p, hsa-miR-1227-5p, hsa-miR-6845-5p,

hsa-miR-6798-5p, hsa-miR-3620-5p, hsa-miR-1915-5p, hsa-miR-4294, hsa-miR-642a-3p, hsa-miR-371a-5p, hsa-miR-940, hsa-miR-4450, hsa-miR-4723-5p, hsa-miR-1469, hsa-miR-6861-5p, hsa-miR-7975, hsa-miR-6879-5p, hsa-miR-6802-5p, hsa-miR-1268b, hsa-miR-663b, hsa-miR-125a-3p, hsa-miR-2861, hsa-miR-6088, hsa-miR-4758-5p, hsa-miR-296-3p, hsa-miR-6738-5p, hsa-miR-671-5p, hsa-miR-4454, hsa-miR-4516, hsa-miR-7845-5p, hsa-miR-4741, hsa-miR-92b-5p, hsa-miR-6795-5p, hsa-miR-6805-3p, hsa-miR-4725-3p, hsa-miR-6782-5p, hsa-miR-4688, hsa-miR-6850-5p, hsa-miR-6777-5p, hsa-miR-6785-5p, hsa-miR-7106-5p, hsa-miR-3663-3p, hsa-miR-6131, hsa-miR-1915-3p, hsa-miR-4532, hsa-miR-6820-5p, hsa-miR-4689, hsa-miR-4638-5p, hsa-miR-3656, hsa-miR-3621, hsa-miR-6769b-5p, hsa-miR-149-3p, hsa-miR-23b-3p, hsa-miR-3135b, hsa-miR-6848-5p, hsa-miR-6769a-5p, hsa-miR-4327, hsa-miR-6765-3p, hsa-miR-6716-5p, hsa-miR-6877-5p, hsa-miR-6727-5p, hsa-miR-4534, hsa-miR-614, hsa-miR-1202, hsa-miR-575, hsa-miR-6870-5p, hsa-miR-6722-3p, hsa-miR-7977, hsa-miR-4649-5p, hsa-miR-4675, hsa-miR-6075, hsa-miR-6779-5p, hsa-miR-4271, hsa-miR-3196, hsa-miR-6803-5p, hsa-miR-6789-5p, hsa-miR-4648, hsa-miR-4508, hsa-miR-4749-5p, hsa-miR-4505, hsa-miR-5698, hsa-miR-1199-5p, hsa-miR-4763-3p, hsa-miR-6836-3p, hsa-miR-3195, hsa-miR-718, hsa-miR-3178, hsa-miR-638, hsa-miR-4497, hsa-miR-6085, hsa-miR-6752-5p and hsa-miR-135a-3p, or a combination thereof, congeners thereof, transcripts thereof, or variants or derivatives thereof: and, optionally in combination therewith, hsa-miR-1231, hsa-miR-1233-5p, hsa-miR-150-3p, hsa-miR-1225-3p, hsa-miR-92a-2-5p, hsa-miR-423-5p, hsa-miR-1268a, hsa-miR-128-2-5p and hsa-miR-24-3p or a combination thereof, congeners thereof, transcripts thereof, or variants or derivatives thereof: and, optionally in combination therewith, hsa-miR-4697-5p, hsa-miR-3197, hsa-miR-675-5p, hsa-miR-4486, hsa-miR-7107-5p, hsa-miR-23a-3p, hsa-miR-4667-5p, hsa-miR-451a, hsa-miR-3940-5p, hsa-miR-8059, hsa-miR-6813-5p, hsa-miR-4492, hsa-miR-4476 and hsa-miR-6090 or a combination thereof, congeners thereof, transcripts thereof, or variants or derivatives thereof.

[0468] The expression level of each target nucleic acid described above is increased or decreased (hereinafter, referred to as "increased/decreased") according to the type of the target nucleic acid in a subject who has colorectal cancer as compared with a healthy subject. Hence, the nucleic acid of the present invention can be effectively used for measuring the expression level of the target nucleic acid described above in a body fluid derived from a subject (e.g., a human) suspected of having colorectal cancer and a body fluid derived from a healthy subject and detecting colorectal cancer by the comparison thereof.

[0469] The nucleic acid probe or the primer that can be used in the present invention is a nucleic acid probe capable of specifically binding to a polynucleotide that consists of a nucleotide sequence represented by at least one of SEQ ID NOs: 1 to 171 and 606 to 614, or a primer for amplifying a polynucleotide that consists of a nucleotide sequence represented by at least one of SEQ ID NOs: 1 to 171 and 606 to 614.

[0470] The nucleic acid probe or the primer that can be further used in the present invention can comprise a nucleic acid probe capable of specifically binding to a polynucleotide consisting of a nucleotide sequence represented by at least one of SEQ ID NOs: 172 to 180, or a primer for amplifying a polynucleotide consisting of a nucleotide sequence represented by at least one of SEQ ID NOs: 172 to 180.

[0471] The nucleic acid probe or the primer that can be further used in the present invention can comprise a nucleic acid probe capable of specifically binding to a polynucleotide consisting of a nucleotide sequence represented by at least one of SEQ ID NOs: 181 to 194, or a primer for amplifying a polynucleotide consisting of a nucleotide sequence represented by at least one of SEQ ID NOs: 181 to 194.

[0472] Specifically, these nucleic acid probes or primers comprise a combination of one or more polynucleotides selected from a polynucleotide group comprising nucleotide sequences represented by any of SEQ ID NOs: 1 to 635 or nucleotide sequences derived from the nucleotide sequences by the replacement of u with t, and a complementary polynucleotide group thereof, a polynucleotide group respectively hybridizing under stringent conditions (mentioned later) to DNAs consisting of nucleotide sequences complementary to these nucleotide sequences, and a complementary polynucleotide group thereof, and a polynucleotide group comprising 15 or more, preferably 17 or more consecutive nucleotides in the nucleotide sequences of these polynucleotide groups. These polynucleotides can be used as nucleic acid probes and primers for detecting the colorectal cancer markers as target nucleic acids.

[0473] More specifically, examples of the nucleic acid probe or the primer that can be used in the present invention include one or more polynucleotide(s) selected from the group consisting of the following polynucleotides (a) to (e):

(a) a polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 1 to 171 and 606 to 614 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,

(b) a polynucleotide comprising a nucleotide sequence represented by any of SEQ ID NOs: 1 to 171 and 606 to 614,

(c) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 1 to 171 and 606 to 614 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,

(d) a polynucleotide comprising a nucleotide sequence complementary to a nucleotide sequence represented by

any of SEQ ID NOs: 1 to 171 and 606 to 614 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, and
(e) a polynucleotide hybridizing under stringent conditions to any of the polynucleotides (a) to (d).

[0474] In addition to at least one or more polynucleotide(s) selected from the polynucleotides (a) to (e), the nucleic acid probe or the primer that can be further used in the present invention can comprise polynucleotides selected from the group consisting of the following polynucleotides (f) to (j):

(f) a polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 172 to 180 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,
(g) a polynucleotide comprising a nucleotide sequence represented by any of SEQ ID NOs: 172 to 180,
(h) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 172 to 180 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,
(i) a polynucleotide comprising a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 172 to 180 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, and
(j) a polynucleotide hybridizing under stringent conditions to any of the polynucleotides (f) to (i).

[0475] In addition to at least one or more polynucleotide(s) selected from the polynucleotides (a) to (j), the nucleic acid probe or the primer that can be further used in the present invention can comprise polynucleotides selected from the group consisting of the following polynucleotides (k) to (o):

(k) a polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 181 to 194 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,
(l) a polynucleotide comprising a nucleotide sequence represented by any of SEQ ID NOs:181 to 194,
(m) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 181 to 194 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,
(n) a polynucleotide comprising a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 181 to 194 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, and
(o) a polynucleotide hybridizing under stringent conditions to any of the polynucleotides (k) to (n).

[0476] For these polynucleotides, the "fragment thereof comprising 15 or more consecutive nucleotides" can contain the number of nucleotides in the range of, for example, from 15 consecutive nucleotides to less than the total number of nucleotides of the sequence, from 17 consecutive nucleotides to less than the total number of nucleotides of the sequence, or from 19 consecutive nucleotides to less than the total number of nucleotides of the sequence, in the nucleotide sequence of each polynucleotide, though the fragment is not limited thereto.

[0477] These polynucleotides or the fragments thereof used in the present invention may each be DNA or may each be RNA.

[0478] The polynucleotides that can be used in the present invention can each be prepared by use of a general technique such as a DNA recombination technique, PCR, or a method using an automatic DNA/RNA synthesizer.

[0479] The DNA recombination technique and the PCR can employ a technique described in, for example, Ausubel et al., Current Protocols in Molecular Biology, John Willey & Sons, US (1993); and Sambrook et al., Molecular Cloning - A Laboratory Manual, Cold Spring Harbor Laboratory Press, US (1989).

[0480] The human-derived hsa-miR-6726-5p, hsa-miR-4257, hsa-miR-6787-5p, hsa-miR-6780b-5p, hsa-miR-3131, hsa-miR-7108-5p, hsa-miR-1343-3p, hsa-miR-1247-3p, hsa-miR-4651, hsa-miR-6757-5p, hsa-miR-3679-5p, hsa-miR-7641, hsa-miR-6746-5p, hsa-miR-8072, hsa-miR-6741-5p, hsa-miR-1908-5p, hsa-miR-6857-5p, hsa-miR-4746-3p, hsa-miR-744-5p, hsa-miR-4792, hsa-miR-564, hsa-miR-6791-5p, hsa-miR-6825-5p, hsa-miR-6826-5p, hsa-miR-4665-3p, hsa-miR-4467, hsa-miR-3188, hsa-miR-6125, hsa-miR-6756-5p, hsa-miR-1228-3p, hsa-miR-8063, hsa-miR-8069, hsa-miR-6875-5p, hsa-miR-3185, hsa-miR-4433b-3p, hsa-miR-6887-5p, hsa-miR-128-1-5p, hsa-miR-6724-5p, hsa-miR-1914-3p, hsa-miR-1225-5p, hsa-miR-4419b, hsa-miR-7110-5p, hsa-miR-187-5p, hsa-miR-3184-5p, hsa-miR-204-3p, hsa-miR-5572, hsa-miR-6729-5p, hsa-miR-615-5p, hsa-miR-6749-5p, hsa-miR-6515-3p, hsa-miR-3937, hsa-miR-6840-3p, hsa-miR-6893-5p, hsa-miR-4728-5p, hsa-miR-6717-5p, hsa-miR-7113-3p, hsa-miR-4665-5p, hsa-miR-642b-3p, hsa-miR-7109-5p, hsa-miR-6842-5p, hsa-miR-4442, hsa-miR-4433-3p, hsa-miR-4707-5p, hsa-miR-6126, hsa-miR-

4449, hsa-miR-4706, hsa-miR-1913, hsa-miR-602, hsa-miR-939-5p, hsa-miR-4695-5p, hsa-miR-711, hsa-miR-6816-5p, hsa-miR-4632-5p, hsa-miR-6721-5p, hsa-miR-7847-3p, hsa-miR-6132, hsa-miR-887-3p, hsa-miR-3679-3p, hsa-miR-6784-5p, hsa-miR-1249, hsa-miR-937-5p, hsa-miR-5195-3p, hsa-miR-6732-5p, hsa-miR-4417, hsa-miR-4281, hsa-miR-4734, hsa-miR-6766-3p, hsa-miR-663a, hsa-miR-4513, hsa-miR-6781-5p, hsa-miR-1227-5p, hsa-miR-6845-5p, hsa-miR-6798-5p, hsa-miR-3620-5p, hsa-miR-1915-5p, hsa-miR-4294, hsa-miR-642a-3p, hsa-miR-371a-5p, hsa-miR-940, hsa-miR-4450, hsa-miR-4723-5p, hsa-miR-1469, hsa-miR-6861-5p, hsa-miR-7975, hsa-miR-6879-5p, hsa-miR-6802-5p, hsa-miR-1268b, hsa-miR-663b, hsa-miR-125a-3p, hsa-miR-2861, hsa-miR-6088, hsa-miR-4758-5p, hsa-miR-296-3p, hsa-miR-6738-5p, hsa-miR-671-5p, hsa-miR-4454, hsa-miR-4516, hsa-miR-7845-5p, hsa-miR-4741, hsa-miR-92b-5p, hsa-miR-6795-5p, hsa-miR-6805-3p, hsa-miR-4725-3p, hsa-miR-6782-5p, hsa-miR-4688, hsa-miR-6850-5p, hsa-miR-6777-5p, hsa-miR-6785-5p, hsa-miR-7106-5p, hsa-miR-3663-3p, hsa-miR-6131, hsa-miR-1915-3p, hsa-miR-4532, hsa-miR-6820-5p, hsa-miR-4689, hsa-miR-4638-5p, hsa-miR-3656, hsa-miR-3621, hsa-miR-6769b-5p, hsa-miR-149-3p, hsa-miR-23b-3p, hsa-miR-3135b, hsa-miR-6848-5p, hsa-miR-6769a-5p, hsa-miR-4327, hsa-miR-6765-3p, hsa-miR-6716-5p, hsa-miR-6877-5p, hsa-miR-6727-5p, hsa-miR-4534, hsa-miR-614, hsa-miR-1202, hsa-miR-575, hsa-miR-6870-5p, hsa-miR-6722-3p, hsa-miR-7977, hsa-miR-4649-5p, hsa-miR-4675, hsa-miR-6075, hsa-miR-6779-5p, hsa-miR-4271, hsa-miR-3196, hsa-miR-6803-5p, hsa-miR-6789-5p, hsa-miR-4648, hsa-miR-4508, hsa-miR-4749-5p, hsa-miR-4505, hsa-miR-5698, hsa-miR-1199-Sp, hsa-miR-4763-3p, hsa-miR-1231, hsa-miR-1233-5p, hsa-miR-150-3p, hsa-miR-1225-3p, hsa-miR-92a-2-5p, hsa-miR-423-5p, hsa-miR-1268a, hsa-miR-128-2-5p, hsa-miR-24-3p, hsa-miR-4697-5p, hsa-miR-3197, hsa-miR-675-5p, hsa-miR-4486, hsa-miR-7107-5p, hsa-miR-23a-3p, hsa-miR-4667-5p, hsa-miR-451a, hsa-miR-3940-5p, hsa-miR-8059, hsa-miR-6813-5p, hsa-miR-4492, hsa-miR-4476, hsa-miR-6090, hsa-miR-6836-3p, hsa-miR-3195, hsa-miR-718, hsa-miR-3178, hsa-miR-638, hsa-miR-4497, hsa-miR-6085, hsa-miR-6752-5p and hsa-miR-135a-3p represented by SEQ ID NOs: 1 to 194 and 606 to 614 are known in the art, and their acquisition methods are also known as mentioned above. Therefore, each polynucleotide that can be used as a nucleic acid probe or a primer in the present invention can be prepared by cloning the gene.

[0481] Such a nucleic acid probe or a primer can be chemically synthesized using an automatic DNA synthesis apparatus. In general, a phosphoramidite method is used in this synthesis, and single-stranded DNA up to approximately 100 nucleotides can be automatically synthesized by this method. The automatic DNA synthesis apparatus is commercially available from, for example, Polygen GmbH, ABI, or Applied Biosystems, Inc.

[0482] Alternatively, the polynucleotide of the present invention can also be prepared by a cDNA cloning method. The cDNA cloning technique can employ, for example, microRNA Cloning Kit Wako.

[0483] In this context, the sequences of the nucleic acid probe and the primer for detecting the polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 1 to 194 and 606 to 614 do not exist as miRNAs or precursors thereof *in vivo.* For example, the nucleotide sequences represented by SEQ ID NO: 11 and SEQ ID NO: 78 are produced from the precursor represented by SEQ ID NO: 205. This precursor has a hairpin-like structure as shown in Figure 1, and the nucleotide sequences represented by SEQ ID NO: 11 and SEQ ID NO: 78 have mismatch sequences with each other. Likewise, a nucleotide sequence completely complementary to the nucleotide sequence represented by SEQ ID NO: 11 or SEQ ID NO: 78 is not naturally produced *in vivo.* Therefore, the nucleic acid probe and the primer for detecting the nucleotide sequence represented by any of SEQ ID NOs: 1 to 194 and 606 to 614 each have an artificial nucleotide sequence that does not exist *in vivo.*

3. Kit or device for detection of colorectal cancer

[0484] The present invention also provides a kit or a device for the detection of colorectal cancer, comprising one or more polynucleotide(s) (which can include a variant, a fragment, and a derivative; hereinafter, also referred to as a polynucleotide for detection) that can be used as a nucleic acid probe or a primer in the present invention for measuring a target nucleic acid as a colorectal cancer marker.

[0485] The target nucleic acid as a colorectal cancer marker according to the present invention is preferably selected from the following group 1:

miR-6726-5p, miR-4257, miR-6787-5p, miR-6780b-5p, miR-3131, miR-7108-5p, miR-1343-3p, miR-1247-3p, miR-4651, miR-6757-5p, miR-3679-5p, miR-7641, miR-6746-5p, miR-8072, miR-6741-5p, miR-1908-5p, miR-6857-5p, miR-4746-3p, miR-744-5p, miR-4792, miR-564, miR-6791-5p, miR-6825-5p, miR-6826-5p, miR-4665-3p, miR-4467, miR-3188, miR-6125, miR-6756-5p, miR-1228-3p, miR-8063, miR-8069, miR-6875-5p, miR-3185, miR-4433b-3p, miR-6887-5p, miR-128-1-5p, miR-6724-5p, miR-1914-3p, miR-1225-5p, miR-4419b, miR-7110-5p, miR-187-5p, miR-3184-5p, miR-204-3p, miR-5572, miR-6729-5p, miR-615-5p, miR-6749-5p, miR-6515-3p, miR-3937, miR-6840-3p, miR-6893-5p, miR-4728-5p, miR-6717-5p, miR-7113-3p, miR-4665-5p, miR-642b-3p, miR-7109-5p, miR-6842-5p, miR-4442, miR-4433-3p, miR-4707-5p, miR-6126, miR-4449, miR-4706, miR-1913, miR-602, miR-939-5p, miR-4695-5p, miR-711, miR-6816-5p, miR-4632-5p, miR-6721-5p, miR-7847-3p, miR-6132, miR-887-3p, miR-3679-3p, miR-6784-5p, miR-1249, miR-937-5p, miR-5195-3p, miR-6732-5p, miR-4417, miR-4281, miR-4734,

miR-6766-3p, miR-663a, miR-4513, miR-6781-5p, miR-1227-5p, miR-6845-5p, miR-6798-5p, miR-3620-5p, miR-1915-5p, miR-4294, miR-642a-3p, miR-371a-5p, miR-940, miR-4450, miR-4723-5p, miR-1469, miR-6861-5p, miR-7975, miR-6879-5p, miR-6802-5p, miR-1268b, miR-663b, miR-125a-3p, miR-2861, miR-6088, miR-4758-5p, miR-296-3p, miR-6738-5p, miR-671-5p, miR-4454, miR-4516, miR-7845-5p, miR-4741, miR-92b-5p, miR-6795-5p, miR-6805-3p, miR-4725-3p, miR-6782-5p, miR-4688, miR-6850-5p, miR-6777-5p, miR-6785-5p, miR-7106-5p, miR-3663-3p, miR-6131, miR-1915-3p, miR-4532, miR-6820-5p, miR-4689, miR-4638-5p, miR-3656, miR-3621, miR-6769b-5p, miR-149-3p, miR-23b-3p, miR-3135b, miR-6848-5p, miR-6769a-5p, miR-4327, miR-6765-3p, miR-6716-5p, miR-6877-5p, miR-6727-5p, miR-4534, miR-614, miR-1202, miR-575, miR-6870-5p, miR-6722-3p, miR-7977, miR-4649-5p, miR-4675, miR-6075, miR-6779-5p, miR-4271, miR-3196, miR-6803-5p, miR-6789-5p, miR-4648, miR-4508, miR-4749-5p, miR-4505, miR-5698, miR-1199-5p, miR-4763-3p, miR-6836-3p, miR-3195, miR-718, miR-3178, miR-638, miR-4497, miR-6085, miR-6752-5p and miR-135a-3p.

[0486] An additional target nucleic acid that can be optionally used in the measurement is selected from the following group 2: miR-1231, miR-1233-5p, miR-150-3p, miR-1225-3p, miR-92a-2-5p, miR-423-5p, miR-1268a, miR-128-2-5p and miR-24-3p.

[0487] An additional target nucleic acid that can be optionally further used in the measurement is selected from the following group 3: miR-4697-5p, miR-3197, miR-675-5p, miR-4486, miR-7107-5p, miR-23a-3p, miR-4667-5p, miR-451a, miR-3940-5p, miR-8059, miR-6813-5p, miR-4492, miR-4476, and miR-6090.

[0488] The kit or the device of the present invention comprises one or more nucleic acid(s) capable of specifically binding to any of the target nucleic acids as the colorectal cancer markers described above, preferably one or more polynucleotide(s) selected from the nucleic acid probes or the primers described in the preceding Section 2, specifically, the polynucleotides described in the preceding Section 2, or variant(s) thereof.

[0489] Specifically, the kit or the device of the present invention can comprise at least one or more polynucleotide(s) comprising (or consisting of) a nucleotide sequence represented by any of SEQ ID NOs: 1 to 171 and 606 to 614 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, polynucleotide(s) comprising (or consisting of) a complementary sequence thereof, polynucleotide(s) hybridizing under stringent conditions to any of these polynucleotides, or variant(s) or fragment(s) comprising 15 or more consecutive nucleotides of any of these polynucleotide sequences.

[0490] The kit or the device of the present invention can further comprise one or more polynucleotide(s) comprising (or consisting of) a nucleotide sequence represented by any of SEQ ID NOs: 172 to 180 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, polynucleotide(s) comprising (or consisting of) a complementary sequence thereof, polynucleotide(s) hybridizing under stringent conditions to any of these polynucleotides, variant(s) or fragment(s) comprising 15 or more consecutive nucleotides of any of these polynucleotide sequences.

[0491] The kit or the device of the present invention can further comprise one or more polynucleotide(s) comprising (or consisting of) a nucleotide sequence represented by any of SEQ ID NOs: 181 to 194 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, polynucleotide(s) comprising (or consisting of) a complementary sequence thereof, polynucleotide(s) hybridizing under stringent conditions to any of these polynucleotides, variant(s) or fragment(s) comprising 15 or more consecutive nucleotides of any of these polynucleotide sequences.

[0492] The fragment that can be contained in the kit or the device of the present invention is, for example, one or more, preferably two or more polynucleotides selected from the group consisting of the following polynucleotides (1) to (3):

(1) a polynucleotide comprising 15 or more consecutive nucleotides in a nucleotide sequence derived from a nucleotide sequence represented by any of SEQ ID NOs: 1 to 171 and 606 to 614 by the replacement of u with t, or a complementary sequence thereof;

(2) a polynucleotide comprising 15 or more consecutive nucleotides in a nucleotide sequence derived from a nucleotide sequence represented by any of SEQ ID NOs: 172 to 180 by the replacement of u with t, or a complementary sequence thereof; and

(3) a polynucleotide comprising 15 or more consecutive nucleotides in a nucleotide sequence derived from a nucleotide sequence represented by any of SEQ ID NOs: 181 to 194 by the replacement of u with t, or a complementary sequence thereof.

[0493] In a preferred embodiment, the polynucleotide is a polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 1 to 171 and 606 to 614 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a polynucleotide consisting of a complementary sequence thereof, a polynucleotide hybridizing under stringent conditions to any of these polynucleotides, or a variant thereof comprising 15 or more, preferably 17 or more, more preferably 19 or more consecutive nucleotides.

[0494] In a preferred embodiment, the polynucleotide is a polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 172 to 180 or a nucleotide sequence derived from the nucleotide sequence by the

replacement of u with t, a polynucleotide consisting of a complementary sequence thereof, a polynucleotide hybridizing under stringent conditions to any of these polynucleotides, or a variant thereof comprising 15 or more, preferably 17 or more, more preferably 19 or more consecutive nucleotides.

[0495] In a preferred embodiment, the polynucleotide is a polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 181 to 194 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a polynucleotide consisting of a complementary sequence thereof, a polynucleotide hybridizing under stringent conditions to any of these polynucleotides, or a variant thereof comprising 15 or more, preferably 17 or more, more preferably 19 or more consecutive nucleotides.

[0496] In a preferred embodiment, the fragment can be a polynucleotide comprising 15 or more, preferably 17 or more, more preferably 19 or more consecutive nucleotides.

[0497] In the present invention, the size of the polynucleotide fragment is the number of bases in the range of, for example, from 15 consecutive nucleotides to less than the total number of bases of the sequence, from 17 consecutive nucleotides to less than the total number of bases of the sequence, or from 19 consecutive nucleotides to less than the total number of nucleotides of the sequence, in the nucleotide sequence of each polynucleotide.

[0498] Specific examples of the aforementioned polynucleotide combination constituting the kit or the device of the present invention can include combinations of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more of the polynucleotides consisting of nucleotide sequences represented by SEQ ID NOs shown in Table 1 (SEQ ID NOs: 1 to 194 and 606 to 614 corresponding to the miRNA markers in the table). However, these are given merely for illustrative purposes, and various other possible combinations are included in the present invention.

[0499] The combination constituting the kit or the device for discriminating a colorectal cancer patient from a healthy subject according to the present invention is desirably, for example, a combination of two or more of the polynucleotides consisting of nucleotide sequences represented by SEQ ID NOs shown in Table 1. Usually, a combination of two of these polynucleotides can produce adequate performance.

[0500] The specific combination of two polynucleotides consisting of the nucleotide sequences or the complementary sequences thereof for discriminating a colorectal cancer patient from a healthy subject is preferably a combination comprising at least one or more of newly found polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 171, among the combinations constituted by two of the aforementioned polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 194 and 606 to 614. More specifically, a combination comprising at least one of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 5, 15, 24, 32, 38, 45, 55, 64, 96, 97, and 162, among the combinations of the polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 194 and 606 to 614, is more preferred.

[0501] The combination of polynucleotides with cancer type specificity capable of discriminating a colorectal cancer patient not only from a healthy subject but also from other cancer patients is preferably, for example, a combination of multiple polynucleotides comprising at least one polynucleotide selected from the group consisting of polynucleotides of SEQ ID NOs: 5, 13, 15, 24, 32, 38, 41, 45, 55, 57, 64, 72, 75, 77, 96, 97, 115, 162, 163, 173, 189, 606, 607, 608, 609, 610, 611, 612, 613 and 614 (hereinafter, this group is referred to as "cancer type-specific polynucleotide group 1"), with any of the polynucleotides of the other SEQ ID NOs.

[0502] The combination of polynucleotides with cancer type specificity capable of discriminating a colorectal cancer patient not only from a healthy subject but also from other cancer patients is more preferably a combination of multiple polynucleotides selected from the cancer type-specific polynucleotide group 1.

[0503] The combination of polynucleotides with cancer type specificity capable of discriminating a colorectal cancer patient not only from a healthy subject but also from other cancer patients is more preferably a combination comprising at least one or more polynucleotide(s) selected from the group consisting of polynucleotides of SEQ ID NOs: 5, 45, 57, 96, and 606 (hereinafter, this group is referred to as "cancer type-specific polynucleotide group 2") included in the cancer type-specific polynucleotide group 1, among the combinations of multiple polynucleotides selected from the cancer type-specific polynucleotide group 1.

[0504] The number of the aforementioned polynucleotides with cancer type specificity in the combination can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more for the combination and is more preferably 6 or more for the combination. Usually, the combination of 5 or 6 of these polynucleotides can produce adequate performance.

[0505] Non-limiting examples of the combination of the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 5 or a complementary sequence thereof with polynucleotides consisting of nucleotide sequences represented by SEQ ID NOs of four or five polynucleotides selected from the cancer type-specific polynucleotide group 1 or complementary sequences thereof will be listed.

[0506]

(1) a combination of SEQ ID NOs: 5, 45, 57, 75, and 607 (markers: hsa-miR-3131, hsa-miR-204-3p, hsa-miR-4665-5p, hsa-miR-7847-3p, and hsa-miR-3195);

(2) a combination of SEQ ID NOs: 5, 45, 96, 606, and 607 (markers: hsa-miR-3131, hsa-miR-204-3p, hsa-miR-

4294, hsa-miR-6836-3p, and hsa-miR-3195);
(3) a combination of SEQ ID NOs: 5, 45, 57, 97, 115, and 607 (markers: hsa-miR-3131, hsa-miR-204-3p, hsa-miR-4665-5p, hsa-miR-642a-3p, hsa-miR-671-5p, and hsa-miR-3195);
(4) a combination of SEQ ID NOs: 5, 45, 57, 97, 162, and 607 (markers: hsa-miR-3131, hsa-miR-204-3p, hsa-miR-4665-5p, hsa-miR-642a-3p, hsa-miR-3196, and hsa-miR-3195);
(5) a combination of SEQ ID NOs: 5, 45, 57, 162, 607, and 613 (markers: hsa-miR-3131, hsa-miR-204-3p, hsa-miR-4665-5p, hsa-miR-3196, hsa-miR-3195, and hsa-miR-6752-5p);
(6) a combination of SEQ ID NOs: 5, 45, 57, 97, 607, and 612 (markers: hsa-miR-3131, hsa-miR-204-3p, hsa-miR-4665-5p, hsa-miR-642a-3p, hsa-miR-3195, and hsa-miR-6085);
(7) a combination of SEQ ID NOs: 5, 13, 45, 57, 606, and 607 (markers: hsa-miR-3131, hsa-miR-6746-5p, hsa-miR-204-3p, hsa-miR-4665-5p, hsa-miR-6836-3p, and hsa-miR-3195);
(8) a combination of SEQ ID NOs: 5, 45, 96, 189, 606, and 608 (markers: hsa-miR-3131, hsa-miR-204-3p, hsa-miR-4294, hsa-miR-3940-5p, hsa-miR-6836-3p, and hsa-miR-718);
(9) a combination of SEQ ID NOs: 5, 45, 57, 96, 189, and 606 (markers: hsa-miR-3131, hsa-miR-204-3p, hsa-miR-4665-5p, hsa-miR-4294, hsa-miR-3940-5p, and hsa-miR-6836-3p);
(10) a combination of SEQ ID NOs: 5, 24, 45, 57, 96, and 608 (markers: hsa-miR-3131, hsa-miR-6826-5p, hsa-miR-204-3p, hsa-miR-4665-5p, hsa-miR-4294, and hsa-miR-718);
(11) a combination of SEQ ID NOs: 5, 45, 57, 162, 607, and 610 (markers: hsa-miR-3131, hsa-miR-204-3p, hsa-miR-4665-5p, hsa-miR-3196, hsa-miR-3195, and hsa-miR-638); and
(12) a combination of SEQ ID NOs: 5, 45, 57, 189, 606, and 607 (markers: hsa-miR-3131, hsa-miR-204-3p, hsa-miR-4665-5p, hsa-miR-3940-5p, hsa-miR-6836-3p, and hsa-miR-3195).

[0507] Non-limiting examples of the combination of the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 45 or a complementary sequence thereof with polynucleotides consisting of nucleotide sequences represented by SEQ ID NOs of four or five polynucleotides selected from the cancer type-specific polynucleotide group 1 or complementary sequences thereof will be further listed.

[0508]

(1) a combination of SEQ ID NOs: 5, 45, 96, 606, and 607 (markers: hsa-miR-3131, hsa-miR-204-3p, hsa-miR-4294, hsa-miR-6836-3p, and hsa-miR-3195);
(2) a combination of SEQ ID NOs: 5, 45, 57, 75, and 607 (markers: hsa-miR-3131, hsa-miR-204-3p, hsa-miR-4665-5p, hsa-miR-7847-3p, and hsa-miR-3195);
(3) a combination of SEQ ID NOs: 5, 45, 57, 75, 606, and 607 (markers: hsa-miR-3131, hsa-miR-204-3p, hsa-miR-4665-5p, hsa-miR-7847-3p, hsa-miR-6836-3p, and hsa-miR-3195);
(4) a combination of SEQ ID NOs: 5, 45, 57, 77, 607, and 613 (markers: hsa-miR-3131, hsa-miR-204-3p, hsa-miR-4665-5p, hsa-miR-887-3p, hsa-miR-3195, and hsa-miR-6752-5p);
(5) a combination of SEQ ID NOs: 5, 45, 57, 97, 606, and 607 (markers: hsa-miR-3131, hsa-miR-204-3p, hsa-miR-4665-5p, hsa-miR-642a-3p, hsa-miR-6836-3p, and hsa-miR-3195);
(6) a combination of SEQ ID NOs: 5, 45, 57, 75, 77, and 607 (markers: hsa-miR-3131, hsa-miR-204-3p, hsa-miR-4665-5p, hsa-miR-7847-3p, hsa-miR-887-3p, and hsa-miR-3195);
(7) a combination of SEQ ID NOs: 5, 32, 45, 57, 96, and 606 (markers: hsa-miR-3131, hsa-miR-8069, hsa-miR-204-3p, hsa-miR-4665-5p, hsa-miR-4294, and hsa-miR-6836-3p);
(8) a combination of SEQ ID NOs: 5, 24, 45, 57, 96, and 606 (markers: hsa-miR-3131, hsa-miR-6826-5p, hsa-miR-204-3p, hsa-miR-4665-5p, hsa-miR-4294, and hsa-miR-6836-3p);
(9) a combination of SEQ ID NOs: 5, 45, 57, 96, 162, and 606 (markers: hsa-miR-3131, hsa-miR-204-3p, hsa-miR-4665-5p, hsa-miR-4294, hsa-miR-3196, and hsa-miR-6836-3p);
(10) a combination of SEQ ID NOs: 5, 15, 45, 75, 96, and 606 (markers: hsa-miR-3131, hsa-miR-6741-5p, hsa-miR-204-3p, hsa-miR-7847-3p, hsa-miR-4294, and hsa-miR-6836-3p);
(11) a combination of SEQ ID NOs: 5, 32, 45, 57, 162, and 607 (markers: hsa-miR-3131, hsa-miR-8069, hsa-miR-204-3p, hsa-miR-4665-5p, hsa-miR-3196, and hsa-miR-3195); and
(12) a combination of SEQ ID NOs: 38, 45, 96, 606, 608, and 611 (markers: hsa-miR-6724-5p, hsa-miR-204-3p, hsa-miR-4294, hsa-miR-6836-3p, hsa-miR-718, and hsa-miR-4497).

[0509] Non-limiting examples of the combination of the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 57 or a complementary sequence thereof with polynucleotides consisting of nucleotide sequences represented by SEQ ID NOs of four or five polynucleotides selected from the cancer type-specific polynucleotide group 1 or complementary sequences thereof will be further listed.

[0510]

(1) a combination of SEQ ID NOs: 24, 41, 57, 45, and 96 (markers: hsa-miR-6826-5p, hsa-miR-4419b, hsa-miR-4665-5p, hsa-miR-204-3p, and hsa-miR-4294);
(2) a combination of SEQ ID NOs: 5, 45, 57, 607, and 612 (markers: hsa-miR-3131, hsa-miR-204-3p, hsa-miR-4665-5p, hsa-miR-3195, and hsa-miR-6085);
(3) a combination of SEQ ID NOs: 5, 45, 57, 606, 607, and 608 (markers: hsa-miR-3131, hsa-miR-204-3p, hsa-miR-4665-5p, hsa-miR-6836-3p, hsa-miR-3195, and hsa-miR-718);
(4) a combination of SEQ ID NOs: 5, 13, 45, 57, 75, and 607 (markers: hsa-miR-3131, hsa-miR-6746-5p, hsa-miR-204-3p, hsa-miR-4665-5p, hsa-miR-7847-3p, and hsa-miR-3195);
(5) a combination of SEQ ID NOs: 5, 45, 57, 64, 75, and 607 (markers: hsa-miR-3131, hsa-miR-204-3p, hsa-miR-4665-5p, hsa-miR-6126, hsa-miR-7847-3p, and hsa-miR-3195);
(6) a combination of SEQ ID NOs: 5, 45, 55, 57, 607, and 613 (markers: hsa-miR-3131, hsa-miR-204-3p, hsa-miR-6717-5p, hsa-miR-4665-5p, hsa-miR-3195, and hsa-miR-6752-5p);
(7) a combination of SEQ ID NOs: 5, 45, 55, 57, 75, and 607 (markers: hsa-miR-3131, hsa-miR-204-3p, hsa-miR-6717-5p, hsa-miR-4665-5p, hsa-miR-7847-3p, and hsa-miR-3195);
(8) a combination of SEQ ID NOs: 5, 38, 45, 57, 96, and 607 (markers: hsa-miR-3131, hsa-miR-6724-5p, hsa-miR-204-3p, hsa-miR-4665-5p, hsa-miR-4294, and hsa-miR-3195);
(9) a combination of SEQ ID NOs: 5, 45, 57, 75, 162, and 607 (markers: hsa-miR-3131, hsa-miR-204-3p, hsa-miR-4665-5p, hsa-miR-7847-3p, hsa-miR-3196, and hsa-miR-3195);
(10) a combination of SEQ ID NOs: 5, 45, 57, 75, 162, and 609 (markers: hsa-miR-3131, hsa-miR-204-3p, hsa-miR-4665-5p, hsa-miR-7847-3p, hsa-miR-3196, and hsa-miR-3178);
(11) a combination of SEQ ID NOs: 5, 45, 57, 64, 96, and 607 (markers: hsa-miR-3131, hsa-miR-204-3p, hsa-miR-4665-5p, hsa-miR-6126, hsa-miR-4294, and hsa-miR-3195); and
(12) a combination of SEQ ID NOs: 57, 64, 96, 606, 608, and 611 (markers: hsa-miR-4665-5p, hsa-miR-6126, hsa-miR-4294, hsa-miR-6836-3p, hsa-miR-718, and hsa-miR-4497).

[0511] Non-limiting examples of the combination of the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 96 or a complementary sequence thereof with polynucleotides consisting of nucleotide sequences represented by SEQ ID NOs of four or five polynucleotides selected from the cancer type-specific polynucleotide group 1 or complementary sequences thereof will be further listed below.

[0512]

(1) a combination of SEQ ID NOs: 38, 96, 606, 608, and 611 (markers: hsa-miR-6724-5p, hsa-miR-4294, hsa-miR-6836-3p, hsa-miR-718, and hsa-miR-4497);
(2) a combination of SEQ ID NOs: 5, 45, 57, 96, and 607 (markers: hsa-miR-3131, hsa-miR-204-3p, hsa-miR-4665-5p, hsa-miR-4294, and hsa-miR-3195);
(3) a combination of SEQ ID NOs: 38, 72, 96, 606, 608, and 611 (markers: hsa-miR-6724-5p, hsa-miR-6816-5p, hsa-miR-4294, hsa-miR-6836-3p, hsa-miR-718, and hsa-miR-4497);
(4) a combination of SEQ ID NOs: 32, 38, 96, 606, 608, and 611 (markers: hsa-miR-8069, hsa-miR-6724-5p, hsa-miR-4294, hsa-miR-6836-3p, hsa-miR-718, and hsa-miR-4497);
(5) a combination of SEQ ID NOs: 38, 96, 163, 606, 608, and 611 (markers: hsa-miR-6724-5p, hsa-miR-4294, hsa-miR-6803-5p, hsa-miR-6836-3p, hsa-miR-718, and hsa-miR-4497);
(6) a combination of SEQ ID NOs: 64, 72, 96, 162, 609, and 611 (markers: hsa-miR-6126, hsa-miR-6816-5p, hsa-miR-4294, hsa-miR-3196, hsa-miR-3178, and hsa-miR-4497);
(7) a combination of SEQ ID NOs: 38, 64, 96, 163, 606, and 608 (markers: hsa-miR-6724-5p, hsa-miR-6126, hsa-miR-4294, hsa-miR-6803-5p, hsa-miR-6836-3p, and hsa-miR-718);
(8) a combination of SEQ ID NOs: 5, 45, 57, 75, 96, and 606 (markers: hsa-miR-3131, hsa-miR-204-3p, hsa-miR-4665-5p, hsa-miR-7847-3p, hsa-miR-4294, and hsa-miR-6836-3p);
(9) a combination of SEQ ID NOs: 5, 15, 45, 57, 96, and 606 (markers: hsa-miR-3131, hsa-miR-6741-5p, hsa-miR-204-3p, hsa-miR-4665-5p, hsa-miR-4294, and hsa-miR-6836-3p);
(10) a combination of SEQ ID NOs: 5, 41, 45, 57, 96, and 606 (markers: hsa-miR-3131, hsa-miR-4419b, hsa-miR-204-3p, hsa-miR-4665-5p, hsa-miR-4294, and hsa-miR-6836-3p);
(11) a combination of SEQ ID NOs: 5, 41, 45, 96, 189, and 606 (markers: hsa-miR-3131, hsa-miR-4419b, hsa-miR-204-3p, hsa-miR-4294, hsa-miR-3940-5p, and hsa-miR-6836-3p); and
(12) a combination of SEQ ID NOs: 5, 45, 75, 96, 189, and 606 (markers: hsa-miR-3131, hsa-miR-204-3p, hsa-miR-7847-3p, hsa-miR-4294, hsa-miR-3940-5p, and hsa-miR-6836-3p).

[0513] Non-limiting examples of the combination of the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 606 or a complementary sequence thereof with polynucleotides consisting of nucleotide sequences

represented by SEQ ID NOs of three polynucleotides selected from the cancer type-specific polynucleotide group 1 or complementary sequences thereof will be further listed.

[0514]

(1) a combination of SEQ ID NOs: 5, 24, 45, 96, 189, and 606 (markers: hsa-miR-3131, hsa-miR-6826-5p, hsa-miR-204-3p, hsa-miR-4294, hsa-miR-3940-5p, and hsa-miR-6836-3p);
(2) a combination of SEQ ID NOs: 5, 15, 45, 96, 189, and 606 (markers: hsa-miR-3131, hsa-miR-6741-5p, hsa-miR-204-3p, hsa-miR-4294, hsa-miR-3940-5p, and hsa-miR-6836-3p);
(3) a combination of SEQ ID NOs: 5, 45, 96, 189, 606, and 613 (markers: hsa-miR-3131, hsa-miR-204-3p, hsa-miR-4294, hsa-miR-3940-5p, hsa-miR-6836-3p, and hsa-miR-6752-5p);
(4) a combination of SEQ ID NOs: 5, 45, 72, 96, 189, and 606 (markers: hsa-miR-3131, hsa-miR-204-3p, hsa-miR-6816-5p, hsa-miR-4294, hsa-miR-3940-5p, and hsa-miR-6836-3p); and
(5) a combination of SEQ ID NOs: 5, 15, 32, 45, 96, and 606 (markers: hsa-miR-3131, hsa-miR-6741-5p, hsa-miR-8069, hsa-miR-204-3p, hsa-miR-4294, and hsa-miR-6836-3p).

[0515] The kit or the device of the present invention can also contain a polynucleotide that is already known or that will be found in the future, to enable detection of colorectal cancer, in addition to the polynucleotide(s) (which can include a variant, a fragment, and a derivative) according to the present invention described above.

[0516] The kit of the present invention can also contain an antibody for measuring a marker for colorectal cancer examination known in the art, such as CEA or CA19-9, in addition to the polynucleotide(s) according to the present invention described above.

[0517] These polynucleotides contained in the kit of the present invention can be packaged in different containers either individually or in any combination.

[0518] The kit of the present invention can contain a kit for extracting a nucleic acid (e.g., total RNA) from body fluids, cells, or tissues, a fluorescent material for labeling, an enzyme and a medium for nucleic acid amplification, an instruction manual, etc.

[0519] The device of the present invention is a device for cancer marker measurement in which nucleic acids such as the polynucleotides according to the present invention described above are bonded or attached to, for example, a solid phase. Examples of the material for the solid phase include plastics, paper, glass, and silicon. The material for the solid phase is preferably a plastic from the viewpoint of easy processability. The solid phase has any shape and is, for example, square, round, reed-shaped, or film-shaped. The device of the present invention includes, for example, a device for measurement by a hybridization technique. Specific examples thereof include blotting devices and nucleic acid arrays (e.g., microarrays, DNA chips, and RNA chips).

[0520] The nucleic acid array technique is a technique which involves binding or attaching the nucleic acids one by one by use of a method [e.g., a method of spotting the nucleic acids using a high-density dispenser called spotter or arrayer onto the surface of the solid phase surface-treated, if necessary, by coating with L-lysine or the introduction of a functional group such as an amino group or a carboxyl group, a method of spraying the nucleic acids onto the solid phase using an inkjet which injects very small liquid droplets by a piezoelectric element or the like from a nozzle, or a method of sequentially synthesizing nucleotides on the solid phase] to prepare an array such as a chip and measuring a target nucleic acid through the use of hybridization using this array.

[0521] The kit or the device of the present invention comprises nucleic acids capable of specifically binding to the polynucleotides of at least one or more, preferably at least two or more, more preferably at least three or more, most preferably at least five or more to all of the colorectal cancer marker miRNAs, respectively, of group 1 described above. The kit or the device of the present invention can optionally further comprise nucleic acids capable of specifically binding to the polynucleotides of at least one or more, preferably at least two or more, more preferably at least three or more, most preferably at least five or more to all of the colorectal cancer marker miRNAs, respectively, of group 2 described above. The kit or the device of the present invention can optionally further comprise nucleic acids capable of specifically binding to the polynucleotides of at least one or more, preferably at least two or more, more preferably at least three or more, most preferably at least five or more to all of the colorectal cancer marker miRNAs, respectively, of group 3 described above.

[0522] The kit or the device of the present invention can be used for detecting colorectal cancer as described in the Section 4 below.

4. Method for detecting colorectal cancer

[0523] The present invention further provides a method for detecting colorectal cancer, comprising using the kit or the device of the present invention (including the nucleic acid(s) that can be used in the present invention) described in the preceding Section 3 above to measure an expression level of one or more colorectal cancer-derived gene(s) represented

by an expression level of colorectal cancer-derived gene(s) selected from the following group: miR-6726-5p, miR-4257, miR-6787-5p, miR-6780b-5p, miR-3131, miR-7108-5p, miR-1343-3p, miR-1247-3p, miR-4651, miR-6757-5p, miR-3679-5p, miR-7641, miR-6746-5p, miR-8072, miR-6741-5p, miR-1908-5p, miR-6857-5p, miR-4746-3p, miR-744-5p, miR-4792, miR-564, miR-6791-5p, miR-6825-5p, miR-6826-5p, miR-4665-3p, miR-4467, miR-3188, miR-6125, miR-6756-5p, miR-1228-3p, miR-8063, miR-8069, miR-6875-5p, miR-3185, miR-4433b-3p, miR-6887-5p, miR-128-1-5p, miR-6724-5p, miR-1914-3p, miR-1225-5p, miR-4419b, miR-7110-5p, miR-187-5p, miR-3184-5p, miR-204-3p, miR-5572, miR-6729-5p, miR-615-5p, miR-6749-5p, miR-6515-3p, miR-3937, miR-6840-3p, miR-6893-5p, miR-4728-5p, miR-6717-5p, miR-7113-3p, miR-4665-5p, miR-642b-3p, miR-7109-5p, miR-6842-5p, miR-4442, miR-4433-3p, miR-4707-5p, miR-6126, miR-4449, miR-4706, miR-1913, miR-602, miR-939-5p, miR-4695-5p, miR-711, miR-6816-5p, miR-4632-5p, miR-6721-5p, miR-7847-3p, miR-6132, miR-887-3p, miR-3679-3p, miR-6784-5p, miR-1249, miR-937-5p, miR-5195-3p, miR-6732-5p, miR-4417, miR-4281, miR-4734, miR-6766-3p, miR-663a, miR-4513, miR-6781-5p, miR-1227-5p, miR-6845-5p, miR-6798-5p, miR-3620-5p, miR-1915-5p, miR-4294, miR-642a-3p, miR-371a-5p, miR-940, miR-4450, miR-4723-5p, miR-1469, miR-6861-5p, miR-7975, miR-6879-5p, miR-6802-5p, miR-1268b, miR-663b, miR-125a-3p, miR-2861, miR-6088, miR-4758-5p, miR-296-3p, miR-6738-5p, miR-671-5p, miR-4454, miR-4516, miR-7845-5p, miR-4741, miR-92b-5p, miR-6795-5p, miR-6805-3p, miR-4725-3p, miR-6782-5p, miR-4688, miR-6850-5p, miR-6777-5p, miR-6785-5p, miR-7106-5p, miR-3663-3p, miR-6131, miR-1915-3p, miR-4532, miR-6820-5p, miR-4689, miR-4638-5p, miR-3656, miR-3621, miR-6769b-5p, miR-149-3p, miR-23b-3p, miR-3135b, miR-6848-5p, miR-6769a-5p, miR-4327, miR-6765-3p, miR-6716-5p, miR-6877-5p, miR-6727-5p, miR-4534, miR-614, miR-1202, miR-575, miR-6870-5p, miR-6722-3p, miR-7977, miR-4649-5p, miR-4675, miR-6075, miR-6779-5p, miR-4271, miR-3196, miR-6803-5p, miR-6789-5p, miR-4648, miR-4508, miR-4749-5p, miR-4505, miR-5698, miR-1199-5p, miR-4763-3p, miR-6836-3p, miR-3195, miR-718, miR-3178, miR-638, miR-4497, miR-6085, miR-6752-5p and miR-135a-3p, optionally an expression level of colorectal cancer-derived gene(s) selected from the following group: miR-1231, miR-1233-5p, miR-150-3p, miR-1225-3p, miR-92a-2-5p, miR-423-5p, miR-1268a, miR-128-2-5p and miR-24-3p, and optionally an expression level of colorectal cancer-derived gene(s) selected from the following group: miR-4697-5p, miR-3197, miR-675-5p, miR-4486, miR-7107-5p, miR-23a-3p, miR-4667-5p, miR-451a, miR-3940-5p, miR-8059, miR-6813-5p, miR-4492, miR-4476, and miR-6090 in a sample *in vitro,* further comparing, for example, the expression level of the aforementioned gene in the sample (e.g., blood, serum, or plasma) collected from a subject suspected of having colorectal cancer with a control expression level in the sample collected from a healthy subject (including a non-colorectal cancer patient), and evaluating the subject as having colorectal cancer when the expression level of the target nucleic acid is statistically significantly different between the samples.

[0524] This method of the present invention permits lowly-invasive early diagnosis of cancer with high sensitivity and specificity and thereby brings about early treatment and improved prognosis. In addition, exacerbation of the disease or the effectiveness of surgical, radiotherapeutic, and chemotherapeutic treatments can be monitored.

[0525] The method for extracting the colorectal cancer-derived gene from the sample such as blood, serum, or plasma according to the present invention is particularly preferably prepared by the addition of a reagent for RNA extraction in 3D-Gene(™) RNA extraction reagent from liquid sample kit (Toray Industries, Inc.). A general acidic phenol method (acid guanidinium-phenolchloroform (AGPC)) may be used, or Trizol(™) (Life Technologies Corp.) may be used. The colorectal cancer-derived gene may be prepared by the addition of a reagent for RNA extraction containing acidic phenol, such as Trizol (Life Technologies Corp.) or Isogen (Nippon Gene Co., Ltd.). Alternatively, a kit such as miRNeasy(™) Mini Kit (Qiagen N.V.) can be used, though the method is not limited thereto.

[0526] The present invention also provides use of the kit or the device of the present invention for detecting *in vitro* an expression product of a colorectal cancer-derived miRNA gene in a sample derived from a subject.

[0527] In the method of the present invention, a kit or a device comprising, each alone or in every possible composition, the polynucleotides that can be used in the present invention as described above is used as the kit or the device.

[0528] In the detection or (genetic) diagnosis of colorectal cancer according to the present invention, each polynucleotide contained in the kit or the device of the present invention can be used as a probe or a primer. In the case of using the polynucleotide as a primer, TaqMan(™) MicroRNA Assays from Life Technologies Corp., miScript PCR System from Qiagen N.V., or the like can be used, though the method is not limited thereto.

[0529] The polynucleotide contained in the kit or the device of the present invention can be used as a primer or a probe according to a routine method in a method known in the art for specifically detecting the particular gene, for example, a hybridization technique such as Northern blot, Southern blot, *in situ* hybridization, Northern hybridization, or Southern hybridization, or a quantitative amplification technique such as quantitative RT-PCR. A body fluid such as blood, serum, plasma, or urine from a subject is collected as a sample to be assayed according to the type of the detection method used. Alternatively, total RNA prepared from such a body fluid by the method described above may be used, and various polynucleotides including cDNA prepared on the basis of the RNA may be used.

[0530] The kit or the device of the present invention is useful for the diagnosis of colorectal cancer or the detection of the presence or absence of colorectal cancer. Specifically, the detection of colorectal cancer using the kit or the device can be performed by detecting *in vitro* an expression level of a gene using the nucleic acid probe or the primer contained

in the kit or the device in a sample such as blood, serum, plasma, or urine from a subject suspected of having colorectal cancer. The subject suspected of having colorectal cancer can be evaluated as having colorectal cancer when the expression level of a target miRNA marker measured using polynucleotide(s) (including a variant, a fragment, and a derivative thereof) consisting of a nucleotide sequence represented by at least one or more of SEQ ID NOs: 1 to 171 and 606 to 614 or a complementary sequence thereof, optionally a nucleotide sequence represented by one or more of SEQ ID NOs: 172 to 180 or a complementary sequence thereof, and optionally a nucleotide sequence represented by one or more of SEQ ID NOs: 181 to 194 or a complementary sequence thereof in the sample such as blood, serum, plasma, or urine of the subject is statistically significantly different from the expression level thereof in the sample such as blood, serum, or plasma, or urine of a healthy subject.

[0531] The method of the present invention can be combined with fecal occult blood, rectal examination, and colonoscopy as well as a diagnostic imaging method such as barium enema, CT, MRI, or bone scintigraphy. The method of the present invention is capable of specifically detecting colorectal cancer and can substantially discriminate colorectal cancer from other cancers.

[0532] The method for detecting the absence of an expression product of a colorectal cancer-derived gene or the presence of the expression product of a colorectal cancer-derived gene in a sample using the kit or the device of the present invention comprises; collecting a body fluid such as blood, serum, plasma, or urine from a subject, measuring the expression level of the target gene that contains therein using one or more polynucleotide(s) (including a variant, a fragment, and a derivative) selected from the polynucleotide group of the present invention, and evaluating the presence or absence of colorectal cancer or detecting colorectal cancer. Using the method for detecting colorectal cancer according to the present invention, for example, the presence or absence of amelioration of the disease or the degree of amelioration thereof in a colorectal cancer patient given a therapeutic drug for the amelioration of the disease can be also evaluated or diagnosed.

[0533] The method of the present invention can comprise, for example, the following steps (a), (b), and (c):

(a) a step of contacting a sample derived from a subject with a polynucleotide in the kit or the device of the present invention *in vitro*;
(b) a step of measuring an expression level of the target nucleic acid in the sample using the polynucleotide as a nucleic acid probe or a primer; and
(c) a step of evaluating the presence or absence of colorectal cancer (cells) in the subject on the basis of the step (b).

[0534] Specifically, the present invention provides a method for detecting colorectal cancer, comprising measuring an expression level of a target nucleic acid in a sample of a subject using a nucleic acid capable of specifically binding to at least one or more (preferably at least two or more) polynucleotide(s) selected from the group consisting of miR-6726-5p, miR-4257, miR-6787-5p, miR-6780b-5p, miR-3131, miR-7108-5p, miR-1343-3p, miR-1247-3p, miR-4651, miR-6757-5p, miR-3679-5p, miR-7641, miR-6746-5p, miR-8072, miR-6741-5p, miR-1908-5p, miR-6857-5p, miR-4746-3p, miR-744-5p, miR-4792, miR-564, miR-6791-5p, miR-6825-5p, miR-6826-5p, miR-4665-3p, miR-4467, miR-3188, miR-6125, miR-6756-5p, miR-1228-3p, miR-8063, miR-8069, miR-6875-5p, miR-3185, miR-4433b-3p, miR-6887-5p, miR-128-1-5p, miR-6724-5p, miR-1914-3p, miR-1225-5p, miR-4419b, miR-7110-5p, miR-187-5p, miR-3184-5p, miR-204-3p, miR-5572, miR-6729-5p, miR-615-5p, miR-6749-5p, miR-6515-3p, miR-3937, miR-6840-3p, miR-6893-5p, miR-4728-5p, miR-6717-5p, miR-7113-3p, miR-4665-5p, miR-642b-3p, miR-7109-5p, miR-6842-5p, miR-4442, miR-4433-3p, miR-4707-5p, miR-6126, miR-4449, miR-4706, miR-1913, miR-602, miR-939-5p, miR-4695-5p, miR-711, miR-6816-5p, miR-4632-5p, miR-6721-5p, miR-7847-3p, miR-6132, miR-887-3p, miR-3679-3p, miR-6784-5p, miR-1249, miR-937-5p, miR-5195-3p, miR-6732-5p, miR-4417, miR-4281, miR-4734, miR-6766-3p, miR-663a, miR-4513, miR-6781-5p, miR-1227-5p, miR-6845-5p, miR-6798-5p, miR-3620-5p, miR-1915-5p, miR-4294, miR-642a-3p, miR-371a-5p, miR-940, miR-4450, miR-4723-5p, miR-1469, miR-6861-5p, miR-7975, miR-6879-5p, miR-6802-5p, miR-1268b, miR-663b, miR-125a-3p, miR-2861, miR-6088, miR-4758-5p, miR-296-3p, miR-6738-5p, miR-671-5p, miR-4454, miR-4516, miR-7845-5p, miR-4741, miR-92b-5p, miR-6795-5p, miR-6805-3p, miR-4725-3p, miR-6782-5p, miR-4688, miR-6850-5p, miR-6777-5p, miR-6785-5p, miR-7106-5p, miR-3663-3p, miR-6131, miR-1915-3p, miR-4532, miR-6820-5p, miR-4689, miR-4638-5p, miR-3656, miR-3621, miR-6769b-5p, miR-149-3p, miR-23b-3p, miR-3135b, miR-6848-5p, miR-6769a-5p, miR-4327, miR-6765-3p, miR-6716-5p, miR-6877-5p, miR-6727-5p, miR-4534, miR-614, miR-1202, miR-575, miR-6870-5p, miR-6722-3p, miR-7977, miR-4649-5p, miR-4675, miR-6075, miR-6779-5p, miR-4271, miR-3196, miR-6803-5p, miR-6789-5p, miR-4648, miR-4508, miR-4749-5p, miR-4505, miR-5698, miR-1199-5p and miR-4763-3p, miR-6836-3p, miR-3195, miR-718, miR-3178, miR-638, miR-4497, miR-6085, miR-6752-5p and miR-135a-3p and evaluating *in vitro* whether or not the subject has colorectal cancer using the measured expression level and a control expression level of a healthy subject measured in the same way as above.

[0535] As used herein, the term "evaluation" is evaluation support based on results of *in vitro* examination, not physician's judgment.

[0536] As described above, as for the target nucleic acids in a preferred embodiment of the method of the present

invention, specifically, miR-6726-5p is hsa-miR-6726-5p, miR-4257 is hsa-miR-4257, miR-6787-5p is hsa-miR-6787-5p, miR-6780b-5p is hsa-miR-6780b-5p, miR-3131 is hsa-miR-3131, miR-7108-5p is hsa-miR-7108-5p, miR-1343-3p is hsa-miR-1343-3p, miR-1247-3p is hsa-miR-1247-3p, miR-4651 is hsa-miR-4651, miR-6757-5p is hsa-miR-6757-5p, miR-3679-5p is hsa-miR-3679-5p, miR-7641 is hsa-miR-7641, miR-6746-5p is hsa-miR-6746-5p, miR-8072 is hsa-miR-8072, miR-6741-5p is hsa-miR-6741-5p, miR-1908-5p is hsa-miR-1908-5p, miR-6857-5p is hsa-miR-6857-5p, miR-4746-3p is hsa-miR-4746-3p, miR-744-5p is hsa-miR-744-5p, miR-4792 is hsa-miR-4792, miR-564 is hsa-miR-564, miR-6791-5p is hsa-miR-6791-5p, miR-6825-5p is hsa-miR-6825-5p, miR-6826-5p is hsa-miR-6826-5p, miR-4665-3p is hsa-miR-4665-3p, miR-4467 is hsa-miR-4467, miR-3188 is hsa-miR-3188, miR-6125 is hsa-miR-6125, miR-6756-5p is hsa-miR-6756-5p, miR-1228-3p is hsa-miR-1228-3p, miR-8063 is hsa-miR-8063, miR-8069 is hsa-miR-8069, miR-6875-5p is hsa-miR-6875-5p, miR-3185 is hsa-miR-3185, miR-4433b-3p is hsa-miR-4433b-3p, miR-6887-5p is hsa-miR-6887-5p, miR-128-1-5p is hsa-miR-128-1-5p, miR-6724-5p is hsa-miR-6724-5p, miR-1914-3p is hsa-miR-1914-3p, miR-1225-5p is hsa-miR-1225-5p, miR-4419b is hsa-miR-4419b, miR-7110-5p is hsa-miR-7110-5p, miR-187-5p is hsa-miR-187-5p, miR-3184-5p is hsa-miR-3184-5p, miR-204-3p is hsa-miR-204-3p, miR-5572 is hsa-miR-5572, miR-6729-5p is hsa-miR-6729-5p, miR-615-5p is hsa-miR-615-5p, miR-6749-5p is hsa-miR-6749-5p, miR-6515-3p is hsa-miR-6515-3p, miR-3937 is hsa-miR-3937, miR-6840-3p is hsa-miR-6840-3p, miR-6893-5p is hsa-miR-6893-5p, miR-4728-5p is hsa-miR-4728-5p, miR-6717-5p is hsa-miR-6717-5p, miR-7113-3p is hsa-miR-7113-3p, miR-4665-5p is hsa-miR-4665-5p, miR-642b-3p is hsa-miR-642b-3p, miR-7109-5p is hsa-miR-7109-5p, miR-6842-5p is hsa-miR-6842-5p, miR-4442 is hsa-miR-4442, miR-4433-3p is hsa-miR-4433-3p, miR-4707-5p is hsa-miR-4707-5p, miR-6126 is hsa-miR-6126, miR-4449 is hsa-miR-4449, miR-4706 is hsa-miR-4706, miR-1913 is hsa-miR-1913, miR-602 is hsa-miR-602, miR-939-5p is hsa-miR-939-5p, miR-4695-5p is hsa-miR-4695-5p, miR-711 is hsa-miR-711, miR-6816-5p is hsa-miR-6816-5p, miR-4632-5p is hsa-miR-4632-5p, miR-6721-5p is hsa-miR-6721-5p, miR-7847-3p is hsa-miR-7847-3p, miR-6132 is hsa-miR-6132, miR-887-3p is hsa-miR-887-3p, miR-3679-3p is hsa-miR-3679-3p, miR-6784-5p is hsa-miR-6784-5p, miR-1249 is hsa-miR-1249, miR-937-5p is hsa-miR-937-5p, miR-5195-3p is hsa-miR-5195-3p, miR-6732-5p is hsa-miR-6732-5p, miR-4417 is hsa-miR-4417, miR-4281 is hsa-miR-4281, miR-4734 is hsa-miR-4734, miR-6766-3p is hsa-miR-6766-3p, miR-663a is hsa-miR-663a, miR-4513 is hsa-miR-4513, miR-6781-5p is hsa-miR-6781-5p, miR-1227-5p is hsa-miR-1227-5p, miR-6845-5p is hsa-miR-6845-5p, miR-6798-5p is hsa-miR-6798-5p, miR-3620-5p is hsa-miR-3620-5p, miR-1915-5p is hsa-miR-1915-5p, miR-4294 is hsa-miR-4294, miR-642a-3p is hsa-miR-642a-3p, miR-371a-5p is hsa-miR-371a-5p, miR-940 is hsa-miR-940, miR-4450 is hsa-miR-4450, miR-4723-5p is hsa-miR-4723-5p, miR-1469 is hsa-miR-1469, miR-6861-5p is hsa-miR-6861-5p, miR-7975 is hsa-miR-7975, miR-6879-5p is hsa-miR-6879-5p, miR-6802-5p is hsa-miR-6802-5p, miR-1268b is hsa-miR-1268b, miR-663b is hsa-miR-663b, miR-125a-3p is hsa-miR-125a-3p, miR-2861 is hsa-miR-2861, miR-6088 is hsa-miR-6088, miR-4758-5p is hsa-miR-4758-5p, miR-296-3p is hsa-miR-296-3p, miR-6738-5p is hsa-miR-6738-5p, miR-671-5p is hsa-miR-671-5p, miR-4454 is hsa-miR-4454, miR-4516 is hsa-miR-4516, miR-7845-5p is hsa-miR-7845-5p, miR-4741 is hsa-miR-4741, miR-92b-5p is hsa-miR-92b-5p, miR-6795-5p is hsa-miR-6795-5p, miR-6805-3p is hsa-miR-6805-3p, miR-4725-3p is hsa-miR-4725-3p, miR-6782-5p is hsa-miR-6782-5p, miR-4688 is hsa-miR-4688, miR-6850-5p is hsa-miR-6850-5p, miR-6777-5p is hsa-miR-6777-5p, miR-6785-5p is hsa-miR-6785-5p, miR-7106-5p is hsa-miR-7106-5p, miR-3663-3p is hsa-miR-3663-3p, miR-6131 is hsa-miR-6131, miR-1915-3p is hsa-miR-1915-3p, miR-4532 is hsa-miR-4532, miR-6820-5p is hsa-miR-6820-5p, miR-4689 is hsa-miR-4689, miR-4638-5p is hsa-miR-4638-5p, miR-3656 is hsa-miR-3656, miR-3621 is hsa-miR-3621, miR-6769b-5p is hsa-miR-6769b-5p, miR-149-3p is hsa-miR-149-3p, miR-23b-3p is hsa-miR-23b-3p, miR-3135b is hsa-miR-3135b, miR-6848-5p is hsa-miR-6848-5p, miR-6769a-5p is hsa-miR-6769a-5p, miR-4327 is hsa-miR-4327, miR-6765-3p is hsa-miR-6765-3p, miR-6716-5p is hsa-miR-6716-5p, miR-6877-5p is hsa-miR-6877-5p, miR-6727-5p is hsa-miR-6727-5p, miR-4534 is hsa-miR-4534, miR-614 is hsa-miR-614, miR-1202 is hsa-miR-1202, miR-575 is hsa-miR-575, miR-6870-5p is hsa-miR-6870-5p, miR-6722-3p is hsa-miR-6722-3p, miR-7977 is hsa-miR-7977, miR-4649-5p is hsa-miR-4649-5p, miR-4675 is hsa-miR-4675, miR-6075 is hsa-miR-6075, miR-6779-5p is hsa-miR-6779-5p, miR-4271 is hsa-miR-4271, miR-3196 is hsa-miR-3196, miR-6803-5p is hsa-miR-6803-5p, miR-6789-5p is hsa-miR-6789-5p, miR-4648 is hsa-miR-4648, miR-4508 is hsa-miR-4508, miR-4749-5p is hsa-miR-4749-5p, miR-4505 is hsa-miR-4505, miR-5698 is hsa-miR-5698, miR-1199-5p is hsa-miR-1199-5p, miR-4763-3p is hsa-miR-4763-3p, miR-6836-3p is hsa-miR-6836-3p, miR-3195 is hsa-miR-3195, miR-718 is hsa-miR-718, miR-3178 is hsa-miR-3178, miR-638 is hsa-miR-638, miR-4497 is hsa-miR-4497, miR-6085 is hsa-miR-6085, miR-6752-5p is hsa-miR-6752-5p, and miR-135a-3p is hsa-miR-135a-3p.

[0537] In a preferred embodiment of the method of the present invention, specifically, the nucleic acid (specifically, probe or primer) is selected from the group consisting of the following polynucleotides (a) to (e):

(a) a polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 1 to 171 and 606 to 614 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,

(b) a polynucleotide comprising a nucleotide sequence represented by any of SEQ ID NOs: 1 to 171 and 606 to 614,

(c) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by

any of SEQ ID NOs: 1 to 171 and 606 to 614 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,

(d) a polynucleotide comprising a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 1 to 171 and 606 to 614 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, and

(e) a polynucleotide hybridizing under stringent conditions to any of the polynucleotides (a) to (d).

[0538] The method of the present invention can further employ a nucleic acid capable of specifically binding to at least one or more polynucleotide(s) selected from the group consisting of miR-1231, miR-1233-5p, miR-150-3p, miR-1225-3p, miR-92a-2-5p, miR-423-5p, miR-1268a, miR-128-2-5p and miR-24-3p.

[0539] As for such a nucleic acid, specifically, miR-1231 is hsa-miR-1231, miR-1233-5p is hsa-miR-1233-5p, miR-150-3p is hsa-miR-150-3p, miR-1225-3p is hsa-miR-1225-3p, miR-92a-2-5p is hsa-miR-92a-2-5p, miR-423-5p is hsa-miR-423-5p, miR-1268a is hsa-miR-1268a, miR-128-2-5p is hsa-miR-128-2-5p, and miR-24-3p is hsa-miR-24-3p.

[0540] In a preferred embodiment, such a nucleic acid is specifically selected from the group consisting of the following polynucleotides (f) to (j):

(f) a polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 172 to 180 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,

(g) a polynucleotide comprising a nucleotide sequence represented by any of SEQ ID NOs: 172 to 180,

(h) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 172 to 180 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,

(i) a polynucleotide comprising a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 172 to 180 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, and

(j) a polynucleotide hybridizing under stringent conditions to any of the polynucleotides (f) to (i).

[0541] The nucleic acid further used in the method of the present invention can comprise a nucleic acid capable of specifically binding to at least one or more polynucleotide(s) selected from the group consisting of miR-4697-5p, miR-3197, miR-675-5p, miR-4486, miR-7107-5p, miR-23a-3p, miR-4667-5p, miR-451a, miR-3940-5p, miR-8059, miR-6813-5p, miR-4492, miR-4476 andmiR-6090.

[0542] As for such a nucleic acid, specifically, miR-4697-5p is hsa-miR-4697-5p, miR-3197 is hsa-miR-3197, miR-675-5p is hsa-miR-675-5p, miR-4486 is hsa-miR-4486, miR-7107-5p is hsa-miR-7107-5p, miR-23a-3p is hsa-miR-23a-3p, miR-4667-5p is hsa-miR-4667-5p, miR-451a is hsa-miR-451a, miR-3940-5p is hsa-miR-3940-5p, miR-8059 is hsa-miR-8059, miR-6813-5p is hsa-miR-6813-5p, miR-4492 is hsa-miR-4492, miR-4476 is hsa-miR-4476, and miR-6090 is hsa-miR-6090.

[0543] In a preferred embodiment, such a nucleic acid is specifically a polynucleotide selected from the group consisting of the following polynucleotides (k) to (o):

(k) a polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 181 to 194 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,

(l) a polynucleotide comprising a nucleotide sequence represented by any of SEQ ID NOs: 181 to 194,

(m) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 181 to 194 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,

(n) a polynucleotide comprising a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 181 to 194 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, and

(o) a polynucleotide hybridizing under stringent conditions to any of the polynucleotides (k) to (n).

[0544] Examples of the sample used in the method of the present invention can include samples prepared from a living tissue (preferably a colorectal tissue) or a body fluid such as blood, serum, plasma, or urine from the subject. Specifically, for example, an RNA-containing sample prepared from the tissue, a polynucleotide-containing sample further prepared therefrom, a body fluid such as blood, serum, plasma, or urine, a portion or the whole of a living tissue collected from the subject by biopsy or the like, or a living tissue excised by surgery can be used, and the sample for

measurement can be prepared therefrom.

[0545] As used herein, the subject refers to a mammal, for example, a human, a monkey, a mouse and a rat without any limitation, and is preferably a human.

[0546] The steps of the method of the present invention can be changed according to the type of the sample to be assayed.

[0547] In the case of using RNA as an analyte, the detection of colorectal cancer (cells) can comprise, for example, the following steps (a), (b), and (c):

(a) a step of binding RNA prepared from the sample of the subject or a complementary polynucleotide (cDNA) transcribed therefrom to a polynucleotide in the kit or the device of the present invention;
(b) a step of measuring the sample-derived RNA or the cDNA synthesized from the RNA, bound with the polynucleotide by hybridization using the polynucleotide as a nucleic acid probe or by quantitative RT-PCR using the polynucleotide as a primer; and
(c) a step of evaluating the presence or absence of colorectal cancer (or colorectal cancer-derived gene expression) on the basis of the measurement results of the step (b).

[0548] For example, various hybridization methods can be used for detecting, examining, evaluating, or diagnosing colorectal cancer (or colorectal cancer-derived gene expression) *in vitro* according to the present invention. For example, Northern blot, Southern blot, RT-PCR, DNA chip analysis, *in situ* hybridization, Northern hybridization, or Southern hybridization can be used as such a hybridization method.

[0549] In the case of using the Northern blot, the presence or absence of expression of each gene or the expression level thereof in the RNA can be detected or measured by use of the nucleic acid probe that can be used in the present invention. Specific examples thereof can include a method which involves labeling the nucleic acid probe (or its complementary strand) with a radioisotope (^{32}P, ^{33}P, ^{35}S, etc.), a fluorescent material, or the like, that hybridizes the labeled product with the living tissue-derived RNA from a subject transferred to a nylon membrane or the like according to a routine method, and then detecting and measuring a signal derived from the label (radioisotope or fluorescent material) on the formed DNA/RNA duplex using a radiation detector (examples thereof can include BAS-1800 II (Fujifilm Corp.)) or a fluorescence detector (examples thereof can include STORM 865 (GE Healthcare Japan Corp.)).

[0550] In the case of using the quantitative RT-PCR, the presence or absence of expression of each gene or the expression level thereof in the RNA can be detected or measured by use of the primer that can be used in the present invention. Specific examples thereof can include a method which involves; preparing cDNA from the living tissue-derived RNA of a subject according to a routine method, hybridizing a pair of primers (consisting of a plus strand and a reverse strand binding to the cDNA) of the present invention with the cDNA such that the region of each target gene can be amplified with the cDNA as a template, and performing PCR according to a routine method to detect the obtained double-stranded DNA. The method for detecting the double-stranded DNA can include a method of performing the PCR using the primers labeled in advance with a radioisotope or a fluorescent material, a method of electrophoresing the PCR product on an agarose gel and staining the double-stranded DNA with ethidium bromide or the like for detection, and a method of transferring the produced double-stranded DNA to a nylon membrane or the like according to a routine method and hybridizing the double-stranded DNA to a labeled nucleic acid probe for detection.

[0551] In the case of using the nucleic acid array analysis, an RNA chip or a DNA chip in which the nucleic acid probes (single-stranded or double-stranded) of the present invention is attached to a substrate (solid phase) is used. Regions that have the attached nucleic acid probes are referred to as probe spots, and regions that have no attached nucleic acid probe are referred to as blank spots. A gene group immobilized on a solid-phase substrate is generally called a nucleic acid chip, a nucleic acid array, a microarray, or the like. The DNA or RNA array includes a DNA or RNA macroarray and a DNA or RNA microarray. The term "chip" used herein includes all of these arrays. 3D-Gene(™) Human miRNA Oligo chip (Toray Industries, Inc.) can be used as the DNA chip, though the DNA chip is not limited thereto.

[0552] Examples of the measurement using the DNA chip can include, but are not limited to, a method of detecting and measuring a signal derived from the label on the nucleic acid probes using an image detector (examples thereof can include Typhoon 9410 (GE Healthcare Japan Corp.) and 3D-Gene(™) scanner (Toray Industries, Inc.)).

[0553] The "stringent conditions" used herein are, as mentioned above, conditions under which a nucleic acid probe hybridizes to its target sequence to a larger extent (e.g., a measurement value equal to or larger than a mean of background measurement values + a standard deviation of the background measurement values × 2) than that for other sequences.

[0554] The stringent conditions are defined by hybridization and subsequent washing conditions. The hybridization conditions involve, for example, but not limited to, 30°C to 60°C for 1 to 24 hours in a solution containing SSC, a surfactant, formamide, dextran sulfate, a blocking agent, etc. In this context, 1 × SSC is an aqueous solution (pH 7.0) containing 150 mM sodium chloride and 15 mM sodium citrate. The surfactant includes, for example, SDS (sodium dodecyl sulfate), Triton, or Tween. The hybridization conditions more preferably involve 3 to 10 × SSC and 0.1 to 1% SDS. Examples of

the conditions of the washing, following the hybridization, which is another condition to define the stringent conditions, can include conditions involving continuous washing at 30°C in a solution containing 0.5 × SSC and 0.1% SDS, at 30°C in a solution containing 0.2 × SSC and 0.1% SDS, and at 30°C in a 0.05 × SSC solution. It is desirable that the complementary strand should maintain its hybridized state with a target plus strand even by the washing under such conditions. Specifically, examples of such a complementary strand can include a strand consisting of a nucleotide sequence in a completely complementary relationship with the nucleotide sequence of the target plus strand, and a strand consisting of a nucleotide sequence having at least 80%, preferably at least 85%, more preferably at least 90% or at least 95%, for example, at least 98% or at least 99% identity to the strand.

[0555] Other examples of the "stringent conditions" for the hybridization are described in, for example, Sambrook, J. & Russel, D., Molecular Cloning, A LABORATORY MANUAL, Cold Spring Harbor Laboratory Press, published on January 15, 2001, Vol. 1, 7.42 to 7.45 and Vol. 2, 8.9 to 8.17, and can be used in the present invention.

[0556] Examples of the conditions for carrying out PCR using a polynucleotide fragment in the kit of the present invention as a primer include treatment for approximately 15 seconds to 1 minute at 5 to 10°C plus a Tm value calculated from the sequence of the primer, using a PCR buffer having composition such as 10 mM Tris-HCL (pH 8.3), 50 mM KCL, and 1 to 2 mM $MgCl_2$. Examples of the method for calculating such a Tm value include Tm value = 2 × (the number of adenine residues + the number of thymine residues) + 4 × (the number of guanine residues + the number of cytosine residues).

[0557] In the case of using the quantitative RT-PCR, a commercially available kit for measurement specially designed for quantitatively measuring miRNA, such as TaqMan(™) MicroRNA Assays (Life Technologies Corp.); LNA(™)-based MicroRNA PCR (Exiqon); or Ncode(™) miRNA qRT-PCT kit (Invitrogen Corp.) may be used.

[0558] For the calculation of gene expression levels, statistical analysis described in, for example, Statistical analysis of gene expression microarray data (Speed T., Chapman and Hall/CRC), and A beginner's guide Microarray gene expression data analysis (Causton H.C. et al., Blackwell publishing) can be used in the present invention, though the calculation method is not limited thereto. For example, twice, preferably 3 times, more preferably 6 times the standard deviation of the measurement values of the blank spots are added to the average measurement value of the blank spots on the DNA chip, and probe spots having a signal value equal to or larger than the resulting value can be regarded as detection spots. Alternatively, the average measurement value of the blank spots is regarded as a background and can be subtracted from the measurement values of the probe spots to determine gene expression levels. A missing value for a gene expression level can be excluded from the analyte, preferably replaced with the smallest value of the gene expression level in each DNA chip, or more preferably replaced with a value obtained by subtracting 0.1 from a logarithmic value of the smallest value of the gene expression level. In order to eliminate low-signal genes, only a gene having a gene expression level of 2^6, preferably 2^8, more preferably 2^{10} or larger, in 20% or more, preferably 50%, more preferably 80% or more of the number of measurement samples can be selected as the analyte. Examples of the normalization of the gene expression level include, but are not limited to, global normalization and quantile normalization (Bolstad, B. M. et al., 2003, Bioinformatics, Vol. 19, p. 185-193).

[0559] The present invention also provides a method comprising measuring a target gene or gene expression level in a sample derived from a subject using the polynucleotide, the kit, or the device (e.g., chip) for detection of the present invention, or a combination thereof, preparing a discriminant (discriminant function) with gene expression levels in a sample derived from a colorectal cancer patient and a sample derived from a healthy subject as supervising samples, and determining or evaluating the presence and/or absence of the colorectal cancer-derived gene in the sample.

[0560] Specifically, the present invention further provides the method comprising: a first step of measuring *in vitro* an expression level of a target gene (target nucleic acid) in multiple samples known to determine or evaluate the presence and/or absence of the colorectal cancer-derived gene in the samples, using the polynucleotide, the kit, or the device (e.g., chip) for detection of the present invention, or a combination thereof; a second step of preparing a discriminant with the measurement values of the expression level of the target gene obtained in the first step as supervising samples; a third step of measuring *in vitro* an expression level of the target gene in a sample derived from a subject in the same way as in the first step; and a fourth step of assigning the measurement value of the expression level of the target gene obtained in the third step into the discriminant obtained in the second step, and determining or evaluating the presence or absence of the colorectal cancer-derived gene in the sample on the basis of the results obtained from the discriminant, wherein the target gene can be detected using the polynucleotide or using a polynucleotide for detection contained in the kit or the device (e.g., chip). In this context, the discriminant can be prepared by use of Fisher's discriminant analysis, nonlinear discriminant analysis based on Mahalanobis' distance, neural network, Support Vector Machine (SVM), or the like, though the method is not limited thereto.

[0561] When a clustering boundary is a straight line or a hyperplane, the linear discriminant analysis is a method for determining the association of a cluster using Formula 1 as a discriminant. In Formula 1, x represents an explanatory variable, w represents a coefficient of the explanatory variable, and w0 represents a constant term.

$$f(x) = w_0 + \sum_{i=1}^{n} w_i x_i \qquad \text{Formula 1}$$

[0562] Values obtained from the discriminant are referred to as discriminant scores. The measurement values of a newly offered data set can be assigned as explanatory variables to the discriminant to determine clusters by the signs of the discriminant scores.

[0563] The Fisher's discriminant analysis, one type of linear discriminant analysis, is a dimensionality reduction method for selecting a dimension suitable for discriminating classes, and constructs synthetic variable with highly discriminant performance by focusing on the variance of synthetic variables and minimizing the variance of data having the same label (Venables, W.N. et al., Modern Applied Statistics with S. Fourth edition. Springer., 2002). In the Fisher's discriminant analysis, direction w of projection is determined so as to maximize Formula 2. In this Formula, μ represents an average input, ng represents the number of data associated to class g, and μg represents an average input of the data associated to class g. The numerator and the denominator are the inter-classe variance and the intra-classe variance, respectively, when each data is projected in the direction of the vector w. Discriminant coefficient wi is determined by maximizing this ratio (Takafumi Kanamori et al., "Pattern Recognition", Kyoritsu Shuppan Co., Ltd. (2009); and Richard O. et al., Pattern Classification Second Edition., Wiley-Interscience, 2000).

$$J(w) = \frac{\sum_{g=1}^{G} n_g \left(w^T \mu_g - w^T \mu\right)\left(w^T \mu_g - w^T \mu\right)^T}{\sum_{g=1}^{G} \sum_{i:y_i=g} \left(w^T x_i - w^T \mu_g\right)\left(w^T x_i - w^T \mu_g\right)} \qquad \text{Formula 2}$$

subject to

$$\mu = \sum_{i=1}^{n} \frac{x_i}{n}, \quad \mu_g = \sum_{i:u_i=g}^{n} \frac{x_i}{n_g}$$

[0564] The Mahalanobis' distance is calculated according to Formula 3 in consideration of data correlation and can be used as nonlinear discriminant analysis for determining a cluster having a closer Mahalanobis' distance from each cluster as an associated cluster. In this Formula 3, μ represents a central vector of each cluster, and S-1 represents an inverse matrix of the variance-covariance matrix of the cluster. The central vector is calculated from explanatory variable x, and an average vector, a median value vector, or the like can be used.

$$D(x, \mu) = \left\{(x-\mu)^t S^{-1} (x-\mu)\right\}^{\frac{1}{2}} \qquad \text{Formula 3}$$

[0565] SVM is a discriminant analysis method devised by V. Vapnik (The Nature of Statistical Leaning Theory, Springer, 1995). Particular data points of a data set having known classes are defined as explanatory variables, and classes are defined as objective variables. A boundary plane called hyperplane for correctly classifying the data set into the known classes is determined, and a discriminant for data classification is determined using the boundary plane. Then, the measurement values of a newly offered data set can be assigned as explanatory variables to the discriminant to determine classes. In this respect, the result of the discriminant analysis may be classes, may be a probability of being classified into correct classes, or may be the distance from the hyperplane. In SVM, a method of nonlinearly converting a feature vector to a high dimension and performing linear discriminant analysis in the space is known as a method for tackling nonlinear problems. An expression in which an inner product of two factors in a nonlinearly mapped space is expressed only by inputs in their original spaces is called kernel. Examples of the kernel can include a linear kernel, a RBF (Radial Basis Function) kernel, and a Gaussian kernel. While highly dimensional mapping is performed according to the kernel, the optimum discriminant, i.e., a discriminant, can be actually constructed by mere calculation according to the kernel, which avoids calculating features in the mapped space (e.g., Hideki Aso et al., Frontier of Statistical Science 6 "Statistics of pattern recognition and learning - New concepts and approaches", Iwanami Shoten, Publishers (2004); Nello Cristianini et al., Introduction to SVM, Kyoritsu Shuppan Co., Ltd. (2008)).

[0566] C-support vector classification (C-SVC), one type of SVM, involves preparing a hyperplane by supervising with the explanatory variables of two groups and classifying an unknown data set into either of the groups (C. Cortes et al.,

1995, Machine Learning, Vol. 20, p. 273-297).

[0567] Exemplary calculation of the C-SVC discriminant that can be used in the method of the present invention will be given below. First, all subjects are divided into two groups, i.e., a colorectal cancer patient group and a healthy subject group. For example, colorectal tissue examination can be used for each subject to be confirmed either as a colorectal cancer patient or as a healthy subject.

[0568] Next, a data set consisting of comprehensive gene expression levels of serum-derived samples of the two divided groups (hereinafter, this data set is referred to as a training cohort) is prepared, and a C-SVC discriminant is determined by using explanatory variables that are genes found to differ clearly in their gene expression levels between the two groups, and objective variables (e.g., -1 and +1) that are the grouping. An optimizing objective function is represented by Formula 4 wherein e represents all input vectors, y represents an objective variable, a represents a Lagrange's undetermined multiplier vector, Q represents a positive definite matrix, and C represents a parameter for adjusting constrained conditions.

$$\min_{a} \quad \frac{1}{2}a^T Qa - e^T a$$
$$subject\ to \quad y^T a = 0, \quad 0 \le a_i \le C, \quad i = 1,...,l, \qquad \text{Formula 4}$$

[0569] Formula 5 is a finally obtained discriminant, and an associated group can be determined on the basis of the sign of a value obtained according to the discriminant. In this Formula, x represents a support vector, y represents a label indicating the association of a group, a represents the corresponding coefficient, b represents a constant term, and K represents a kernel function.

$$f(x) = \mathrm{sgn}\left(\sum_{i=1}^{l} y_i a_i K(x_i, x) + b \right) \qquad \text{Formula 5}$$

[0570] For example, a RBF kernel defined by Formula 6 can be used as the kernel function. In this Formula, x represents a support vector, and y represents a kernel parameter for adjusting the complexity of the hyperplane.

$$K(x_i, x_j) = \exp\left(-r\left\|x_i - x_j\right\|^2\right), \quad r < 0 \qquad \text{Formula 6}$$

[0571] In addition, an approach such as neural network, k-nearest neighbor algorithms, decision trees, or logistic regression analysis can be selected as a method for determining or evaluating the presence and/or absence of expression of a colorectal cancer-derived target gene in a sample derived from a subject, or for evaluating the expression level thereof by comparison with a control derived from a healthy subject.

[0572] The method of the present invention can comprise, for example, the following steps (a), (b), and (c):

(a) a step of measuring an expression level of a target gene in tissues containing colorectal cancer-derived genes derived from colorectal cancer patients and/or samples already known to be tissues containing no colorectal cancer-derived gene derived from healthy subjects, using the polynucleotide, the kit, or the device (e.g., DNA chip) for detection according to the present invention;

(b) a step of preparing the discriminants of Formulas 1 to 3, 5, and 6 described above from the measurement values of the expression level measured in the step (a); and

(c) measuring an expression level of the target gene in a sample derived from a subject using the polynucleotide, the kit, or the device (e.g., DNA chip) for detection according to the present invention, assigning the obtained measurement value to the discriminants prepared in the step (b), and determining or evaluating the presence and/or absence of the colorectal cancer-derived target gene in the sample, or evaluating the expression level thereof by comparison with a healthy subject-derived control, on the basis of the obtained results. In this context, in the discriminants of Formulas 1 to 3, 5, and 6, x represents an explanatory variable and includes a value obtained by measuring a polynucleotide selected from the polynucleotides described in Section 2 above, or a fragment thereof, etc. Specifically, the explanatory variable for discriminating a colorectal cancer patient from a healthy subject according to the present invention is a gene expression level selected from, for example, the following expression levels (1) to (3):

[0573]

(1) a gene expression level in the serum of a colorectal cancer patient or a healthy subject measured by any DNA comprising 15 or more consecutive nucleotides in a nucleotide sequence represented by any of SEQ ID NOs: 1 to 171 and 606 to 614 or a complementary sequence thereof,
(2) a gene expression level in the serum of a colorectal cancer patient or a healthy subject measured by any DNA comprising 15 or more consecutive nucleotides in a nucleotide sequence represented by any of SEQ ID NOs: 172 to 180 or a complementary sequence thereof, and
(3) a gene expression level in the serum of a colorectal cancer patient or a healthy subject measured by any DNA comprising 15 or more consecutive nucleotides in a nucleotide sequence represented by any of SEQ ID NOs: 181 to 194 or a complementary sequence thereof.

[0574] As described above, for the method for determining or evaluating the presence and/or absence of a colorectal cancer-derived gene in a sample derived from a subject, the preparation of a discriminant requires a discriminant constructed from a training cohort. For enhancing the discriminant accuracy of the discriminant, it is necessary for the discriminant to use genes that show clear difference between two groups in the training cohort.

[0575] Each gene that is used for an explanatory variable in a discriminant is preferably determined as follows. First, comprehensive gene expression levels of a colorectal cancer patient group and comprehensive gene expression levels of a healthy subject group in a training cohort are used as a data set, the degree of difference in the expression level of each gene between the two groups is determined through the use of, for example, the P value of t test, which is parametric analysis, or the P value of Mann-Whitney's U test or Wilcoxon test, which is nonparametric analysis.

[0576] The gene can be regarded as being statistically significant when the critical rate (significance level) of the P value obtained by the test is smaller than, for example, 5%, 1%, or 0.01%.

[0577] In order to correct an increased probability of type I error attributed to the repetition of a test, a method known in the art, for example, Bonferroni or Holm method, can be used for the correction (e.g., Yasushi Nagata et al., "Basics of statistical multiple comparison methods", Scientist Press Co., Ltd. (2007)). As an example of the Bonferroni correction, for example, the P value obtained by a test is multiplied by the number of repetitions of the test, i.e., the number of genes used in the analysis, and the obtained value can be compared with a desired significance level to suppress a probability of causing type I error in the whole test.

[0578] Instead of the statistical test, the absolute value (fold change) of an expression ratio of a median value of each gene expression level between gene expression levels of a colorectal cancer patient group and gene expression levels of a healthy subject group may be calculated to select a gene that is used for an explanatory variable in a discriminant. Alternatively, ROC curves may be prepared using gene expression levels of a colorectal cancer patient group and a healthy subject group, and a gene that is used for an explanatory variable in a discriminant can be selected on the basis of an AUROC value.

[0579] Next, a discriminant that can be calculated by various methods described above is constructed using any number of genes that show large difference in their gene expression levels determined here. Examples of the method for constructing a discriminant that produces the largest discriminant accuracy include a method of constructing a discriminant in every combination of genes that satisfy the significance level of P value, and a method of repetitively evaluating the genes for use in the construction of a discriminant while increasing the number of genes one by one in a descending order of the difference in gene expression level (Furey TS. et al., 2000, Bioinformatics., Vol. 16, p. 906-14). A gene expression level of another independent colorectal cancer patient or healthy subject is assigned as an explanatory variable to this discriminant, and a result of the discriminant analysis regarding the group to which this independent colorectal cancer patient or healthy subject associated, is calculated. Specifically, the found gene set for diagnosis and the discriminant constructed using the gene set for diagnosis can be evaluated in an independent sample group to find a more universal gene set for diagnosis capable of detecting colorectal cancer and a more universal method for discriminating colorectal cancer.

[0580] Split-sample method is preferably used for evaluating the discriminant performance (generality) of the discriminant. Specifically, a data set is divided into a training cohort and a validation cohort, and gene selection by a statistical test and discriminant construction are performed in the training cohort. Accuracy, sensitivity, and specificity are calculated using results of discriminating a validation cohort according to the discriminant and a true group to which the validation cohort associated, to evaluate the discriminant performance. On the other hand, instead of dividing a data set, gene selection by a statistical test and discriminant preparation may be performed using all of samples, and accuracy, sensitivity, and specificity can be calculated by the discriminant of newly prepared samples according to the discriminant to evaluate the discriminant performance.

[0581] The present invention provides a polynucleotide for detection or for disease diagnosis useful in the diagnosis and treatment of colorectal cancer, a method for detecting colorectal cancer using the polynucleotide, and a kit and a device for the detection of colorectal cancer, comprising the polynucleotide. Particularly, in order to select a gene for

diagnosis and prepare a discriminant so as to exhibit accuracy beyond a colorectal cancer diagnosis method using existing tumor markers CEA, a gene set for diagnosis and a discriminant for the method of the present invention can be constructed, which exhibit accuracy beyond CEA, for example, by comparing genes expressed in serum derived from a patient confirmed to be negative using CEA but finally found to have colorectal cancer by detailed examination such as computed tomography using a contrast medium, with genes expressed in serum derived from a patient who has no colorectal cancer.

[0582] For example, the gene set for diagnosis is set to any combination selected from one or two or more of the polynucleotides based on a nucleotide sequence represented by any of SEQ ID NOs: 1 to 171 and 606 to 614 or a complementary sequence thereof as described above, optionally one or two or more of the polynucleotides based on a nucleotide sequence represented by any of SEQ ID NOs: 172 to 180 or a complementary sequence thereof, and optionally one or two or more of the polynucleotides based on a nucleotide sequence represented by any of SEQ ID NOs: 181 to 194 or a complementary sequence thereof. Further, a discriminant is constructed using expression levels of the gene set for diagnosis in samples derived from class I colorectal cancer patients and samples derived from class II healthy subjects as a result of tissue diagnosis. As a result, the presence or absence of colorectal cancer-derived genes in an unknown sample can be determined with 100% accuracy at the maximum by measuring expression levels of the gene set for diagnosis in the unknown sample.

Examples

[0583] Hereinafter, the present invention will be described further specifically with reference to Examples below. However, the scope of the present invention is not intended to be limited by these Examples.

[Reference Example 1]

<Collection of samples from colorectal cancer patients and healthy subjects>

[0584] Serum was collected using VENOJECT II vacuum blood collecting tube VP-AS109K60 (Terumo Corp.) from each of 100 healthy subjects and 34 colorectal cancer patients (15 cases with stage I, 6 cases with stage IIA, 4 cases with stage IIIA, 6 cases with stage IIIB, 2 cases with stage IIIC, and 1 case with stage IV) who were confirmed to have no primary cancer other than colorectal cancer after acquisition of informed consent, and used as a training cohort. Likewise, serum was collected using VENOJECT II vacuum blood collecting tube VP-AS109K60 (Terumo Corp.) from each of 50 healthy subjects and 16 colorectal cancer patients (3 cases with stage I, 4 cases with stage IIA, 1 case with stage IIB, 2 cases with stage IIIB, 2 cases with stage IIIC, and 4 cases with stage IV) who were confirmed to have no primary cancer other than colorectal cancer after acquisition of informed consent, and used as a validation cohort.

<Extraction of total RNA>

[0585] Total RNA was obtained from 300 μL of the serum sample obtained from each of 200 persons in total of 150 healthy subjects and 50 colorectal cancer patients included in the training cohort and the validation cohort, using a reagent for RNA extraction in 3D-Gene(™) RNA extraction reagent from liquid sample kit (Toray Industries, Inc.) according to the protocol provided by the manufacturer.

<Measurement of gene expression level>

[0586] miRNAs in the total RNA obtained from the serum sample of each of 200 persons in total of 150 healthy subjects and 50 colorectal cancer patients included in the training cohort and the validation cohort were fluorescently labeled using 3D-Gene(™) miRNA Labeling kit (Toray Industries, Inc.) according to the protocol (ver 2.20) provided by the manufacturer. The oligo DNA chip used was 3D-Gene(™) Human miRNA Oligo chip (Toray Industries, Inc.) with attached probes having sequences complementary to 2,555 miRNAs among the miRNAs registered in miRBase Release 20. Hybridization between the miRNAs in the total RNA and the probes on the DNA chip under stringent conditions and washing following the hybridization were performed according to the protocol provided by the manufacturer. The DNA chip was scanned using 3D-Gene(™) scanner (Toray Industries, Inc.) to obtain images. Fluorescence intensity was digitized using 3D-Gene(™) Extraction (Toray Industries, Inc.). The digitized fluorescence intensity was converted to a logarithmic value with a base of 2 and used as a gene expression level, from which a blank value was subtracted. A missing value was replaced with a value obtained by subtracting 0.1 from a logarithmic value of the smallest value of the gene expression level in each DNA chip. As a result, the comprehensive gene expression levels of the miRNAs in the serum were obtained for the 50 colorectal cancer patients and the 150 healthy subjects. Calculation and statistical analysis using the digitized gene expression levels of the miRNAs were carried out using R language 3.0.2 (R Devel-

opment Core Team (2013). R: A language and environment for statistical computing. R Foundation for Statistical Computing, URL http://www.R-project.org/.) and MASS package 7.3-30 (Venables, W. N. & Ripley, B. D. (2002) Modern Applied Statistics with S. Fourth Edition. Springer, New York. ISBN 0-387-95457-0).

[Reference Example 2]

<Collection of samples from patients with cancer other than colorectal cancer>

[0587] Serum was collected using VENOJECT II vacuum blood collecting tube VP-AS109K60 (Terumo Corp.) from each of 69 pancreatic cancer patients, 66 biliary tract cancer patients, 30 stomach cancer patients, 33 esophageal cancer patients, 32 liver cancer patients, and 15 benign pancreaticobiliary disease patients who were confirmed to have no cancer in other organs after acquisition of informed consent, and used as a training cohort together with the samples of 34 colorectal cancer patients and 103 healthy subjects of Reference Example 1. Likewise, serum was collected using VENOJECT II vacuum blood collecting tube VP-AS109K60 (Terumo Corp.) from each of 30 pancreatic cancer patients, 33 bile duct cancer patients, 20 stomach cancer patients, 17 esophageal cancer patients, 20 liver cancer patients, and 6 benign pancreaticobiliary disease patients who were confirmed to have no cancer in other organs after acquisition of informed consent, and used as a validation cohort together with the samples of 16 colorectal cancer patients confirmed to have no cancer in organs other than the large intestine and 47 healthy subjects of Reference Example 1. Subsequent operations were conducted in the same way as in Reference Example 1.

[Example 1]

<Selection of gene marker using samples in the training cohort, and method for evaluating colorectal cancer discriminant performance of single gene marker using samples of in the validation cohort>

[0588] In this Example, a gene marker for discriminating a colorectal cancer patient from a healthy subject was selected in the training cohort and studied in samples in the validation cohort independent of the training cohort, for a method for evaluating the colorectal cancer discriminant performance of each selected gene marker alone.

[0589] Specifically, first, the miRNA expression levels of the training cohort and the validation cohort obtained in the preceding Reference Examples were combined and normalized by quantile normalization.

[0590] Next, genes for diagnosis were selected using the training cohort. Here, in order to acquire diagnostic markers with higher reliability, only genes that show a gene expression level of 2^6 or higher in 50% or more of the samples in either of the colorectal cancer patient group in the training cohort or the healthy subj ect group in the training cohort were selected. In order to further acquire statistically significant genes for discriminating a colorectal cancer patient group from a healthy subject group, the P value obtained by two-tailed t-test assuming equal variance as to each gene expression level was corrected by the Bonferroni method, and genes that satisfied $p < 0.01$ were acquired as gene markers for use in explanatory variables of a discriminant. The obtained genes are described in Table 2.

[0591] In this way, hsa-miR-6726-5p, hsa-miR-4257, hsa-miR-6787-5p, hsa-miR-6780b-5p, hsa-miR-3131, hsa-miR-7108-5p, hsa-miR-1343-3p, hsa-miR-1247-3p, hsa-miR-4651, hsa-miR-6757-5p, hsa-miR-3679-5p, hsa-miR-7641, hsa-miR-6746-5p, hsa-miR-8072, hsa-miR-6741-5p, hsa-miR-1908-5p, hsa-miR-6857-5p, hsa-miR-4746-3p, hsa-miR-744-5p, hsa-miR-4792, hsa-miR-564, hsa-miR-6791-5p, hsa-miR-6825-5p, hsa-miR-6826-5p, hsa-miR-4665-3p, hsa-miR-4467, hsa-miR-3188, hsa-miR-6125, hsa-miR-6756-5p, hsa-miR-1228-3p, hsa-miR-8063, hsa-miR-8069, hsa-miR-6875-5p, hsa-miR-3185, hsa-miR-4433b-3p, hsa-miR-6887-5p, hsa-miR-128-1-5p, hsa-miR-6724-5p, hsa-miR-1914-3p, hsa-miR-1225-5p, hsa-miR-4419b, hsa-miR-7110-5p, hsa-miR-187-5p, hsa-miR-3184-5p, hsa-miR-204-3p, hsa-miR-5572, hsa-miR-6729-5p, hsa-miR-615-5p, hsa-miR-6749-5p, hsa-miR-6515-3p, hsa-miR-3937, hsa-miR-6840-3p, hsa-miR-6893-5p, hsa-miR-4728-5p, hsa-miR-6717-5p, hsa-miR-7113-3p, hsa-miR-4665-5p, hsa-miR-642b-3p, hsa-miR-7109-5p, hsa-miR-6842-5p, hsa-miR-4442, hsa-miR-4433-3p, hsa-miR-4707-5p, hsa-miR-6126, hsa-miR-4449, hsa-miR-4706, hsa-miR-1913, hsa-miR-602, hsa-miR-939-5p, hsa-miR-4695-5p, hsa-miR-711, hsa-miR-6816-5p, hsa-miR-4632-5p, hsa-miR-6721-5p, hsa-miR-7847-3p, hsa-miR-6132, hsa-miR-887-3p, hsa-miR-3679-3p, hsa-miR-6784-5p, hsa-miR-1249, hsa-miR-937-5p, hsa-miR-5195-3p, hsa-miR-6732-5p, hsa-miR-4417, hsa-miR-4281, hsa-miR-4734, hsa-miR-6766-3p, hsa-miR-663a, hsa-miR-4513, hsa-miR-6781-5p, hsa-miR-1227-5p, hsa-miR-6845-5p, hsa-miR-6798-5p, hsa-miR-3620-5p, hsa-miR-1915-5p, hsa-miR-4294, hsa-miR-642a-3p, hsa-miR-371a-5p, hsa-miR-940, hsa-miR-4450, hsa-miR-4723-5p, hsa-miR-1469, hsa-miR-6861-5p, hsa-miR-7975, hsa-miR-6879-5p, hsa-miR-6802-5p, hsa-miR-1268b, hsa-miR-663b, hsa-miR-125a-3p, hsa-miR-2861, hsa-miR-6088, hsa-miR-4758-5p, hsa-miR-296-3p, hsa-miR-6738-5p, hsa-miR-671-5p, hsa-miR-4454, hsa-miR-4516, hsa-miR-7845-5p, hsa-miR-4741, hsa-miR-92b-5p, hsa-miR-6795-5p, hsa-miR-6805-3p, hsa-miR-4725-3p, hsa-miR-6782-5p, hsa-miR-4688, hsa-miR-6850-5p, hsa-miR-6777-5p, hsa-miR-6785-5p, hsa-miR-7106-5p, hsa-miR-3663-3p, hsa-miR-6131, hsa-miR-1915-3p, hsa-miR-4532, hsa-miR-6820-5p, hsa-miR-4689, hsa-miR-4638-5p, hsa-miR-3656, hsa-miR-3621, hsa-miR-6769b-5p, hsa-miR-

149-3p, hsa-miR-23b-3p, hsa-miR-3135b, hsa-miR-6848-5p, hsa-miR-6769a-5p, hsa-miR-4327, hsa-miR-6765-3p, hsa-miR-6716-5p, hsa-miR-6877-5p, hsa-miR-6727-5p, hsa-miR-4534, hsa-miR-614, hsa-miR-1202, hsa-miR-575, hsa-miR-6870-5p, hsa-miR-6722-3p, hsa-miR-7977, hsa-miR-4649-5p, hsa-miR-4675, hsa-miR-6075, hsa-miR-6779-5p, hsa-miR-4271, hsa-miR-3196, hsa-miR-6803-5p, hsa-miR-6789-5p, hsa-miR-4648, hsa-miR-4508, hsa-miR-4749-5p, hsa-miR-4505, hsa-miR-5698, hsa-miR-1199-5p and hsa-miR-4763-3p, hsa-miR-1231, hsa-miR-1233-5p, hsa-miR-150-3p, hsa-miR-1225-3p, hsa-miR-92a-2-5p, hsa-miR-423-5p, hsa-miR-1268a, hsa-miR-128-2-5p and hsa-miR-24-3p genes, and polynucleotides consisting of the nucleotide sequences of SEQ ID NOs: 1 to 180 related thereto were found.

[0592] Among them, genes newly found as markers for examining the presence or absence of colorectal cancer are polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 171.

[0593] A discriminant for determining the presence or absence of colorectal cancer was further prepared by Fisher's discriminant analysis with the expression levels of these genes as an index. Specifically, any polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 1 to 180 found in the training cohort was applied to Formula 2 above to construct a discriminant. Calculated accuracy, sensitivity, and specificity are shown in Table 3. In this respect, a discriminant coefficient and a constant term are shown in Table 4.

[0594] Accuracy, sensitivity, and specificity in the validation cohort were calculated using the discriminant thus prepared, and the discriminant performance of the selected polynucleotides was validated using independent samples (Table 3). For example, the expression level measurement value of the nucleotide sequence represented by SEQ ID NO: 1 was compared between the healthy subjects (100 persons) and the colorectal cancer patients (34 persons) in the training cohort. As a result, the gene expression level measurement values were found to be significantly lower in the colorectal cancer patient group than in the healthy subject group (see the left diagram of Figure 2). These results were also reproducible for the healthy subjects (50 persons) and the colorectal cancer patients (16 persons) in the validation cohort (see the right diagram of Figure 2). Likewise, the results obtained about the other polynucleotides shown in SEQ ID NOs: 2 to 180 showed that the gene expression level measurement values were significantly lower (-) or higher (+) in the colorectal cancer patient group than in the healthy subject group (Table 2). These results were able to be validated in the validation cohort. For example, as for this nucleotide sequence represented by SEQ ID NO: 1, the number of samples that correctly identified in the detection of colorectal cancer in the validation cohort was calculated using the threshold (9.43) that was set in the training cohort and discriminated between the two groups. As a result, 16 true positives, 50 true negatives, 0 false positives, and 0 false negatives were obtained. From these values, 100% accuracy, 100% sensitivity, and 100% specificity were obtained as detection performance. In this way, the detection performance was calculated as to all of the polynucleotides shown in SEQ ID NOs: 1 to 180, and described in Table 3.

[0595] For example, 110 polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 49, 50, 51, 52, 53, 55, 56, 57, 58, 59, 60, 61, 62, 63, 65, 66, 67, 68, 69, 71, 72, 73, 74, 76, 77, 78, 79, 80, 81, 83, 84, 86, 87, 88, 90, 92, 93, 95, 96, 97, 99, 100, 101, 102, 107, 109, 110, 111, 113, 114, 115, 118, 120, 122, 124, 126, 134, 136, 142, 153, 172, 173 and 175 exhibited sensitivity of 100%, 100%, 100%, 75%, 93.8%, 75%, 87.5%, 75%, 93.8%, 68.8%, 81.2%, 100%, 75%, 50%, 75%, 75%, 68.8%, 75%, 81.2%, 81.2%, 75%, 62.5%, 75%, 56.2%, 75%, 68.8%, 56.2%, 62.5%, 68.8%, 75%, 68.8%, 68.8%, 56.2%, 68.8%, 62.5%, 68.8%, 62.5%, 50%, 56.2%, 56.2%, 56.2%, 75%, 50%, 68.8%, 68.8%, 68.8%, 50%, 56.2%, 62.5%, 62.5%, 50%, 62.5%, 68.8%, 56.2%, 56.2%, 43.8%, 75%, 62.5%, 62.5%, 56.2%, 62.5%, 62.5%, 56.2%, 62.5%, 56.2%, 56.2%, 56.2%, 56.2%, 43.8%, 43.8%, 50%, 68.8%, 56.2%, 62.5%, 62.5%, 43.8%, 62.5%, 56.2%, 62.5%, 62.5%, 50%, 56.2%, 43.8%, 50%, 43.8%, 50%, 43.8%, 56.2%, 43.8%, 50%, 50%, 50%, 50%, 50%, 50%, 43.8%, 50%, 43.8%, 50%, 50%, 50%, 43.8%, 43.8%, 50%, 43.8%, 43.8%, 50%, 81.2%, 68.8% and 56.2%, respectively in the validation cohort (Table 3). As seen from Comparative Example mentioned later, the existing markers CEA had sensitivity of 43.75% in the validation cohort (Tables 5-1 and 5-2), demonstrating that the 110 polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 49, 50, 51, 52, 53, 55, 56, 57, 58, 59, 60, 61, 62, 63, 65, 66, 67, 68, 69, 71, 72, 73, 74, 76, 77, 78, 79, 80, 81, 83, 84, 86, 87, 88, 90, 92, 93, 95, 96, 97, 99, 100, 101, 102, 107, 109, 110, 111, 113, 114, 115, 118, 120, 122, 124, 126, 134, 136, 142, 153, 172, 173 and 175 can discriminate, each alone, colorectal cancer in the validation cohort with sensitivity beyond CEA.

[0596] For example, 14 polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1, 2, 3, 10, 14, 17, 21, 23, 32, 36, 47, 59, 65, and 101 were able to correctly determine colorectal cancer as to all of three stage 1 colorectal cancer samples that were contained in the validation cohort. Thus, these polynucleotides can detect even early colorectal cancer and contribute to the early diagnosis of colorectal cancer.

[0597] For example, 12 polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1, 2, 3, 5, 7, 10, 14, 39, 46, 73, 81, and 148 were able to correctly determine colorectal cancer as to all of one cecal cancer case and 3 ascending colon cancer cases, which were cancer cases in the upper large intestine that are reportedly difficult to detect by the fecal occult blood test, in the validation cohort. Thus, these polynucleotides can detect colorectal cancer regardless of where colorectal cancer develops.

[Example 2]

<Method for evaluating colorectal cancer discriminant performance by combination of multiple gene markers using samples in the validation cohort>

[0598] In this Example, a method for evaluating colorectal cancer discriminant performance by a combination of the gene markers selected in Example 1 was studied. Specifically, Fisher's discriminant analysis was conducted as to 16,074 combinations of two polynucleotides comprising at least one or more of the expression level measurement values of the newly found polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 171 among the polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 180 selected in Example 1, to construct a discriminant for determining the presence or absence of colorectal cancer. Next, accuracy, sensitivity, and specificity in the validation cohort were calculated using the discriminant thus prepared, and the discriminant performance of the selected polynucleotides was validated using independent samples.

[0599] For example, the expression level measurement values of the nucleotide sequences represented by SEQ ID NO: 1 and SEQ ID NO: 2 were compared between the healthy subjects (100 persons) and the colorectal cancer patients (34 persons) in the training cohort. As a result, a scatter diagram that significantly separated the gene expression level measurement values of the colorectal cancer patient group from those of the healthy subject group was obtained (see the left diagram of Figure 3). These results were also reproducible for the healthy subjects (50 persons) and the colorectal cancer patients (16 persons) in the validation cohort (see the right diagram of Figure 3). Likewise, a scatter diagram that significantly separated the gene expression level measurement values of the colorectal cancer patient group from those of the healthy subject group was also obtained as to the other combinations of two expression level measurement values comprising at least one or more of the expression level measurement values of the newly found polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 171 among the polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 180. These results were able to be validated in the validation cohort. For example, as for these nucleotide sequences represented by SEQ ID NO: 1 and SEQ ID NO: 2, the number of samples that correctly identified in the detection of colorectal cancer was calculated using the function (0 = 1.26x + y - 18.06) that was set in the training cohort and discriminated between the two groups. As a result, 16 true positives, 50 true negatives, 0 false positives, and 0 false negatives were obtained. From these values, 100% accuracy, 100% sensitivity, and 100% specificity were obtained as detection performance. In this way, the detection performance was calculated as to all of the combinations of two expression level measurement values comprising at least one or more of the expression level measurement values of the newly found polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 171 among the polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 180. Among them, 179 combinations comprising the expression level measurement value of the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 1 and the detection performance thereof were described in Table 6 as an example. For example, all of combinations of the expression level measurement values of the polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 and 2, SEQ ID NOs: 1 and 3, SEQ ID NOs: 1 and 4, and SEQ ID NOs: 1 and 5 exhibited sensitivity of 100% in the validation cohort (Table 6). Further, combinations of two polynucleotides consisting of nucleotide sequences other than SEQ ID NO: 1 were described in Table 7 as an example. As specific combinations of two polynucleotides, for example, combinations represented by SEQ ID NOs: 5 and 6, SEQ ID NOs: 5 and 11, SEQ ID NOs: 5 and 38, SEQ ID NOs: 15 and 16, SEQ ID NOs: 15 and 21, SEQ ID NOs: 15 and 64, SEQ ID NOs: 24 and 25, SEQ ID NOs: 24 and 30, SEQ ID NOs: 24 and 32, SEQ ID NOs: 2 and 32, SEQ ID NOs: 32 and 36, SEQ ID NOs: 15 and 32, SEQ ID NOs: 3 and 38, SEQ ID NOs: 38 and 39, SEQ ID NOs: 38 and 64, SEQ ID NOs: 3 and 45, SEQ ID NOs: 45 and 58, SEQ ID NOs: 45 and 64, SEQ ID NOs: 2 and 55, SEQ ID NOs: 6 and 55, SEQ ID NOs: 55 and 64, SEQ ID NOs: 2 and 64, SEQ ID NOs: 4 and 64, SEQ ID NOs: 2 and 96, SEQ ID NOs: 7 and 96, SEQ ID NOs: 96 and 97, SEQ ID NOs: 2 and 97, SEQ ID NOs: 3 and 97, SEQ ID NOs: 5 and 97, SEQ ID NOs: 2 and 162, SEQ ID NOs: 3 and 162, and SEQ ID NOs: 5 and 162, exhibited accuracy of 75% or higher for discriminating the colorectal cancer patients from the healthy subjects in both of the training cohort and the validation cohort. In this way, 14,598 combinations of the expression level measurement values of two polynucleotides that have sensitivity beyond the existing marker CEA (43.8% in Table 5-2) were obtained in the validation cohort. All of the nucleotide sequences 1 to 180 described in Table 2 obtained in Example 1 were employed at least once in these combinations. These results demonstrated that the combined use of two of the polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 180 can also discriminate colorectal cancer with excellent performance beyond the existing marker.

[0600] Markers for the detection of colorectal cancer with better sensitivity are obtained by combining 3, 4, 5, 6, 7, 8, 9, 10 or more of the expression level measurement values of the polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 180. For example, the newly found polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 171 among the polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 180 selected in Example 1 were measured to obtain their expression levels between

the healthy subject group and the colorectal cancer group in the validation cohort. All of the polynucleotides were ranked in the descending order of their P values obtained by the Student's t-test, which indicates statistical significance of difference between groups (i.e., one having the lowest P value was ranked in the first place), and colorectal cancer detection sensitivity was evaluated using combinations of one or more polynucleotides to which the polynucleotides were added to the combination one by one from the top to the bottom according to the rank. In short, the order in which the polynucleotides were combined in this evaluation is in reverse in terms of SEQ ID NOs, from SEQ ID NO: 171 to SEQ ID NOs: 170, 169, ... as shown in Table 2. As a result, the sensitivity in the validation cohort was 12.5% for 1 polynucleotide (SEQ ID NO: 171), 18.8% for 2 polynucleotides (SEQ ID NOs: 170 and 171), 25.0% for 4 polynucleotides (SEQ ID NOs: 168 to 171), 31.2% for 5 polynucleotides (SEQ ID NOs: 167 to 171), 37.5% for 7 polynucleotides (SEQ ID NOs: 165 to 171), 87.5% for 10 polynucleotides (SEQ ID NOs: 162 to 171), 100% for 20 polynucleotides (SEQ ID NOs: 152 to 171), 100% for 30 polynucleotides (SEQ ID NOs: 142 to 171), 100% for 80 polynucleotides (SEQ ID NOs: 92 to 171), 100% for 170 polynucleotides (SEQ ID NOs: 2 to 171), and 100% for 171 polynucleotides (SEQ ID NOs: 1 to 171).

[0601] These results demonstrated that a combination of multiple polynucleotides can produce higher colorectal cancer discriminant performance than that of each polynucleotide alone or a combination of a fewer number of polynucleotides. In this context, the combinations of multiple polynucleotides are not limited to the combinations of the polynucleotides added in the order of statistically significant difference as described above, and any combination of multiple polynucleotides can be used in the detection of colorectal cancer.

[0602] From these results, it can be concluded that all of the polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 180 serve as excellent markers for the detection of colorectal cancer.

[Table 2]

SEQ ID NO:	Gene name	P value after Bonferroni correction	Expression level in colorectal cancer patient with respect to healthy subject
1	hsa-miR-6726-5p	5.20.E-41	-
2	hsa-miR-4257	7.54.E-40	-
3	hsa-miR-6787-5p	1.72.E-30	-
4	hsa-miR-6780b-5p	3.42.E-30	+
5	hsa-miR-3131	1.62.E-27	-
6	hsa-miR-7108-5p	5.42.E-27	+
7	hsa-miR-1343-3p	2.12.E-26	-
8	hsa-miR-1247-3p	9.98.E-26	+
9	hsa-miR-4651	3.90.E-24	-
10	hsa-miR-6757-5p	2.25.E-23	-
11	hsa-miR-3679-5p	2.55.E-23	+
12	hsa-miR-7641	9.71.E-22	-
13	hsa-miR-6746-5p	1.64.E-21	-
14	hsa-miR-8072	4.09.E-21	+
15	hsa-miR-6741-5p	7.23.E-21	-
16	hsa-miR-1908-5p	2.12.E-20	+
17	hsa-miR-6857-5p	2.70.E-20	+
18	hsa-miR-4746-3p	3.58.E-20	+
19	hsa-miR-744-5p	4.23.E-20	+
20	hsa-miR-4792	8.25.E-20	+
21	hsa-miR-564	1.78.E-19	-
22	hsa-miR-6791-5p	3.80.E-19	+
23	hsa-miR-6825-5p	5.93.E-19	+

(continued)

SEQ ID NO:	Gene name	P value after Bonferroni correction	Expression level in colorectal cancer patient with respect to healthy subject
24	hsa-miR-6826-5p	8.67.E-19	-
25	hsa-miR-4665-3p	1.92.E-18	+
26	hsa-miR-4467	5.55.E-18	+
27	hsa-miR-3188	8.48.E-18	+
28	hsa-miR-6125	1.09.E-17	+
29	hsa-miR-6756-5p	1.24.E-17	-
30	hsa-miR-1228-3p	1.68.E-17	+
31	hsa-miR-8063	2.70.E-17	-
32	hsa-miR-8069	3.58.E-17	+
33	hsa-miR-6875-5p	6.07.E-17	+
34	hsa-miR-3185	5.07.E-16	+
35	hsa-miR-4433b-3p	1.22.E-15	+
36	hsa-miR-6887-5p	1.30.E-15	-
37	hsa-miR-128-1-5p	3.61.E-15	+
38	hsa-miR-6724-5p	3.81.E-15	+
39	hsa-miR-1914-3p	1.05.E-14	-
40	hsa-miR-1225-5p	3.93.E-14	+
41	hsa-miR-4419b	5.90.E-14	-
42	hsa-miR-7110-5p	6.01.E-14	+
43	hsa-miR-187-5p	8.57.E-14	-
44	hsa-miR-3184-5p	1.40.E-13	+
45	hsa-miR-204-3p	2.23.E-13	-
46	hsa-miR-5572	2.34.E-13	+
47	hsa-miR-6729-5p	3.33.E-13	+
48	hsa-miR-615-5p	4.27.E-13	-
49	hsa-miR-6749-5p	5.30.E-13	-
50	hsa-miR-6515-3p	7.31.E-13	+
51	hsa-miR-3937	8.10.E-13	+
52	hsa-miR-6840-3p	1.15.E-12	-
53	hsa-miR-6893-5p	1.34.E-12	-
54	hsa-miR-4728-5p	2.48.E-12	-
55	hsa-miR-6717-5p	4.45.E-12	-
56	hsa-miR-7113-3p	5.11.E-12	+
57	hsa-miR-4665-5p	5.33.E-12	-
58	hsa-miR-642b-3p	6.74.E-12	-
59	hsa-miR-7109-5p	6.88.E-12	-
60	hsa-miR-6842-5p	6.91.E-12	+

(continued)

SEQ ID NO:	Gene name	P value after Bonferroni correction	Expression level in colorectal cancer patient with respect to healthy subject
61	hsa-miR-4442	8.87.E-12	-
62	hsa-miR-4433-3p	9.88.E-12	+
63	hsa-miR-4707-5p	1.19.E-11	+
64	hsa-miR-6126	1.27.E-11	+
65	hsa-miR-4449	1.32.E-11	+
66	hsa-miR-4706	2.85.E-11	-
67	hsa-miR-1913	3.15.E-11	+
68	hsa-miR-602	4.98.E-11	+
69	hsa-miR-939-5p	6.08.E-11	+
70	hsa-miR-4695-5p	8.15.E-11	+
71	hsa-miR-711	1.23.E-10	+
72	hsa-miR-6816-5p	1.29.E-10	+
73	hsa-miR-4632-5p	1.50.E-10	+
74	hsa-miR-6721-5p	1.98.E-10	+
75	hsa-miR-7847-3p	2.14.E-10	-
76	hsa-miR-6132	2.68.E-10	+
77	hsa-miR-887-3p	2.81.E-10	+
78	hsa-miR-3679-3p	3.07.E-10	+
79	hsa-miR-6784-5p	3.20.E-10	+
80	hsa-miR-1249	3.40.E-10	+
81	hsa-miR-937-5p	5.57.E-10	-
82	hsa-miR-5195-3p	6.88.E-10	-
83	hsa-miR-6732-5p	7.27.E-10	+
84	hsa-miR-4417	7.95.E-10	+
85	hsa-miR-4281	9.35.E-10	-
86	hsa-miR-4734	1.04.E-09	+
87	hsa-miR-6766-3p	1.07.E-09	+
88	hsa-miR-663a	2.19.E-09	+
89	hsa-miR-4513	3.03.E-09	-
90	hsa-miR-6781-5p	5.11.E-09	+
91	hsa-miR-1227-5p	6.16.E-09	+
92	hsa-miR-6845-5p	6.49.E-09	+
93	hsa-miR-6798-5p	8.99.E-09	+
94	hsa-miR-3620-5p	1.09.E-08	+
95	hsa-miR-1915-5p	1.78.E-08	-
96	hsa-miR-4294	2.30.E-08	-
97	hsa-miR-642a-3p	2.61.E-08	-

(continued)

SEQ ID NO:	Gene name	P value after Bonferroni correction	Expression level in colorectal cancer patient with respect to healthy subject
98	hsa-miR-371a-5p	3.15.E-08	-
99	hsa-miR-940	3.18.E-08	+
100	hsa-miR-4450	3.25.E-08	-
101	hsa-miR-4723-5p	4.21.E-08	-
102	hsa-miR-1469	4.26.E-08	+
103	hsa-miR-6861-5p	4.71.E-08	-
104	hsa-miR-7975	7.28.E-08	-
105	hsa-miR-6879-5p	7.64.E-08	+
106	hsa-miR-6802-5p	9.22.E-08	-
107	hsa-miR-1268b	1.08.E-07	+
108	hsa-miR-663b	1.12.E-07	-
109	hsa-miR-125a-3p	1.16.E-07	-
110	hsa-miR-2861	1.87.E-07	-
111	hsa-miR-6088	2.97.E-07	-
112	hsa-miR-4758-5p	3.12.E-07	-
113	hsa-miR-296-3p	3.43.E-07	-
114	hsa-miR-6738-5p	4.05.E-07	-
115	hsa-miR-671-5p	5.76.E-07	-
116	hsa-miR-4454	6.68.E-07	-
117	hsa-miR-4516	1.04.E-06	-
118	hsa-miR-7845-5p	1.10.E-06	+
119	hsa-miR-4741	1.52.E-06	+
120	hsa-miR-92b-5p	1.63.E-06	+
121	hsa-miR-6795-5p	2.31.E-06	-
122	hsa-miR-6805-3p	3.95.E-06	+
123	hsa-miR-4725-3p	5.35.E-06	+
124	hsa-miR-6782-5p	5.69.E-06	+
125	hsa-miR-4688	8.95.E-06	-
126	hsa-miR-6850-5p	1.66.E-05	+
127	hsa-miR-6777-5p	1.74.E-05	-
128	hsa-miR-6785-5p	1.89.E-05	-
129	hsa-miR-7106-5p	1.94.E-05	-
130	hsa-miR-3663-3p	2.08.E-05	-
131	hsa-miR-6131	2.29.E-05	-
132	hsa-miR-1915-3p	3.16.E-05	+
133	hsa-miR-4532	3.46.E-05	-
134	hsa-miR-6820-5p	3.81.E-05	-

(continued)

SEQ ID NO:	Gene name	P value after Bonferroni correction	Expression level in colorectal cancer patient with respect to healthy subject
135	hsa-miR-4689	4.54.E-05	-
136	hsa-miR-4638-5p	4.70.E-05	-
137	hsa-miR-3656	5.75.E-05	+
138	hsa-miR-3621	6.34.E-05	-
139	hsa-miR-6769b-5p	6.63.E-05	-
140	hsa-miR-149-3p	1.01.E-04	-
141	hsa-miR-23b-3p	1.11.E-04	-
142	hsa-miR-3135b	1.16.E-04	-
143	hsa-miR-6848-5p	1.17.E-04	+
144	hsa-miR-6769a-5p	1.23.E-04	-
145	hsa-miR-4327	1.40.E-04	+
146	hsa-miR-6765-3p	1.50.E-04	-
147	hsa-miR-6716-5p	1.51.E-04	+
148	hsa-miR-6877-5p	1.52.E-04	-
149	hsa-miR-6727-5p	2.04.E-04	-
150	hsa-miR-4534	2.10.E-04	-
151	hsa-miR-614	3.18.E-04	-
152	hsa-miR-1202	4.86.E-04	-
153	hsa-miR-575	4.92.E-04	-
154	hsa-miR-6870-5p	5.55.E-04	+
155	hsa-miR-6722-3p	7.07.E-04	+
156	hsa-miR-7977	7.17.E-04	-
157	hsa-miR-4649-5p	7.70.E-04	-
158	hsa-miR-4675	9.21.E-04	-
159	hsa-miR-6075	1.03.E-03	+
160	hsa-miR-6779-5p	1.04.E-03	-
161	hsa-miR-4271	1.43.E-03	-
162	hsa-miR-3196	1.45.E-03	+
163	hsa-miR-6803-5p	1.46.E-03	+
164	hsa-miR-6789-5p	1.71.E-03	+
165	hsa-miR-4648	1.90.E-03	+
166	hsa-miR-4508	3.41.E-03	+
167	hsa-miR-4749-5p	3.52.E-03	+
168	hsa-miR-4505	4.01.E-03	+
169	hsa-miR-5698	4.99.E-03	-
170	hsa-miR-1199-5p	5.88.E-03	-
171	hsa-miR-4763-3p	8.40.E-03	+

(continued)

SEQ ID NO:	Gene name	P value after Bonferroni correction	Expression level in colorectal cancer patient with respect to healthy subject
172	hsa-miR-1231	7.36.E-25	+
173	hsa-miR-1233-5p	1.21.E-22	-
174	hsa-miR-150-3p	5.76.E-07	-
175	hsa-miR-1225-3p	1.44.E-06	+
176	hsa-miR-92a-2-5p	2.36.E-05	+
177	hsa-miR-423-5p	4.62.E-05	-
178	hsa-miR-1268a	4.30.E-04	+
179	hsa-miR-128-2-5p	6.64.E-04	-
180	hsa-miR-24-3p	1.31.E-03	-

[Table 3]

	Training cohort			Validation cohort		
SEQ ID NO:	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
1	99.3	100	99	100	100	100
2	96.3	88.2	99	100	100	100
3	96.3	91.2	98	98.5	100	98
4	93.3	85.3	96	93.9	75	100
5	97	91.2	99	97	93.8	98
6	94	82.4	98	90.9	75	96
7	96.3	88.2	99	95.5	87.5	98
8	92.5	82.4	96	89.4	75	94
9	93.3	85.3	96	97	93.8	98
10	91.8	79.4	96	92.4	68.8	100
11	94.8	91.2	96	95.5	81.2	100
12	90.3	82.4	93	97	100	96
13	89.6	79.4	93	90.9	75	96
14	91	73.5	97	80.3	50	90
15	94	79.4	99	89.4	75	94
16	88.1	73.5	93	89.4	75	94
17	91	85.3	93	87.9	68.8	94
18	91	79.4	95	92.4	75	98
19	90.3	76.5	95	93.9	81.2	98
20	91.8	88.2	93	92.4	81.2	96
21	87.3	58.8	97	92.4	75	98
22	88.1	73.5	93	89.4	62.5	98
23	87.3	79.4	90	87.9	75	92
24	90.3	67.6	98	89.4	56.2	100

(continued)

	Training cohort			Validation cohort		
SEQ ID NO:	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
25	89.6	67.6	97	84.8	75	88
26	83.6	70.6	88	89.4	68.8	96
27	91.8	76.5	97	87.9	56.2	98
28	91	82.4	94	87.9	62.5	96
29	88.8	67.6	96	83.3	68.8	88
30	91.8	85.3	94	86.4	75	90
31	87.3	79.4	90	87.9	68.8	94
32	87.3	64.7	95	89.4	68.8	96
33	91	79.4	95	80.3	56.2	88
34	89.6	76.5	94	89.4	68.8	96
35	89.6	79.4	93	78.8	62.5	84
36	88.1	55.9	99	92.4	68.8	100
37	85.1	61.8	93	80.3	62.5	86
38	86.6	70.6	92	78.8	50	88
39	88.1	70.6	94	81.8	56.2	90
40	91	76.5	96	84.8	56.2	94
41	86.6	58.8	96	87.9	56.2	98
42	84.3	64.7	91	86.4	75	90
43	84.3	52.9	95	86.4	50	98
44	87.3	70.6	93	87.9	68.8	94
45	87.3	61.8	96	77.3	68.8	80
46	83.6	70.6	88	84.8	68.8	90
47	86.6	52.9	98	86.4	50	98
48	88.8	58.8	99	81.8	31.2	98
49	87.3	61.8	96	87.9	56.2	98
50	86.6	73.5	91	77.3	62.5	82
51	86.6	64.7	94	87.9	62.5	96
52	84.3	52.9	95	84.8	50	96
53	88.8	64.7	97	87.9	62.5	96
54	81.3	50	92	77.3	31.2	92
55	88.8	58.8	99	90.9	68.8	98
56	84.2	66.7	90	83.3	56.2	92
57	84.3	58.8	93	80.3	56.2	88
58	85.1	50	97	86.4	43.8	100
59	82.8	55.9	92	89.4	75	94
60	87.3	64.7	95	87.9	62.5	96
61	81.3	52.9	91	84.8	62.5	92

(continued)

	Training cohort			Validation cohort		
SEQ ID NO:	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
62	82.8	67.6	88	80.3	56.2	88
63	82.1	55.9	91	84.8	62.5	92
64	78.4	38.2	92	83.3	37.5	98
65	86.6	61.8	95	87.9	62.5	96
66	85.1	58.8	94	84.8	56.2	94
67	83.6	61.8	91	80	62.5	85.7
68	85.1	61.8	93	84.8	56.2	94
69	80.6	64.7	86	80.3	56.2	88
70	81.3	52.9	91	78.8	31.2	94
71	85.1	58.8	94	87.9	56.2	98
72	83.6	64.7	90	83.3	56.2	92
73	87.3	55.9	98	84.8	43.8	98
74	83.6	64.7	90	77.3	43.8	88
75	82.7	33.3	99	84.8	37.5	100
76	83.6	44.1	97	86.4	50	98
77	85.8	73.5	90	83.3	68.8	88
78	83.6	52.9	94	81.8	56.2	90
79	83.6	67.6	89	81.8	62.5	88
80	85	58.8	93.9	83.3	62.5	90
81	84.3	50	96	83.3	43.8	96
82	81.3	44.1	94	81.8	37.5	96
83	82.1	61.8	89	78.8	62.5	84
84	90.3	70.6	97	84.8	56.2	94
85	83.6	55.9	93	80.3	31.2	96
86	80.6	41.2	94	86.4	62.5	94
87	83.6	50	95	83.3	62.5	90
88	84.3	52.9	95	83.3	50	94
89	84.3	44.1	98	77.3	12.5	98
90	82.8	50	94	81.8	56.2	90
91	79.9	38.2	94	75.8	31.2	90
92	84.3	50	96	78.8	43.8	90
93	82.8	61.8	90	75.8	50	84
94	84.3	55.9	94	77.3	31.2	92
95	82.1	41.2	96	83.3	43.8	96
96	85.1	55.9	95	81.8	50	92
97	78.4	38.2	92	78.8	43.8	90
98	82.8	50	94	75.8	37.5	88

(continued)

	Training cohort			Validation cohort		
SEQ ID NO:	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
99	81.3	47.1	93	86.4	56.2	96
100	85.1	47.1	98	83.3	43.8	96
101	87.3	58.8	97	83.3	50	94
102	80.6	38.2	95	80.3	50	90
103	83.6	47.1	96	80.3	37.5	94
104	79.1	35.3	94	78.8	37.5	92
105	82.8	38.2	98	84.8	37.5	100
106	82.8	44.1	96	81.8	37.5	96
107	74.6	32.4	89	75.8	50	84
108	83.6	47.1	96	83.3	31.2	100
109	85.1	44.1	99	87.9	50	100
110	82.8	52.9	93	84.8	50	96
111	78.4	44.1	90	81.8	50	92
112	84.3	44.1	98	80.3	25	98
113	82.8	50	94	80.3	43.8	92
114	82.8	52.9	93	83.3	50	94
115	82.1	44.1	95	84.8	43.8	98
116	79.9	41.2	93	77.3	31.2	92
117	87.3	50	100	84.8	37.5	100
118	88.1	58.8	98	81.8	50	92
119	78.4	29.4	95	77.3	25	94
120	78.4	41.2	91	84.8	50	96
121	80.6	26.5	99	80.3	18.8	100
122	77.6	38.2	91	83.3	50	94
123	76.1	26.5	93	74.2	12.5	94
124	83.6	44.1	97	83.3	43.8	96
125	77.6	35.3	92	74.2	18.8	92
126	80.6	41.2	94	78.8	43.8	90
127	79.1	23.5	98	83.3	31.2	100
128	80.6	38.2	95	80.3	31.2	96
129	78.4	23.5	97	80.3	25	98
130	78.4	29.4	95	80.3	31.2	96
131	81.3	35.3	97	83.3	37.5	98
132	80.6	35.3	96	80.3	25	98
133	82.8	44.1	96	80.3	37.5	94
134	83.6	41.2	98	83.3	50	94
135	79.9	29.4	97	81.8	25	100

(continued)

	Training cohort			Validation cohort		
SEQ ID NO:	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
136	83.6	41.2	98	86.4	43.8	100
137	79.9	38.2	94	77.3	12.5	98
138	76.1	26.5	93	77.3	25	94
139	79.1	26.5	97	78.8	18.8	98
140	76.9	23.5	95	77.3	25	94
141	79.1	26.5	97	75.8	18.8	94
142	83.6	38.2	99	86.4	43.8	100
143	77.6	26.5	95	78.8	25	96
144	74.6	17.6	94	80.3	31.2	96
145	79.1	41.2	92	75.8	25	92
146	78.4	32.4	94	80.3	31.2	96
147	79.1	29.4	96	77.3	31.2	92
148	73.9	20.6	92	71.2	6.2	92
149	79.1	38.2	93	81.8	31.2	98
150	78.4	23.5	97	74.2	25	90
151	76.1	32.4	91	77.3	25	94
152	81.3	29.4	99	81.8	25	100
153	82.1	29.4	100	87.9	50	100
154	81.3	35.3	97	84.8	37.5	100
155	79.1	29.4	96	78.8	31.2	94
156	78.9	24.2	97	77.3	25	94
157	79.9	29.4	97	83.3	31.2	100
158	80.6	35.3	96	84.8	37.5	100
159	82.1	35.3	98	81.8	31.2	98
160	78.4	20.6	98	81.8	31.2	98
161	78.4	26.5	96	81.8	25	100
162	79.1	29.4	96	77.3	18.8	96
163	74.6	26.5	91	63.6	0	84
164	76.1	20.6	95	71.2	12.5	90
165	77.6	23.5	96	81.8	25	100
166	78.4	29.4	95	69.7	6.2	90
167	78.4	14.7	100	75.8	0	100
168	78.2	21.2	97	78.8	12.5	100
169	78.4	23.5	97	77.3	6.2	100
170	73.9	2.9	98	77.3	6.2	100
171	80.6	26.5	99	78.8	12.5	100
172	93.3	85.3	96	90.9	81.2	94

(continued)

	Training cohort			Validation cohort		
SEQ ID NO:	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
173	91	76.5	96	90.9	68.8	98
174	82.1	35.3	98	77.3	31.2	92
175	87.3	52.9	99	89.4	56.2	100
176	74.6	29.4	90	78.8	37.5	92
177	79.9	35.3	95	69.7	12.5	88
178	73.9	17.6	93	71.2	6.2	92
179	81.3	32.4	98	84.8	37.5	100
180	76.9	11.8	99	81.8	25	100

[Table 4]

SEQ ID NO:	Discriminant coefficient	Constant term
1	3.451	32.537
2	2.778	17.111
3	3.893	32.032
4	3.208	29.340
5	2.408	15.716
6	4.760	44.132
7	1.872	13.040
8	4.189	26.554
9	5.692	61.192
10	2.915	20.140
11	2.801	19.585
12	1.247	8.323
13	3.434	21.316
14	5.315	65.956
15	3.971	26.352
16	4.335	50.272
17	1.843	9.956
18	2.796	18.550
19	2.726	19.273
20	2.151	14.586
21	1.432	7.567
22	4.810	44.500
23	2.202	14.554
24	1.787	9.999
25	4.048	23.773

(continued)

SEQ ID NO:	Discriminant coefficient	Constant term
26	2.353	23.473
27	3.139	19.203
28	5.364	64.417
29	5.274	42.891
30	4.406	27.813
31	2.590	20.814
32	6.586	84.911
33	3.426	31.099
34	2.365	16.821
35	3.810	30.817
36	2.245	13.547
37	2.667	20.060
38	4.817	48.162
39	4.582	33.609
40	3.409	25.092
41	2.180	12.620
42	1.846	14.493
43	2.092	20.352
44	2.237	18.151
45	1.808	22.979
46	2.361	15.747
47	8.658	108.735
48	1.910	11.860
49	4.384	43.382
50	4.476	30.075
51	4.069	35.285
52	2.888	24.905
53	2.016	16.544
54	4.690	32.139
55	2.207	13.044
56	3.152	18.319
57	3.384	31.679
58	2.167	19.956
59	5.078	36.907
60	3.628	21.525
61	3.373	31.520
62	3.836	28.118
63	4.332	31.744

(continued)

SEQ ID NO:	Discriminant coefficient	Constant term
64	2.949	32.215
65	3.709	24.031
66	3.738	28.272
67	3.638	22.448
68	3.013	19.232
69	2.461	18.582
70	4.311	32.255
71	3.548	29.298
72	4.499	45.352
73	4.079	32.445
74	3.995	30.128
75	2.483	15.148
76	3.479	27.463
77	2.342	16.975
78	3.352	20.098
79	3.684	46.309
80	3.835	22.808
81	3.983	32.779
82	2.904	19.401
83	3.426	29.138
84	5.296	43.216
85	3.793	43.429
86	5.582	66.478
87	3.815	22.562
88	4.509	45.905
89	2.269	12.804
90	5.547	57.838
91	6.325	60.270
92	3.946	37.787
93	2.967	30.962
94	3.865	30.606
95	1.266	7.550
96	2.410	24.206
97	2.733	20.281
98	3.561	25.772
99	3.064	19.551
100	1.188	6.373
101	2.565	22.283

(continued)

SEQ ID NO:	Discriminant coefficient	Constant term
102	5.084	51.748
103	3.700	26.315
104	2.224	21.832
105	3.135	25.894
106	4.526	37.574
107	3.166	31.384
108	2.839	24.460
109	1.007	6.029
110	5.545	68.155
111	3.299	33.145
112	6.271	53.263
113	2.148	12.402
114	3.608	25.322
115	2.758	17.059
116	2.175	25.025
117	3.823	49.903
118	2.725	18.024
119	3.890	38.378
120	3.506	27.825
121	2.582	15.075
122	2.476	18.382
123	4.084	39.823
124	2.978	18.190
125	3.980	27.914
126	5.916	67.040
127	2.075	13.104
128	2.317	20.667
129	2.093	12.035
130	4.219	50.899
131	1.841	19.246
132	3.960	43.646
133	3.277	38.660
134	2.733	19.515
135	3.239	30.244
136	1.482	8.655
137	4.554	52.325
138	5.175	61.317
139	3.430	21.115

(continued)

SEQ ID NO:	Discriminant coefficient	Constant term
140	5.430	50.527
141	1.168	6.718
142	2.311	17.824
143	4.599	33.779
144	3.921	24.668
145	4.968	43.118
146	1.700	14.753
147	3.593	23.332
148	4.307	30.486
149	6.087	77.329
150	2.704	17.759
151	1.757	11.661
152	2.635	16.886
153	1.214	6.968
154	3.201	23.463
155	6.593	55.857
156	2.177	21.212
157	2.411	24.700
158	2.636	19.709
159	3.045	25.772
160	5.593	39.283
161	3.606	29.381
162	6.360	76.890
163	6.727	74.567
164	4.350	42.883
165	1.256	7.389
166	6.503	84.138
167	3.665	29.142
168	4.233	35.592
169	1.766	10.169
170	1.955	12.693
171	3.328	27.665
172	3.674	24.498
173	2.869	31.161
174	1.758	11.388
175	2.132	11.850
176	2.148	20.104
177	2.169	15.443

(continued)

SEQ ID NO:	Discriminant coefficient	Constant term
178	3.124	34.907
179	2.552	27.422
180	1.417	8.536

[Table 5-1]

Training cohort			
Sample name	Cancer stage	CEA(ng/mL)	CA19-9(U/mL)
CC03	I	1.6	13.5
CC04	I	2	30.6
CC05	I	1.3	3.2
CC06	I	1.7	13.5
CC07	IIIA	4.4	0.1
CC09	IIIB	0.9	4.4
CC10	I	1.5	13.2
CC12	I	0.9	13.2
CC13	I	0.8	3.1
CC15	I	1.6	5.6
CC17	IIIA	2.7	21.7
CC18	I	3.2	16.4
CC19	IVL	6.2	45.9
CC20	IIIC	9.4	5.4
CC23	I	2.3	7.9
CC24	IIA	8.8	106.7
CC25	IIA	6.2	29.6
CC26	I	4.5	18.6
CC27	IIIC	17.3	14.4
CC29	IIA	2.1	6.9
CC30	IIIA	3.2	13.2
CC31	IIIB	6	5.7
CC32	IIIA	2.4	26.7
CC34	I	0.6	9.3
CC36	I	6.7	0.1
CC38	IIA	1.2	6.1
CC40	IIIB	2.1	7.6
CC41	I	2.8	10.6
CC42	IIIB	46.7	3524
CC45	I	2.2	38.4

(continued)

Training cohort			
Sample name	Cancer stage	CEA(ng/mL)	CA19-9(U/mL)
CC47	IIIB	1.7	7.1
CC48	IIA	2	19.1
CC49	IIIB	0.9	8.1
CC50	IIA	7.6	12.2
	Sensitivity	26.5%	12%

[Table 5-2]

Validation cohort			
Sample name	Cancer stage	CEA(ng/mL)	CA19-9(U/mL)
CC01	I	2.2	13.9
CC02	I	3.9	16
CC08	IVH	15.4	9.5
CC11	IIIC	7.2	8
CC14	I	0.6	14
CC16	IVL	10.1	106.7
CC21	IIIB	6.7	23.6
CC22	IIIC	2.9	42.4
CC28	IIIB	35.5	71
CC33	IIB	5	-
CC35	IVH	20.3	552
CC37	IIA	0.1	8.1
CC39	IVHLu	267.7	269.6
CC43	IIA	2	10.3
CC44	IIA	3.7	14
CC46	IIA	1.7	4.2
	Sensitivity	43.8%	31%

[Table 6]

	Training cohort			Validation cohort		
SEQ ID NO:	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
1_2	100	100	100	100	100	100
1_3	99.3	97.1	100	100	100	100
1_4	100	100	100	100	100	100
1_5	100	100	100	100	100	100
1_6	100	100	100	100	100	100
1_7	100	100	100	100	100	100

(continued)

	Training cohort			Validation cohort		
SEQ ID NO:	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
1_8	100	100	100	100	100	100
1_9	98.5	100	98	98.5	100	98
1_10	100	100	100	100	100	100
1_11	99.3	100	99	100	100	100
1_12	99.3	100	99	98.5	100	98
1_13	99.3	100	99	100	100	100
1_14	100	100	100	98.5	100	98
1_15	99.3	97.1	100	97	100	96
1_16	100	100	100	100	100	100
1_17	97.8	94.1	99	100	100	100
1_18	99.3	100	99	100	100	100
1_19	98.5	100	98	100	100	100
1_20	100	100	100	100	100	100
1_21	99.3	100	99	100	100	100
1_22	98.5	97.1	99	100	100	100
1_23	99.3	100	99	100	100	100
1_24	98.5	94.1	100	100	100	100
1_25	99.3	100	99	98.5	100	98
1_26	99.3	100	99	100	100	100
1_27	98.5	94.1	100	100	100	100
1_28	100	100	100	98.5	100	98
1_29	98.5	97.1	99	100	100	100
1_30	100	100	100	100	100	100
1_31	98.5	97.1	99	100	100	100
1_32	99.3	100	99	98.5	100	98
1_33	98.5	97.1	99	100	100	100
1_34	97.8	97.1	98	100	100	100
1_35	98.5	97.1	99	98.5	100	98
1_36	100	100	100	100	100	100
1_37	97.8	97.1	98	98.5	100	98
1_38	98.5	97.1	99	100	100	100
1_39	99.3	97.1	100	100	100	100
1_40	97.8	97.1	98	100	100	100
1_41	99.3	100	99	100	100	100
1_42	98.5	100	98	98.5	100	98
1_43	100	100	100	100	100	100
1_44	97.8	97.1	98	100	100	100

(continued)

	Training cohort			Validation cohort		
SEQ ID NO:	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
1_45	98.5	100	98	100	100	100
1_46	98.5	100	98	100	100	100
1_47	100	100	100	98.5	100	98
1_48	99.3	100	99	100	100	100
1_49	97.8	97.1	98	98.5	100	98
1_50	100	100	100	98.5	100	98
1_51	98.5	97.1	99	100	100	100
1_52	97.8	94.1	99	98.5	100	98
1_53	98.5	100	98	100	100	100
1_54	100	100	100	98.5	93.8	100
1_55	99.3	97.1	100	100	100	100
1_56	100	100	100	98.5	100	98
1_57	99.3	100	99	100	100	100
1_58	98.5	97.1	99	100	100	100
1_59	99.3	100	99	100	100	100
1_60	99.3	100	99	100	100	100
1_61	99.3	100	99	98.5	100	98
1_62	99.3	100	99	100	100	100
1_63	99.3	100	99	100	100	100
1_64	100	100	100	98.5	100	98
1_65	99.3	100	99	98.5	100	98
1_66	99.3	97.1	100	100	100	100
1_67	99.3	100	99	98.5	100	98
1_68	100	100	100	98.5	100	98
1_69	98.5	100	98	98.5	100	98
1_70	99.3	100	99	100	100	100
1_71	99.3	100	99	100	100	100
1_72	99.3	100	99	100	100	100
1_73	97.8	97.1	98	100	100	100
1_74	98.5	97.1	99	98.5	100	98
1_75	99.2	100	99	98.5	100	98
1_76	98.5	100	98	100	100	100
1_77	99.3	100	99	98.5	100	98
1_78	99.3	100	99	98.5	100	98
1_79	99.3	100	99	98.5	100	98
1_80	98.5	100	98	98.5	100	98
1_81	98.5	97.1	99	98.5	100	98

(continued)

	Training cohort			Validation cohort		
SEQ ID NO:	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
1_82	99.3	100	99	100	100	100
1_83	99.3	100	99	98.5	100	98
1_84	98.5	97.1	99	100	100	100
1_85	98.5	97.1	99	100	100	100
1_86	99.3	100	99	100	100	100
1_87	99.3	97.1	100	100	100	100
1_88	98.5	100	98	100	100	100
1_89	99.3	100	99	100	100	100
1_90	100	100	100	100	100	100
1_91	99.3	100	99	100	100	100
1_92	99.3	100	99	100	100	100
1_93	99.3	100	99	98.5	100	98
1_94	98.5	97.1	99	100	100	100
1_95	99.3	100	99	100	100	100
1_96	99.3	100	99	100	100	100
1_97	99.3	100	99	98.5	100	98
1_98	99.3	100	99	98.5	100	98
1_99	98.5	100	98	100	100	100
1_100	97	97.1	97	100	100	100
1_101	98.5	97.1	99	100	100	100
1_102	99.3	100	99	98.5	100	98
1_103	97.8	97.1	98	98.5	100	98
1_104	100	100	100	100	100	100
1_105	98.5	100	98	100	100	100
1_106	98.5	97.1	99	98.5	100	98
1_107	99.3	100	99	100	100	100
1_108	97.8	97.1	98	100	100	100
1_109	98.5	97.1	99	100	100	100
1_110	98.5	97.1	99	100	100	100
1_111	98.5	100	98	100	100	100
1_112	98.5	97.1	99	100	100	100
1_113	99.3	97.1	100	98.5	93.8	100
1_114	97.8	97.1	98	98.5	100	98
1_115	99.3	100	99	100	100	100
1_116	100	100	100	100	100	100
1_117	97.8	94.1	99	98.5	100	98
1_118	99.3	100	99	98.5	100	98

(continued)

	Training cohort			Validation cohort		
SEQ ID NO:	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
1_119	99.3	100	99	100	100	100
1_120	98.5	100	98	97	93.8	98
1_121	99.3	97.1	100	100	100	100
1_122	98.5	100	98	98.5	100	98
1_123	97.8	97.1	98	100	100	100
1_124	98.5	100	98	100	100	100
1_125	98.5	97.1	99	98.5	93.8	100
1_126	99.3	100	99	100	100	100
1_127	99.3	100	99	100	100	100
1_128	99.3	100	99	98.5	100	98
1_129	99.3	100	99	100	100	100
1_130	97.8	97.1	98	100	100	100
1_131	97	94.1	98	100	100	100
1_132	97.8	97.1	98	98.5	100	98
1_133	99.3	100	99	100	100	100
1_134	99.3	100	99	100	100	100
1_135	98.5	97.1	99	100	100	100
1_136	97.8	100	97	100	100	100
1_137	99.3	100	99	100	100	100
1_138	99.3	100	99	100	100	100
1_139	98.5	97.1	99	97	100	96
1_140	98.5	94.1	100	100	100	100
1_141	99.3	100	99	100	100	100
1_142	98.5	100	98	100	100	100
1_143	98.5	97.1	99	100	100	100
1_144	99.3	100	99	100	100	100
1_145	97.8	97.1	98	100	100	100
1_146	100	100	100	100	100	100
1_147	99.3	100	99	100	100	100
1_148	99.3	100	99	100	100	100
1_149	98.5	97.1	99	98.5	100	98
1_150	99.3	100	99	100	100	100
1_151	99.3	100	99	100	100	100
1_152	98.5	97.1	99	100	100	100
1_153	99.3	100	99	100	100	100
1_154	99.3	100	99	100	100	100
1_155	98.5	100	98	100	100	100

(continued)

	Training cohort			Validation cohort		
SEQ ID NO:	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
1_156	100	100	100	100	100	100
1_157	97.8	97.1	98	98.5	100	98
1_158	98.5	97.1	99	100	100	100
1_159	97.8	97.1	98	100	100	100
1_160	99.3	100	99	98.5	100	98
1_161	98.5	100	98	100	100	100
1_162	99.3	100	99	100	100	100
1_163	97.8	100	97	100	100	100
1_164	99.3	100	99	100	100	100
1_165	98.5	97.1	99	100	100	100
1_166	99.3	100	99	98.5	100	98
1_167	99.3	100	99	100	100	100
1_168	99.2	100	99	100	100	100
1_169	99.3	100	99	100	100	100
1_170	99.3	100	99	100	100	100
1_171	97.8	100	97	100	100	100
1_172	98.5	97.1	99	98.5	100	98
1_173	99.3	100	99	100	100	100
1_174	99.3	100	99	100	100	100
1_175	98.5	97.1	99	100	100	100
1_176	100	100	100	98.5	100	98
1_177	98.5	97.1	99	100	100	100
1_178	99.3	100	99	98.5	93.8	100
1_179	99.3	100	99	98.5	100	98
1_180	99.3	100	99	100	100	100

[Table 7]

	Training cohort			Validation cohort		
SEQ ID NO:	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
5_6	98.5	97.1	99.0	93.9	87.5	96.0
5_11	98.5	97.1	99.0	97.0	87.5	100
5_38	97.0	97.1	97.0	95.5	87.5	98.0
15_16	93.3	82.4	97.0	92.4	75.0	98.0
15_21	97.8	97.1	98.0	95.5	93.8	96.0
15_64	91.0	70.6	98.0	90.9	68.8	98.0
24_25	97.8	94.1	99.0	95.5	81.2	100

(continued)

	Training cohort			Validation cohort		
SEQ ID NO:	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
24_30	96.3	91.2	98.0	89.4	75.0	94.0
24_32	90.3	70.6	97.0	90.9	68.8	98.0
2_32	97.0	88.2	100	100	100	100
32_36	94.8	82.4	99.0	89.4	68.8	96.0
15_32	92.5	76.5	98.0	95.5	87.5	98.0
3_38	97.0	97.1	97.0	97.0	100	96.0
38_39	93.3	82.4	97.0	87.9	75.0	92.0
38_64	87.3	61.8	96.0	87.9	62.5	96.0
3_45	96.3	85.3	100	97.0	100	96.0
45_58	96.3	91.2	98.0	83.3	75.0	86.0
45_64	95.5	94.1	96.0	95.5	87.5	98.0
2_55	96.3	88.2	99.0	100	100	100
6_55	95.5	85.3	99.0	90.9	81.2	94.0
55_64	88.1	61.8	97.0	84.8	56.2	94.0
2_64	97.0	91.2	99.0	100	100	100
4_64	94.8	85.3	98.0	97.0	87.5	100
2_96	97.8	94.1	99.0	98.5	100	98.0
7_96	98.5	100	98.0	93.9	93.8	94.0
96_97	85.1	61.8	93.0	77.3	31.2	92.0
2_97	96.3	88.2	99.0	100	100	100
3_97	98.5	97.1	99.0	98.5	100	98.0
5_97	96.3	91.2	98.0	97.0	93.8	98.0
2_162	96.3	88.2	99.0	98.5	100	98.0
3_162	97.8	94.1	99.0	100	100	100
5_162	97.8	94.1	99.0	98.5	93.8	100

[Example 3]

<Selection of gene marker using all samples and method for evaluating colorectal cancer discriminant performance of acquired gene marker>

[0603] In this Example, the samples in the training cohort and the validation cohort used in Examples 1 and 2 were integrated, and selection of a gene marker and evaluation of its colorectal cancer discriminant performance were conducted using all of the samples.

[0604] Specifically, the miRNA expression levels in the serum of the 50 colorectal cancer patients and the 150 healthy subjects obtained in the preceding Reference Examples were normalized by quantile normalization. In order to acquire diagnostic markers with higher reliability, only genes having a gene expression level of 2^6 or higher in 50% or more of the samples in either of the colorectal cancer patient group or the healthy subject group were selected in the gene marker selection. In order to further acquire statistical significance for discriminating a colorectal cancer patient group from a healthy subject group, the P value obtained by two-tailed t-test assuming equal variance as to each gene expression level was corrected by the Bonferroni method, and genes that satisfied $p < 0.01$ were selected as gene markers for use in explanatory variables of a discriminant, and the obtained genes are described in Table 8. In this way, hsa-miR-4697-5p,

hsa-miR-3197, hsa-miR-675-5p, hsa-miR-4486, hsa-miR-7107-5p, hsa-miR-23a-3p, hsa-miR-4667-5p, hsa-miR-451a, hsa-miR-3940-5p, hsa-miR-8059, hsa-miR-6813-5p, hsa-miR-4492, hsa-miR-4476 and hsa-miR-6090 genes, and the nucleotide sequences of SEQ ID NOs: 181 to 194 related thereto were found in addition to the genes described in Table 2. As with the nucleotide sequences of SEQ ID NOs: 1 to 180, the results obtained about the polynucleotides shown in SEQ ID NOs: 181 to 194 also showed that the gene measurement values were significantly lower (-) or higher (+) in the colorectal cancer patient group than in the healthy subject group (Table 8). These results were able to be validated in the validation cohort. Thus, the presence or absence of colorectal cancer in the newly obtained samples can be determined by the methods described in Examples 1 and 2 by using the gene expression level measurement values described in Table 8 either alone or in combination with the gene expression level measurement values described in Table 2.

[Table 8]

SEQ ID NO:	Gene name	P value after Bonferroni correction	Expression level in colorectal cancer patient with respect to healthy subject
1	hsa-miR-6726-5p	5.31.E-62	-
2	hsa-miR-4257	1.09.E-61	-
3	hsa-miR-6787-5p	2.44.E-47	-
4	hsa-miR-6780b-5p	2.11.E-42	+
5	hsa-miR-3131	4.30.E-42	-
6	hsa-miR-7108-5p	3.00.E-35	+
7	hsa-miR-1343-3p	4.27.E-43	-
8	hsa-miR-1247-3p	9.79.E-35	+
9	hsa-miR-4651	9.99.E-39	-
10	hsa-miR-6757-5p	2.24.E-34	-
11	hsa-miR-3679-5p	3.50.E-37	+
12	hsa-miR-7641	5.56.E-34	-
13	hsa-miR-6746-5p	1.02.E-31	-
14	hsa-miR-8072	1.54.E-27	+
15	hsa-miR-6741-5p	2.21.E-31	-
16	hsa-miR-1908-5p	4.52.E-29	+
17	hsa-miR-6857-5p	3.92.E-22	+
18	hsa-miR-4746-3p	3.57.E-31	+
19	hsa-miR-744-5p	7.34.E-32	+
20	hsa-miR-4792	1.24.E-27	+
21	hsa-miR-564	2.13.E-30	-
22	hsa-miR-6791-5p	2.90.E-27	+
23	hsa-miR-6825-5p	4.61.E-29	+
24	hsa-miR-6826-5p	2.05.E-29	-
25	hsa-miR-4665-3p	7.74.E-29	+
26	hsa-miR-4467	5.07.E-27	+
27	hsa-miR-3188	5.96.E-29	+
28	hsa-miR-6125	2.14.E-23	+
29	hsa-miR-6756-5p	2.14.E-22	-
30	hsa-miR-1228-3p	7.24.E-25	+

(continued)

SEQ ID NO:	Gene name	P value after Bonferroni correction	Expression level in colorectal cancer patient with respect to healthy subject
31	hsa-miR-8063	1.63.E-24	-
32	hsa-miR-8069	9.97.E-22	+
33	hsa-miR-6875-5p	6.41.E-21	+
34	hsa-miR-3185	1.30.E-24	+
35	hsa-miR-4433b-3p	2.47.E-20	+
36	hsa-miR-6887-Sp	5.17.E-26	-
37	hsa-miR-128-1-5p	3.06.E-18	+
38	hsa-miR-6724-5p	4.44.E-21	+
39	hsa-miR-1914-3p	2.19.E-16	-
40	hsa-miR-1225-5p	9.96.E-22	+
41	hsa-miR-4419b	2.99.E-22	-
42	hsa-miR-7110-5p	1.00.E-22	+
43	hsa-miR-187-5p	1.62.E-19	-
44	hsa-miR-3184-5p	2.98.E-20	+
45	hsa-miR-204-3p	1.12.E-17	-
46	hsa-miR-5572	5.88.E-21	+
47	hsa-miR-6729-5p	6.07.E-18	+
48	hsa-miR-615-5p	3.71.E-19	-
49	hsa-miR-6749-5p	1.52.E-19	-
50	hsa-miR-6515-3p	1.14.E-15	+
51	hsa-miR-3937	1.06.E-20	+
52	hsa-miR-6840-3p	3.27.E-16	-
53	hsa-miR-6893-5p	3.70.E-20	-
54	hsa-miR-4728-5p	1.49.E-16	-
55	hsa-miR-6717-5p	5.86.E-21	-
56	hsa-miR-7113-3p	1.99.E-19	+
57	hsa-miR-4665-5p	4.71.E-16	-
58	hsa-miR-642b-3p	1.28.E-15	-
59	hsa-miR-7109-5p	6.89.E-19	-
60	hsa-miR-6842-5p	5.06.E-19	+
61	hsa-miR-4442	9.22.E-16	-
62	hsa-miR-4433-3p	2.94.E-16	+
63	hsa-miR-4707-5p	1.21.E-17	+
64	hsa-miR-6126	3.89.E-16	+
65	hsa-miR-4449	3.16.E-20	+
66	hsa-miR-4706	1.73.E-16	-
67	hsa-miR-1913	3.48.E-16	+

(continued)

SEQ ID NO:	Gene name	P value after Bonferroni correction	Expression level in colorectal cancer patient with respect to healthy subject
68	hsa-miR-602	1.60.E-16	+
69	hsa-miR-939-5p	4.02.E-16	+
70	hsa-miR-4695-5p	2.61.E-14	+
71	hsa-miR-711	1.79.E-16	+
72	hsa-miR-6816-5p	5.98.E-14	+
73	hsa-miR-4632-5p	4.56.E-14	+
74	hsa-miR-6721-5p	5.64.E-13	+
75	hsa-miR-7847-3p	7.52.E-17	-
76	hsa-miR-6132	6.77.E-16	+
77	hsa-miR-887-3p	3.26.E-14	+
78	hsa-miR-3679-3p	5.22.E-14	+
79	hsa-miR-6784-5p	6.38.E-13	+
80	hsa-miR-1249	1.62.E-14	+
81	hsa-miR-937-5p	8.71.E-13	-
82	hsa-miR-5195-3p	2.51.E-14	-
83	hsa-miR-6732-5p	2.71.E-13	+
84	hsa-miR-4417	4.13.E-15	+
85	hsa-miR-4281	1.09.E-13	-
86	hsa-miR-4734	7.65.E-15	+
87	hsa-miR-6766-3p	1.32.E-13	+
88	hsa-miR-663a	1.12.E-14	+
90	hsa-miR-6781-5p	1.88.E-11	+
91	hsa-miR-1227-5p	6.26.E-12	+
92	hsa-miR-6845-5p	1.06.E-14	+
93	hsa-miR-6798-5p	2.72.E-08	+
94	hsa-miR-3620-5p	7.80.E-10	+
95	hsa-miR-1915-5p	1.02.E-11	-
96	hsa-miR-4294	1.22.E-12	-
97	hsa-miR-642a-3p	5.69.E-12	-
98	hsa-miR-371a-5p	2.55.E-09	-
99	hsa-miR-940	2.85.E-14	+
100	hsa-miR-4450	2.15.E-13	-
101	hsa-miR-4723-5p	8.73.E-13	-
102	hsa-miR-1469	5.67.E-12	+
103	hsa-miR-6861-5p	2.03.E-12	-
104	hsa-miR-7975	1.02.E-09	-
105	hsa-miR-6879-5p	6.99.E-11	+

(continued)

SEQ ID NO:	Gene name	P value after Bonferroni correction	Expression level in colorectal cancer patient with respect to healthy subject
106	hsa-miR-6802-5p	1.21.E-10	-
107	hsa-miR-1268b	8.63.E-11	+
108	hsa-miR-663b	1.02.E-10	-
109	hsa-miR-125a-3p	1.21.E-12	-
110	hsa-miR-2861	4.18.E-13	-
111	hsa-miR-6088	6.31.E-12	-
112	hsa-miR-4758-5p	1.17.E-10	-
113	hsa-miR-296-3p	1.20.E-08	-
114	hsa-miR-673 8-Sp	1.29.E-09	-
115	hsa-miR-671-5p	8.62.E-11	-
116	hsa-miR-4454	4.34.E-10	-
117	hsa-miR-4516	3.61.E-10	-
118	hsa-miR-7845-5p	7.69.E-09	+
119	hsa-miR-4741	2.27.E-09	+
120	hsa-miR-92b-5p	2.68.E-09	+
121	hsa-miR-6795-5p	1.14.E-09	-
122	hsa-miR-6805-3p	1.59.E-11	+
123	hsa-miR-4725-3p	6.13.E-07	+
124	hsa-miR-6782-5p	1.59.E-08	+
125	hsa-miR-4688	5.22.E-07	-
126	hsa-miR-6850-5p	7.32.E-08	+
127	hsa-miR-6777-5p	7.19.E-11	-
128	hsa-miR-6785-5p	1.41.E-07	-
129	hsa-miR-7106-5p	6.63.E-09	-
130	hsa-miR-3663-3p	3.69.E-09	-
131	hsa-miR-6131	1.40.E-09	-
132	hsa-miR-1915-3p	6.80.E-08	+
133	hsa-miR-4532	2.71.E-07	-
134	hsa-miR-6820-5p	1.32.E-07	-
135	hsa-miR-4689	3.51.E-09	-
136	hsa-miR-4638-5p	2.60.E-07	-
137	hsa-miR-3656	1.23.E-07	+
138	hsa-miR-3621	6.72.E-07	-
139	hsa-miR-6769b-5p	7.12.E-08	-
140	hsa-miR-149-3p	1.99.E-07	-
141	hsa-miR-23b-3p	1.65.E-07	-
142	hsa-miR-3135b	1.27.E-07	-

(continued)

SEQ ID NO:	Gene name	P value after Bonferroni correction	Expression level in colorectal cancer patient with respect to healthy subject
143	hsa-miR-6848-5p	3.54.E-06	+
144	hsa-miR-6769a-5p	5.27.E-08	-
145	hsa-miR-4327	4.27.E-06	+
146	hsa-miR-6765-3p	2.60.E-07	-
147	hsa-miR-6716-5p	1.00.E-06	+
148	hsa-miR-6877-5p	1.64.E-06	-
149	hsa-miR-6727-5p	3.79.E-06	-
150	hsa-miR-4534	4.38.E-06	-
151	hsa-miR-614	2.94.E-06	-
152	hsa-miR-1202	3.36.E-07	-
153	hsa-miR-575	5.28.E-08	-
154	hsa-miR-6870-5p	3.19.E-08	+
155	hsa-miR-6722-3p	8.34.E-06	+
156	hsa-miR-7977	6.56.E-05	-
157	hsa-miR-4649-5p	1.23.E-05	-
158	hsa-miR-4675	3.15.E-07	-
159	hsa-miR-6075	6.53.E-05	+
160	hsa-miR-6779-5p	5.68.E-07	-
161	hsa-miR-4271	1.02.E-05	-
162	hsa-miR-3196	2.40.E-06	+
163	hsa-miR-6803-5p	3.32.E-03	+
164	hsa-miR-6789-5p	1.02.E-06	+
165	hsa-miR-4648	7.63.E-08	+
167	hsa-miR-4749-5p	3.78.E-05	+
168	hsa-miR-4505	7.82.E-05	+
169	hsa-miR-5698	2.28.E-04	-
170	hsa-miR-1199-Sp	2.58.E-04	-
171	hsa-miR-4763-3p	1.20.E-03	+
172	hsa-miR-1231	2.42.E-35	+
173	hsa-miR-1233-Sp	4.01.E-32	-
174	hsa-miR-150-3p	4.05.E-09	-
175	hsa-miR-1225-3p	3.42.E-13	+
176	hsa-miR-92a-2-Sp	3.89.E-08	+
177	hsa-miR-423-5p	1.73.E-06	-
178	hsa-miR-1268a	2.52.E-05	+
179	hsa-miR-128-2-5p	5.33.E-06	-
180	hsa-miR-24-3p	1.01.E-07	-

(continued)

SEQ ID NO:	Gene name	P value after Bonferroni correction	Expression level in colorectal cancer patient with respect to healthy subject
181	hsa-miR-4697-5p	4.79.E-05	-
182	hsa-miR-3197	1.62.E-04	+
183	hsa-miR-675-5p	2.19.E-04	-
184	hsa-miR-4486	4.27.E-04	+
185	hsa-miR-7107-5p	4.72.E-04	-
186	hsa-miR-23a-3p	1.53.E-03	-
187	hsa-miR-4667-5p	2.51.E-03	+
188	hsa-miR-451a	3.74.E-03	-
189	hsa-miR-3940-5p	4.95.E-03	+
190	hsa-miR-8059	5.22.E-03	-
191	hsa-miR-6813-5p	5.33.E-03	+
192	hsa-miR-4492	9.03.E-03	+
193	hsa-miR-4476	9.04.E-03	-
194	hsa-miR-6090	9.46.E-03	+

[Example 4]

<Method for evaluating colorectal cancer-specific discriminant performance by combination of multiple gene markers using samples in the validation cohort>

[0605] In this Example, a gene for diagnosis is selected by comparing gene expression levels of miRNAs in serum between colorectal cancer patients and a control group that consist of healthy subjects, pancreatic cancer patients, bile duct cancer patients, stomach cancer patients, esophageal cancer patients, liver cancer patients, and benign pancreaticobiliary disease patients in the same way as the method described in Example 1, using the gene markers selected in Example 1, and targeting the training cohort as the sample group described in Reference Example 2. The polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 606 to 614 thus selected were further combined therewith to study a method for evaluating colorectal cancer-specific discriminant performance.

[0606] Specifically, first, the miRNA expression levels in the training cohort and the validation cohort obtained in Reference Example 2 were combined and normalized by quantile normalization. Next, Fisher's discriminant analysis was conducted as to combinations of 1 to 6 expression level measurement values comprising at least one or more of the expression level measurement values of the polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 171 and 606 to 614, to construct a discriminant for determining the presence or absence of colorectal cancer. Next, accuracy, sensitivity, and specificity in the validation cohort were calculated using the discriminant thus prepared, with the colorectal cancer patient group as a positive sample group and, on the other hand, the healthy subject group, the pancreatic cancer patient group, the bile duct cancer patient group, the stomach cancer patient group, the esophageal cancer patient group, the liver cancer patient group, and the benign pancreaticobiliary disease patient group as a negative sample group. The discriminant performance of the selected polynucleotides was validated using independent samples.

[0607] Most of polynucleotides consisting of the nucleotide sequences represented by these SEQ ID NOs (SEQ ID NOs: 1 to 194 and 606 to 614 corresponding to the miRNA markers of Table 1) or complementary sequences thereof were able to provide relatively high accuracy, sensitivity, and specificity in the determination of the presence or absence of colorectal cancer, and furthermore, were able to specifically discriminate colorectal cancer from the other cancers. For example, among the combinations of multiple polynucleotides selected from the group consisting of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 5, 13, 15, 24, 32, 38, 41, 45, 55, 57, 64, 72, 75, 77, 96, 97, 115, 162, 163, 173, 189, 606, 607, 608, 609, 610, 611, 612, 613 and 614, or complementary sequences thereof (the cancer type-specific polynucleotide group 1) as polynucleotides capable of specifically binding to target markers, combinations comprising at least one or more polynucleotide(s) selected from the group consisting of polynu-

cleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 5, 45, 57, 96, and 606, or complementary sequences thereof (the cancer type-specific polynucleotide group 2) included in the cancer type-specific polynucleotide group 1 were able to specifically discriminate colorectal cancer from the other cancers with high accuracy.

[0608] The number of the aforementioned polynucleotides with cancer type specificity in the combination can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more for the combination. The combinations of 6 or more of these polynucleotides were able to exhibit discriminant accuracy of 90% or higher.

[0609] Specifically, the discriminant accuracy of the measurement using the polynucleotide that consists of the nucleotide sequence represented by SEQ ID NO: 5 or a complementary sequence thereof is shown in Table 9-1. The measurement using the combination of one polynucleotide comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 5 or a complementary sequence thereof exhibited the highest accuracy of 90.1% in the training cohort and accuracy of 87.6% in the validation cohort. Also, for example, the measurement using the combinations of two polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 5 or a complementary sequence thereof exhibited the highest accuracy of 91.7% in the training cohort and accuracy of 88.8% in the validation cohort. Furthermore, for example, the measurement using the combinations of three polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 5 or a complementary sequence thereof exhibited the highest accuracy of 94.0% in the training cohort and accuracy of 91.2% in the validation cohort. Furthermore, for example, the measurement using the combinations of four polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 5 or a complementary sequence thereof exhibited the highest accuracy of 95.6% in the training cohort and accuracy of 93.6% in the validation cohort. Furthermore, for example, the measurement using the combinations of five polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 5 or a complementary sequence thereof exhibited the highest accuracy of 96.4% in the training cohort and accuracy of 94.8% in the validation cohort. Furthermore, for example, the measurement using the combinations of six polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 5 or a complementary sequence thereof exhibited the highest accuracy of 96.9% in the training cohort and accuracy of 94.7% in the validation cohort.

[0610] The discriminant accuracy of the measurement using the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 45 or a complementary sequence thereof is shown in Table 9-2. The measurement using the combination of one polynucleotide comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 45 or a complementary sequence thereof exhibited the highest accuracy of 56.7% in the training cohort and accuracy of 55.4% in the validation cohort. Also, for example, the measurement using the combinations of two polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 45 or a complementary sequence thereof exhibited the highest accuracy of 90.7% in the training cohort and accuracy of 88.4% in the validation cohort. Furthermore, for example, the measurement using the combinations of three polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 45 or a complementary sequence thereof exhibited the highest accuracy of 94.0% in the training cohort and accuracy of 89.6% in the validation cohort. Furthermore, for example, the measurement using the combinations of four polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 45 or a complementary sequence thereof exhibited the highest accuracy of 95.2% in the training cohort and accuracy of 91.6% in the validation cohort. Furthermore, for example, the measurement using the combinations of five polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 45 or a complementary sequence thereof exhibited the highest accuracy of 96.4% in the training cohort and accuracy of 94.4% in the validation cohort. Furthermore, for example, the measurement using the combinations of six polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 45 or a complementary sequence thereof exhibited the highest accuracy of 97.6% in the training cohort and accuracy of 92.6% in the validation cohort.

[0611] The discriminant accuracy of the measurement using the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 57 or a complementary sequence thereof is shown in Table 9-3. The measurement using the combination of one polynucleotide comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 57 or a complementary sequence thereof exhibited the highest accuracy of 60.2% in the training cohort and accuracy of 60.6% in the validation cohort. Also, for example, the measurement using the combinations of two polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 57 or a complementary sequence thereof exhibited the highest accuracy of 86.7% in the training cohort and accuracy of 83.7% in the validation cohort. Furthermore, for example, the measurement using the combinations of three polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 57 or a complementary sequence thereof exhibited the highest accuracy of 92.4% in the training cohort and accuracy of 90.0% in the validation cohort. Furthermore, for example, the measurement using the combinations of four polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID

NO: 57 or a complementary sequence thereof exhibited the highest accuracy of 95.2% in the training cohort and accuracy of 91.2% in the validation cohort. Furthermore, for example, the measurement using the combinations of five polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 57 or a complementary sequence thereof exhibited the highest accuracy of 96.2% in the training cohort and accuracy of 94.8% in the validation cohort. Furthermore, for example, the measurement using the combinations of six polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 57 or a complementary sequence thereof exhibited the highest accuracy of 96.9% in the training cohort and accuracy of 93.6% in the validation cohort.

[0612] The discriminant accuracy of the measurement using the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 96 or a complementary sequence thereof is shown in Table 9-4. The measurement using the combination of one polynucleotide comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 96 or a complementary sequence thereof exhibited the highest accuracy of 57.9% in the training cohort and accuracy of 59.4% in the validation cohort. Also, for example, the measurement using the combinations of two polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 96 or a complementary sequence thereof exhibited the highest accuracy of 85.9% in the training cohort and accuracy of 83.7% in the validation cohort. Furthermore, for example, the measurement using the combinations of three polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 96 or a complementary sequence thereof exhibited the highest accuracy of 92.6% in the training cohort and accuracy of 90.4% in the validation cohort. Furthermore, for example, the measurement using the combinations of four polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 96 or a complementary sequence thereof exhibited the highest accuracy of 94.4% in the training cohort and accuracy of 91.2% in the validation cohort. Furthermore, for example, the measurement using the combinations of five polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 96 or a complementary sequence thereof exhibited the highest accuracy of 96.0% in the training cohort and accuracy of 94.0% in the validation cohort. Furthermore, for example, the measurement using the combinations of six polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 96 or a complementary sequence thereof exhibited the highest accuracy of 96.3% in the training cohort and accuracy of 93.6% in the validation cohort.

[0613] The discriminant accuracy of the measurement using the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 606 or a complementary sequence thereof is shown in Table 9-5. The measurement using the combination of one polynucleotide comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 606 or a complementary sequence thereof exhibited the highest accuracy of 59.4% in the training cohort and accuracy of 58.6% in the validation cohort. Also, for example, the measurement using the combinations of two polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 606 or a complementary sequence thereof exhibited the highest accuracy of 86.6% in the training cohort and accuracy of 82.9% in the validation cohort. Furthermore, for example, the measurement using the combinations of three polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 606 or a complementary sequence thereof exhibited the highest accuracy of 92.6% in the training cohort and accuracy of 91.2% in the validation cohort. Furthermore, for example, the measurement using the combinations of four polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 606 or a complementary sequence thereof exhibited the highest accuracy of 94.8% in the training cohort and accuracy of 90.0% in the validation cohort. Furthermore, for example, the measurement using the combinations of five polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 606 or a complementary sequence thereof exhibited the highest accuracy of 96.0% in the training cohort and accuracy of 93.6% in the validation cohort. Furthermore, for example, the measurement using the combinations of six polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 606 or a complementary sequence thereof exhibited the highest accuracy of 95.3% in the training cohort and accuracy of 93.6% in the validation cohort.

[0614] The expression level measurement values of the nucleotide sequences represented by SEQ ID NOs: 5, 45, 57, 75, 162, and 607 were compared among 34 colorectal cancer patients, 103 healthy subject, 69 pancreatic cancer patients, 66 bile duct cancer patients, 30 stomach cancer patients, 33 esophageal cancer patients, 32 liver cancer patients, and 15 benign pancreaticobiliary disease patients in the training cohort. As a result, a scatter diagram that significantly separated the discriminant score of the colorectal cancer patient group from the discriminant scores of the other groups was obtained in the training cohort (see the upper diagram of Figure 4). These results were also reproducible in the validation cohort (see the lower diagram of Figure 4).

[Table 9-1]

SEQ ID NO:	Training cohort			Validation cohort		
	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
5	90.1	100	89.3	87.6	87.5	87.7
5_608	91.7	91.2	91.7	88.8	62.5	90.6
5_45_607	94	91.2	94.2	91.2	75	92.3
5_45_57_607	95.6	88.2	96.2	93.6	62.5	95.7
5_45_57_75_607	96.3	84.8	97.4	93.1	62.5	95.9
5_45_96_606_607	96.4	97.1	96.4	94.8	87.5	95.3
5_45_57_97_115_607	96.9	88.2	97.7	94.7	75.0	96.5
5_45_57_97_162_607	96.9	88.2	97.7	94.1	68.8	96.5
5_45_57_162_607_613	96.9	88.2	97.7	94.1	62.5	97.1
5_45_57_97_607_612	96.9	94.1	97.1	94.1	81.2	95.3
5_13_45_57_606_607	96.9	91.2	97.4	93.6	68.8	95.9
5_45_96_189_606_608	95.3	94.1	95.4	94.7	75	96.5
5_45_57_96_189_606	96.3	97.1	96.3	93.6	75	95.3
5_24_45_57_96_608	95.3	94.1	95.4	92.6	56.2	95.9
5_45_57_162_607_610	95.8	85.3	96.8	93.6	62.5	96.5
5_45_57_189_606_607	96.1	91.2	96.6	93.6	75	95.3

[Table 9-2]

SEQ ID NO:	Training cohort			Validation cohort		
	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
45	56.7	61.8	56.3	55.4	56.2	55.3
5_45	90.7	100	90	88.4	87.5	88.5
5_45_57	94	94.1	94	89.6	81.2	90.2
5_45_57_97	95.2	94.1	95.3	91.6	81.2	92.3
5_45_96_606_607	95.5	91.2	96.0	95.2	87.5	95.9
5_45_57_75_607	96.4	87.9	97	94.4	62.5	96.6
5_45_57_75_606_607	97.6	87.9	98.6	92.6	62.5	95.3
5_45_57_77_607_613	97.4	94.1	97.7	94.1	75.0	95.9
5_45_57_97_606_607	97.1	94.1	97.4	94.1	81.2	95.3
5_45_57_75_77_607	97.1	90.9	97.7	93.1	68.8	95.3
5_32_45_57_96_606	96.3	97.1	96.3	93.6	68.8	95.9
5_24_45_57_96_606	96.1	97.1	96	93.1	68.8	95.3
5_45_57_96_162_606	95.5	91.2	96	94.7	81.2	95.9
5_15_45_75_96_606	95.5	100	95.1	93.6	81.2	94.8
5_32_45_57_162_607	95.8	85.3	96.8	93.6	62.5	96.5

(continued)

SEQ ID NO:	Training cohort			Validation cohort		
	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
38_45_96_606_608_611	87.1	88.2	87.0	86.2	68.8	87.8

[Table 9-3]

SEQ ID NO:	Training cohort			Validation cohort		
	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
57	60.2	70.6	59.5	60.6	56.2	60.9
24_57	86.7	91.2	86.4	83.7	62.5	85.1
5_57_608	92.4	88.2	92.8	90	68.8	91.5
5_45_57_608	95.2	91.2	95.5	91.2	62.5	93.2
24_41_57_45_96	94.5	94.1	94.5	88.8	56.2	91.9
5_45_57_607_612	96.2	94.1	96.4	94.8	68.8	96.6
5_45_57_606_607_608	96.9	91.2	97.4	93.6	68.8	95.9
5_13_45_57_75_607	96.9	90.9	97.4	93.1	68.8	95.3
5_45_57_64_75_607	96.9	90.9	97.4	92.6	68.8	94.8
5_45_55_57_607_613	96.9	91.2	97.4	92.6	68.8	94.8
5_45_55_57_75_607	96.6	87.9	97.4	92.6	68.8	94.8
5_38_45_57_96_607	96.3	88.2	97.1	94.1	68.8	96.5
5_45_57_75_162_607	96.6	87.9	97.4	94.1	62.5	97.1
5_45_57_75_162_609	94.2	97	94	91.5	62.5	94.2
5_45_57_64_96_607	95.5	88.2	96.3	94.7	75	96.5
57_64_96_606_608_611	90.6	91.2	90.5	88.3	75.0	89.5

[Table 9-4]

SEQ ID NO:	Training cohort			Validation cohort		
	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
96	57.9	58.8	57.8	59.4	62.5	59.1
41_96	85.9	88.2	85.7	83.7	62.5	85.1
5_96_606	92.6	100	92.1	90.4	87.5	90.6
5_45_57_96	94.4	91.2	94.7	91.2	75	92.3
38_96_606_608_611	86.4	91.2	85.9	85.6	75	86.6
5_45_57_96_607	96	91.2	96.4	94	68.8	95.7
38_72_96_606_608_611	89.0	88.2	89.0	87.7	75.0	88.9
32_38_96_606_608_611	89.8	88.2	89.9	86.7	68.8	88.4
38_96_163_606_608_611	87.4	85.3	87.6	85.1	68.8	86.6

(continued)

	Training cohort			Validation cohort		
SEQ ID NO:	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
64_72_96_162_609_611	81.9	85.3	81.6	81.8	81.2	81.9
38_64_96_163_606_608	87.4	91.2	87.1	86.7	68.8	88.4
5_45_57_75_96_606	96.3	93.9	96.6	93.6	81.2	94.8
5_15_45_57_96_606	95.5	91.2	96	94.1	87.5	94.8
5_41_45_57_96_606	94.8	91.2	95.1	94.1	87.5	94.8
5_41_45_96_189_606	94.5	100	94	93.1	75	94.8
5_45_75_96_189_606	94.8	97	94.5	94.7	75	96.5

[Table 9-5]

606	Training cohort			Validation cohort		
SEQ ID NO:	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
606	59.4	61.8	59.3	58.6	50	59.1
75_606	86.6	84.8	86.8	82.9	62.5	84.3
5_606_610	92.6	97.1	92.3	91.2	81.2	91.9
5_45_96_606	94.8	100	94.5	90	87.5	90.2
64_96_606_608_611	86.4	91.2	85.9	85.6	75.0	86.6
5_45_57_606_610	96	94.1	96.2	93.6	68.8	95.3
64_96_162_609_610_611	81.9	85.3	81.6	81.4	81.2	81.4
38_64_96_606_608_611	88.7	88.2	88.8	87.8	75.0	89.0
64_72_96_606_608_611	89.0	88.2	89.0	88.2	75.0	89.5
64_96_97_606_608_611	89.7	88.2	89.9	89.4	75.0	90.7
45_64_96_606_608_611	89.8	88.2	89.9	88.8	75.0	90.1
5_24_45_96_189_606	95.3	100	94.8	93.6	62.5	96.5
5_15_45_96_189_606	94	94.1	94	94.1	75	95.9
5_45_96_189_606_613	95	97.1	94.8	94.7	81.2	95.9
5_45_72_96_189_606	95	97.1	94.8	94.7	81.2	95.9
5_15_32_45_96_606	95.3	97.1	95.1	93.6	68.8	95.9

[Comparative Example 1]

<Colorectal cancer discriminant performance of an existing tumor marker in blood>

[0615] The concentration of the existing tumor marker CEA in blood was measured in the training cohort and the validation cohort obtained in the preceding Reference Examples. When the concentration of the tumor marker in blood is higher than the reference value described in Non Patent Literature 4 (CEA: 5 ng/mL), subjects are generally suspected of having cancer. Thus, whether or not the concentration of CEA in blood exceeded its reference value was confirmed for each sample, and the results were assessed for the ability of the tumor marker to detect cancer in colorectal cancer patients. The sensitivity of the existing marker in the training cohort and the validation cohort was calculated. The results

are shown in Tables 5-1 and 5-2. The sensitivity of CEA was as low as 26.5% in the training cohort and was as low as 43.8% in the validation cohort, demonstrating that the marker is not useful in the detection of colorectal cancer (Tables 5-1 and 5-2).

[0616] On the other hand, as shown above in Tables 3 and 6 of Examples 1 and 2, it can be concluded that in all of the polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 180, combinations of 1 or 2 polynucleotides exhibiting sensitivity beyond the existing colorectal cancer marker are present, and thus such polynucleotides serve as excellent diagnosis markers.

[0617] As shown in these Examples and Comparative Example, the kit, etc., and the method of the present invention can detect colorectal cancer more sensitively than the existing tumor marker and therefore permit early detection and treatment of colorectal cancer. As a result, improvement in survival rate and a therapeutic option of endoscopic operation, which places less burden on patients, can also be provided.

Industrial Applicability

[0618] According to the present invention, colorectal cancer can be effectively detected by a simple and inexpensive method. This enables early detection, diagnosis and treatment of colorectal cancer. The method of the present invention can detect colorectal cancer with limited invasiveness using the blood of a patient and therefore allows colorectal cancer to be detected conveniently and rapidly.

[0619] All publications, patents, and patent applications cited herein are incorporated herein by reference in their entirety.

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National Cancer Center

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agaggugggg acugagccuu aguugg 86

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ccuugucucc uuucccuag 79

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ccgccuccgc uccagucgcc 80

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uccgccccgg cccccgcccc 80

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gcacaugcug uugccacuaa ccucaaccuu acucgguc 98

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gcgcacaucu cugc 74

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gggcggcgcc guguccgcga ccgcguaccc ugac 94

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<210> 218
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uagugcaaug uuuaagcucc ccucucuuuc cuguucag 98

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uagcccccgc cacaucggg 79

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ugugcggaua cggggcugga ggccu 85

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cggaaggcgg agcggcggau cuggacaccc agcggu 96

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cag 63

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ccucgccccc cag 73

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agucggggcu uuacugcuuu u 81

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ugggggcggu cggcguaacu caggga 86

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uccauguc 68

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ccuag 65

<210> 232
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cggucucuuu uucagcugcu uc 82

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guagcucccg aggcccgagc cgcgacccgc gg 92

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gcacugggag gggcccucac 80

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ggacugacug agccccugug ccgccccccag 90

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uugagccu 68

<210> 237
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ucucucucuc ucccacuucc cugcag 86

<210> 238
<211> 109
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<400> 238
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cucugacccc ucgugucuug uguugcagcc ggagggacgc agguccgca 109

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cccucagccu aacuu 75

<210> 240
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auaugaagga ggcugggaag gcaaagggac guucaauugu caucacuggc 110

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<400> 241
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ccagccuggg gcaucgguug gggugcaggg gucugcuggu gaugcuuucc aucucuuugc 120

uuuguccuga uuguagc 137

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cucag 65

<210> 243
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<212> RNA
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uccgagccug ggucucccuc uucccccccaa cccccc 96

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cuggcccag 69

<210> 245
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<400> 245
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<210> 246
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<212> RNA
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acaggcggcu guagcaaugg ggggcuggau gggcaucuca augugc 106

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<210> 248
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accugccag 69

<210> 249
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agggacccuc ccaacuc 77

<210> 253
<211> 65
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<400> 253
gucuccuggg gggaggagac ccugcucucc cuggcagcaa gccucuccug cccuuccaga 60

uuagc 65

<210> 254
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<212> RNA
<213> Homo sapiens

<400> 254
agcccuggggg guggucucua gccaaggcuc ugggggucuca cccuuggcug gucucugcuc 60

cgcag 65

<210> 255
<211> 67
<212> RNA
<213> Homo sapiens

<400> 255
gcgcccuccc ucucucccccg gugugcaaau gugugugugc gguguuaugc cggacaagag 60

ggaggug 67

<210> 256
<211> 81
<212> RNA
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<400> 256
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gggugggaca uaaggaggau a 81

<210> 257
<211> 80
<212> RNA
<213> Homo sapiens

<400> 257
gguuccggag ccccggcgcg ggcggguucu ggggguguaga cgcugcuggc cagcccgccc 60

cagccgaggu ucucggcacc 80

<210> 258

<211> 89
<212> RNA
<213> Homo sapiens

<400> 258
agccuguggg aaagagaaga gcagggcagg gugaaggccc ggcggagaca cucugcccac 60

cccacacccu gccuaugggc cacacagcu 89

<210> 259
<211> 66
<212> RNA
<213> Homo sapiens

<400> 259
agcagcccuc ggcggcccgg ggggcgggcg gcggugcccg ucccggggcu gcgcgaggca 60

caggcg 66

<210> 260
<211> 82
<212> RNA
<213> Homo sapiens

<400> 260
gcuacgggga gcggggagga agugggcgcu gcuucugcgu uaucuggaag gagcagccca 60

cuccuguccu gggcucugug gu 82

<210> 261
<211> 80
<212> RNA
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gcugcugcca aguggcuggu 80

<210> 262
<211> 98
<212> RNA
<213> Homo sapiens

<400> 262
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gcgucuccug ucaggcaagg gagagcagag ccccccug 98

<210> 263
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<400> 263
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ugcucccccag ugucugaccg cg 82

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<211> 74
<212> RNA
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gcugccuccu uccc 74

<210> 265
<211> 76
<212> RNA
<213> Homo sapiens

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uaagugaggg gagaug 76

<210> 266
<211> 66
<212> RNA
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<400> 266
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ccacag 66

<210> 267
<211> 61
<212> RNA
<213> Homo sapiens

<400> 267
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g 61

<210> 268
<211> 87
<212> RNA
<213> Homo sapiens

<400> 268
cccucaucuc ugggcagggg cuuauuguag gagucucuga agagagcugu ggacugaccu 60

gcuuuaaccc uucccccaggu ucccauu 87

<210> 269
<211> 103
<212> RNA
<213> Homo sapiens

<400> 269

gugucggcug uggcgugacu gucccucugu gucccccacu aggcccacug cucaguggag 60

cguggaggac gaggaggagg ccguccacga gcaaugccag cau 103

<210> 270
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<212> RNA
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<400> 270
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cccaguccug ccccugcugc uaccuagucc agccucaccg caucccaga 109

<210> 271
<211> 79
<212> RNA
<213> Homo sapiens

<400> 271
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aucccgaggc uuugcacag 79

<210> 272
<211> 67
<212> RNA
<213> Homo sapiens

<400> 272
uacaggccgg ggcuuugggu gagggacccc cggagucugu cacggucuca ccccaacucu 60

gccccag 67

<210> 273
<211> 66
<212> RNA
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<400> 273
gggaggaggg aggagauggg ccaaguuccc ucuggcugga acgcccuucc cccccuucuu 60

caccug 66

<210> 274
<211> 86
<212> RNA
<213> Homo sapiens

<400> 274
agcacugccc ccggugaguc aggguggggc uggcccccug cuucgugccc auccgcgcuc 60

ugacucucug cccaccugca ggagcu 86

<210> 275
<211> 115
<212> RNA

<213> Homo sapiens

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accugaccca uccaguucuc ugagggggcu cuuguguguu cuacaagguu guuca 115

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<211> 60
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<210> 277
<211> 73
<212> RNA
<213> Homo sapiens

<400> 277
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ccuaccacgu uug 73

<210> 278
<211> 62
<212> RNA
<213> Homo sapiens

<400> 278
gcuggggguc ccccgacagu guggagcugg ggccgggucc cggggagggg gguucugggc 60

ag 62

<210> 279
<211> 70
<212> RNA
<213> Homo sapiens

<400> 279
cucgggcccg accgcgccgg cccgcaccuc ccggcccgga gcugcgggcu gcggucaggg 60

cgaucccggg 70

<210> 280
<211> 72
<212> RNA
<213> Homo sapiens

<400> 280
augagcgggu gggagcagau cuuauugaga guuccuucuc cugcuccuga uugucuuccc 60

ccacccucac ag 72

<210> 281
<211> 93

<212> RNA
<213> Homo sapiens

<400> 281
ccuuccggcg ucccaggcgg ggcgccgcgg gaccgcccuc gugucugugg cggugggauc 60

ccgcggccgu guuuuccugg uggcccggcc aug 93

<210> 282
<211> 86
<212> RNA
<213> Homo sapiens

<400> 282
auucuaggug gggagacuga cggcuggagg cccauaagcu gucuaaaacu ucggccccca 60

gauuucuggu cuccccacuu cagaac 86

<210> 283
<211> 64
<212> RNA
<213> Homo sapiens

<400> 283
aaccccgggc cggaggucaa gggcgucgcu ucucccuaau guugccucuu uuccacggcc 60

ucag 64

<210> 284
<211> 88
<212> RNA
<213> Homo sapiens

<400> 284
gugggggccag gcgguggugg gcacugcugg ggugggcaca gcagccaugc agagcgggca 60

uuugaccccg ugccacccuu uuccccag 88

<210> 285
<211> 61
<212> RNA
<213> Homo sapiens

<400> 285
aacugcgggg ccagagcaga gagcccuugc acaccaccag ccucuccucc cugugcccca 60

g 61

<210> 286
<211> 67
<212> RNA
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<400> 286
ggcagccagg gggaugggcg agcuugggcc cauuccuuuc cuuacccuac cccccauccc 60

ccuguag 67

<210> 287
<211> 79
<212> RNA
<213> Homo sapiens

<400> 287
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cccugcaucc cgcacccag 79

<210> 288
<211> 80
<212> RNA
<213> Homo sapiens

<400> 288
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ggcgggggcg gcccuagcga 80

<210> 289
<211> 76
<212> RNA
<213> Homo sapiens

<400> 289
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ucccagguuu cggugc 76

<210> 290
<211> 97
<212> RNA
<213> Homo sapiens

<400> 290
aucugaguug ggagggcccc ucuccaaaug ugucuugggg ugggggauca agacacauuu 60

ggagagggaa ccucccaacu cggccucugc caucauu 97

<210> 291
<211> 67
<212> RNA
<213> Homo sapiens

<400> 291
guggcacuca aacugugggg gcacuuucug cucucuggug aaagugccgc caucuuuuga 60

guguuac 67

<210> 292
<211> 94
<212> RNA
<213> Homo sapiens

<400> 292
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aggcagggcc cccgcucccc gggccugacc ccac 94

<210> 293
<211> 65
<212> RNA
<213> Homo sapiens

<400> 293
ugucugggga uuuggagaag uggugagcgc aggucuuugg caccaucucc ccuggucccu 60

uggcu 65

<210> 294
<211> 81
<212> RNA
<213> Homo sapiens

<400> 294
aguugguggg ggagccauga gauaagagca ccuccuagag aauguugaac uaaaggugcc 60

cucucuggcu ccuccccaaa g 81

<210> 295
<211> 47
<212> RNA
<213> Homo sapiens

<400> 295
cucggcgcgg ggcgcgggcu ccggguuggg gcgagccaac gccgggg 47

<210> 296
<211> 64
<212> RNA
<213> Homo sapiens

<400> 296
gaggcacugg guaggugggg cuccagggcu ccugacaccu ggaccucucc uccccaggcc 60

caca 64

<210> 297
<211> 68
<212> RNA
<213> Homo sapiens

<400> 297
gugcaaagag caggaggaca ggggauuuau cucccaaggg aggucccccug auccuaguca 60

cggcacca 68

<210> 298
<211> 66
<212> RNA
<213> Homo sapiens

<400> 298

cagagcaggg cagggaaggu gggagagggg cccagcugac ccuccuguca cccgcuccuu 60

gcccag 66

<210> 299
<211> 65
<212> RNA
<213> Homo sapiens

<400> 299
gagggcuagg ugggggggcuu gaagccccga gaugccucac gucuucaccc cucucaccua 60

agcag 65

<210> 300
<211> 50
<212> RNA
<213> Homo sapiens

<400> 300
acccgggcgu gguggugggg gugggugccu guaauuccag cuaguuggga 50

<210> 301
<211> 115
<212> RNA
<213> Homo sapiens

<400> 301
ggugccgagg gccguccggc auccuaggcg ggucgcugcg guaccucccu ccugucugug 60

gcgggugggau cccguggccg uguuuuccug guggcccggc cgugccugag guuuc 115

<210> 302
<211> 86
<212> RNA
<213> Homo sapiens

<400> 302
ugccagucuc uaggucccug agacccuuua accugugagg acauccaggg ucacagguga 60

gguucuuggg agccuggcgu cuggcc 86

<210> 303
<211> 90
<212> RNA
<213> Homo sapiens

<400> 303
ggcgccucug cagcuccggc ucccccuggc cucucgggaa cuacaagucc caggggggccu 60

ggcgggugggc ggcgggcgga agaggcgggg 90

<210> 304
<211> 51
<212> RNA
<213> Homo sapiens

<400> 304
agagaugaag cgggggggcg gggucuugcu cuauugccua cgcugaucuc a 51

<210> 305
<211> 71
<212> RNA
<213> Homo sapiens

<400> 305
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ccacccuccc c 71

<210> 306
<211> 80
<212> RNA
<213> Homo sapiens

<400> 306
aggacccuuc cagagggccc ccccucaauc cuguugugcc uaauucagag gguuggggugg 60

aggcucuccu gaagggcucu 80

<210> 307
<211> 64
<212> RNA
<213> Homo sapiens

<400> 307
gaaggcgagg gguagaagag cacaggggguu cugauaaacc cuucugccug cauucuacuc 60

ccag 64

<210> 308
<211> 118
<212> RNA
<213> Homo sapiens

<400> 308
gcaggugaac uggcaggcca ggaagaggag gaagcccugg aggggcugga ggugauggau 60

guuuuccucc gguucucagg gcuccaccuc uuucgggccg uagagccagg gcuggugc 118

<210> 309
<211> 55
<212> RNA
<213> Homo sapiens

<400> 309
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<210> 310
<211> 86
<212> RNA
<213> Homo sapiens

<400> 310

agggagaagg gucggggcag ggagggcagg gcaggcucug ggguggggggg ucugugaguc 60

agccacggcu cugcccacgu cucccc 86

<210> 311
<211> 99
<212> RNA
<213> Homo sapiens

<400> 311
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gcuggucgcc gaccuccgac ccuccacuag augccuggc 99

<210> 312
<211> 90
<212> RNA
<213> Homo sapiens

<400> 312
cgggcggggc ggguccggcc gccuccgagc ccggccggca gccccccggcc uuaaagcgcg 60

ggcuguccgg aggggucggc uuucccaccg 90

<210> 313
<211> 96
<212> RNA
<213> Homo sapiens

<400> 313
cgggccccgg gcgggcggga gggacgggac gcggugcagu guuguuuuuu ccccccgccaa 60

uauugcacuc gucccggccu ccggcccccc cggccc 96

<210> 314
<211> 68
<212> RNA
<213> Homo sapiens

<400> 314
aggguuggggg ggacaggaug agaggcuguc uucauucccu cuugaccacc ccucguuucu 60

ucccccag 68

<210> 315
<211> 62
<212> RNA
<213> Homo sapiens

<400> 315
uggccuaggg ggcggcuugu ggaguguaug ggcugagccu ugcucugcuc ccccgccccc 60

ag 62

<210> 316
<211> 90
<212> RNA

<213> Homo sapiens

<400> 316
gugucucucu ggagacccug cagccuuccc acccaccagg gagcuuucca ugggcugugg 60

ggaaggcguc agugucgggu gagggaacac 90

<210> 317
<211> 69
<212> RNA
<213> Homo sapiens

<400> 317
uggggguaggg gugggggaau ucaggggugu cgaacucaug gcugccaccu uuguguccc 60

auccugcag 69

<210> 318
<211> 83
<212> RNA
<213> Homo sapiens

<400> 318
gucuacuccc agggugccaa gcuguuucgu guucccuccc uaggggaucc cagguagggg 60

cagcagagga ccugggccug gac 83

<210> 319
<211> 61
<212> RNA
<213> Homo sapiens

<400> 319
gugcggaacg cuggccgggg cgggagggga agggacgccc ggccggaacg ccgcacucac 60

g 61

<210> 320
<211> 66
<212> RNA
<213> Homo sapiens

<400> 320
ucaagacggg gagucaggca gugguggaga uggagagccc ugagccucca cucuccuggc 60

ccccag 66

<210> 321
<211> 81
<212> RNA
<213> Homo sapiens

<400> 321
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acaucgcccc accuucccca g 81

<210> 322
<211> 65
<212> RNA
<213> Homo sapiens

<400> 322
gcuucuggga ggaggggauc uugggaguga ucccaacagc ugagcucccu gaaucccugu 60

cccag 65

<210> 323
<211> 97
<212> RNA
<213> Homo sapiens

<400> 323
cccgggaccu ugguccaggc gcuggucugc guggugcucg gguggauaag ucugaucuga 60

gcaccacaca ggccgggcgc cgggaccaag ggggcuc 97

<210> 324
<211> 109
<212> RNA
<213> Homo sapiens

<400> 324
ucccgcauuc ccucugcuuu ggucaggugg ugcccuccuu ccauggguag agccagagau 60

gguggguucu ggcuggucag augggagugg acagagaccc gggguccuc 109

<210> 325
<211> 51
<212> RNA
<213> Homo sapiens

<400> 325
acagaccccg gggagcccgg cggugaagcu ccugguaucc ugggugucug a 51

<210> 326
<211> 62
<212> RNA
<213> Homo sapiens

<400> 326
ccuucugcgg cagagcuggg gucaccagcc cucauguacu ugugacuucu ccccugccac 60

ag 62

<210> 327
<211> 70
<212> RNA
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<400> 327
gguuucuccu ugaggagaca uggugggggc cggucaggca gcccaugcca uguguccuca 60

uggagaggcc 70

<210> 328
<211> 68
<212> RNA
<213> Homo sapiens

<400> 328
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caggggguc 68

<210> 329
<211> 69
<212> RNA
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<400> 329
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gguggggagg 69

<210> 330
<211> 85
<212> RNA
<213> Homo sapiens

<400> 330
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ccgcgccuuu gucugugucc cacag 85

<210> 331
<211> 62
<212> RNA
<213> Homo sapiens

<400> 331
cuuccuggug gguggggagg agaagugccg uccucaugag ccccucucug ucccacccau 60

ag 62

<210> 332
<211> 89
<212> RNA
<213> Homo sapiens

<400> 332
gccggcgccc gagcucuggc uccgugucuu cacucccgug cuuguccgag gagggaggga 60

gggacggggg cugugcuggg gcagcugga 89

<210> 333
<211> 97
<212> RNA
<213> Homo sapiens

<400> 333
cucaggugcu cuggcugcuu ggguuccugg caugcugauu ugugacuuaa gauuaaaauc 60

acauugccag ggauuaccac gcaaccacga ccuuggc 97

<210> 334
<211> 68
<212> RNA
<213> Homo sapiens

<400> 334
ugcccaggcu ggagcgagug caguggugca gucaguccua gcucacugca gccucgaacu 60
ccugggcu 68

<210> 335
<211> 70
<212> RNA
<213> Homo sapiens

<400> 335
gucccuggggg gcugggaugg gccauggugu gcucugaucc cccuguggguc ucuuggcccc 60
caggaacucc 70

<210> 336
<211> 73
<212> RNA
<213> Homo sapiens

<400> 336
aggccaggug gguauggagg agcccucaua uggcaguugg cgagggccca gugagccccu 60
cucugcucuc cag 73

<210> 337
<211> 85
<212> RNA
<213> Homo sapiens

<400> 337
ggccuggggua ggcuugcaug ggggacuggg aagagaccau gaacagguua guccagggag 60
uucucaucaa gccuuuacuc aguag 85

<210> 338
<211> 87
<212> RNA
<213> Homo sapiens

<400> 338
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ggacgcucac cuggcuggcc cgcccag 87

<210> 339
<211> 80
<212> RNA
<213> Homo sapiens

<400> 339
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auuccucugc agagcgcucu 80

<210> 340
<211> 64
<212> RNA
<213> Homo sapiens

<400> 340
aguucagggc cgaagggugg aagcugcugg ugcucaucuc agccucugcc cuuggccucc 60

ccag 64

<210> 341
<211> 65
<212> RNA
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<400> 341
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cgcag 65

<210> 342
<211> 60
<212> RNA
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<400> 342
ugugaaugac ccccuuccag agccaaaauc accagggaug gaggaggggu cuuggguacu 60

<210> 343
<211> 90
<212> RNA
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uguucuugcc agguggcaga agguugcugc 90

<210> 344
<211> 83
<212> RNA
<213> Homo sapiens

<400> 344
ccugcugcag aggugccagc ugcagugggg gaggcacugc cagggcugcc cacucugcuu 60

agccagcagg ugccaagaac agg 83

<210> 345
<211> 94
<212> RNA

<213> Homo sapiens

<400> 345
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gagccaguug gacaggagca gugccacuca acuc 94

<210> 346
<211> 60
<212> RNA
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<400> 346
caaggugggg gagaugggggg uugaacuuca uuucucaugc ucaucccccau cuccuuucag 60

<210> 347
<211> 78
<212> RNA
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<400> 347
ggccucaggc aggcgcaccc gaccacaugc auggcuggug gcggcgugca ggggucgggu 60

gggccaggcu gugggggcg 78

<210> 348
<211> 49
<212> RNA
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<400> 348
uucccagcca acgcaccaaa aaugauaugg gucuguuguc uggagaaac 49

<210> 349
<211> 64
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<213> Homo sapiens

<400> 349
ucugggcgag gggugggcuc ucagaggggc uggcaguacu gcucugaggc cugccucucc 60

ccag 64

<210> 350
<211> 77
<212> RNA
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<400> 350
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cagcaggacu ucucaug 77

<210> 351
<211> 95
<212> RNA
<213> Homo sapiens

<400> 351
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ugcagcacca cggcccaggc ggcauuggug ucacc 95

<210> 352
<211> 64
<212> RNA
<213> Homo sapiens

<400> 352
gagcucuggg aggggcuggg uuuggcagga caguuuccaa gcccugucuc cucccaucuu 60

ccag 64

<210> 353
<211> 67
<212> RNA
<213> Homo sapiens

<400> 353
aaaucucucu ccauaucuuu ccugcagccc ccaggugggg gggaagaaaa ggugggggaau 60

uagauuc 67

<210> 354
<211> 64
<212> RNA
<213> Homo sapiens

<400> 354
ggguggggggc ggggcggcag gggccucccc cagugccagg ccccauucug cuucucuccc 60

agcu 64

<210> 355
<211> 65
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Claims

1. A kit for the detection of colorectal cancer, comprising a nucleic acid capable of specifically binding to at least one or more polynucleotide(s) selected from the group consisting of colorectal cancer markers miR-6726-5p, miR-4257, miR-6787-5p, miR-6780b-5p, miR-3131, miR-7108-5p, miR-1343-3p, miR-1247-3p, miR-4651, miR-6757-5p, miR-3679-5p, miR-7641, miR-6746-5p, miR-8072, miR-6741-5p, miR-1908-5p, miR-6857-5p, miR-4746-3p, miR-744-5p, miR-4792, miR-564, miR-6791-5p, miR-6825-5p, miR-6826-5p, miR-4665-3p, miR-4467, miR-3188, miR-6125, miR-6756-5p, miR-1228-3p, miR-8063, miR-8069, miR-6875-5p, miR-3185, miR-4433b-3p, miR-6887-5p, miR-128-1-5p, miR-6724-5p, miR-1914-3p, miR-1225-5p, miR-4419b, miR-7110-5p, miR-187-5p, miR-3184-5p, miR-204-3p, miR-5572, miR-6729-5p, miR-615-5p, miR-6749-5p, miR-6515-3p, miR-3937, miR-6840-3p, miR-6893-5p, miR-4728-5p, miR-6717-5p, miR-7113-3p, miR-4665-5p, miR-642b-3p, miR-7109-5p, miR-6842-5p, miR-4442, miR-4433-3p, miR-4707-5p, miR-6126, miR-4449, miR-4706, miR-1913, miR-602, miR-939-5p, miR-4695-5p, miR-711, miR-6816-5p, miR-4632-5p, miR-6721-5p, miR-7847-3p, miR-6132, miR-887-3p, miR-3679-3p, miR-6784-5p, miR-1249, miR-937-5p, miR-5195-3p, miR-6732-5p, miR-4417, miR-4281, miR-4734, miR-6766-3p, miR-663a, miR-4513, miR-6781-5p, miR-1227-5p, miR-6845-5p, miR-6798-5p, miR-3620-5p, miR-1915-5p, miR-4294, miR-642a-3p, miR-371a-5p, miR-940, miR-4450, miR-4723-5p, miR-1469, miR-6861-5p, miR-7975, miR-6879-5p, miR-6802-5p, miR-1268b, miR-663b, miR-125a-3p, miR-2861, miR-6088, miR-4758-5p, miR-296-3p, miR-6738-5p, miR-671-5p, miR-4454, miR-4516, miR-7845-5p, miR-4741, miR-92b-5p, miR-6795-5p, miR-6805-3p, miR-4725-3p, miR-6782-5p, miR-4688, miR-6850-5p, miR-6777-5p, miR-6785-5p, miR-7106-5p, miR-3663-3p, miR-6131, miR-1915-3p, miR-4532, miR-6820-5p, miR-4689, miR-4638-5p, miR-3656, miR-3621, miR-6769b-5p, miR-149-3p, miR-23b-3p, miR-3135b, miR-6848-5p, miR-6769a-5p, miR-4327, miR-6765-3p, miR-6716-5p, miR-6877-5p, miR-6727-5p, miR-4534, miR-614, miR-1202, miR-575, miR-6870-5p, miR-6722-3p, miR-7977, miR-4649-5p, miR-4675, miR-6075, miR-6779-5p, miR-4271, miR-3196, miR-6803-5p, miR-6789-5p, miR-4648, miR-4508, miR-4749-5p, miR-4505, miR-5698, miR-1199-5p, miR-4763-3p, miR-6836-3p, miR-3195, miR-718, miR-3178, miR-638, miR-4497, miR-6085, miR-6752-5p and miR-135a-3p.

2. The kit according to claim 1, wherein miR-6726-5p is hsa-miR-6726-5p, miR-4257 is hsa-miR-4257, miR-6787-5p is hsa-miR-6787-5p, miR-6780b-5p is hsa-miR-6780b-5p, miR-3131 is hsa-miR-3131, miR-7108-5p is hsa-miR-7108-5p, miR-1343-3p is hsa-miR-1343-3p, miR-1247-3p is hsa-miR-1247-3p, miR-4651 is hsa-miR-4651, miR-6757-5p is hsa-miR-6757-5p, miR-3679-5p is hsa-miR-3679-5p, miR-7641 is hsa-miR-7641, miR-6746-5p is hsa-miR-6746-5p, miR-8072 is hsa-miR-8072, miR-6741-5p is hsa-miR-6741-5p, miR-1908-5p is hsa-miR-1908-5p, miR-6857-5p is hsa-miR-6857-5p, miR-4746-3p is hsa-miR-4746-3p, miR-744-5p is hsa-miR-744-5p, miR-4792 is hsa-miR-4792, miR-564 is hsa-miR-564, miR-6791-5p is hsa-miR-6791-5p, miR-6825-5p is hsa-miR-6825-5p, miR-6826-5p is hsa-miR-6826-5p, miR-4665-3p is hsa-miR-4665-3p, miR-4467 is hsa-miR-4467, miR-3188 is hsa-miR-3188, miR-6125 is hsa-miR-6125, miR-6756-5p is hsa-miR-6756-5p, miR-1228-3p is hsa-miR-1228-3p, miR-8063 is hsa-miR-8063, miR-8069 is hsa-miR-8069, miR-6875-5p is hsa-miR-6875-5p, miR-3185 is hsa-miR-3185, miR-4433b-3p is hsa-miR-4433b-3p, miR-6887-5p is hsa-miR-6887-5p, miR-128-1-Sp is hsa-miR-128-1-5p, miR-6724-5p is hsa-miR-6724-5p, miR-1914-3p is hsa-miR-1914-3p, miR-1225-5p is hsa-miR-1225-5p, miR-4419b is hsa-miR-4419b, miR-7110-5p is hsa-miR-7110-5p, miR-187-5p is hsa-miR-187-5p, miR-3184-5p is hsa-miR-3184-5p, miR-204-3p is hsa-miR-204-3p, miR-5572 is hsa-miR-5572, miR-6729-5p is hsa-miR-6729-5p, miR-615-5p is hsa-miR-615-5p, miR-6749-5p is hsa-miR-6749-5p, miR-6515-3p is hsa-miR-6515-3p, miR-3937 is hsa-miR-3937, miR-6840-3p is hsa-miR-6840-3p, miR-6893-5p is hsa-miR-6893-5p, miR-4728-5p is hsa-miR-4728-5p, miR-6717-5p is hsa-miR-6717-5p, miR-7113-3p is hsa-miR-7113-3p, miR-4665-5p is hsa-miR-4665-5p, miR-642b-3p is hsa-miR-642b-3p, miR-7109-5p is hsa-miR-7109-5p, miR-6842-5p is hsa-miR-6842-5p, miR-4442 is hsa-miR-4442, miR-4433-3p is hsa-miR-4433-3p, miR-4707-5p is hsa-miR-4707-5p, miR-6126 is hsa-miR-6126, miR-4449 is hsa-miR-4449, miR-4706 is hsa-miR-4706, miR-1913 is hsa-miR-1913, miR-602 is hsa-miR-602, miR-939-5p is hsa-miR-939-5p, miR-4695-5p is hsa-miR-4695-5p, miR-711 is hsa-miR-711, miR-6816-5p is hsa-miR-6816-5p, miR-4632-5p is hsa-miR-4632-5p, miR-6721-5p is hsa-miR-6721-5p, miR-7847-3p is hsa-miR-7847-3p, miR-6132 is hsa-miR-6132, miR-887-3p is hsa-miR-887-3p, miR-3679-3p is hsa-miR-3679-3p, miR-6784-5p is hsa-miR-6784-5p, miR-1249 is hsa-miR-1249, miR-937-5p is hsa-miR-937-5p, miR-5195-3p is hsa-miR-5195-3p, miR-6732-5p is hsa-miR-6732-5p, miR-4417 is hsa-miR-4417, miR-4281 is hsa-miR-4281, miR-4734 is hsa-miR-4734, miR-6766-3p is hsa-miR-6766-3p, miR-663a is hsa-miR-663a, miR-4513 is hsa-miR-4513, miR-6781-5p is hsa-miR-6781-5p, miR-1227-5p is hsa-miR-1227-5p, miR-6845-5p is hsa-miR-6845-5p, miR-6798-5p is hsa-miR-6798-5p, miR-3620-5p is hsa-miR-3620-5p, miR-1915-5p is hsa-miR-1915-5p, miR-4294 is hsa-miR-4294, miR-642a-3p is hsa-miR-642a-3p, miR-371a-5p is hsa-miR-371a-5p, miR-940 is hsa-miR-940, miR-4450 is hsa-miR-4450, miR-4723-5p is hsa-miR-4723-5p, miR-1469 is hsa-miR-1469, miR-6861-5p is hsa-miR-6861-5p, miR-7975 is hsa-miR-7975, miR-6879-5p is hsa-miR-6879-5p, miR-6802-5p is hsa-miR-6802-5p, miR-1268b is hsa-miR-1268b, miR-663b is hsa-miR-663b, miR-125a-3p is hsa-miR-125a-3p, miR-2861 is hsa-miR-2861, miR-6088 is hsa-

miR-6088, miR-4758-5p is hsa-miR-4758-5p, miR-296-3p is hsa-miR-296-3p, miR-6738-5p is hsa-miR-6738-5p, miR-671-5p is hsa-miR-671-5p, miR-4454 is hsa-miR-4454, miR-4516 is hsa-miR-4516, miR-7845-5p is hsa-miR-7845-5p, miR-4741 is hsa-miR-4741, miR-92b-5p is hsa-miR-92b-5p, miR-6795-5p is hsa-miR-6795-5p, miR-6805-3p is hsa-miR-6805-3p, miR-4725-3p is hsa-miR-4725-3p, miR-6782-5p is hsa-miR-6782-5p, miR-4688 is hsa-miR-4688, miR-6850-5p is hsa-miR-6850-5p, miR-6777-5p is hsa-miR-6777-5p, miR-6785-5p is hsa-miR-6785-5p, miR-7106-5p is hsa-miR-7106-5p, miR-3663-3p is hsa-miR-3663-3p, miR-6131 is hsa-miR-6131, miR-1915-3p is hsa-miR-1915-3p, miR-4532 is hsa-miR-4532, miR-6820-5p is hsa-miR-6820-5p, miR-4689 is hsa-miR-4689, miR-4638-5p is hsa-miR-4638-5p, miR-3656 is hsa-miR-3656, miR-3621 is hsa-miR-3621, miR-6769b-5p is hsa-miR-6769b-5p, miR-149-3p is hsa-miR-149-3p, miR-23b-3p is hsa-miR-23b-3p, miR-3135b is hsa-miR-3135b, miR-6848-5p is hsa-miR-6848-5p, miR-6769a-5p is hsa-miR-6769a-5p, miR-4327 is hsa-miR-4327, miR-6765-3p is hsa-miR-6765-3p, miR-6716-5p is hsa-miR-6716-5p, miR-6877-5p is hsa-miR-6877-5p, miR-6727-5p is hsa-miR-6727-5p, miR-4534 is hsa-miR-4534, miR-614 is hsa-miR-614, miR-1202 is hsa-miR-1202, miR-575 is hsa-miR-575, miR-6870-5p is hsa-miR-6870-5p, miR-6722-3p is hsa-miR-6722-3p, miR-7977 is hsa-miR-7977, miR-4649-5p is hsa-miR-4649-5p, miR-4675 is hsa-miR-4675, miR-6075 is hsa-miR-6075, miR-6779-5p is hsa-miR-6779-5p, miR-4271 is hsa-miR-4271, miR-3196 is hsa-miR-3196, miR-6803-5p is hsa-miR-6803-5p, miR-6789-5p is hsa-miR-6789-5p, miR-4648 is hsa-miR-4648, miR-4508 is hsa-miR-4508, miR-4749-5p is hsa-miR-4749-5p, miR-4505 is hsa-miR-4505, miR-5698 is hsa-miR-5698, miR-1199-5p is hsa-miR-1199-5p, miR-4763-3p is hsa-miR-4763-3p, miR-6836-3p is hsa-miR-6836-3p, miR-3195 is hsa-miR-3195, miR-718 is hsa-miR-718, miR-3178 is hsa-miR-3178, miR-638 is hsa-miR-638, miR-4497 is hsa-miR-4497, miR-6085 is hsa-miR-6085, miR-6752-5p is hsa-miR-6752-5p, and miR-135a-3p is hsa-miR-135a-3p.

3. The kit according to claim 1 or 2, wherein the nucleic acid is a polynucleotide selected from the group consisting of the following polynucleotides (a) to (e):

(a) a polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 1 to 171 and 606 to 614 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,
(b) a polynucleotide comprising a nucleotide sequence represented by any of SEQ ID NOs: 1 to 171 and 606 to 614,
(c) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 1 to 171 and 606 to 614 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,
(d) a polynucleotide comprising a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 1 to 171 and 606 to 614 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, and
(e) a polynucleotide hybridizing under stringent conditions to any of the polynucleotides (a) to (d).

4. The kit according to any one of claims 1 to 3, wherein the kit further comprises a nucleic acid capable of specifically binding to at least one or more polynucleotide(s) selected from the group consisting of other colorectal cancer markers miR-1231, miR-1233-5p, miR-150-3p, miR-1225-3p, miR-92a-2-5p, miR-423-5p, miR-1268a, miR-128-2-5p and miR-24-3p.

5. The kit according to claim 4, wherein miR-1231 is hsa-miR-1231, miR-1233-5p is hsa-miR-1233-5p, miR-150-3p is hsa-miR-150-3p, miR-1225-3p is hsa-miR-1225-3p, miR-92a-2-5p is hsa-miR-92a-2-5p, miR-423-5p is hsa-miR-423-5p, miR-1268a is hsa-miR-1268a, miR-128-2-5p is hsa-miR-128-2-5p, and miR-24-3p is hsa-miR-24-3p.

6. The kit according to claim 4 or 5, wherein the nucleic acid is a polynucleotide selected from the group consisting of the following polynucleotides (f) to (j):

(f) a polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 172 to 180 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,
(g) a polynucleotide comprising a nucleotide sequence represented by any of SEQ ID NOs: 172 to 180,
(h) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 172 to 180 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,

(i) a polynucleotide comprising a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 172 to 180 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, and
(j) a polynucleotide hybridizing under stringent conditions to any of the polynucleotides (f) to (i).

7. The kit according to any one of claims 1 to 6, wherein the kit further comprises a nucleic acid capable of specifically binding to at least one or more polynucleotide(s) selected from the group consisting of other colorectal cancer markers miR-4697-5p, miR-3197, miR-675-5p, miR-4486, miR-7107-5p, miR-23a-3p, miR-4667-5p, miR-451a, miR-3940-5p, miR-8059, miR-6813-5p, miR-4492, miR-4476 and miR-6090.

8. The kit according to claim 7, wherein miR-4697-5p is hsa-miR-4697-5p, miR-3197 is hsa-miR-3197, miR-675-5p is hsa-miR-675-5p, miR-4486 is hsa-miR-4486, miR-7107-5p is hsa-miR-7107-5p, miR-23a-3p is hsa-miR-23a-3p, miR-4667-5p is hsa-miR-4667-5p, miR-451a is hsa-miR-451a, miR-3940-5p is hsa-miR-3940-5p, miR-8059 is hsa-miR-8059, miR-6813-5p is hsa-miR-6813-5p, miR-4492 is hsa-miR-4492, miR-4476 is hsa-miR-4476, and miR-6090 is hsa-miR-6090.

9. The kit according to claim 7 or 8, wherein the nucleic acid is a polynucleotide selected from the group consisting of the following polynucleotides (k) to (o):

(k) a polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 181 to 194 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,
(l) a polynucleotide comprising a nucleotide sequence represented by any of SEQ ID NOs: 181 to 194,
(m) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 181 to 194 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,
(n) a polynucleotide comprising a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 181 to 194 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, and
(o) a polynucleotide hybridizing under stringent conditions to any of the polynucleotides (k) to (n).

10. The kit according to any one of claims 1 to 9, wherein the kit comprises at least two or more nucleic acids capable of specifically binding to at least two or more polynucleotides, respectively, selected from all of the colorectal cancer markers according to claim 1 or 2.

11. A device for the detection of colorectal cancer, comprising a nucleic acid capable of specifically binding to at least one or more polynucleotide(s) selected from the group consisting of colorectal cancer markers miR-6726-5p, miR-4257, miR-6787-5p, miR-6780b-5p, miR-3131, miR-7108-5p, miR-1343-3p, miR-1247-3p, miR-4651, miR-6757-5p, miR-3679-5p, miR-7641, miR-6746-5p, miR-8072, miR-6741-5p, miR-1908-5p, miR-6857-5p, miR-4746-3p, miR-744-5p, miR-4792, miR-564, miR-6791-5p, miR-6825-5p, miR-6826-5p, miR-4665-3p, miR-4467, miR-3188, miR-6125, miR-6756-5p, miR-1228-3p, miR-8063, miR-8069, miR-6875-5p, miR-3185, miR-4433b-3p, miR-6887-5p, miR-128-1-5p, miR-6724-5p, miR-1914-3p, miR-1225-5p, miR-4419b, miR-7110-5p, miR-187-5p, miR-3184-5p, miR-204-3p, miR-5572, miR-6729-5p, miR-615-5p, miR-6749-5p, miR-6515-3p, miR-3937, miR-6840-3p, miR-6893-5p, miR-4728-5p, miR-6717-5p, miR-7113-3p, miR-4665-5p, miR-642b-3p, miR-7109-5p, miR-6842-5p, miR-4442, miR-4433-3p, miR-4707-5p, miR-6126, miR-4449, miR-4706, miR-1913, miR-602, miR-939-5p, miR-4695-5p, miR-711, miR-6816-5p, miR-4632-5p, miR-6721-5p, miR-7847-3p, miR-6132, miR-887-3p, miR-3679-3p, miR-6784-5p, miR-1249, miR-937-5p, miR-5195-3p, miR-6732-5p, miR-4417, miR-4281, miR-4734, miR-6766-3p, miR-663a, miR-4513, miR-6781-5p, miR-1227-5p, miR-6845-5p, miR-6798-5p, miR-3620-5p, miR-1915-5p, miR-4294, miR-642a-3p, miR-371a-Sp, miR-940, miR-4450, miR-4723-5p, miR-1469, miR-6861-5p, miR-7975, miR-6879-5p, miR-6802-5p, miR-1268b, miR-663b, miR-125a-3p, miR-2861, miR-6088, miR-4758-5p, miR-296-3p, miR-6738-5p, miR-671-5p, miR-4454, miR-4516, miR-7845-5p, miR-4741, miR-92b-5p, miR-6795-5p, miR-6805-3p, miR-4725-3p, miR-6782-5p, miR-4688, miR-6850-5p, miR-6777-5p, miR-6785-5p, miR-7106-5p, miR-3663-3p, miR-6131, miR-1915-3p, miR-4532, miR-6820-5p, miR-4689, miR-4638-5p, miR-3656, miR-3621, miR-6769b-5p, miR-149-3p, miR-23b-3p, miR-3135b, miR-6848-5p, miR-6769a-5p, miR-4327, miR-6765-3p, miR-6716-5p, miR-6877-5p, miR-6727-5p, miR-4534, miR-614, miR-1202, miR-575, miR-6870-5p, miR-6722-3p, miR-7977, miR-4649-5p, miR-4675, miR-6075, miR-6779-5p, miR-4271, miR-3196, miR-6803-5p, miR-6789-5p, miR-4648, miR-4508, miR-4749-5p, miR-4505, miR-5698, miR-1199-5p, miR-4763-3p, miR-6836-3p, miR-3195, miR-718, miR-

3178, miR-638, miR-4497, miR-6085, miR-6752-5p andmiR-135a-3p.

12. The device according to claim 11, wherein miR-6726-5p is hsa-miR-6726-5p, miR-4257 is hsa-miR-4257, miR-6787-5p is hsa-miR-6787-5p, miR-6780b-5p is hsa-miR-6780b-5p, miR-3131 is hsa-miR-3131, miR-7108-5p is hsa-miR-7108-5p, miR-1343-3p is hsa-miR-1343-3p, miR-1247-3p is hsa-miR-1247-3p, miR-4651 is hsa-miR-4651, miR-6757-5p is hsa-miR-6757-5p, miR-3679-5p is hsa-miR-3679-5p, miR-7641 is hsa-miR-7641, miR-6746-5p is hsa-miR-6746-5p, miR-8072 is hsa-miR-8072, miR-6741-5p is hsa-miR-6741-5p, miR-1908-5p is hsa-miR-1908-5p, miR-6857-5p is hsa-miR-6857-5p, miR-4746-3p is hsa-miR-4746-3p, miR-744-5p is hsa-miR-744-Sp, miR-4792 is hsa-miR-4792, miR-564 is hsa-miR-564, miR-6791-5p is hsa-miR-6791-5p, miR-6825-5p is hsa-miR-6825-5p, miR-6826-5p is hsa-miR-6826-5p, miR-4665-3p is hsa-miR-4665-3p, miR-4467 is hsa-miR-4467, miR-3188 is hsa-miR-3188, miR-6125 is hsa-miR-6125, miR-6756-5p is hsa-miR-6756-5p, miR-1228-3p is hsa-miR-1228-3p, miR-8063 is hsa-miR-8063, miR-8069 is hsa-miR-8069, miR-6875-5p is hsa-miR-6875-5p, miR-3185 is hsa-miR-3185, miR-4433b-3p is hsa-miR-4433b-3p, miR-6887-5p is hsa-miR-6887-5p, miR-128-1-5p is hsa-miR-128-1-5p, miR-6724-5p is hsa-miR-6724-5p, miR-1914-3p is hsa-miR-1914-3p, miR-1225-5p is hsa-miR-1225-5p, miR-4419b is hsa-miR-4419b, miR-7110-5p is hsa-miR-7110-5p, miR-187-5p is hsa-miR-187-5p, miR-3184-5p is hsa-miR-3184-5p, miR-204-3p is hsa-miR-204-3p, miR-5572 is hsa-miR-5572, miR-6729-5p is hsa-miR-6729-5p, miR-615-5p is hsa-miR-615-5p, miR-6749-5p is hsa-miR-6749-5p, miR-6515-3p is hsa-miR-6515-3p, miR-3937 is hsa-miR-3937, miR-6840-3p is hsa-miR-6840-3p, miR-6893-5p is hsa-miR-6893-5p, miR-4728-5p is hsa-miR-4728-5p, miR-6717-5p is hsa-miR-6717-5p, miR-7113-3p is hsa-miR-7113-3p, miR-4665-5p is hsa-miR-4665-5p, miR-642b-3p is hsa-miR-642b-3p, miR-7109-5p is hsa-miR-7109-5p, miR-6842-5p is hsa-miR-6842-5p, miR-4442 is hsa-miR-4442, miR-4433-3p is hsa-miR-4433-3p, miR-4707-5p is hsa-miR-4707-5p, miR-6126 is hsa-miR-6126, miR-4449 is hsa-miR-4449, miR-4706 is hsa-miR-4706, miR-1913 is hsa-miR-1913, miR-602 is hsa-miR-602, miR-939-5p is hsa-miR-939-5p, miR-4695-5p is hsa-miR-4695-5p, miR-711 is hsa-miR-711, miR-6816-5p is hsa-miR-6816-5p, miR-4632-5p is hsa-miR-4632-5p, miR-6721-5p is hsa-miR-6721-5p, miR-7847-3p is hsa-miR-7847-3p, miR-6132 is hsa-miR-6132, miR-887-3p is hsa-miR-887-3p, miR-3679-3p is hsa-miR-3679-3p, miR-6784-5p is hsa-miR-6784-5p, miR-1249 is hsa-miR-1249, miR-937-5p is hsa-miR-937-5p, miR-5195-3p is hsa-miR-5195-3p, miR-6732-5p is hsa-miR-6732-5p, miR-4417 is hsa-miR-4417, miR-4281 is hsa-miR-4281, miR-4734 is hsa-miR-4734, miR-6766-3p is hsa-miR-6766-3p, miR-663a is hsa-miR-663a, miR-4513 is hsa-miR-4513, miR-6781-5p is hsa-miR-6781-5p, miR-1227-5p is hsa-miR-1227-5p, miR-6845-5p is hsa-miR-6845-5p, miR-6798-5p is hsa-miR-6798-5p, miR-3620-5p is hsa-miR-3620-5p, miR-1915-5p is hsa-miR-1915-5p, miR-4294 is hsa-miR-4294, miR-642a-3p is hsa-miR-642a-3p, miR-371a-5p is hsa-miR-371a-5p, miR-940 is hsa-miR-940, miR-4450 is hsa-miR-4450, miR-4723-5p is hsa-miR-4723-5p, miR-1469 is hsa-miR-1469, miR-6861-5p is hsa-miR-6861-5p, miR-7975 is hsa-miR-7975, miR-6879-5p is hsa-miR-6879-5p, miR-6802-5p is hsa-miR-6802-5p, miR-1268b is hsa-miR-1268b, miR-663b is hsa-miR-663b, miR-125a-3p is hsa-miR-125a-3p, miR-2861 is hsa-miR-2861, miR-6088 is hsa-miR-6088, miR-4758-5p is hsa-miR-4758-5p, miR-296-3p is hsa-miR-296-3p, miR-6738-5p is hsa-miR-6738-5p, miR-671-5p is hsa-miR-671-5p, miR-4454 is hsa-miR-4454, miR-4516 is hsa-miR-4516, miR-7845-5p is hsa-miR-7845-5p, miR-4741 is hsa-miR-4741, miR-92b-5p is hsa-miR-92b-5p, miR-6795-5p is hsa-miR-6795-5p, miR-6805-3p is hsa-miR-6805-3p, miR-4725-3p is hsa-miR-4725-3p, miR-6782-5p is hsa-miR-6782-5p, miR-4688 is hsa-miR-4688, miR-6850-5p is hsa-miR-6850-5p, miR-6777-5p is hsa-miR-6777-5p, miR-6785-5p is hsa-miR-6785-5p, miR-7106-5p is hsa-miR-7106-5p, miR-3663-3p is hsa-miR-3663-3p, miR-6131 is hsa-miR-6131, miR-1915-3p is hsa-miR-1915-3p, miR-4532 is hsa-miR-4532, miR-6820-5p is hsa-miR-6820-5p, miR-4689 is hsa-miR-4689, miR-4638-5p is hsa-miR-4638-5p, miR-3656 is hsa-miR-3656, miR-3621 is hsa-miR-3621, miR-6769b-5p is hsa-miR-6769b-5p, miR-149-3p is hsa-miR-149-3p, miR-23b-3p is hsa-miR-23b-3p, miR-3135b is hsa-miR-3135b, miR-6848-5p is hsa-miR-6848-5p, miR-6769a-5p is hsa-miR-6769a-5p, miR-4327 is hsa-miR-4327, miR-6765-3p is hsa-miR-6765-3p, miR-6716-5p is hsa-miR-6716-5p, miR-6877-5p is hsa-miR-6877-5p, miR-6727-5p is hsa-miR-6727-5p, miR-4534 is hsa-miR-4534, miR-614 is hsa-miR-614, miR-1202 is hsa-miR-1202, miR-575 is hsa-miR-575, miR-6870-5p is hsa-miR-6870-5p, miR-6722-3p is hsa-miR-6722-3p, miR-7977 is hsa-miR-7977, miR-4649-5p is hsa-miR-4649-5p, miR-4675 is hsa-miR-4675, miR-6075 is hsa-miR-6075, miR-6779-5p is hsa-miR-6779-5p, miR-4271 is hsa-miR-4271, miR-3196 is hsa-miR-3196, miR-6803-5p is hsa-miR-6803-5p, miR-6789-5p is hsa-miR-6789-5p, miR-4648 is hsa-miR-4648, miR-4508 is hsa-miR-4508, miR-4749-5p is hsa-miR-4749-5p, miR-4505 is hsa-miR-4505, miR-5698 is hsa-miR-5698, miR-1199-5p is hsa-miR-1199-5p, miR-4763-3p is hsa-miR-4763-3p, miR-6836-3p is hsa-miR-6836-3p, miR-3195 is hsa-miR-3195, miR-718 is hsa-miR-718, miR-3178 is hsa-miR-3178, miR-638 is hsa-miR-638, miR-4497 is hsa-miR-4497, miR-6085 is hsa-miR-6085, miR-6752-5p is hsa-miR-6752-5p, and miR-135a-3p is hsa-miR-135a-3p.

13. The device according to claim 11 or 12, wherein the nucleic acid is a polynucleotide selected from the group consisting of the following polynucleotides (a) to (e):

(a) a polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 1 to 171 and 606 to 614 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,
(b) a polynucleotide comprising a nucleotide sequence represented by any of SEQ ID NOs: 1 to 171 and 606 to 614,
(c) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 1 to 171 and 606 to 614 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,
(d) a polynucleotide comprising a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 1 to 171 and 606 to 614 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, and
(e) a polynucleotide hybridizing under stringent conditions to any of the polynucleotides (a) to (d).

14. The device according to any one of claims 11 to 13, wherein the device further comprises a nucleic acid capable of specifically binding to at least one or more polynucleotide(s) selected from the group consisting of other colorectal cancer markers miR-1231, miR-1233-5p, miR-150-3p, miR-1225-3p, miR-92a-2-5p, miR-423-5p, miR-1268a, miR-128-2-5p and miR-24-3p.

15. The device according to claim 14, wherein miR-1231 is hsa-miR-1231, miR-1233-5p is hsa-miR-1233-5p, miR-150-3p is hsa-miR-150-3p, miR-1225-3p is hsa-miR-1225-3p, miR-92a-2-5p is hsa-miR-92a-2-5p, miR-423-5p is hsa-miR-423-5p, miR-1268a is hsa-miR-1268a, miR-128-2-5p is hsa-miR-128-2-5p, and miR-24-3p is hsa-miR-24-3p.

16. The device according to claim 14 or 15, wherein the nucleic acid is a polynucleotide selected from the group consisting of the following polynucleotides (f) to (j):

(f) a polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 172 to 180 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,
(g) a polynucleotide comprising a nucleotide sequence represented by any of SEQ ID NOs: 172 to 180,
(h) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 172 to 180 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,
(i) a polynucleotide comprising a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 172 to 180 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, and
(j) a polynucleotide hybridizing under stringent conditions to any of the polynucleotides (f) to (i).

17. The device according to any one of claims 11 to 16, wherein the device further comprises a nucleic acid capable of specifically binding to at least one or more polynucleotide(s) selected from the group consisting of other colorectal cancer markers miR-4697-5p, miR-3197, miR-675-5p, miR-4486, miR-7107-5p, miR-23a-3p, miR-4667-5p, miR-451a, miR-3940-5p, miR-8059, miR-6813-5p, miR-4492, miR-4476 and miR-6090.

18. The device according to claim 17, wherein miR-4697-5p is hsa-miR-4697-5p, miR-3197 is hsa-miR-3197, miR-675-5p is hsa-miR-675-5p, miR-4486 is hsa-miR-4486, miR-7107-5p is hsa-miR-7107-5p, miR-23a-3p is hsa-miR-23a-3p, miR-4667-5p is hsa-miR-4667-5p, miR-451a is hsa-miR-451a, miR-3940-5p is hsa-miR-3940-5p, miR-8059 is hsa-miR-8059, miR-6813-5p is hsa-miR-6813-5p, miR-4492 is hsa-miR-4492, miR-4476 is hsa-miR-4476, and miR-6090 is hsa-miR-6090.

19. The device according to claim 17 or 18, wherein the nucleic acid is a polynucleotide selected from the group consisting of the following polynucleotides (k) to (o):

(k) a polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 181 to 194 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,
(l) a polynucleotide comprising a nucleotide sequence represented by any of SEQ ID NOs: 181 to 194,

(m) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 181 to 194 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,
(n) a polynucleotide comprising a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 181 to 194 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, and
(o) a polynucleotide hybridizing under stringent conditions to any of the polynucleotides (k) to (n).

20. The device according to any one of claims 11 to 19, wherein the device is a device for measurement by a hybridization technique.

21. The device according to claim 20, wherein the hybridization technique is a nucleic acid array technique.

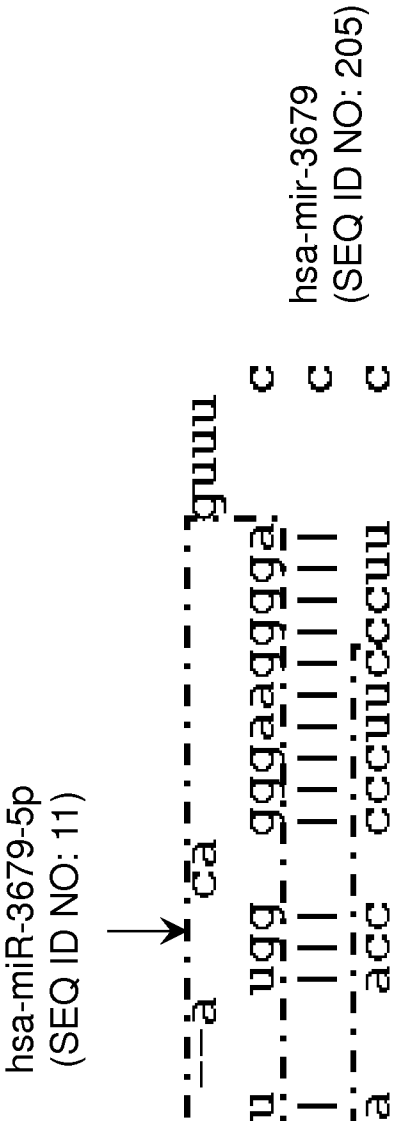
22. The device according to any one of claims 11 to 21, wherein the device comprises at least two or more nucleic acids capable of specifically binding to at least two or more polynucleotides, respectively, selected from all of the colorectal cancer markers according to claim 11 or 12.

23. A method for detecting colorectal cancer, comprising measuring an expression level of a target nucleic acid in a sample from a subject using a kit according to any one of claims 1 to 10 or a device according to any one of claims 11 to 22, and evaluating *in vitro* whether or not the subject has colorectal cancer using both of the measured expression level and a control expression level in a sample from a healthy subject measured in the same way.

24. The method according to claim 23, wherein the subject is a human.

25. The method according to claim 23 or 24, wherein the sample is blood, serum, or plasma.

Fig. 1


hsa-miR-3679-5p
(SEQ ID NO: 11)
hsa-mir-3679
(SEQ ID NO: 205)
hsa-miR-3679-3p
(SEQ ID NO: 78)

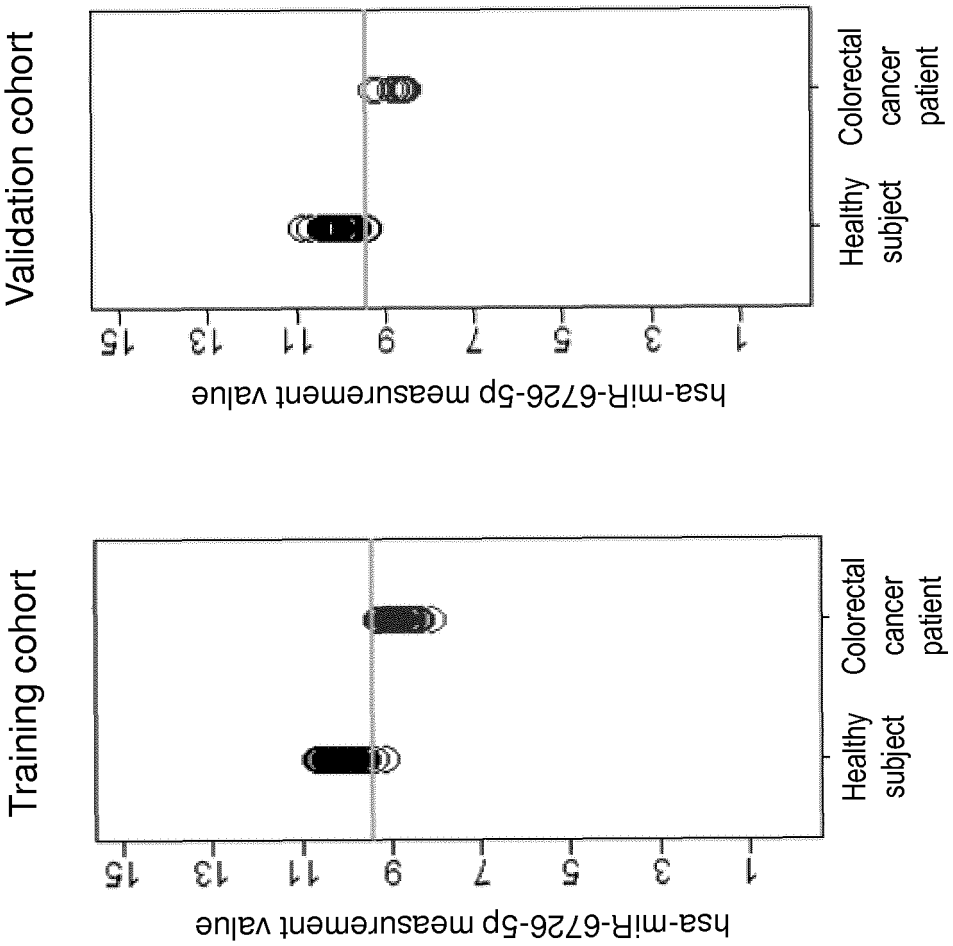

Validation cohort
hsa-miR-6726-5p measurement value
1
3
5
7
9
11
13
15
Healthy subject
Colorectal cancer patient
Training cohort
hsa-miR-6726-5p measurement value
1
3
5
7
9
11
13
15
Healthy subject
Colorectal cancer patient

Fig. 2

Fig. 3

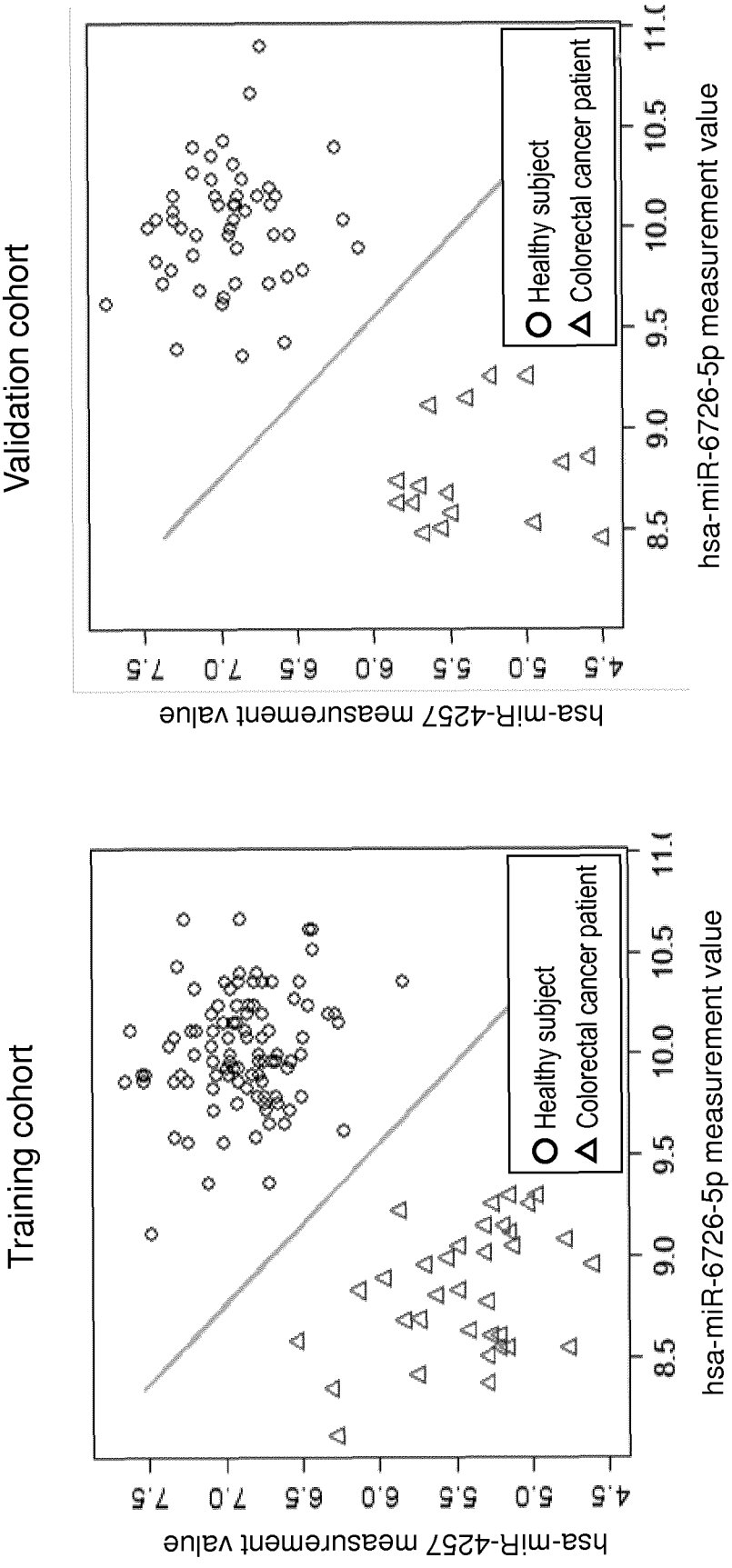
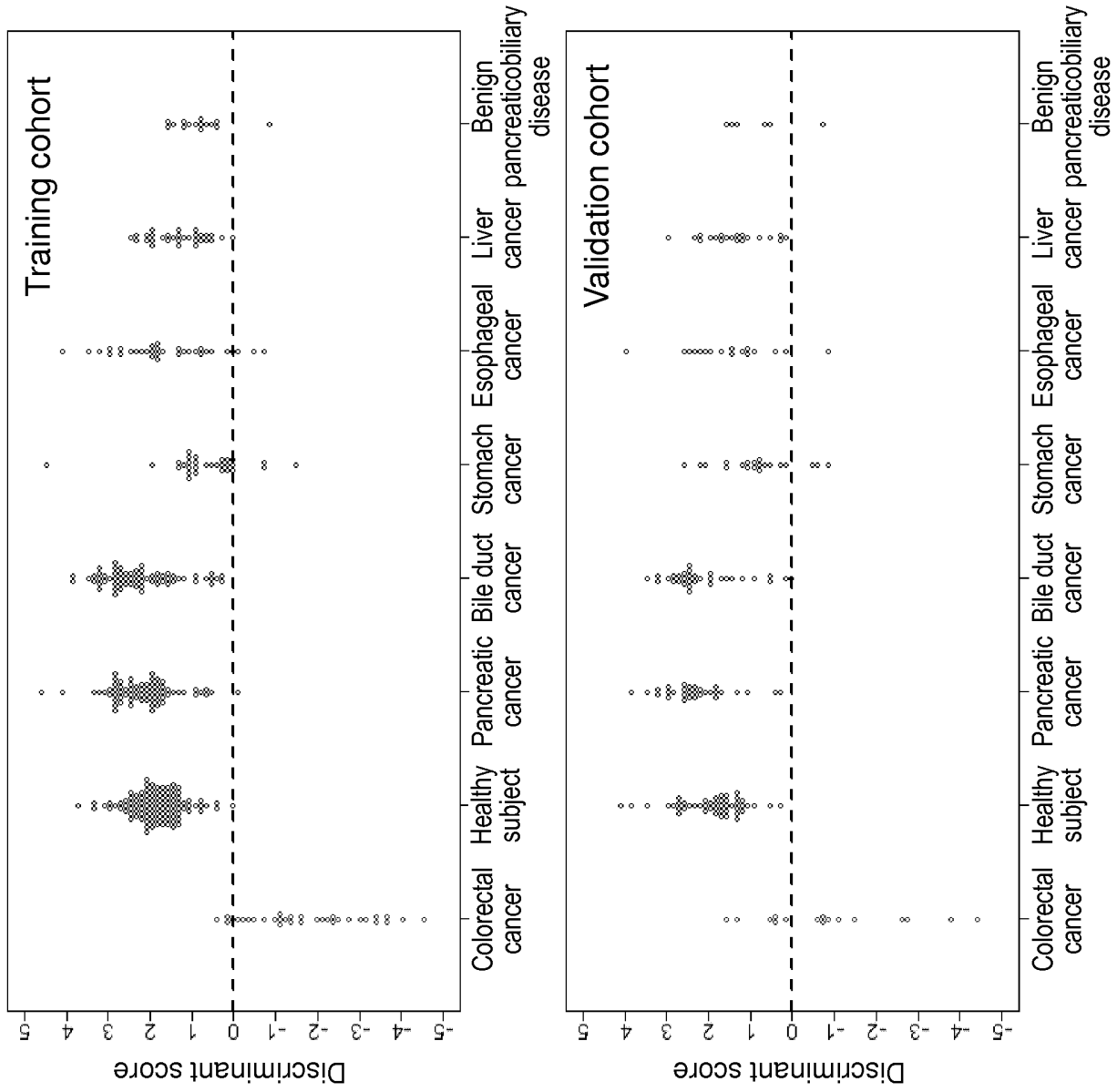

Training cohort
Validation cohort
hsa-miR-4257 measurement value
hsa-miR-6726-5p measurement value
Healthy subject
Colorectal cancer patient
4.5
5.0
5.5
6.0
6.5
7.0
7.5
8.5
9.0
9.5
10.0
10.5

Fig. 4


Training cohort
Validation cohort
Discriminant score
5
4
3
2
1
0
-1
-2
-3
-4
-5
Colorectal cancer
Healthy subject
Pancreatic cancer
Bile duct cancer
Stomach cancer
Esophageal cancer
Liver cancer
Benign pancreaticobiliary disease

INTERNATIONAL SEARCH REPORT

International application No.
PCT/JP2015/066970

A. CLASSIFICATION OF SUBJECT MATTER
C12Q1/68(2006.01)i, *C12M1/00*(2006.01)i, *C12N15/09*(2006.01)i, *C12N15/113*(2010.01)i, *G01N33/53*(2006.01)i, *G01N33/574*(2006.01)i

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

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
C12Q1/68, C12M1/00, C12N15/09, C12N15/113, G01N33/53, G01N33/574

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
Jitsuyo Shinan Koho 1922-1996 Jitsuyo Shinan Toroku Koho 1996-2015
Kokai Jitsuyo Shinan Koho 1971-2015 Toroku Jitsuyo Shinan Koho 1994-2015

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
JSTPlus/JMEDPlus/JST7580(JDreamIII), CAplus/MEDLINE/EMBASE/BIOSIS(STN)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	JP 2009-531019 A (The Ohio State University Research Foundation), 03 September 2009 (03.09.2009), claims & JP 2013-46612 A & JP 5395439 B2 & JP 2014-60993 A & US 2008/0306006 A1 & EP 1969147 A2 & CA 2633754 A & CN 101389770 A & AU 2007205163 A & ES 2440787 T & HK 1132302 A	1-22

☒ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:
"A" document defining the general state of the art which is not considered to be of particular relevance
"E" earlier application or patent but published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed
"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
27 August 2015 (27.08.15)	08 September 2015 (08.09.15)
Name and mailing address of the ISA/ Japan Patent Office 3-4-3,Kasumigaseki,Chiyoda-ku, Tokyo 100-8915,Japan	Authorized officer Telephone No.

Form PCT/ISA/210 (second sheet) (July 2009)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/JP2015/066970

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	US 2013/0102487 A1 (HOSPITAL CLINIC DE BARCELONA), 25 April 2013 (25.04.2013), claims & JP 2014-530619 A & US 2015/0087525 A1 & WO 2013/093635 A2 & EP 2768986 A2 & AU 2012356317 A & CA 2852850 A & KR 10-2014-0097195 A & CN 104145024 A & AU 2015201072 A	1-22
Y	US 2012/0088687 A1 (GOEL, A., et al.), 12 April 2012 (12.04.2012), claims & WO 2012/048236 A1 & EP 2625293 A1 & AU 2011311881 A & CA 2814081 A & TW 201303026 A & AR 84723 A1	1-22
Y	KOZOMARA, A., et al., miRBase: annotating high confidence microRNAs using deep sequencing data, Nucleic Acids Research, 2014, Vol. 42, Database issue, pp. D68-D73, (Published online 2013.11. 25)	1-22
Y	Satoko TAKIZAWA et al., "DNA Chip 3D-Gene(R) ni yoru FFPE·Kessei Kentai deno Tashu miRNA Doji Kaiseki", BIO Clinica, 2013, vol.28, no.9, pages 872 to 873	1-22
Y	TAKIZAWA, S., et al., The difference of serum RNA profile: RNA extraction and detection method, Cancer Research, 2013.04, Vol. 73, No. 8(Suppl. 1), Abstract No. 5294	1-22

Form PCT/ISA/210 (continuation of second sheet) (July 2009)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/JP2015/066970

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.: 23-25
because they relate to subject matter not required to be searched by this Authority, namely:
(See extra sheet)

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
See extra sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
Parts of claims 1-25, wherein the colorectal cancer marker is miR-6726-5p.

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☐ No protest accompanied the payment of additional search fees.

Form PCT/ISA/210 (continuation of first sheet (2)) (July 2009)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/JP2015/066970

Continuation of Box No.II-1 of continuation of first sheet(2)

In claims 23-25, the criteria for determining whether or not a subject is suffering from colorectal cancer by employing the expression amount of a target nucleic acid in a sample from the subject and a control, i.e., the expression amount of the target nucleic acid in a sample from a normal person, are not described, and a step of judging by a physician is involved in the determination. Therefore, these claims relate to a method for diagnosing a human body.

Continuation of Box No.III of continuation of first sheet(2)

In claim 1, 180 types of miR are described. Therefore, 180 inventions are included in claim 1.

The 180 inventions share a common technical feature "a kit for detecting colorectal cancer, which contains a nucleic acid capable of specifically binding to a miR polynucleotide that can serve as a colorectal cancer marker".

However, the above-said technical feature cannot be considered to be a special technical feature, since the technical feature does not make a contribution over the prior art in the light of the contents disclosed in the following documents.

Further, there is no other same or corresponding special technical feature among these inventions.

Furthermore, the 180 types of miR share no common nucleotide sequence.

Accordingly, the following one hundred and eighty inventions (invention groups) are involved in claims.

(Invention 1) Parts of the inventions described in claims 1-25, wherein the colorectal cancer marker is miR-6726-5p.

(Invention 2) Parts of the inventions described in claims 1-25, wherein the colorectal cancer marker is miR-4257.

(Invention 3) Parts of the inventions described in claims 1-25, wherein the colorectal cancer marker is miR-6787-5p.

...

(Invention 179) Parts of the inventions described in claims 1-25, wherein the colorectal cancer marker is miR-6752-5p.

(Invention 180) Parts of the inventions described in claims 1-25, wherein the colorectal cancer marker is miR-135a-3p.

Because an additional search fee has not been paid, the international search report was prepared only on "(Invention 1) Parts of the inventions described in claims 1-25, wherein the colorectal cancer marker is miR-6726-5p" which correspond to inventions which are firstly described in the claims.

[List of Documents]

Document 1: JP 2009-531019 A (The Ohio State University Research Foundation), 03 September 2009 (03.09.2009), claims

Document 2: US 2013/0102487 A1 (HOSPITAL CLINIC DE BARCELONA), 25 April 2013 (25.04.2013), claims

Document 3: US 2012/0088687 A1 (GOEL, A., et al.), 12 April 2012 (12.04.2012), claims

Form PCT/ISA/210 (extra sheet) (July 2009)

REFERENCES CITED IN THE DESCRIPTION

This list of references cited by the applicant is for the reader's convenience only. It does not form part of the European patent document. Even though great care has been taken in compiling the references, errors or omissions cannot be excluded and the EPO disclaims all liability in this regard.

Patent documents cited in the description

- WO 2007081740 A **[0012]**
- US 2013102487 A **[0012]**
- US 2012088687 A **[0012]**
- JP 2009531019 A **[0012]**

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专利名称(译)	结肠直肠癌检测试剂盒或装置，以及检测方法		
公开(公告)号	EP3156499A1	公开(公告)日	2017-04-19
申请号	EP2015806013	申请日	2015-06-12
[标]申请(专利权)人(译)	东丽株式会社 NAT癌症CENT		
申请(专利权)人(译)	TORAY INDUSTRIES，INC. 国家癌症中心		
当前申请(专利权)人(译)	TORAY INDUSTRIES，INC. 国家癌症中心		
[标]发明人	KOZONO SATOKO NOBUMASA HITOSHI KONDOU SATOSHI SUDO HIROKO KAWAUCHI JUNPEI OCHIAI ATSUSHI KOJIMA MOTOHIRO		
发明人	KOZONO SATOKO NOBUMASA HITOSHI KONDOU SATOSHI SUDO HIROKO KAWAUCHI JUNPEI OCHIAI ATSUSHI KOJIMA MOTOHIRO		
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CPC分类号	C12M1/00 C12N15/09 C12N15/113 C12Q1/68 G01N33/53 G01N33/574 C12Q1/6834 C12Q1/6886 C12Q2600/158 C12Q2600/178 C12Q2600/118		
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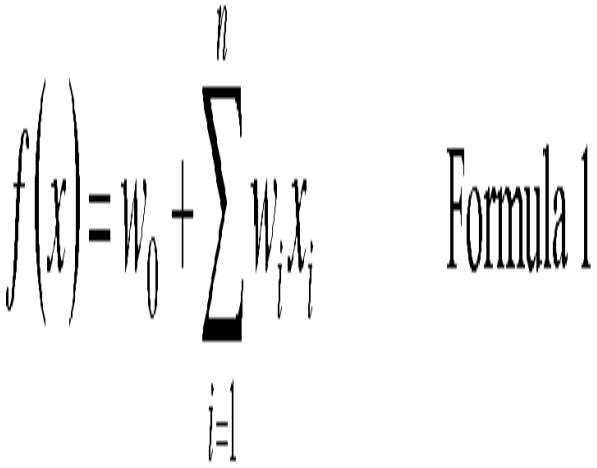
摘要(译)

旨在提供用于检测结肠直肠癌的试剂盒或装置以及用于检测结肠直肠癌的方法。本发明提供用于检测结肠直肠癌的试剂盒或装置，其包含能够特异性结合来自受试者的样品中的miRNA的核酸，以及用于检测结肠直肠癌的方法，包括在体外测量miRNA。



Formula 1